Araştırma Makalesi *BAUN Fen Bil. Enst. Dergisi, 27(1), 269-281, (2025)*

DOI:10.25092/baunfbed. 1594230 *J. BAUN Inst. Sci. Technol., 27(1), 269-281, (2025)*

Erythemato-squamous diseases diagnosis and prediction using artificial intelligence

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Geliş Tarihi (Received Date): 10.11.2024
Kabul Tarihi (Accepted Date): 20.12.2024

Abstract

In this study, artificial intelligence was applied to accurately diagnose and predict erythemato-squamous diseases (ESDs). Feature selection was performed for 34 features in the dataset with the wrapper feature selection method. 18 features were selected using the feature selection method. In the analyses performed with machine learning algorithms, results were obtained and compared with both the initial 34 features and the selected 18 features. Six different machine learning classification algorithms were compared for erythemato-squamous diseases. Naive Bayes algorithm was determined as the most successful algorithm in the diagnosis and prediction of erythemato-squamous diseases with an accuracy rate of 99.45%. In addition, it was determined that the applied feature selection method increased the performance of all algorithms. When the results obtained in the study are examined, it is seen that wrapper feature selection plays an important role in improving the performance of machine learning models.

Keywords: *Artificial intelligence, machine learning, attribute selection. erythemato-squamous.*

Yapay zeka kullanılarak erythemato-squamous hastalıklarının tanısı ve tahmini

Öz

Bu çalışmada, erythemato-squamous hastalıklarını (ESDs) doğru bir şekilde tahmin etmek için yapay zeka uygulanmıştır. Veri setinde bulunan 34 özellik için wrapper nitelik seçim yöntemi ile özellik seçimi yapılmıştır. Analiz sonrasında 18 özellik seçilmiştir. Makine öğrenmesi algoritmaları ile gerçekleştirilen analizlerde hem başlangıçtaki 34 özellikle hem de seçilen 18 özellikle sonuçlar alınıp karşılaştırılmıştır. Erythemato-squamous hastalıklar için altı farklı makine öğrenmesi sınıflandırma algoritması

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karşılaştırılmıştır. Naive Bayes algoritması, 99.45% doğruluk oranıyla erythemato-squamous hastalık tahmininde en başarılı algoritma olarak tespit edilmiştir. Bunun yanı sıra, uygulanan özellik seçim yönteminin tüm algoritmaların performansını yükselttiği tespit edilmiştir. Çalışmada elde edilen sonuçlar incelendiğinde, wrapper nitelik seçiminin makine öğrenmesi modellerinin performansının iyileştirilmesinde önemli bir rol oynadığı görülmektedir.

Anahtar kelimeler: *Yapay zeka, makine öğrenmesi, özellik seçimi, erythemato-squamous.*

1. Introduction

In recent years, the use of artificial intelligence (AI) in healthcare has attracted great interest, especially in the areas of disease treatment and diagnosis [1]. AI algorithms have the potential to help healthcare professionals and analyze complex medical data make more accurate and timely decisions. AI can increase the efficiency of healthcare, improve patient outcomes, and reduce healthcare costs. AI-powered imaging systems can help radiologists detect tumors and other abnormalities earlier and more accurately. AI can also play an important role in the development of personalized medicine. AI algorithms can be used to create treatment plans tailored to a patient's genetic makeup, lifestyle, and medical history [2, 3].

Machine Learning (ML), a field of Artificial Intelligence, can learn from large datasets and perform various tasks such as medical diagnoses, personalized treatment plans, and prediction of disease outcomes [4]. ML models can be trained on a variety of medical data, including genomic data, medical images, and electronic health records. The performance of ML-based systems depends on the algorithm used, the quality of the dataset, and feature selection. Metrics such as accuracy, precision, recall, and F1 score are widely used to evaluate and compare the performance of ML algorithms [5, 6]. The application of ML in healthcare can provide significant benefits for patient care and the efficiency of healthcare services [7]. ML algorithms provide solutions for skin diseases that are difficult to diagnose due to their distinctive features, such as erythemato-squamous diseases (ESDs) [8]. These algorithms can identify different types of ESDs by analyzing various factors such as clinical features (e.g. erythema, scaling, pruritus), histopathological features (e.g. fibrosis of papillary dermis, thinning of subpapillary epidermis), and age of the patient. The performance of these algorithms varies depending on the feature selection methods and hyperparameter settings used [5, 6, 9].

This study introduces a machine learning approach designed to address the classification problems of erythemato-squamous diseases. The method developed in the study offers a promising path to advance the field of skin diseases. This study makes a significant contribution to the healthcare field by providing higher performance predictions than the state-of-the-art studies in the field of skin diseases. This paper is structured in six sections. A review of related studies is presented in the second section, while the third section focuses on the methods and materials used. The fourth section explains machine learning algorithms, and the fifth section discusses the comparative results. Finally, the sixth section summarizes the conclusions reached in light of the findings.

2. Related Works

Erythemato-squamous diseases were first discussed by [10] who also donated the dataset. In the study, the differential diagnosis of erythemato-squamous diseases was aimed with an expert system. Analyses were performed using Naive Bayes and support vector machine algorithms. In [11], a diagnosis model based on association rules, support vector machines, and particle swarm optimization is proposed. The model consists of two stages, firstly, the appropriate feature subset is selected and then the analysis is performed with the most suitable parameters. In [12], researchers have tried to obtain the best features with three embedded feature selection methods and four different filtering methods. They have applied ensemble learning based machine learning methods with skin disease datasets.

In [1, 5], Random Forest algorithm was used for feature selection. Logistic regression, support vector machines, and K-Nearest neighbor classifiers were applied in the study where the best 15 features were selected. In another study [4], a hybrid ensemble learning model was used and successful results were obtained with 10-fold cross-validation. In this study, SVM, DT, LR, and kNN classifiers were combined to overcome the limitations of a single model and create a more powerful prediction model. Although successful algorithms have been proposed for erythemato-squamous disease in the literature, different algorithms need to be applied to provide effective solutions, so research on erythemato-squamous problems is needed.

3. Material and method

This section details the material and methodology used, including dataset description, attribute selection, and evaluation metrics approach.

3.1 Dataset description

ESDs are a group of skin diseases characterized by scaly red lesions, including pityriasis rubra pilaris, chronic dermatitis, pityriasis rosea, lichen planus, seborrheic dermatitis, and psoriasis. ESDs are challenging to diagnose because of their similar histopathological and clinical features. This difficulty has led to the use of machine learning (ML) in the classification of ESDs.

The dataset, which is publicly available on the University of California, Irvine (UCI) Machine Learning Repository website, has been widely used in the development of ML algorithms to support the diagnosis and classification of ESDs. The dataset contains information from 366 patients and is defined by 34 predictor variables. These variables cover 22 histopathological features and 12 clinical features.

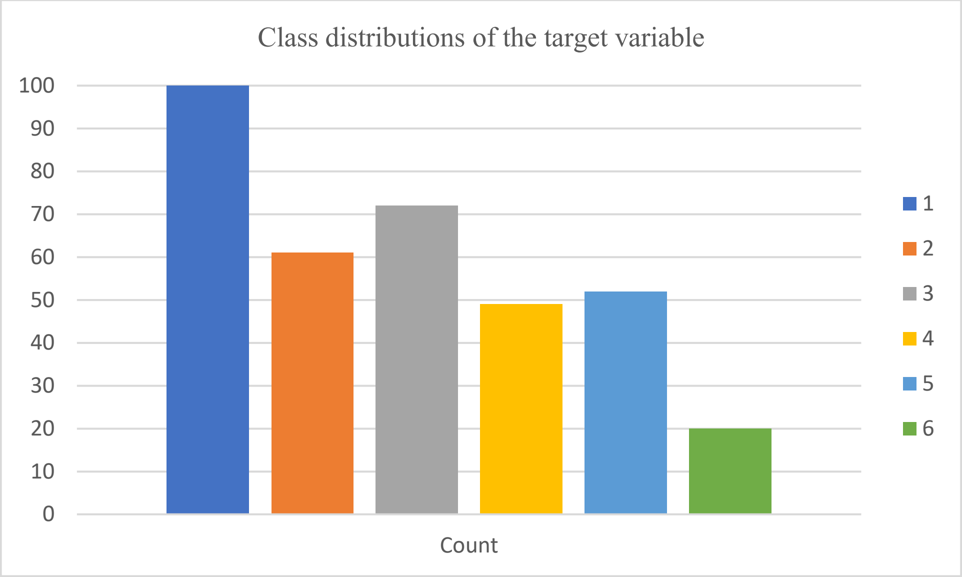


Figure 1. Class distributions of the target variable

The frequencies of each class are clearly indicated in the bar chart in Figure 1. The class distribution of the target variable is important to understand how the samples in the data set are distributed among different classes.

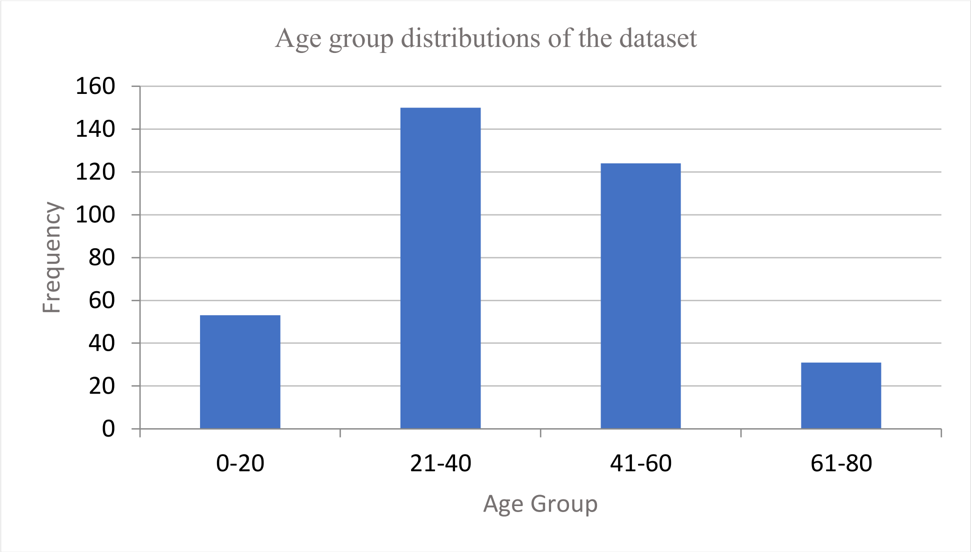


Figure 2. Age group distributions of the dataset

The distribution of patients according to age groups provides important information about which age groups dermatological disorders are more common. Figure 2 illustrates the Age Group Distributions of The Dataset. According to the distribution in the dataset, the 21-40 age group has the highest frequency with 150 patients, and this age range stands out as the period in which dermatological disorders are most frequently seen. The presence of 124 patients in the 41-60 age group indicates that dermatological disorders are also significantly prevalent in the middle age group. In contrast, the frequency decreased to 31 in the 61-80 age group, suggesting that the prevalence of dermatological disorders may decrease in elderly individuals. Finally, the presence of 53 patients in the

0-20 age group indicates the possibility of encountering dermatological problems at an early age, but this group appears to be less affected than other groups.

3.2 Attribute selection

The prediction success of classification algorithms is affected by the data and the attributes of this data. The goal of attribute selection is to select meaningful and relevant attributes with maximum discriminatory ability. The attribute selection process reduces data dimensions by removing meaningless and irrelevant features from the data space. In this way, the data structure becomes simpler, the amount of data decreases, the execution time of the analysis decreases, and the prediction performance increases.

In our study, attribute selection was performed using the Wrapper Attribute Selection method. Wrapper Attribute Selection method is a popular attribute selection technique that evaluates the performance of the algorithm by using a powerful learning algorithm with different subsets of the selected attributes. The number of attributes, which was 34 in the original data set, was determined as 18 after applying the Wrapper Attribute Selection method. Table 1 indicates the importance values of the selected attributes.

Table 1. Importance values of the selected attribute.

Id	Attribute	Importance
13	thinning_of_the_suprapapillary_epidermis	0.13304
7	fibrosis_of_the_papillary_dermis	0.10354
11	clubbing_of_the_rete_ridges	0.10119
14	focal_hypergranulosis	0.09500
1	koebner_phenomenon	0.08751
14	saw-tooth_appearance_of_retes	0.07556
12	elongation_of_the_rete_ridges	0.06674
16	spongiosis	0.05655
2	follicular_papules	0.05516
6	PNL_infiltrate	0.05400
3	oral_mucosal_involvement	0.05318
15	disappearance_of_the_granular_layer	0.03243
4	scalp_involvement	0.02948
10	parakeratosis	0.01711
8	acanthosis	0.01128
9	hyperkeratosis	0.01075
5	eosinophils_in_the_infiltrate	0.00943
18	inflammatory_monoluclear_inflitrate	0.00806

When the values in Table 1 are examined, it is seen that the first three attributes with the highest values are thinning_of_the_suprapapillary_epidermis (0,13304), fibrosis_of_the_papillary_dermis (0,10354), and clubbing_of_the_rete_ridges (0,10119), respectively.

3.3 Evaluation metrics

We used the 10-fold cross-validation approach to train and evaluate our classification model. In the evaluation step, we used standard metrics to evaluate the performance of the proposed method along various dimensions. These metrics include accuracy, precision, recall, and F-measure. Each metric provides unique insights into different aspects of the model. The mathematical formulas for these metrics using true positives (TP), true negatives (TN), false positives (FP), and false negatives (FN) are presented in Equations (1) to (4) as follows:

$$\text{Accuracy} = \frac{\text{TP+TN}}{\text{TP+TN+FP+FN}} \tag{1}$$

$$\text{Precision} = \frac{\text{TP}}{\text{TP+FP}} \tag{2}$$

$$\text{Recall} = \frac{\text{TP}}{\text{TP+FN}} \tag{3}$$

$$\text{F} - \text{measure} = \frac{\text{2TP}}{\text{2TP+FP+FN}} \tag{4}$$

4. Machine learning algorithms

In this study, erythemato-squamous diseases were diagnosed and predicted using various machine learning algorithms. The machine learning algorithms preferred in the analyses performed within the scope of the study are Decision Tree, Kstar, Support Vector Machine, Random Tree, Naive Bayes, and Random Forest. This section includes explanations about the mentioned algorithms.

Decision tree algorithm is a tree-based algorithm that is widely used for classification tasks. The results obtained for the classification task are similar to a flowchart. The nodes of the decision tree represent the feature conditions while the branches hold the target values. The algorithm has a learning process based on the importance of the features in the data. First, a feature is selected as the root node of the tree and then the other features come [13-15]. Kstar algorithm is an example-based machine learning classifier. It performs the classification and prediction tasks by selecting the distance measures and parameters. The algorithm, which uses the entropy distance measure as the distance measure, aims to include each example in the cluster with the closest mean. [16, 17]. Naive Bayes algorithm is a frequently used and well-known machine learning method. The Naive Bayes algorithm, which can be applied to both discrete and continuous data, is based on feature independence and probability theory. It stands out as an interpretable algorithm that can be applied to different fields [18].

The Random Forest algorithm represents a set of classification trees that perform well and are effective for classification tasks. The algorithm makes decisions by combining the predictions of many independent decision trees. It is robust to problems such as overfitting and data pollution, which are frequently encountered in classification [13-15]. The Random Tree algorithm, a supervised learning algorithm, is effective in both regression and classification problems. It is a linear algorithm that performs the classification task by creating a decision tree [15]. The Support Vector Machine algorithm is one of the most widely used supervised learning algorithms. It provides effective results in solving classification problems. It classifies a new sample by drawing the most appropriate support vector called a hyperplane [11, 19].

5. Results

The interdependencies between the attributes of the EDSs dataset used in our study were analyzed with the heatmap [20]. The results obtained for the heatmap and Clinical and Histopathological Features in ESDs are presented in Figure 3. When Figure 3 is examined, it is seen that there is a significant positive correlation between "thinning_of_the_suprapapillary_epidermis" and "clubbing_of_the_rete_ridges". Similarly, a high level of positive correlation was detected between "focal_hypergranulosis" and "oral_mucosal_involvement". The positive correlation between the attributes means that the tendency of the variables to increase together is strong.

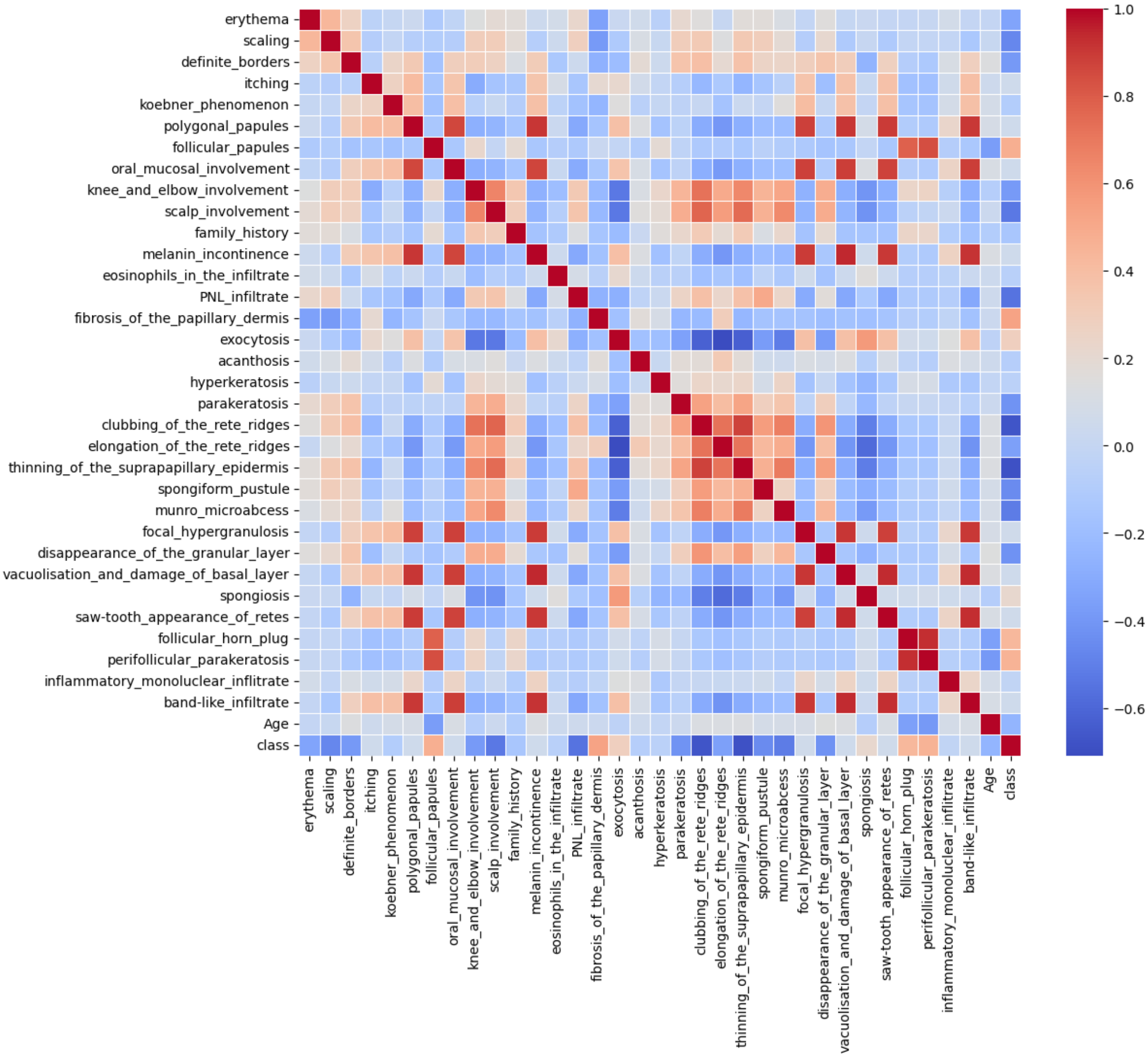


Figure 3. Heatmap of clinical and histopathological features in ESDs.

Table 2 evaluates the performance (%) of various machine learning (ML) algorithms before applying wrapper attribute selection, using different metrics.

Table 2. Performance comparison of ML algorithms before Wrapper attribute selection in all metrics (%).

ML Algorithm	Accuracy	Precision	Recall	F-Measure
Decision Tree	93.99	94.00	94.00	94.00
Kstar	94.26	94.40	94.43	94.43
Naive Bayes	**97.27**	**97.40**	**97.30**	**97.30**
Random Forest	95.90	95.90	95.90	95.90
Random Tree	87.43	87.50	87.40	87.40
Support Vector Machine	95.36	95.40	95.40	95.40

Examining Table 2, it is evident that the Naive Bayes algorithm exhibits the highest performance with an accuracy rate of 97.27%. This is followed by the Random Forest and SVM algorithms with accuracy rates of 95.90% and 95.36%, respectively. The Random Tree algorithm shows the lowest performance with an accuracy rate of 87.43%.

Table 3 evaluates the performance (%) of various machine learning (ML) algorithms after applying wrapper attribute selection, using different metrics. Wrapper Attribute Selection is a technique used to select the most relevant features to maximize the performance of an ML algorithm [21].

Table 3. Performance comparison of ML algorithms after Wrapper attribute selection in all metrics (%).

ML Algorithm	Accuracy	Precision	Recall	F-Measure
Decision Tree	95.63	95.70	95.60	95.60
Kstar	95.36	95.40	95.40	95.40
Naive Bayes	**99.45**	**99.50**	**99.50**	**99.50**
Random Forest	96.45	96.50	96.40	96.40
Random Tree	90.16	90.20	90.20	90.10
Support Vector Machine	98.09	98.10	98.10	98.11

Table 3 evaluates the performance of different machine learning algorithms on various metrics (%) after applying wrapper attribute selection. As seen in the table, Naive Bayes algorithm shows the highest performance with an accuracy rate of 99.45%. This is followed by SVM and Random Forest algorithms with accuracies of 98.09% and 96.45% respectively. The lowest performance is shown by Random Tree algorithm with an accuracy rate of 90.16%.

In our study, the results of machine learning algorithms were obtained by performing two different experiments, before and after applying the wrapper attribute selection method. The comparison of the results obtained as a result of the experiments in terms of accuracy metric is presented in Figure 4.

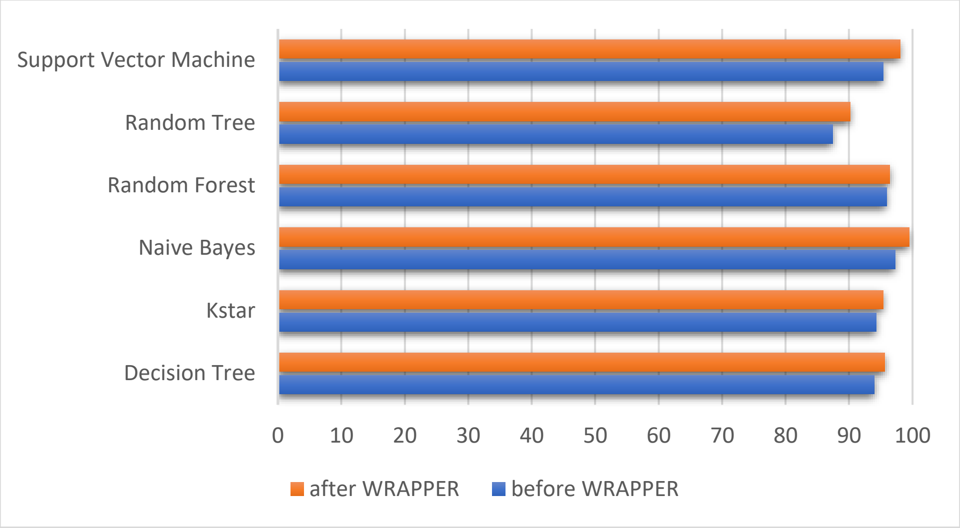


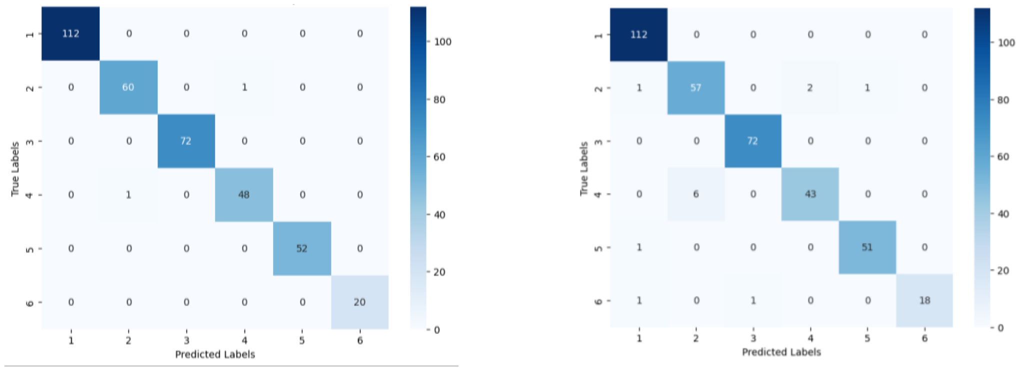
Figure 4. Comparison of ML algorithms performance in terms of accuracy

When Figure 4 is examined, it is seen that the accuracy value of all algorithms showed a remarkable increase after the wrapper attribute selection method was applied. According to the results obtained, it can be said that the wrapper attribute selection method is an effective attributes selection method for prediction performance.

Table 4. Class-based performance comparison of the best algorithm (Naive Bayes)

Class	TP Rate	FP Rate	Precision	Recall	F-Measure
1	1.000	0.000	1.000	1.000	1.000
2	0.984	0.003	0.984	0.984	0.984
3	1.000	0.000	1.000	1.000	1.000
4	0.980	0.003	0.980	0.980	0.980
5	1.000	0.000	1.000	1.000	1.000
6	1.000	0.000	1.000	1.000	1.000
Weighted Avg.	**0.995**	**0.001**	**0.995**	**0.995**	**0.995**

The class-based performance comparison of the Naive Bayes algorithm, which showed the highest performance in the analyses, is given in Table 4. According to Table 4, the most accurate and error-free predictions in terms of all metrics were made in classes 1, 3, 5 and 6. The Naive Bayes algorithm performed with a False Positive Rate of 0.003 and a True Positive Rate of 0.984 in class 2, while it performed with a False Positive Rate of 0.003 and a True Positive Rate of 0.980 in class 4.

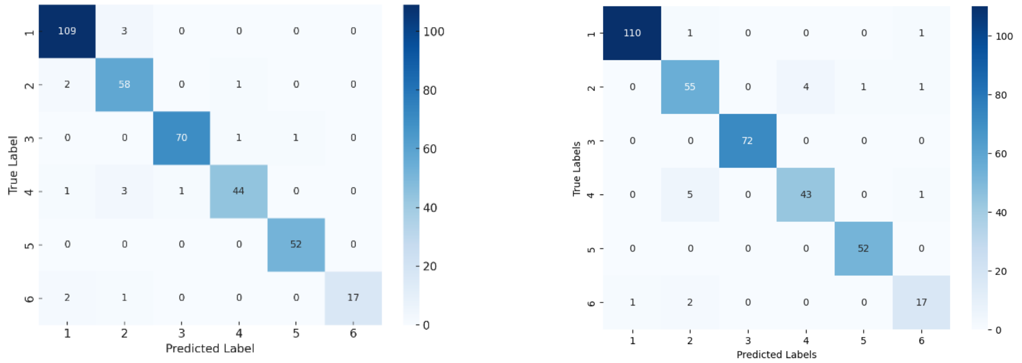


	1	2	3	4	5	6
1	112	0	0	0	0	0
2	0	60	0	1	0	0
3	0	0	72	0	0	0
4	0	1	0	48	0	0
5	0	0	0	0	52	0
6	0	0	0	0	0	20

(a) Confusion Matrix for Naive Bayes

	1	2	3	4	5	6
1	112	0	0	0	0	0
2	1	57	0	2	1	0
3	0	0	72	0	0	0
4	0	6	0	43	0	0
5	1	0	0	0	51	0
6	1	0	1	0	0	18

(b) Confusion Matrix for Random Forest

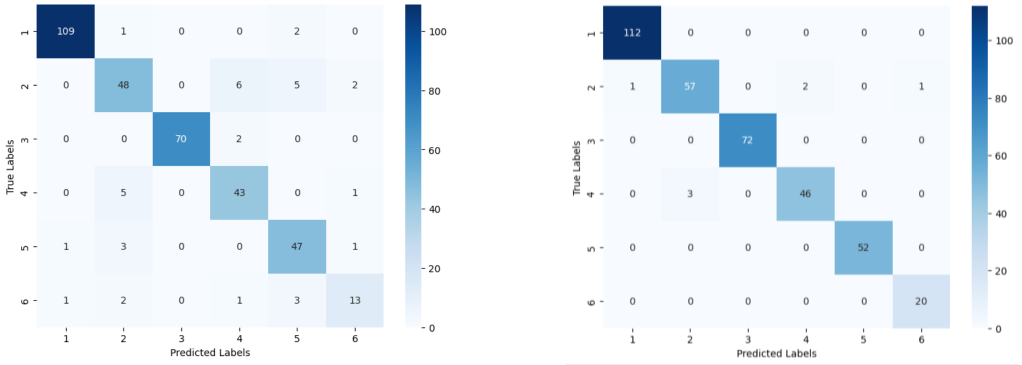


	1	2	3	4	5	6
1	109	3	0	0	0	0
2	2	58	0	1	0	0
3	0	0	70	1	1	0
4	1	3	1	44	0	0
5	0	0	0	0	52	0
6	2	1	0	0	0	17

(c) Confusion Matrix for Decision Tree

	1	2	3	4	5	6
1	110	1	0	0	0	1
2	0	55	0	4	1	1
3	0	0	72	0	0	0
4	0	5	0	43	0	1
5	0	0	0	0	52	0
6	1	2	0	0	0	17

(d) Confusion Matrix for Kstar



	1	2	3	4	5	6
1	109	1	0	0	2	0
2	0	48	0	6	5	2
3	0	0	70	2	0	0
4	0	5	0	43	0	1
5	1	3	0	0	47	1
6	1	2	0	1	3	13

(e) Confusion Matrix for Random Tree

	1	2	3	4	5	6
1	112	0	0	0	0	0
2	1	57	0	2	0	1
3	0	0	72	0	0	0
4	0	3	0	46	0	0
5	0	0	0	0	52	0
6	0	0	0	0	0	20

(f) Confusion Matrix for Support Vector Machine

Figure 5. Confusion matrix for ML algorithms

Confusion Matrices of all ML algorithms applied within the scope of the study are shown in Figure 5. Confusion Matrix is used to evaluate and visualize the prediction performances of the algorithms. In Confusion Matrix, correct classifications are located along the first diagonal. Incorrect classifications are all other values that are not diagonal. For example, according to the Confusion Matrix of Random Tree algorithm in Figure 5(e), 13 elements that should be in class 2 were classified incorrectly, while 48 elements were classified as they should be. According to the Confusion Matrix of Naive Bayes algorithm shown in Figure 5(a), only 2 elements were classified incorrectly for all classes, and all other elements were classified correctly.

6. Conclusion

In this study, artificial intelligence-based analyses were performed for the prediction and diagnosis of erythemato-squamous diseases and the results were presented by comparing them. The results obtained with machine learning algorithms supported by the wrapper attribute selection method within the scope of the study are more successful than previous studies [1, 2, 4, 5, 9, 12, 19, 21]. Wrapper attribute selection aims to find the most appropriate feature subset to increase the performance of machine learning models. This method uses a specific ML algorithm to evaluate candidate attribute subsets and select the best performing one. This plays an important role in increasing the accuracy and efficiency of machine learning models [9, 12, 21]. The results obtained in our study show that wrapper attribute selection increases the performance of all algorithms. In particular, the Naive Bayes algorithm exhibited a high performance of 99.45% after attribute selection. This shows that genetic algorithms are an effective search strategy to find the most relevant features and Bayesian network is a powerful classifier by exploiting these features. As a result, wrapper feature selection plays an important role in improving the performance of machine learning models. The results presented in this study provide an example of this effect and show how Naive Bayes algorithm can show strong performance in classifying complex datasets with feature selection.

There are some limitations to the study. The dataset has a relatively small sample size, which may affect the performance of some ML models. In addition, the dataset may not be representative of the population since it was collected from a single center. Despite these limitations, the Erythemato-squamous dataset is a valuable resource for the development of ML algorithms for automatic diagnosis and classification of ESDs. Future studies can address these limitations and further improve the diagnosis and prediction of ESDs by using larger, more diverse and better-defined datasets.

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