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Araştırma Makalesi / Research Article

Examining the Performance of the Bagging Method in Breast Cancer Classification

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Abstract

The aim of this study is to classify breast cancer using the Bagging classifier, which is among the Ensemble methods. To this end, the breast cancer dataset available on the Kaggle database was used. The dataset consists of 569 observations and 32 variables, with 212 (37.3 %) being benign and 357 (62.7 %) malignant. Initially, the gain ratio feature selection method was used to determine the important variables. The performance of the method was then examined according to the number of variables and using 2-fold, 5-fold, and 10-fold cross-validation methods. The analyses were performed using the WEKA program. As a result of the analysis, both with all variables included and after removing insignificant variables, the performance metrics were determined as follows: accuracy was 95.0791, with precision, recall, and F-measure values of 0.951, and the ROC area value was 0.988. Moreover, it was observed that when all variables were used and when insignificant variables were removed, the method's performance was similar, except for the time variable, and it showed better performance compared to other variable numbers. Additionally, it can be said that the 2-fold cross-validation method showed slightly better classification performance in all metrics except for the ROC area measure. It is recommended that the Bagging method be used in the classification of different diseases.

Keywords: Breast cancer, classification, bagging, machine learning

1. Introduction

Cancer ranks as the second leading cause of death worldwide. Among women, the most common type of cancer is cervical cancer, followed by breast cancer (Naisen et al., 2022). In 2022, the number of deaths due to breast cancer globally was recorded as 670,000. Breast cancer is also identified as the most common cancer among women in 158 out of 185 countries. This cancer can be described as a disease where abnormal breast cells grow out of control, forming tumors. If not controlled, the spread of these tumors throughout the body can result in death (WHO, 2024). Early diagnosis of such a serious and widespread disease will not only reduce the number of deaths but also increase life expectancy. In recent years, machine learning methods have started to be used in the diagnosis and prediction of the disease (Divyavani and Kalpana, 2021). Using machine learning methods, it is possible to predict the disease with minimal error and high accuracy. Machine learning methods are a collection of techniques that uncover meaningful relationships between models and variables through experience (Bishop, 2006). This study aims to classify breast cancer using the Bagging method, which is part of the Ensemble methods family within machine learning techniques. Additionally, it intends to examine the classification performance of the method according to the number of variables. This study seeks to answer the following questions:

- What are the most important factors affecting breast cancer according to the gain ratio feature selection method?
- How is the prediction performance of the Bagging method in breast cancer?
- Does the performance of the Bagging method vary according to the number of variables used?
- Does the performance of the Bagging method differ according to the cross-validation method used?

In the literature, there are various studies where the dataset used in this study has been analyzed through machine learning methods. The study conducted by Nasien et al. (2022) attempted to predict breast cancer using the Artificial Neural Network (ANN) method. Divyavani and Kalpana (2021) not only employed this method but also applied the Support Vector Machine (SVM) method to diagnose breast cancer. Similarly, Nathiya and Sumitha (2023) utilized both of these methods as well as the Decision Tree (DT) method for this purpose. Assegie (2020), on the other hand, tried to predict breast cancer using the SVM and DT methods. Additionally, Hossin et al. (2023) explored the use of Logistic Regression (LR), Random Forest (RF), K-Nearest Neighbors (KNN), DT, Adaptive Boosting (Adaboost), SVM, Gradient Boosting (GB), and Gaussian Naive Bayes (GNB) methods for the same objective. In a similar vein, the study by Bansal and Singhrova (2021) incorporated linear regression (LiR), LR, DT, GNB, SVM, Perceptron, Multilayer Perceptron (MLP), RF, Bagging, GB, Adaboost, and KNN methods. Prastyo et al. (2020) also employed GNN, KNN, SVM, RF, Adaboost, GB, Extreme Gradient Boosting (XGBoost), and MLP methods for this purpose. Ahmed and Shefat (2022) applied LR, NB, DT, RF, SVM, and KNN methods to achieve the same goal. Assegie, Tulasi, and Kumar (2021) implemented DT and Adaboost methods. On the other hand, the study by Sari, Nabela, and Abdurrohman (2023) used the k-means algorithm to predict breast cancer. The study conducted by Abdulkareem and Abdulkareem (2021) employed RF and XGBoost methods for this purpose. The authors utilized the Recursive Feature Elimination (RFE) method to reduce dimensionality. In their study aimed at classifying breast cancer, Koirunnisa and Faisal (2023) employed ANN, SVM, DT, RF, LR, KNN, and NB methods, and resorted to the Principal Component Analysis (PCA) method for dimensionality reduction. The study by Assegie et al. (2022) examined the performance of Sequential, Embedded, and Chi-square feature selection methods using the mentioned dataset. Furthermore, Mallick et al. employed DT, LR, RF, NB, SVM, and ANN methods to analyze breast cancer data. The literature includes studies that explore the performance of cross-validation methods (Sujana et al., 2017; Battineni et al., 2019; Güre, 2024). The use of the Bagging method for this purpose has been encountered only in a limited number of studies (Bansal and Singhrova, 2021). Moreover, no studies have been found that examine its performance based on the number of variables and cross-validation methods. However, the study conducted by Bezek Güre (2023) employed Adaboost and Bagging methods to classify mathematical achievement and investigated the performance of these methods according to the number of variables and sample sizes.

2. Materials and Methods

The current study utilized the "Breast cancer data set" available on the Kaggle database. The dataset was obtained from the following link: https://www.kaggle.com/datasets/yasserh/breast-cancer-dataset?resource=download. The dataset consists of 569 samples, with 212 (37.3 %) being malignant and 357 (62.7 %) benign, and contains 32 variables. Besides the ID variable, the study includes 31 variables. Due to the large number of variables in the dataset, which contains no missing data, the Gain ratio feature selection method was first used to rank the variables according to their importance. Then, the classification performance of the Bagging method was examined using all variables, as well as using 15, 10, and 5 variables after removing the insignificant ones. The WEKA program was employed for the analysis of the standardized data. Descriptive statistics for the independent variables are presented in Table 1.

Table 1. Descriptive statistics for the variables

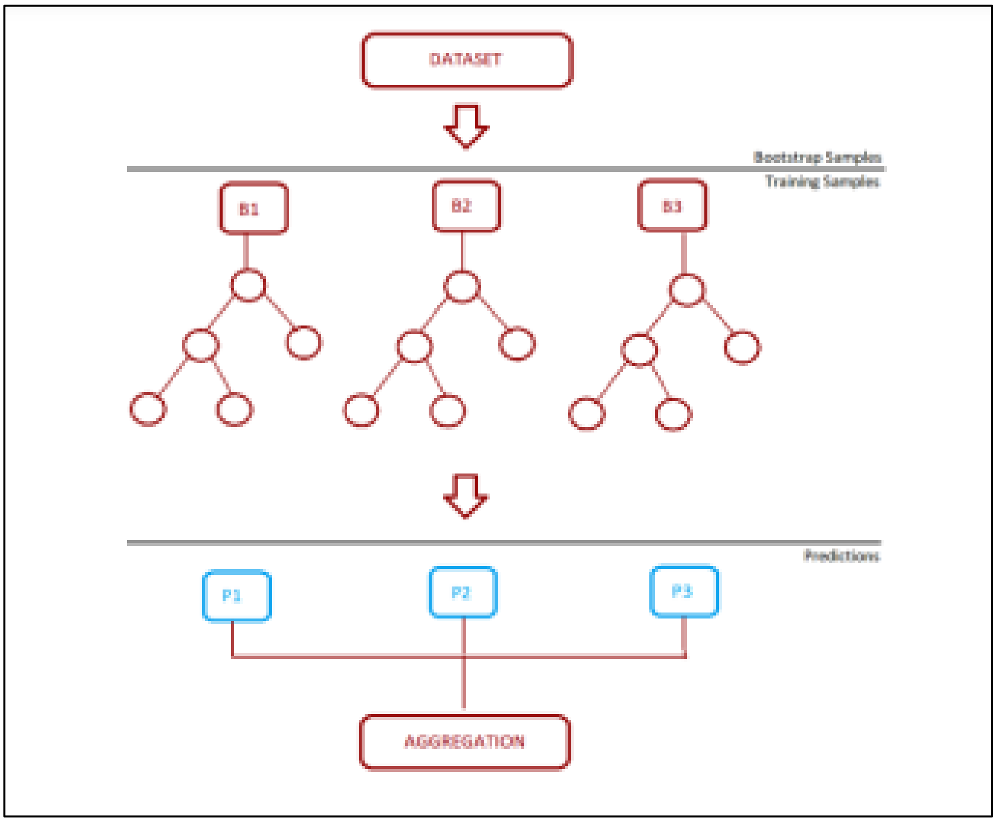
Variables	Minimum	Maximum	Mean	Std. Deviation
radius_mean	6.98	28.11	14.1273	3.52405
texture_mean	9.71	39.28	19.2896	4.30104
perimeter_mean	43.8	188.5	91.969	24.2990
area_mean	144	2501	654.89	351.914
smoothness_mean	0.0526	0.1634	0.096360	0.0140641
compactness_mean	0.0194	0.3454	0.104341	0.0528128
concavity_mean	0.0000	0.4268	0.088799	0.0797198
concave points_mean	0.0000	0.2012	0.048919	0.0388028
symmetry_mean	0.1060	0.3040	0.181162	0.0274143
fractal_dimension_mean	.04996	0.09744	0.0627976	0.00706036
radius_se	0.112	2.873	0.40517	0.277313
texture_se	0.3602	4.8850	1.216853	0.5516484
perimeter_se	0.757	21.980	2.86606	2.021855
area_se	6.8	542.2	40.337	45.4910
smoothness_se	0.001713	0.031130	0.00704098	0.003002518
compactness_se	0.00225	0.13540	0.0254781	0.01790818
concavity_se	0.00000	0.39600	0.0318937	0.03018606
concave points_se	0.00000	0.05279	0.0117961	0.00617029
symmetry_se	.00788	0.07895	0.0205423	0.00826637
fractal_dimension_se	.000895	0.029840	0.00379490	0.002646071
radius_worst	7.93	36.04	16.2692	4.83324
texture_worst	12.02	49.54	25.6772	6.14626
perimeter_worst	50.4	251.2	107.261	33.6025
area_worst	185	4254	880.58	569.357
smoothness_worst	.0712	0.2226	0.132369	0.0228324
compactness_worst	.0273	1.0580	0.254265	0.1573365
concavity_worst	0.0000	1.2520	0.272188	0.2086243
concave points_worst	0.0000	0.2910	.114606	0.0657323
symmetry_worst	.1565	0.6638	0.290076	0.0618675
fractal_dimension_worst	.0550	0.2075	0.083946	0.0180613

2.1. Cross-validation (CV)

Cross-validation is a method used to measure prediction accuracy (Watanabe, 2010; Battineni et al., 2019). This method is employed to enhance prediction accuracy. In this method, the dataset is randomly divided into k subsets. Among these, one is used as test data, while the others are used as training data. It is essential that all classes are almost equally represented. The method uses different test data each time. Then, the overall error rate is calculated by averaging the errors across all classes (Aksu and Doğan, 2018; Bezek Güre, 2023).

2.2. Bagging Method

The Bagging method, proposed by Breiman in 1996, was developed to improve prediction performance. It is part of the ensemble methods family, widely used in statistics and machine learning (Patil et al., 2023). Primarily aiming to reduce variance, the method is included among supervised machine learning techniques (Kadiyala and Kumar, 2018). It is trained by decision trees, which are individual machine learning methods (Ngo et al., 2022). The method is employed for solving both classification and prediction problems. In addition to reducing prediction variance, the method helps prevent overfitting (Oza and Russel, 2001). Prediction techniques are applied by drawing bootstrap samples from the dataset (Sutton, 2005). These numerous samples are then trained and combined in the final model. Bootstrap can be described as a process where small samples are iteratively drawn from the original dataset, with replacement (Ghosh and Prabu, 2019). In regression problems, the final decision is made by averaging, while in classification problems, it is made by majority voting.



Şekil 1. Bagging model (Ghosh ve Prabu, 2019).

2.3. Performance criteria

This study used Accuracy, Precision, Recall, F-measure, and ROC Area as performance criteria, along with the time taken by the method. Table 2 presents the confusion matrix.

Table 2. Confusion matrix

		Estimated Class		
		No	**Yes**	**Total**
Real Class	No	TN	FP	TN+FP
	Yes	FN	TP	FN+TP
	Total	TN+FN	FP+TP	TN+FN+FP+TP

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

$$Precision = \frac{TP}{TP+FP} \quad (2)$$

$$Recall = \frac{TP}{TP+FN} \quad (3)$$

$$F1\ score = 2x\ \frac{(Precision\ x\ \ Recall)}{(Precision+\ Recall)} \quad (4)$$

(Şevgin and Önen, 2022).

ROC Area: Also known as the Area Under the Curve (AUC), this metric ranges between 0 and 1 (Bowers and Zhou, 2019).

3. Results and Discussion

First, the variables affecting breast cancer were ranked according to their importance using the Gain ratio feature selection method, as shown in Table 3.

Table 3. Important variables according to the gain ratio feature selection method

Rank	Variable Importance	Variable Order	Variable Name
1	0.4443	24	perimeterworst
2	0.3872	22	radiusworst
3	0.3851	25	areaworst
4	0.3844	29	concavepointsworst
5	0.3288	9	concavepointsmean
6	0.3195	8	concavitymean
7	0.3127	28	concavityworst
8	0.3123	4	perimetermean
9	0.3061	5	areamean
10	0.2968	2	radiusmean
11	0.266	15	arease
12	0.2156	7	compactnessmean
13	0.215	12	radiusse
14	0.194	14	perimeterse
15	0.1681	27	compactnessworst
16	0.1604	18	concavityse
17	0.1595	3	texturemean
18	0.145	20	symmetryse
19	0.1281	19	concavepointsse
20	0.1256	26	smoothnessworst
21	0.1201	23	textureworst
22	0.1072	30	symmetryworst
23	0.1053	6	smoothnessmean
24	0.1024	17	compactnessse
25	0.0956	31	fractaldimensionworst
26	0.0682	10	symmetrymean
27	0.0346	21	fractaldimensionse
28	0	13	texturese
29	0	11	fractal_dimensionmean
30	0	16	smoothnessse

Table 3 shows that the variables perimeterworst, radiusworst, and areaworst are the most important variables, while texturese, fractal_dimensionmean, and smoothnessse have no impact. Subsequently, the WEKA program was used to apply the Bagging method. To enhance the prediction performance of the method, a 10-fold cross-validation method was employed. The classification performance of the Bagging method according to the performance metrics used in the study is presented in Table 4.

Table 4. Performance of the bagging method based on the number of variables

	Accuracy	Precision	Recall	Fmeasure	RocArea	Time
All Variables	95.0791	0.951	0.951	0.951	0.988	0.18
With Insignificant Variables Removed	95.0791	0.951	0.951	0.951	0.988	0.03
15	93.1459	0.932	0.931	0.931	0.983	0.03
10	94.2004	0.942	0.942	0.942	0.981	0.02
5	94.2004	0.942	0.942	0.942	0.980	0.01

Tablo 4 indicates that the classification performance is similar when using all variables and when insignificant variables are removed, except for the time metric. However, it was determined that the classification performance is better in comparison to the other scenarios. Therefore, in order to compare the performance of the cross-validation methods, analyses were conducted using all variables. The results of the analyses are shown in Table 5.

Table 5. Performance of the bagging method based on different cross-validation amounts

	Accuracy	Precision	Recall	Fmeasure	RocArea	Time
2	95.4306	0.954	0.954	0.954	0.986	0.05
5	93.4974	0.935	0.935	0.935	0.985	0.06
10	95.0791	0.951	0.951	0.951	0.988	0.18

As can be seen from Table 5, when the 2-fold cross-validation method is applied, the method shows slightly better classification performance in all metrics except for the ROC area.

4.Conclusions

This study used the Bagging method to predict breast cancer and also examined its performance based on different numbers of variables. Initially, the study employed the Gain ratio feature selection method to identify the most important factors affecting breast cancer. Then, using the Bagging method, the study evaluated the performance of the method by using all variables, excluding three insignificant variables, and by using the top 15, 10, and 5 most important variables. The analysis results showed that, when all variables were used and when the three insignificant variables were excluded, the performance metrics were as follows: accuracy: 95.0791, precision, recall, and F-measure values were 0.951, and the ROC area value was 0.988. Moreover, it was observed that the performance of the method was similar, regardless of whether all variables or only the significant ones were used, and it performed better compared to scenarios with fewer variables. When 15 variables were used, the classification performance decreased, while an increase in performance was noted when 10 and 5 variables were used. In summary, it can be said that using all variables resulted in better classification performance. The literature contains many studies supporting our findings (Temel et al., 2012; Kanik et al., 2013; Dolgun, 2014; Yabacı, 2017; Kumar and Chong, 2018; Nuray et al., 2021). On the other hand, there are studies that suggest the number of variables does not affect the performance of the methods (Huang and Fang, 2013; Kwon and Sim, 2013; Ceyhan, 2020; Kasap et al., 2021; Bezek Güre, 2023). The literature also includes studies that examine the impact of feature selection methods on the classification performance of methods. The study conducted by Lavanya and Rani (2011) found that using different feature selection methods, the classification performance of the CART method improved (Lavanya and Rani, 2011). Furthermore, according to the analysis results, it can be said that the 2-fold cross-validation method showed slightly better classification performance in all metrics except for the ROC area. Contrary to the results of this study, Sujana, Rao, and Reddy (2017) found that the 10-fold cross-validation method performed better, while Güre (2024) reported that the 20-fold cross-validation method showed better classification performance. The study by Battineni et al. (2019) found no difference in the performance of the NB and LR methods but identified 15-fold cross-validation as more successful in the J48 and RF methods.

The literature contains numerous studies that examine the performance of different machine learning methods using the dataset employed in the current study. In their study, Nasien et al. (2022) attempted to predict breast cancer using the ANN method and reported an accuracy rate of 96.92%. In the study by Divyavani and Kalpana (2021), which utilized both SVM and ANN methods, it was noted that the ANN method performed better, with a correct classification rate of 99 %. In another study, Nathiya and Sumitha (2023) used DT, SVM, and ANN methods for this purpose and concluded that the ANN method provided better predictions.

Hossin et al. (2023) aimed to diagnose breast cancer by employing methods such as LR, RF, KNN, DT, Adaboost, SVM, GB, and GNB. In their study, they observed that the LR method outperformed the others, achieving an accuracy rate of 99.12 %. Similarly, Bansal and Singhrova (2021) applied methods including LiR, LR, DT, GNB, SVM, Perceptron, MLP, RF, Bagging, GB, Adaboost, and KNN, and noted that the SVM algorithm demonstrated a better classification performance with a 96.67 % correct classification rate. This study, akin to our results, reached a 95.71 % correct classification rate using the Bagging method. Prastyo and colleagues (2020), on the other hand, utilized GNN, KNN, SVM, RF, Adaboost, GB, XGBoost, and MLP methods and found that the XGBoost method performed more successfully, with a 97.19 % correct classification rate. Similarly, Ahmed and Shefat (2022) conducted a study where they employed LR, NB, DT, RF, SVM, and KNN methods, and reported that the SVM method yielded the best result with a 97.20 % correct classification rate. Assegie (2020) also used the SVM and DT methods for this purpose and concluded that the SVM method was more successful, with a correct classification rate of 91.92 %. On the other hand, Koirunnisa and Faisal (2023) used ANN, SVM, DT, RF, LR, KNN, and NB methods in their study and determined that the LR method achieved a correct classification rate of 97.3 %. Assegie, Tulasi, and Kumar (2021) employed DT and Adaboost methods for the same goal and found that the Adaboost method performed better, with a correct classification rate of 92.53 %.

On the other hand, the study by Sari, Nabela, and Abdurrohman (2023), which employed the k-means algorithm, achieved an 84.57 % correct classification rate. In the study conducted by Abdulkareem and Abdulkareem (2021), RF and XGBoost methods were applied. The authors implemented the RFE method for dimensionality reduction and reported that the XGBoost method attained a 99.02 % correct classification rate. Similarly, Assegie and colleagues (2022), in their research that examined the performance of Sequential, Embedded, and Chi-square feature selection methods, achieved a 98.3% accuracy rate using the sequential feature selection method. Additionally, Mallick and colleagues utilized DT, LR, RF, NB, SVM, and ANN methods for this purpose, and it was found that the ANN method demonstrated superior performance. The current study employed the Bagging method to diagnose breast cancer. The performance of the Bagging method was assessed based on the number of variables utilized and the cross-validation methods. The performance of other machine learning methods related to this topic could also be explored. Additionally, the Gain ratio method was adopted as the feature selection technique. Future research could involve methods such as Correlation Based, One-R, Relief, and Symmetrical Uncertainty. Similar to the study by Güre (2023), the impact of different feature selection methods on various approaches could be analyzed. It is recommended to apply machine learning methods for predicting and classifying common diseases like breast cancer, and to evaluate their performance based on criteria such as the number of variables, sample size, cross-validation amount, and the percentage of training and test data.

Ethical Committee Approval

The dataset used in the present study was sourced from the publicly accessible Kaggle database; therefore, the research did not necessitate ethical committee approval.

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