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Breast Cancer Prediction with Artificial Intelligence Based Clinical Decision Support System

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Abstract: Breast cancer is caused by uncontrolled cell division and early diagnosis is crucial for successful treatment. Diagnostic methods such as MRI, mammography, ultrasound, biopsy are used in breast cancer diagnosis. AI-based clinical decision support systems can predict treatment outcomes. In this study, a study was conducted to diagnose breast cancer using blood test values data and to improve the performance of performance metrics by applying discretization preprocessing method. Machine learning algorithms such as Naive Bayes, K-Nearest Neighborhood, Random Forest, Multilayer Perceptron classifier algorithms were used. 10-Layer Cross-Validation method was used to compare the performance results. Two data sets with and without discretization were created and a model was built on these data. In breast cancer outcome prediction, the Multilayer Perceptron classification algorithm gave the highest classification performance with a sensitivity value of 0.828 on data without discretization. In the model created by applying discretization, an increase from 55% to 72% was seen in Support Vector Machines.

Keywords: Intelligent decision support systems, Machine learning algorithms, Breast cancer

Yapay Zeka Tabanlı Klinik Karar Destek Sistemi ile Meme Kanseri Tahmini

Özet: Meme kanseri, kontrolsüz hücre bölünmesinden kaynaklanır ve başarılı tedavi için erken teşhisi çok önemlidir. Meme kanseri teşhisinde MR, mamografi, ultrason, biyopsi gibi tanı yöntemleri kullanılmaktadır. AI tabanlı klinik karar destek sistemleri, tedavi sonuçlarını tahmin edebilmektedir. Bu çalışmada, kan tahlil değerleri verileri kullanılarak meme kanserini teşhis etmeyi ve ayrıklaştırma ön işleme yöntemi uygulanılarak performans metriklerinin başarımını artırmayı amaçlayan bir çalışma yapılmıştır. Makine öğrenimi algoritmalarından, Naive Bayes, K-En Yakın Komşuluk, Rastgele Orman, Çok Katmanlı Algılayıcı sınıflandırıcı algoritmaları kullanılmıştır. 10 Katmanlı Çapraz Doğrulama yöntemi kullanılarak performans sonuçları karşılaştırılmıştır. Ayrıklaştırma uygulanmış ve uygulanmamış iki veri seti oluşturulmuş ve bu veriler üzerinden bir model oluşturulmuştur. Meme kanseri sonuç tahmininde en yüksek sınıflandırma performansını, ayrıklaşırma uygulanmamış veriler üzerinde, Çok Katmanlı Algılayıcı sınıflandırma algoritması duyarlık değeri 0.828 ile vermiştir. Ayrıklaştırma uygulanarak oluşturulan modelde ise Destek Vektör Makinelerinde %55'ten %72'ye artış görülmüştür.

Anahtar Kelimeler:Akıllı karar destek sistemleri, Makine öğrenimi algoritmaları, Meme kanseri

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1. INTRODUCTION

Artificial intelligence-based intelligent decision support systems aim to determine the most appropriate treatment for the patient by analyzing the clinical databases of the results of various treatment methods that have been applied before. With the application of these systems, it is possible to quickly diagnose and increase the treatment success rates for diseases whose diagnosis is based on many parameters and whose treatment is sensitive, such as cancer, immune system diseases, neurological diseases. Breast cancer is the most common type of cancer among women. Breast cancer is one of the most important causes of death in women, especially between the ages of 30-59.

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There are many published research articles investigating the effects of decision support systems on treatment decisions in patients at high risk of metastatic breast cancer. One of these studies included 10 oncologists who offered treatment recommendations to an average of 1977 patients evaluated before and after using the therapeutic options offered by the CDSS. The findings of the study show a significant increase in the rate of treatment changes made by physicians after using CDSS, especially in cases of stage IV disease. However, it did not show a statistically significant result in the first stage (P=.022). The researchers suggest that more research is needed to derive overall value, including the impact of CDSS technology on clinical outcomes, patient-physician communication, and other factors such as learning, blood tests, and imaging [1].

In summary, the study suggests that CDSS technology has the potential to positively impact treatment decisions for patients with high-risk breast cancer, but additional research is needed to fully understand its value in clinical practice.

In another study, a model was developed that calculates the probability of positive pregnancy by using the features of the patient who will start IVF treatment. The data consists of 1154 electronic health records performed at Yeditepe University Hospital IVF Clinic between 2013-2019. Five different classification methods on the dataset (Support Vector Machines, Multilayer Perceptron, Random Forest, Extreme Gradient Boost and Light Gradient Boost) were comparatively examined using 5-fold cross validation method. In prediction of pregnancy outcome, the highest classification performance was obtained with the Support Vector Machines method (AUC=0.70), and the estimation accuracy was further improved with the optimization of the decision threshold value in the classification probability results, and the pregnancy outcome was predicted with a rate of 71.7% True Positive and 59.4% True Negative [2].

This study aimed to develop a web-based system for the diagnosis and treatment of headaches using data mining techniques. The study used classification criteria published by the International Headache Society as the basis for the diagnosis and treatment of headaches. The dataset used in the study included 850 patient records obtained from three different cities in Turkey. The study compared the performance of different algorithms, including artificial immune system algorithms, ant colony algorithms, and artificial bee colony algorithms, in terms of accuracy, precision, and recall. The system developed in the study used a rule-based algorithm for classification based on the diagnosis criteria. The results showed that the artificial immune system algorithm performed better than the other two algorithms in terms of accuracy, precision, and recall. The study has important implications for the development of web-based systems for the diagnosis and treatment of headaches. By using data mining techniques, the system can provide more accurate and efficient diagnosis and treatment recommendations to patients. However, it is important to note that the study was limited to a dataset from Turkey, and further research is needed to determine the generalizability of the findings to other populations [3].

Another study has successfully predicted melanoma using a dermoscopic image dataset. VGG-16 aims to build a model using pre-trained networks based on deep learning. The current study provides clinical support to physicians in the medical decision-making process for the diagnosis of melanoma. Accuracy 93.2% and sensitivity 67.4% achieved metrics [4].

The study you mentioned used clinical data from the cBioPortal database and applied data preprocessing to make the data more understandable and applicable. The study evaluated the performance of seven widely used classification algorithms from machine learning, K-Nearest neighbors, Random trees, Gradient boosting, Support vector machine, Logistic regression, Naive Bayes and Decision trees. The study found the best performance of the Gradient boosting algorithm among the seven classifiers with an accuracy of 85.37%. This is interesting as previous studies have shown that the Random trees algorithm tends to perform better. It's important to note that the accuracy of a classifier is not the only factor to consider when choosing a machine learning algorithm for a particular task. Other factors such as the interpretability of the model, computational efficiency, and ability to handle imbalanced data should also be considered. Overall, it seems that the study has contributed to the understanding of the performance of different machine learning algorithms on clinical data and has provided evidence that the Gradient boosting algorithm may be a promising choice for this type of data [5].

Another study proposes a unique feature selection method based on Eagle Strategy Optimization (ESO), Gravity Search Optimization (GSO) algorithm and their hybrid combination. Using Wisconsin as a dataset, feature selection is applied to classify breast cancer into two groups and select the fewest features to achieve maximum accuracy. This study also created a hybrid model that combines two algorithms, ESO and GSO algorithms, while removing unimportant features and reducing complexity. They show that their proposed hybrid algorithm performs well in breast cancer classification. They achieved an accuracy of 98.9578% [6]

In order to support the evaluation process of mammogram images and improve the diagnostic process, this paper presents the design, development and proof of concept of a novel intelligent clinical decision support system based on two predictive approaches operating simultaneously. The first one implements a set of expert systems based on fuzzy inferential engines for the treatment of features associated with the main findings found in mammograms. This allows the identification of a set of risk indicators, Symbolic Risks, related to the risk of developing breast cancer according to different findings. The second applies a classification machine learning algorithm that uses general patient information as well as data on mammography findings to determine the Statistical Risk, another measure linked to the risk of developing breast cancer. These risk indicators are then combined to produce a new indicator, Global Risk. This can then be corrected using a weighting factor according to the BI-RADS category assigned to each patient

by the responsible medical team. Thus, the Corrected Global Risk is obtained, which, once interpreted, can be used to determine the patient's condition and generate personalized recommendations. The proof-of-concept and software implementation of the system was realized using a dataset containing 130 patients from a database from the University of Wisconsin-Madison School of Medicine and Public Health [7].
The study mentioned in the article analyzed the performance of machine learning classification methods on lung and brain cancer datasets. The researchers used Naive Bayes, Bayes NET, kNN, Random Forest, and LSVM for the analysis, and also performed feature selection using genetic algorithm to improve the performance of the Support Vector Machines (SVM) classifier. The results of the study showed that the feature selection process with genetic algorithm significantly increased the performance of the SVM classifier. This finding highlights the importance of feature selection in cancer diagnosis studies using machine learning, as it can improve the accuracy of the classification models. The researchers also provided tables to support their results and interpretations. Overall, this study provides valuable insights into the potential of machine learning and genetic algorithms for cancer diagnosis, and underscores the importance of careful feature selection in developing accurate classification models [8].
In this study, AI-based clinical decision support systems can predict treatment outcomes. In this study, a study was conducted to diagnose breast cancer using blood test values data and to improve the performance of performance metrics by applying a discretization preprocessing method.

2. METHODS

2.1. Data Set Used in The Study

It has 10 features that indicate the presence or absence of breast cancer, all quantitative and one binary dependent variable. It is a data set consisting of 116 person records. The data set from Uci was put into the database in 2018 and is referred to as the Breast Cancer Coimbra Data Set. Predictors are anthropometric data and parameters that can be collected in routine blood analysis. Predictive models based on these predictors, if correct, could potentially be used as a biomarker of breast cancer. Attributes in the data set; age, BMI (kg/m2), glucose (mg/dL), insulin (µU/mL), HOMA, Leptin (ng/mL), Adiponectin (µg/mL), Resistance (ng/mL), MCP-1(pg/dL), labels are expressed as healthy controls and patients [9].

2.2. Created Model

In order to increase the performance metrics of the model, the discretization preprocessing method was applied to the data. Then, Naive Nayes, k-NN, Random Forest, Support Vector Machines, Multilayer Perceptron methods, which are artificial intelligence classification algorithms that will be beneficial in clinical decision support, were applied to the new data set obtained from here. Discretized and non-discretized data were given to the classifier algorithms and the findings were obtained. The model drawing is shown in Figure 1. In the figure, the data written as Breast Canser Datas are two. One is a discretized dataset and the other is a non-discretized dataset.

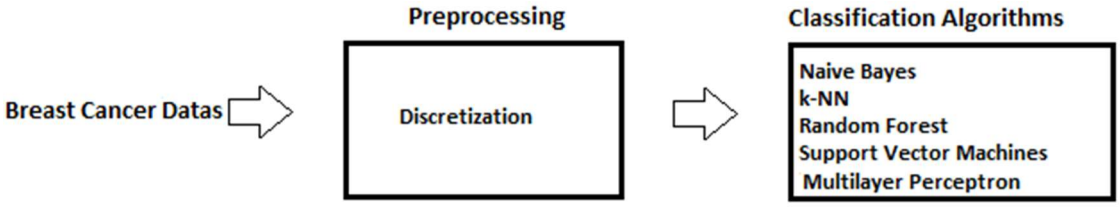

Figure 1. Artificial Intelligence-Based Model in Clinical Decision Support Systems

2.3. Preprocessing Method

2.3.1 Discrete

The filter that separates numerical attributes into nominal attributes using the Fayyad and Irani discretization method can be divided into four steps. The continuous values of the first feature are sorted. A breakpoint is chosen to divide the values into ranges. Continuous ranges of values are split or combined to create the discretized feature. Steps 1-3 are repeated for each continuous feature remaining in the dataset. Discretization is a process that helps reduce the number of values in a continuous attribute by dividing the range of values into intervals. This can generate more accurate and manageable nominal attributes than continuous attributes. The Fayyad and Irani method is a widely used approach for discretization that involves iteratively refining ranges based on a chosen cutoff point and stopping

criteria. Discretization can be useful when working with large datasets with many continuous attributes, as it can reduce dimensionality and increase the accuracy of machine learning models [10].

2.4. Classification Algorithms

Classification is the grouping of data according to their similarities. Classifier algorithms learn the training set and the distribution pattern and apply the class on the imprecise test data [11]. As classification algorithms, machine learning-based classification methods, which are frequently used in solving different problems in the literature, such as Random Forest, Naive Bayes, Bayes Networks, k-Nearest Neighbor (k-NN), Multi-Layer Perceptron (MLP) and Support Vector Machines (SVM) are used. . Its suitability to the problem of detecting anti-CoV peptides was evaluated according to the results obtained.

2.4.1. Naive Bayes

Naive Bayes is a Bayes-based statistical classification technique. This classifier predicts the effect of a feature value in a particular class and decides independently of the values of other features [12]. The naive Bayes classifier is basically the product of all conditional probabilities. A naive Bayes classifier is an algorithm based on Bayes' theorem, which predicts the impact on the class for each feature value independently of the values of the other features. This is called "naive" because it is a pure assumption. This algorithm estimates the probability of the class by the product of conditional probabilities and is often successful in applications such as text classification.

2.4.2. k- Nearest Neighborhood

k-Nearest Neighborhood (k-NN) is multi-label learning and its application consists of examples associated with the class of the relevant example according to the class of k nearest neighbors. It analyzes the training samples with known tag sets and predicts the tag sets of the samples whose class is not known [13]. The nearest neighbors are calculated with the Euclidean distance formula.
Euclidean Distance is a distance metric that measures the linear distance between two points. This distance metric calculates the differences between the coordinates of the points, squares these differences, and then takes the square root to get the result. However, it gives the option to use different distance metrics. Apart from "Euclidean Distance", other distance metrics such as "Manhattan Distance" and "Chebyshev Distance" are also available. These metrics measure distance in different ways and may produce different results in the KNN algorithm. [14].

2.4.3. Random Forest

Random Forest algorithm, an ensemble learning algorithm, is a machine learning classification method that is computationally efficient and can handle large datasets[15]. The algorithm uses resampling techniques, such as bootstrapping with replacement, to select a certain number of samples from the dataset. For each selected sample, a decision tree classifier is constructed to perform bootstrap aggregation. The classifier with the best performance is then selected through majority vote. Additionally, Random Forest randomly selects a subset of attributes for each node in the decision tree and selects the best features from those subsets for classification. Since the Random Forest classifier combines multiple base classifiers, it has a high degree of interference robustness. As the number of base classifiers increases, the classifier tends to have a lower estimation error. In summary, Random Forest is a powerful machine learning algorithm that uses resampling and feature subset selection to create a robust classification model [16].

2.4.4. Support Vector Machines

Support Vector Machines (SVM) were developed in 1979 for solving pattern recognition and classification problems [17]. SVM relies on defining a hyperplane to optimally distinguish between the two classes. In this study, SVM algorithms with linear and radial basis function kernel functions are used. For classification, it is possible to separate the two groups by drawing a boundary between two groups on a plane. The SVM algorithm determines the boundary of the class to which it belongs. The planes on which the support vectors are represented by points are called boundary planes. The plane that passes through the middle of the boundary planes and is equidistant from both planes is referred to as the hyper plane [18].

On a training set consisting of two classes, defined as separable (x1,y1),……,(xr,yr) for r samples; x ϵ RN denotes an N-dimensional space and class labels with y ϵ {+1,-1}. These two classes can be separated by N-1 dimensional hyperplanes [19]. A hyperplane is defined as in equation 2.3.

$$w.xi+b=0 \quad (2.1)$$

xi denotes the point on the hyperplane, w denotes the normal of the hyperplane, and b denotes the bias, expressed as the distance of the hyperplane from the origin.

2.4.5. Multilayer Perceptrons

Multilayer Perceptrons (MLPs) consist of interconnected artificial nerve cells called neurons. Information flow from the connections of artificial nerve cells is provided in the network. It is successful in nonlinear problems [20]. MLP consists of input, intermediate and output layers. Multi-layer sensors consist of one or more hidden and final output layers, which are the input to the system. The MLP system has transitions that propagate forward and backward. In forward propagation, the output produced by the network and the resulting error value are calculated. In backpropagation, the link weight values between the layers are updated to minimize the calculated error value [21]. Generally, back propagation algorithm is used. In the first step, random weights are generated for the inputs. In the input, the inputs are obtained and transmitted to the middleware. The middle layer is one or more and each layer can have a different number of processing elements. In the middleware, the total value is obtained with the weights, inputs and threshold value. It is then passed through the activation function and the net value is formed. The net value is transmitted to the next middleware or output layer. Elements in the middle layer are determined by the activation function. The outputs of the initial inputs and the outputs produced by the network are compared and the difference is accepted as an error. The resulting error value is distributed to the weights of the model and the goal is to reduce the error in the next iteration. Errors are distributed in weights to reduce the error value of each processing element in the output layer. The updating of the weights continues as back propagation up to the input layer, minimizing the error in the output layer.

3. EXPERIMENTAL RESULTS

The k fold cross validation test technique involves dividing the dataset into k equal clusters.The k-value, which is quite common in data mining, is used here to represent the separation into test and training clusters, unlike the k-means method as in clustering algorithms [22]. The k value is taken as 10. For each test, nine of the clusters are used to train the model, while the remaining cluster is used to test the performance of the trained model. This process is repeated ten times, so that each cluster is used for testing once. The performance values obtained from each test are then averaged to obtain the final performance estimate of the model [23]. Class accuracy was assessed using the area under the ROC curve (AUC), Precision, Sensitivity, and Mathew's Coefficient of Correlation (MCC) metrics. These metrics are derived from the complexity matrix shown in Figure 2, namely positive (P), negative (N), true positive (TP), true negative (TN), false positive (FP), and false negative (FN).

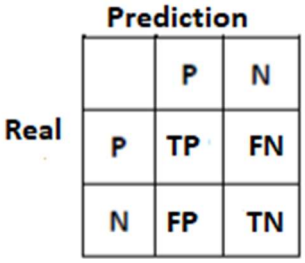

Figure 2. Confusion matrix

Class accuracy gives the ratio of positive and negative correctly predicted values. Precision value shows how stable the model is for the data to be estimated, and the precision value is important in unbalanced data sets. Precision gives the rate at which the target class (TP) is predicted correctly. The AUC is a graph of the ROC curve showing the ratio of sensitivity to specificity minus one. The area under this curve is defined as AUC. It is a value expressed in the range of 0-1. The closer it is to 1, the better the model's performance. MCC is the correlation coefficient between observed and predicted outputs for binary classification. It is a criterion that indicates the strength of the model in problems with two classes [22]. The MCC value is a performance metric that ranges from -1 to +1. The closer the value is to 1, the better prediction is made, 0 indicates a random guess, and closer to -1, it indicates a reverse prediction. The F-

Score is obtained by calculating the harmonic mean of the sensitivity and precision values and maintaining the balance between the two metrics. It is possible to interpret the classification more accurately by looking at the F-Score value. As a result of all testing, performance metrics are averaged. In the developed model, the classification algorithms of Naive Bayes, Random Forest, k-NN, MLP and SVM were tested on the discretized data set and the non discretized data sets. The rate of increase of the metrics was analyzed.

Preprocessing	Algorithm	Accuracy(%)	Recall	Precision	MCC	f-Score	AUC
DSC	Naive Bayes	72,41	0,813	0,724	0,439	0,721	0,744
	k-NN	71,55	0,781	0,715	0,421	0,714	0,732
	Random Forest	71,51	0,797	0,715	0,421	0,713	0,729
	SVM	72,41	0,766	0,723	0,441	0,724	0,719
	MLP	73,27	0,828	0,734	0,457	0,729	0,734
Without applying DSC	Naive Bayes	60,34	0,603	0,662	0,276	0,587	0,735
	k-NN	66,37	0,664	0,676	0,34	0,664	0,695
	Random Forest	74,13	0,797	0,741	0,475	0,74	0,816
	SVM	55,17	0,552	0,552	-	0,711	0,5
	MLP	65,51	0,688	0,655	0,303	0,655	0,749

Table 1. The results of artificial intelligence algorithms to support clinical decisions on discretized data set and non-discrete data set

When looking at the performance values obtained from the data set without DSC and DSC, while DSC works in almost every algorithm, it did not work in the Random Forest algorithm. Random Forest obtained the best value with a success rate of 74.13% on the dataset without DSC. With Naive Bayes DSC, it can be considered as the best working algorithm with a performance increase of 12%. MLP gives the most successful result in the DSC applied data set with a value of 73.27%. When looking at all values, MLP gave the most successful results in the DSC-applied dataset, recall 0.828 in the non-DSC-applied dataset, and precision 0.734. It has shown that the MLP algorithm gives the best result in the model by providing the most successful positive class prediction with the recall value used for the correct prediction of the positive class.

4. CONCLUSIONS

Breast cancer is the most common cancer among women. Early detection through breast cancer screening programs is associated with invasive procedures that cause less aesthetic discomfort, improved overall survival and reduced mortality. Breast cancer is biologically and clinically very heterogeneous. Although there are many risk factors for the development of breast cancer, no risk factor can be identified in 75% of women with breast cancer. The most important risk factor for developing breast cancer is advancing age and a family history of breast cancer. Many experimental and statistical models have been developed to calculate the lifetime risk of developing breast cancer. Early detection and initiation of treatment before further metastasis is important to reduce mortality. By utilizing intelligent decision support systems, it is possible for physicians to prevent early detection and treatment progression.

In this study, performance values are compared with the metrics obtained with the discrete method used as a preprocessing method by utilizing artificial intelligence-based machine learning algorithms in clinical decision support systems. As a result of the comparison of evaluation metrics in the context of this model, it was concluded that Random Forest does not work well with DSC compared to others. Two data sets were created without and with DSC. When we look at the performance values obtained from these datasets, DSC works in almost every algorithm, but not in Random Forest algorithm. Random Forest was also the model that gave the best accuracy in the dataset without DSC. Naive Bayes can be considered as an algorithm that works well when combined with DSC as it increases the performance increase rate. MLP gave the most successful result among all values in the dataset with DSC.

In future studies, other pre-processing methods can be added to dicrete and a new hybrid model can be applied to breast and other cancer types to create and compare different clinical decision aids.

References

[1] Xu, F., Sepúlveda, M. J., Jiang, Z., Wang, H., Li, J., Liu, Z., ... & Rhee, K. (2020). Effect of an artificial intelligence clinical decision support system on treatment decisions for complex breast cancer. JCO Clinical Cancer Informatics, 4, 824-838.

[2] Pacci, Z., Şengül, Y. A., Attar, R., Alagöz, O., & Asli, U. Y. A. R. (2021). Yapay Zeka Tabanlı Klinik Karar Destek Sistemi İle Tüp Bebek Tedavisi Gebelik Sonucu Tahmini. Emo Bilimsel Dergi, 11(22), 27-35.

[3] Çelik, U. (2015). Baş Ağrısı Teşhisi İçin Bir Karar Destek Sisteminin Geliştirilmesi.

[4] Kaplan, A., Güldogan, E., & Arslan, A. K. (2019, September). Prediction Of Melanoma From Dermoscopic İmages Using Deep Learning-Based Artificial İntelligence Techniques. In 2019 International Artificial Intelligence And Data Processing Symposium (Idap) (Pp. 1-5). Ieee.

[5] Atasoy, N. A., & Demiröz, A. Makine Öğrenmesi Algoritmaları Kullanılarak Prostat Kanseri Tümör Oluşumunun İncelenmesi. Avrupa Bilim Ve Teknoloji Dergisi, (29), 87-92.

[6] Singh, L. K., Khanna, M., & Singh, R. (2023). Artificial intelligence based medical decision support system for early and accurate breast cancer prediction. Advances in Engineering Software, 175, 103338.

[7] Casal-Guisande, M., Álvarez-Pazó, A., Cerqueiro-Pequeño, J., Bouza-Rodríguez, J. B., Peláez-Lourido, G., & Comesaña-Campos, A. (2023). Proposal and Definition of an Intelligent Clinical Decision Support System Applied to the Screening and Early Diagnosis of Breast Cancer. Cancers, 15(6), 1711.

[8] Candan, H., Durmuş, A., & Harman, G. (2019). Genetik Algoritma Ve Sınıflandırıcı Yöntemler İle Kanser Tahmini. Veri Bilimi, 2(1), 30-34.

[9] Austria, Y. D., Jay-ar, P. L., Maria Jr, L. B. S., Goh, J. E. E., Goh, M. L. I., & Vicente, H. N. (2019). Comparison of machine learning algorithms in breast cancer prediction using the coimbra dataset. cancer, 7(10), 23-1.

[10] Hall, M. A., & Holmes, G. (2003). Benchmarking attribute selection techniques for discrete class data mining. IEEE Transactions on Knowledge and Data engineering, 15(6), 1437-1447.

[11] Güleryüz, D. (2020). Evaluation of waste management using clustering algorithm in megacity Istanbul. Environmental Research and Technology, 3(3), 102-112.

[12] Candan, H., Durmuş, A., & Harman, G. Genetik Algoritma Ve Sınıflandırıcı Yöntemler İle Kanser Tahmini. Veri Bilimi, 2(1), 30-34.

[13] Zhang, M. L., & Zhou, Z. H. (2007). ML-KNN: A lazy learning approach to multi-label learning. Pattern recognition, 40(7), 2038-2048.

[14] Zhang, Min-Ling, and Zhi-Hua Zhou. "ML-KNN: A lazy learning approach to multi-label learning." Pattern recognition 40.7 (2007): 2038-2048.

[15] Speiser, J. L., Miller, M. E., Tooze, J., & Ip, E. (2019). A comparison of random forest variable selection methods for classification prediction modeling. Expert systems with applications, 134, 93-101.

[16] Leo B. Random forests. Mach Learn 2001; 45(1): 5–32.

[17] Huang, C., Davis L. S., vd. (2002). "An assessment of support vector machines for land cover classification." International Journal of Remote Sensing 23(4): 725-749.

[18] Cervantes, J., Garcia-Lamont, F., Rodríguez-Mazahua, L., & Lopez, A. (2020). A comprehensive survey on support vector machine classification: Applications, challenges and trends. Neurocomputing, 408, 189-215.

[19] Abhishek, L. (2020, June). Optical character recognition using ensemble of SVM, MLP and extra trees classifier. In 2020 International Conference for Emerging Technology (INCET) (pp. 1-4). IEEE.

[20] Khishe, M., & Safari, A. (2019). Classification of sonar targets using an MLP neural network trained by dragonfly algorithm. Wireless Personal Communications, 108(4), 2241-2260.

[21] Davis, J., & Goadrich, M. (2006, June). The relationship between Precision-Recall and ROC curves. In Proceedings of the 23rd international conference on Machine learning (pp. 233-240).

[22] Ozden, E., & Guleryuz, D. (2022). Optimized machine learning algorithms for investigating the relationship between economic development and human capital. Computational Economics, 60(1), 347-373.

[23] Grandini, M., Bagli, E., & Visani, G. (2020). Metrics for multi-class classification: an overview. arXiv preprint arXiv:2008.05756.