RESEARCH ARTICLE

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The Investigation of the Success of Different Machine Learning Methods in Breast Cancer Diagnosis

ABSTRACT

Objective: The aim of this study is to identify cancer earlier in life using machine learning methods.

Methods: For this purpose, the Wisconsin Diagnostic Breast Cancer dataset was classified using Naive Bayes, decision trees, artificial neural networks algorithms and comparison of these machine learning methods was made. KNIME Analytics Platform was used for applications. Before the classification process, the dataset was preprocessed. After the pre-processing stage, three different classifier methods were applied to the dataset. Accuracy, sensitivity, specificity and confusion matrices were used to measure the success of the methods.

Results: The results show that Naive Bayes and artificial neural network methods classify tumors with 96.5% accuracy. The success of the decision tree method in classification was 92.6%.

Conclusions: The machine learning algorithms can be used successfully in breast cancer diagnosis to determine whether the tumors are malign or benign.

Keywords: Breast Cancer Diagnosis, Machine Learning, Naive Bayes, Decision Trees, Artificial Neural Networks, KNIME

Meme Kanseri Tespitinde Farklı Makine Öğrenmesi Yöntemleri Başarısının İncelenmesi

ÖZET

Amaç: Bu çalışmanın amacı, makine öğrenimi yöntemlerini kullanarak kanseri yaşamın erken dönemlerinde belirlemektir.

Gereç ve Yöntem: Bu amaçla, Wisconsin Diagnostic Breast Cancer veri setinin Naive Bayes, karar ağaçları, yapay sinir ağları ile sınıflandırılması yapılmış ve söz konusu makine öğrenme yöntemleri karşılaştırılmıştır. Uygulamalar için 'KNIME Analytics Platform' u kullanılmıştır. Sınıflandırma işlemi yapılmadan önce veri seti ön işlemeden geçirilmiştir. Ön işleme aşamasından sonra, verilere üç farklı sınıflandırıcı yöntem uygulanmıştır. Yöntemlerin başarısını ölçmek için doğruluk, duyarlılık, özgüllük, hata matrisleri ve ROC eğrileri kullanılmıştır.

Bulgular: Uygulama sonuçları, Naive Bayes ve yapay sinir ağı yöntemlerinin tümörleri %96.5 doğrulukla doğru olarak sınıflandırdığını göstermektedir. Karar ağacı yönteminin sınıflandırmadaki başarısı %92.6 olarak elde edilmiştir. Sonuç olarak, her üç modelin üstün doğruluğa sahip sınıflandırma yaptığı söylenebilir.

Sonuç: Makine öğrenme algoritmaları, meme kanseri teşhisinde tümörlerin kötü huylu veya iyi huylu olup olmadığını belirlemek için başarıyla kullanılabilir.

Anahtar Kelimeler: Meme Kanseri Teşhisi, Makine Öğrenmesi, Naive Bayes, Karar Ağaçları, Yapay Sinir Ağları, KNIME

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INTRODUCTION

According to the data of the World Health Organization, approximately 2.3 million women in the world were diagnosed with breast cancer in 2020, and this number corresponds to 11.7% of the total cancer cases. The number of women who died of breast cancer in 2020 was reported to be approximately 685000 (1). This means that one out of every three cases results in death. In our country, it was reported by the World Health Organization that 24175 of 101018 cancer cases seen in women in 2020 were breast cancer (Figure 1). This rate corresponds to approximately 24% of the total cancer cases in women. Despite the high rate of breast cancer cases, researchers have stated that this type of cancer is among the types of cancer that can be treated if diagnosed at an early stage (3). Therefore, early diagnosis and subsequent determination of the appropriate cancer treatment helps to significantly eliminate the risk of death. Breast cancers are classified as benign and malignant according to their radiological and pathological examination. Doctors need support and conducive mechanisms to differentiate these tumors. However, there are cases where the distinction between benign and malign is contradictory. Therefore, automatic diagnosis systems will help for classification of tumors (4).

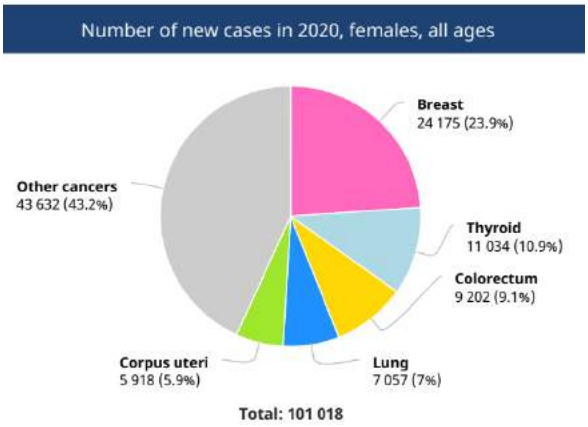


Figure 1. Distribution of cancer cases in women in Turkey (2)

Recently, many studies have been conducted in the era of artificial intelligence to diagnose breast cancer and classify them as benign or malignant. Machine learning algorithms have been applied by the researchers for the diagnosis of cancer and the detection of the tumor type and it has been stated that these algorithms are generally successful (5, 6). When the literature is reviewed, it is seen that various classification methods have been developed and applied for the diagnosis of breast cancer (3-8,15-26). Most studies used the Wisconsin Diagnostic Breast Cancer (WDBC) and Breast Cancer (BC) dataset from the UCI machine learning depository.

Rodrigues (7) examined the performance of Naive Bayes and J48 decision tree machine learning techniques in breast cancer diagnosis using the WDBC dataset containing missing data. It was stated that with the Naive Bayes algorithm, 97.8% accuracy in predictions was achieved while the accuracy was 96.05% with the J48 decision tree algorithm. It was stated that the dataset should be pre-processed before running the Naive Bayes algorithm because it does not operate with lost values, and normalization should be done to achieve better results.

Asri et al. (8) compared the performances of four different machine learning algorithms, which are the Support Vector Machine, C4.5 decision tree, Naive Bayes and k-Nearest Neighborhood, in the diagnosis of breast cancer using the WDBC dataset. The success of each algorithm in classification was evaluated using the values of accuracy, precision, sensitivity and specificity. The experimental results have shown that the Support Vector Machine gives the highest accuracy with a value of about 97.13%. All analyzes were carried out in a simulation environment using WEKA data mining program.

Saygılı (9) classified the WDBC dataset with machine learning methods such as Support Vector Machine, k-Nearest Neighborhood, Naive Bayes, J48 decision tree, random forest and MLP artificial neural networks. After the pre-processing stage, six different classifiers were applied to the dataset with 10-fold cross validation method. Accuracy, sensitivity, specificity, ROC area values and confusion matrices were used to measure the performance of the methods. As a result of the simulations, it was seen that the most successful method was random forest with 98.77% accuracy. The second most successful method is MLP artificial neural network method with 98.41% accuracy.

Ünal and Başçiftçi (10) made an empirical comparison of 10 popular machine learning models for breast cancer prediction. WDBC dataset was used to train the models and advanced accuracy metrics were used for comparison. The experimental results have shown that all models have high accuracy, but the Support Vector Machine algorithm has slightly better performance than other methods. In addition, Logistic Regression, K-Nearest Neighborhood, and artificial neural networks have also been found to be powerful classifiers for predicting breast cancer.

Mohammed et al. (11) targeted to increase the accuracy of the classification made in the diagnosis of breast cancer by processing the missing data in WDBC and BC datasets with the resampling technique. In the study, Decision Trees (J48), Naive Bayes, Sequential Minimal Optimization machine learning algorithms are used. The results obtained showed that the use of the resampling filter in the preprocessing stage increased the performance of the classifier. In this study, the performance of different machine

learning methods to classify tumors as benign or malignant was examined on breast cancer dataset. Data mining has been done with three classification algorithms. Naive Bayes, Decision Trees and MLP Artificial Neural Networks were used as classification algorithms. The application was implemented in version 4.2.3 of the KNIME Analytics Platform data mining program. Accuracy, sensitivity, specificity, precision, confusion matrices and ROC curves were used to measure the success of the methods examined.

METHOD

Dataset: The original dataset (WDBC) used in this study is located in the Machine Learning Repository of the University of California, Irvine (UCI). The dataset was created by Dr. Wolberg at the University of Wisconsin Hospital in the United States of America (12). The WDBC dataset used in this study was taken from Kaggle and consists of 569 samples and 30 cytologic features (13). The features derived from a digital scan of fine needle aspirate (FNA) slides (ref). For digital analysis examinations on the cytology slide, an area containing the most abnormal cells was selected and an image was obtained from this area. Ten major nuclear features were measured for each cell in this image. These features are radius, texture, circumference, area, smoothness, compactness, concave, concave points, symmetry, fractal dimension of the cell nucleus. High values of these features was modeled to correlate with malignancy. The average value of each feature, the worst (average of the three largest values) and standard error were evaluated for each image, resulting in a total of 30 features for each case. The details of the characterization procedures of each nuclear features can be found in (14). Of the 569 samples in the dataset, 357 were classified as benign and 212 as malignant. The summary of the WDBC dataset is shown in Table 1. An example for image of a benign and malignant breast fine needle aspirates is given in Figure 2 and 3, respectfully.

Table 1. The summary of the WDBC dataset (15)

Feature no	Feature name	Average	Standart error	Maximum
1	Radius	6.98-28.11	0.112-2.873	7.92-36.06
2	Texture	9.71-39.28	0.36-4.89	12.02-49.54
3	Circumference	43.79-188.50	0.76-21.98	50.41-251.20
4	Area	143.50-2501.00	6.80-542.20	185.20-4254.00
5	Smoothness	0.053-0.163	0.002-0.031	0.071-0.223
6	Compactness	0.019-0.345	0.002-0.135	0.027-1.058
7	Concave	0.000-0.427	0.000-0.396	0.000-1.252
8	Concave points	0.000-0.201	0.000-0.053	0.000-0.291
9	Symmetry	0.106-0.304	0.008-0.079	0.157-0.664
10	Fractal dimension	0.050-0.097	0.001-0.030	0.055-0.208

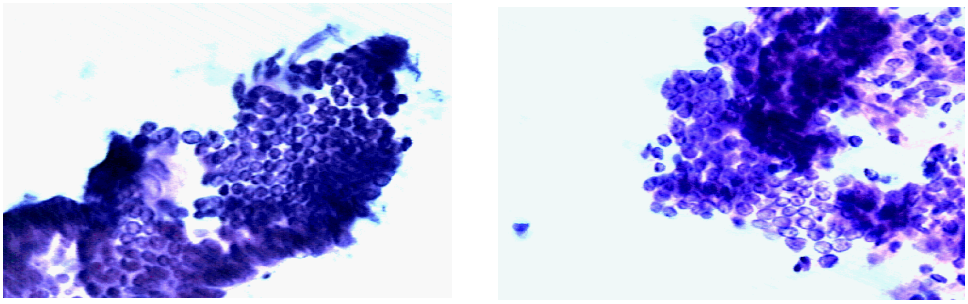


Figure 2. Benign cancer cell sample images (16)

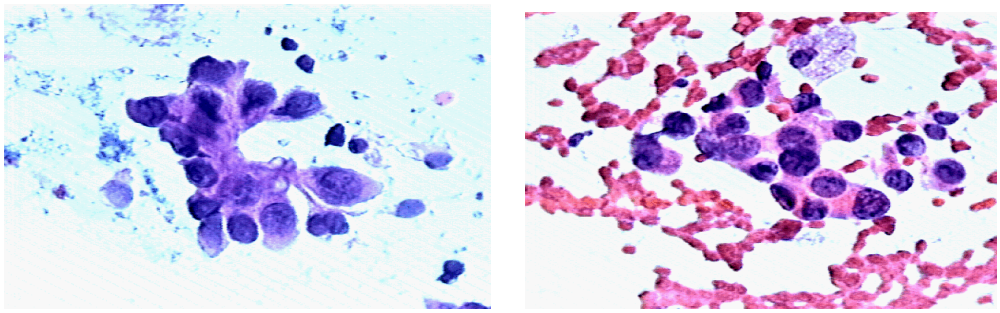


Figure 3. Malignant cancer cell sample images (16)

Machine Learning Methods: The Naive Bayes classifier is based on Bayes' theorem. Bayes theorem was found by Thomas Bayes in 1812 and is based on the conditional probability calculation formula. In the Naive Bayes algorithm, the probability of occurrence of each situation is calculated for a sample and the classification process is made according to the one with the highest probability value.

The basic idea in decision tree algorithms is based on dividing the input dataset into groups with the help of a clustering algorithm. The clustering process continues in depth until all the elements of the group have the same class label. In other words, a decision tree is a structure used to divide a dataset containing a large number of sample into smaller groups by applying a set of decision rules. Decision trees have a predefined target variable. In terms of their structure, they offer a strategy from top to bottom. How the split takes place in decision tree algorithms is one of the factors affecting the accuracy of the tree.

The artificial neural network is a model created by taking into account the working structure of the human nervous system, such as the brain that processes information. Neural networks can be used to model and identify trends that are too complex to be noticed by humans or other computer techniques, with their extraordinary ability to extract meaning from complex or imprecise datasets (4). Unlike the real biological neural network structure, many artificial neural network models have been created with some simplifications. Such simplifications are indispensable for understanding the properties under study and for any mathematical analysis.

KNIME Analytics Platform: KNIME includes modular data flow design and various tools for machine learning and data mining, called nodes. By making associations between nodes, dataset can be processed, visualized, interpreted and reported. Applications in this study were carried out in KNIME 4.2.3 program.

As stated before, the applications have been made on the WDBC file downloaded from Kaggle. First, the dataset was pre-processed. The related file has been transferred to the program with the "File Reader" node under the "IO" category. The 30 features of the sample taken from the patient were measured in the dataset and as a result, it was determined whether the tumor was benign or malignant. Secondly, the total data is divided into two parts in the "Partitioning" node under the "Manipulation" category, as 70% training sets and 30% test sets. The separation of the dataset into two parts was done by random sampling. As a result of the partitioning process, 398 data lines were determined as training sets, while the remaining 171 data lines were determined as training sets. At this stage, the dataset has become suitable for classification algorithms. The training set obtained in the partitioning node is processed in “Learner” node in which the learning takes places. The test set output of the partitioning node is sent to the “Predictor" node. Both nodes are in the "Mining" category. On the other hand, the learning experience gained from the “Learner” node also comes to “Predictor” node. Thus, the “Predictor" node has two entry points. Finally, the "Scorer" node in the "Mining" category was added to evaluate the success of the classifiers. The "Scorer" node provides the assessment of other success criteria, especially the confusion matrix. Also, "ROC Curve (local)" node has been added to view ROC curves.

Figure 4 shows the selections used in the configuration of the "Decision Tree Learner" node related to the decision tree method. This node is the section where the decision tree algorithm performs learning. It is stated that the class to be decided is the "diagnosis" column. While creating the decision tree, Gini index was used as the quality measure in the division process. The tree building process is set to continue until only one item remains on each node, and no pruning will be performed. In addition, multipath splits have been applied instead of binary nominal splits.

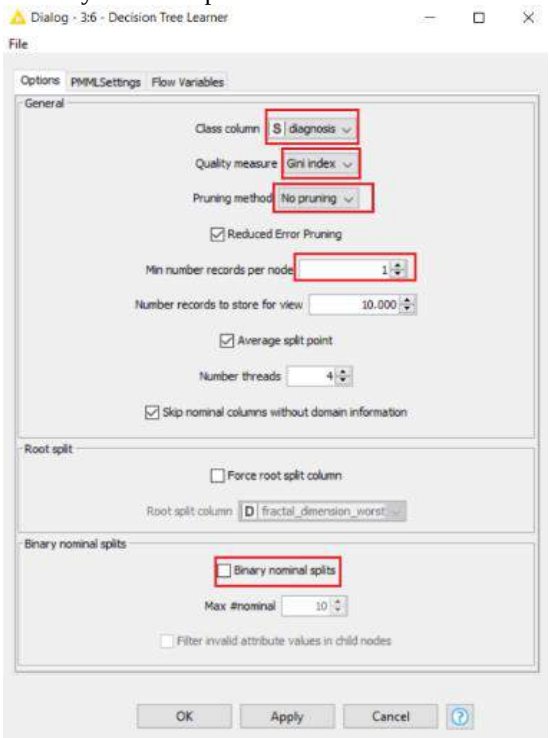


Figure 4. Decision Tree Learner configuration window

In this study, the Multilayer Perceptron (MLP) algorithm also is used as neural networks method. For this purpose, "RProp MLP Learner" and "Multilayer Perceptron Predictor" nodes, which are under the "Mining" category in the KNIME

program, have been used. Prior to this, each set obtained after the Partitioning node is normalized in the "Normalizer" node. Thus, it is aimed to prevent the effect of feature values that may be in different orders to the results. All dataset is subjected to the Min-Max normalization process and arranged so that their values are between 0-1. The normalized training set is connected to the "RProp MLP Learner" node. The values entered in "RProp MLP Learner" configuration are shown in Figure 5. A maximum of 100 iterations will be made to determine the weight coefficients in the learning process. The number of hidden layers is determined as 5 and the number of hidden neurons per layer is determined as 10. The class column to be trained is specified as "diagnosis".

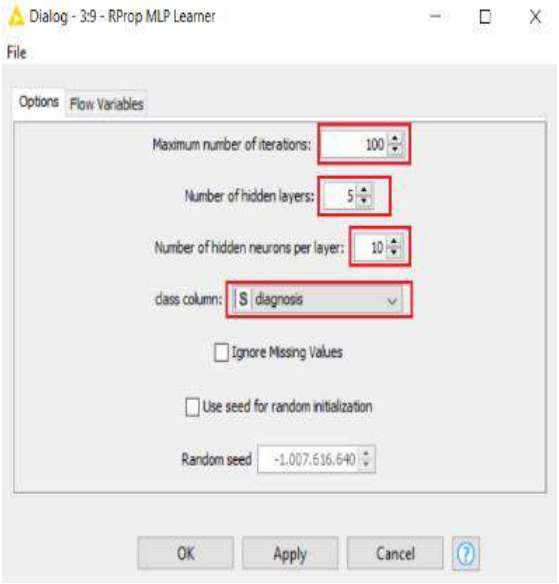


Figure 5. RProp MLP Learner dialog window

Performance Metrics: In this study, the error matrix, accuracy, specificity, sensitivity, precision, F score and ROC curve were used as performance metrics. Confusion matrix is used to measure the performance of machine classification algorithms when the number of class labels is two or more. The confusion matrix is a table made up of four different combinations with predicted and actual values when the number of class labels is two. With the confusion matrix table, the values predicted by the model and the actual values are compared.

Various performance metrics have been developed using the values in the confusion matrix. The most commonly used of these is accuracy. Accuracy is a measure of the correct predictions made by the classifier and provides general information about how many samples were classified as true or false. The accuracy is calculated with the following equation.

$$\text{Accuracy} = \frac{TP + TN}{FP + FN + TP + TN} \quad (1)$$

Sensitivity or Recall is a metric that shows how much of the values that are actually positive are predicted positively and is obtained from Equation 2.

$$\text{Sensitivity, Recall} = \frac{TP}{TP + FN} \quad (2)$$

Another metric derived from the confusion matrix is precision. Precision shows how many of the values are predicted positively are actually positive and is calculated by Equation (3).

$$\text{Precision} = \frac{TP}{TP + FP} \quad (3)$$

Specificity, on the other hand, is an indicator of how much of the values that are actually negative are predicted negatively and is calculated from Equation 4.

$$\text{Specificity} = \frac{TN}{TN + FP} \quad (4)$$

The F-score (F-measure) shows the harmonic mean of the precision and sensitivity values. It is a more successful metric compared to accuracy, especially in datasets that are not evenly distributed. F score can be calculated from Equation 5.

$$F - \text{score}\,(F - \text{measure}) = \frac{2 \times \text{Precision} \times \text{Sensitivity}}{\text{Precision} + \text{Sensitivity}} \quad (5)$$

Another important performance criterion used outside of the above metrics derived from the confusion matrix is the ROC curve. The ROC curve is basically a metric that shows whether the obtained classification models are working well and is calculated as follows.

$$\text{ROC} = \frac{\text{True Positive Rate (TPR)}}{\text{False Positive Rate (FPR)}} = \frac{\text{Sensitivity}}{1 - \text{Specificity}} \quad (6)$$

RESULTS

Figure 6 shows the image of the workflow chart created in the KNIME program within the scope of this study.

The confusion matrices and performance metrics of the three methods are shown together in Table 2. When Table 2 is examined, it is seen that the Naive Bayes algorithm and MLP artificial neural networks algorithm had the same accuracy with 96.5%. In two algorithms, they made 165 correct classifications and 6 incorrect classifications. At the same time, the F-score values were the same in both methods. On the other hand,

the classification accuracy percentage of the decision tree algorithm was obtained as 92.4%. It classified 13 samples of dataset incorrectly and classified 158 samples of dataset correctly. The performance criteria of the decision tree were lower than the other two algorithms.

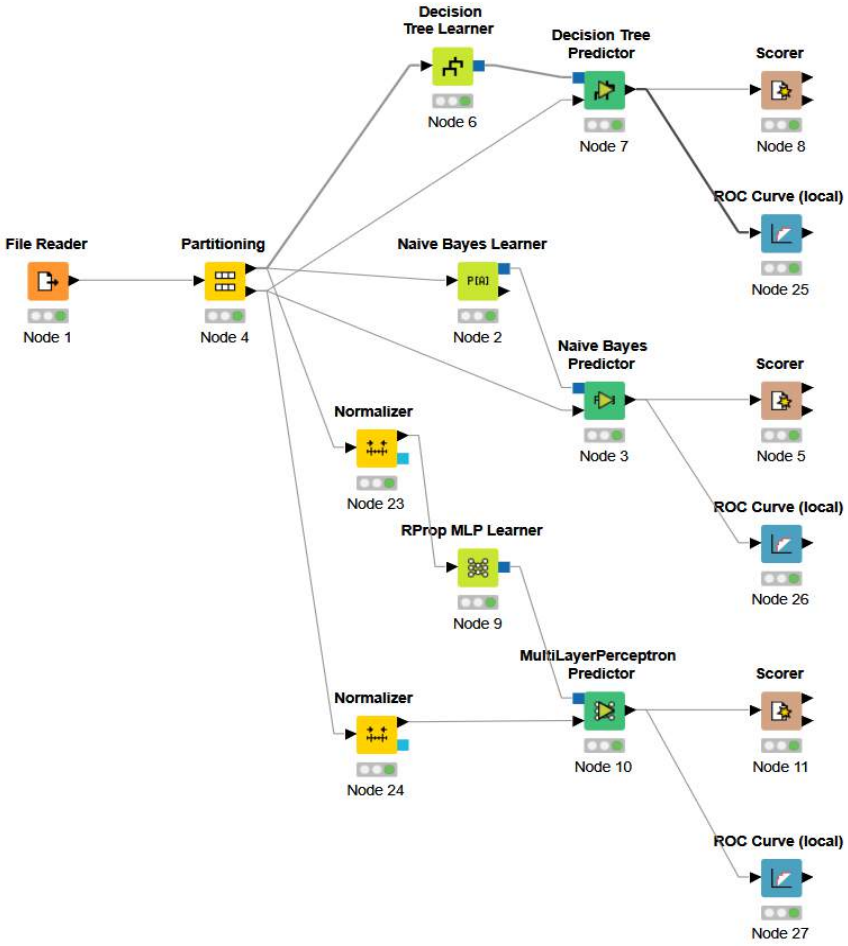


Figure 6. Workflow chart created in KNIME

Table 2. Confusion matrices and performance metrics

Naive Bayes		**Predicted value**		**Performance metrics**				
		Malign	Benign	Accuracy	Sensitivity	Specificity	Precision	F-score
Actual value	Malign	59	4	0.965	0.937	0.981	0.967	0.952
	Benign	2	106		0.981	0.937	0.964	0.972
Decision Tree		**Predicted value**		**Performance metrics**				
		Malign	Benign	Accuracy	Sensitivity	Specificity	Precision	F-score
Actual value	Malign	58	5	0.924	0.921	0.926	0.879	0.899
	Benign	8	100		0.926	0.921	0.952	0.939
MLP Artificial Neural Network		**Predicted value**		**Performance metrics**				
		Malign	Benign	Accuracy	Sensitivity	Specificity	Precision	F-score
Actual value	Malign	60	3	0.965	0.952	0.972	0.952	0.952
	Benign	3	105		0.972	0.952	0.972	0.972

Figure 7 shows the ROC curves obtained in each algorithm for malign and benign tumor classes. The ROC curves of Naive Bayes and MLP artificial neural network algorithms are quite similar to each other. The two curves have a fairly steep slope. The area value under the ROC curve was found to be 0.996 and 0.989 for the Naive Bayes and MLP artificial neural network method, respectively. So it can be said that the Naive Bayes algorithm is slightly more successful than the MLP

artificial neural network algorithm. In the decision tree method, the speed of convergence to 1 is slower than the other two algorithms. In Figure 8, the classified decision tree structure is shown. It is seen that there is a lot of branching in the decision tree. This can affect accuracy as well as complicate the classification algorithm. Here, a simpler tree can be obtained by pruning. In addition, the classification process was made by considering 30 features of the tumor samples. By applying feature selection algorithms, the most effective of those on classification can be selected. Therefore, the decision trees can be created having simple tree structure with more accurate classification.

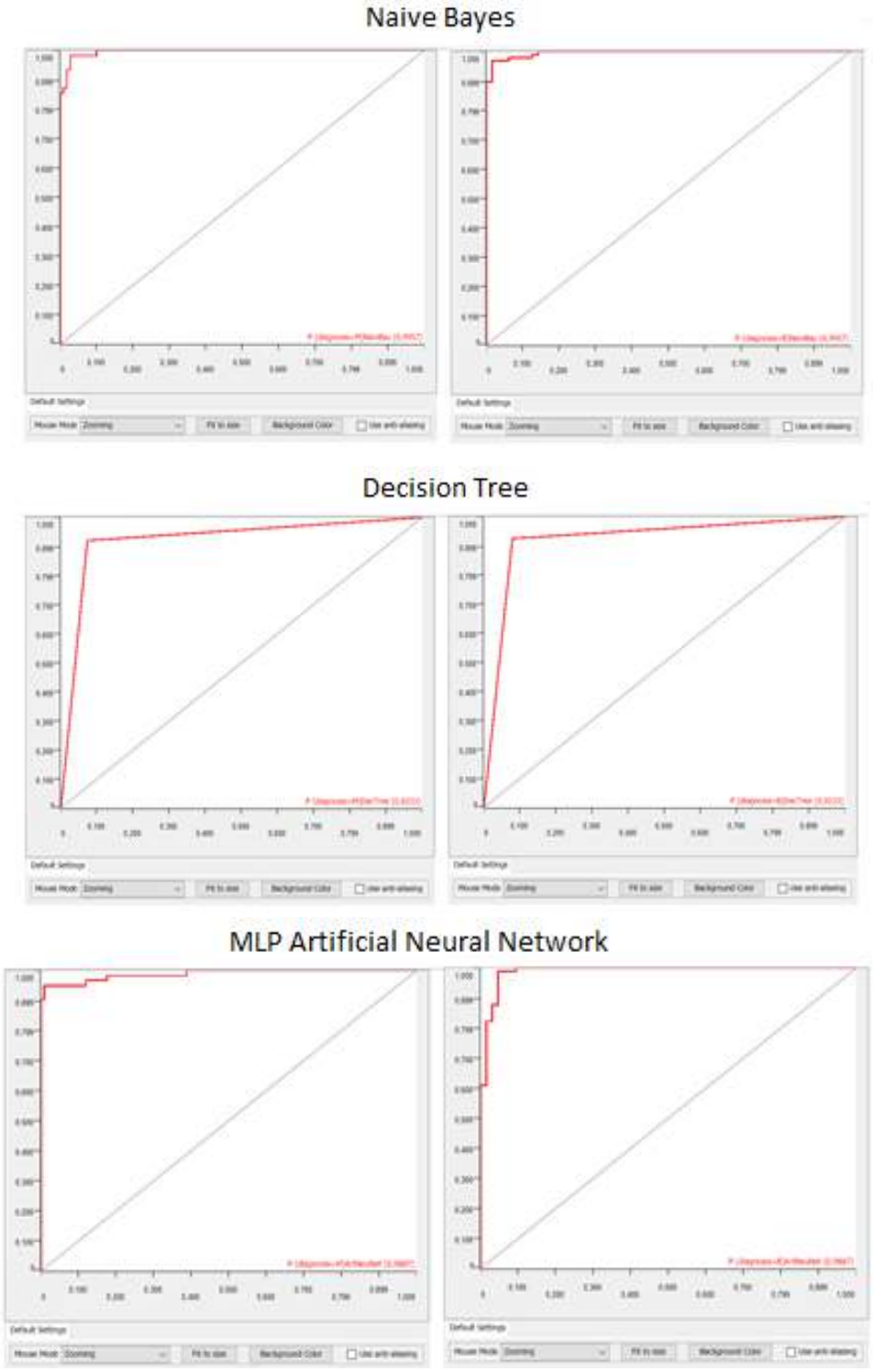


Figure 7. ROC curves

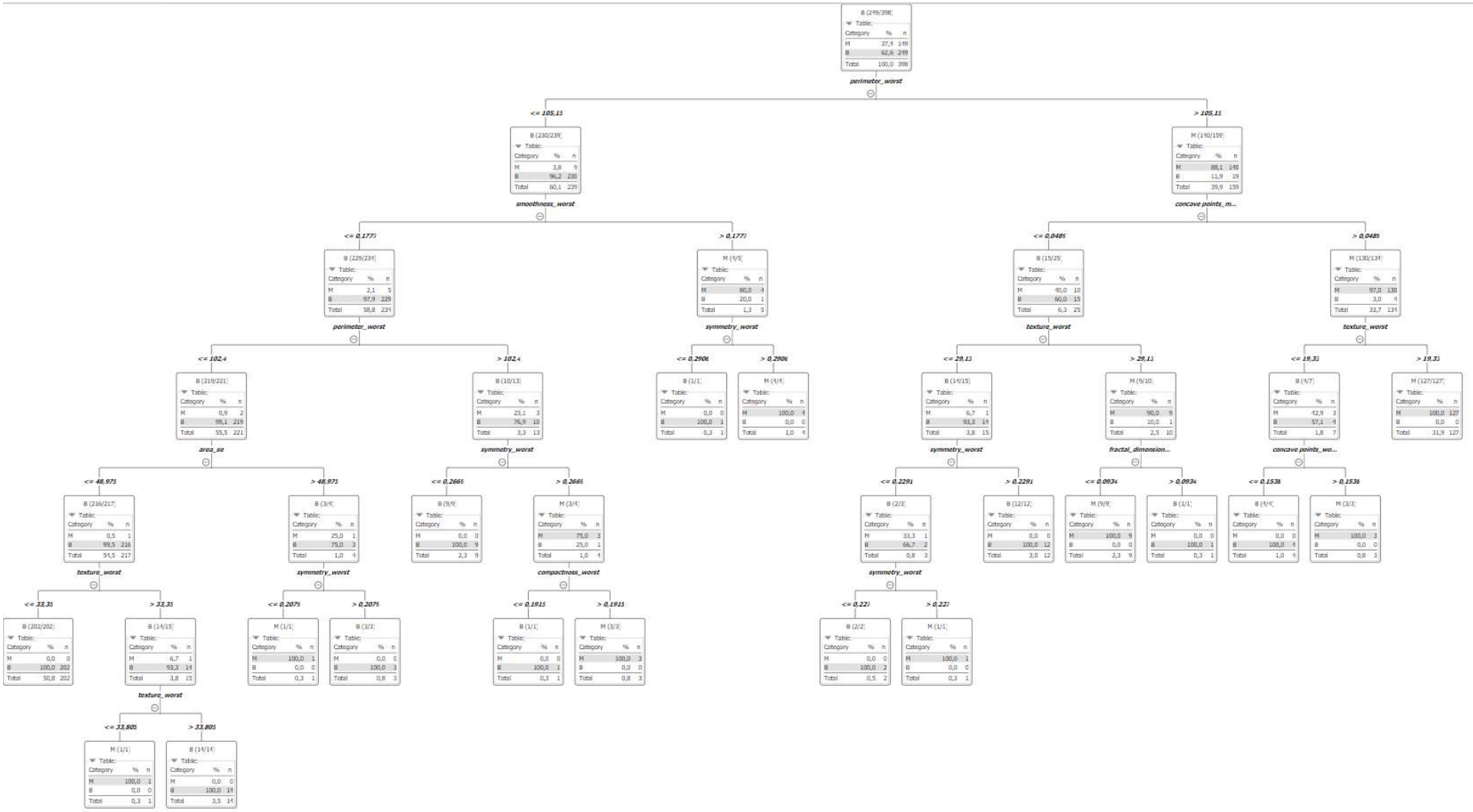


Figure 8. Decision tree structure (M: Malign, B: Benign)

DISCUSSION

In this section, the success rates achieved with various techniques on the WDBC data set in recent years are included. The classification accuracy of the existing studies in Table 6 varies between approximately 88% and 97%. Considering the 92.6% and 96.5% classification accuracies obtained in this study, it can be said that it has a high success among the existing studies in the literature.

Table 3. Methods and classification accuracy rates used in literature

Reference	Method	Classification accuracy (%)
Miao et al. (17)	Rough co-training	88.6
Lavanya and Rani (18)	Decision tree	94.84
Maldonado et al. (19)	Support vector machine	95.25
Koloseni et al. (20)	Differantial evolution	93.64
Astudillo ve Oommen (21)	Tree-based topology oriented self-organizing maps	93.32
Tabakhi et al. (22)	Naive Bayes/Decision tree	93.2/92.94
Lim and Chan (23)	Bandler-Kohout Subproduct	95.26
Rodrigues (7)	Naive Bayes/Decision tree	97.08/96.05
Asri et al. (8)	Support vector machine	97.13
Kong et al. (24)	Jointly sparse discriminant snalysis	93.85
Xu et al. (25)	Particle swarm optimisation	94.74
Nilashi et al. (15)	Fuzzy logic	93.2
Yavuz and Eyupoglu (26)	Generalized Regression Neural Network - Feed Forward Neural Network	94.54

As can be seen in Table 3, the studies have been conducted on the prediction of breast cancer diagnosis of many different machine learning techniques in the literature. It is noteworthy that despite the use of similar machine learning algorithms, the classification accuracies reported by researchers are different. The reason for that the machine learning is still an area with limitations and needs not only knowledge of data mining engineers but also the experience of the domain experts (27). Designing an effective machine learning model requires successful preprocessing, feature selection and classification processes (28). Each process includes different parameter selections and accordingly different solutions (27). Since there are no analytical approaches for parameter selection, the success of the model still depends on the choice of the expert performing the analysis. Therefore, setting the parameters and design of machine learning methods automatically has not been solved yet (28).

CONCLUSION

In this study, the performance of different machine learning methods to classify tumors as benign or malignant was examined on a breast cancer dataset. Data mining has been done with three classification algorithms. Naive Bayes, Decision Trees and Artificial Neural Networks algorithms were used as classification algorithms. The application was implemented in version 4.2.3 of the KNIME Analytics Platform data mining program. Accuracy, sensitivity, specificity, error matrices and ROC curves were used to measure the success of the methods examined. The key results from the study are listed below.

- Naive Bayes algorithm and MLP artificial neural network algorithm have shown similar classification performance. The accuracy value of both methods in classification was found to be 96.5%.
- Decision tree method classified the dataset correctly with 92.4% accuracy.
- Decision tree's success criteria are lower than the other two algorithms.
- It has been observed that the ROC curves of Naive Bayes and MLP artificial neural network algorithms are quite similar to each other and the two curves have a very steep slope. In the decision tree, the speed of convergence to 1 is slower than the other two algorithms.

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