Enhanced Epileptic Seizure diagnosis using EEG Signals with Support vector machine and Bagging Classifiers

Rana Alrawashdeh¹, Mohammad Al-Fawa'reh² and Wail Mardini¹

¹Faculty of Computer and Information Technology, Jordan university of science and technology, Jordan ²Faculty of Information Technology and Computer Science, Yarmouk University, Jordan

Abstract: Many approaches have been proposed using Electroencephalogram (EEG) to detect epilepsy seizures in their early stages. Epilepsy seizure is a severe neurological disease. Practitioners continue to rely on manual testing of EEG signals. Artificial intelligence (AI) and Machine Learning (ML) can effectively deal with this problem. ML can be used to classify EEG signals employing feature extraction techniques. This work focuses on automated detection for epilepsy seizures using ML techniques. Various algorithms are investigated, such as Bagging, Decision Tree (DT), Adaboost, Support vector machine (SVM), K-nearest neighbors(KNN), Artificial neural network(ANN), Naïve Bayes, and Random Forest (RF) to distinguish injected signals from normal ones with high accuracy. In this work, 54 Discrete wavelet transforms (DWTs) are used for feature extraction, and the similarity distance is applied to identify the most powerful features. The features are then selected to form the features matrix. The matrix is subsequently used to train ML. The proposed approach is evaluated through different metrics such as F-measure, precision, accuracy, and Recall. The experimental results show that the SVM and Bagging classifiers in some data set combinations outperforming all other classifiers.

Keywords: Electroencephalogram (EEG), Discrete Wavelet Transform (DWT), Epilepsy, Decision tree, Random Forest, Adaboost, Bagging.

1. Introduction

Numerous diseases affect the human neurological system, leading to severe complications and adverse health and lifestyle problems[1]. One of these diseases is epilepsy. Epilepsy is caused by a defect in brain chemistry or neurotransmitters. The presence of excessive electrical charges characterizes it. This disease occurs in the form of successive epileptic seizures, passing through different seizure states. Epilepsy patients face several challenges and mortal risks, and they must take precautions to avoid danger for themselves and others[2] [3].

An electroencephalogram can detect epileptic seizures. While EEG signals provide essential brain knowledge, the Classification of these signals has not been well established, and they continue to be evaluated manually by clinicians. Diagnostic medicine for epilepsy could be significantly improved by developing accurate automated detection methods to evaluate EEG signals [4][5]. The existing manual system is resource-intensive, entailing financial and time costs for health practitioners and systems, and epilepsy diagnoses without resorting to this method would be a great boon to health providers and patients[6]. The need for a new automated method to diagnosis epileptic seizures has long been acknowledged [7] [8] [9] and provides the rationale for this work. The current research presents a model for the automatic determination of whether signals indicate a seizure attack after a preliminary evaluation.

This paper presents an enhanced method to diagnose epileptic seizures from EEG signals with high accuracy. The work starts with signal preprocessing to remove noise from EEG signals. Features are extracted by analyzing the mother wavelet into sub-signals within a specific domain. This step relies on Multi-DWT [10]. We use all DWT wavelets, divided into: "bior1.1, bior1.3, bior1.5, bior2.2, bior2.2, bior2.4, bior2.6, bior2.8, bior3.1, bior3.3, bior3.7, bior3.9, bior4.4, bior5.5, bior6.8, coif1, coif2, coif3, coif4, coif5, db1, db2, db3, db4, db5, db6, db7, db8, db9, db10, rbior1.1, rbior1.3, rbior1.5, rbior2.2, rbior2.2, rbior2.4, rbior2.6, rbior2.8, rbior3.1, rbior3.3, rbior3.7, rbior3.9, rbior4.4, rbior5.5, rbior6.8, sym2, sym3, sym4, sym5, sym6, sym7, sym8, demy, and Haar" [9]. In the next step, the similarity distance (Euclidean, Manhattan, and cosine distance) is executed to minimize the number of features and select the most critical features from a vast feature set[11]. These selected features subsequently attain the best classification performance. The obtained features from similarity distance train different classifiers such as DT, RF, Adaboost, and Bagging in the last step. The efficiency of the new approach is calculated by using different metrics such as F-measure, precision accuracy, and Recall.

Many machine learning algorithms have been developed to detect epileptic seizures via using the frequency domain. The selection process of powerful features and Classification is done by trial and error in machine learning algorithms. In traditional algorithms of machine learning, most experiments are executed in a Matlab environment. The main goals of our work are as follows: provide complete information on the available datasets and review most works that are done using multiple machine learning models for automated detection of seizures.

The rest of the paper is divided into the following sections. The related work is discussed in Section Two, and section Three contains the proposed methodology. The evaluation metrics are discussed in section Four. Finally, the experimental results are discussed in section Five.

2. Related Work

Chen et al. [9] supposed that the primary target of the proposed discrete wavelet transform (DWT) is to split the required signal into small signals called sub-signals and then to extract the required features from each one. Their work proposed a new EEG data approach based mainly on Multi DWT variants, divided into seven families. Each family type contains several DWTs, each of which aims to split the EEG data into the maximum level of the mother wavelet. The authors presented four elements that affect seizure detection accuracy: mother wavelet type, level of decomposition for each DWT, the frequency band for each DWT, and the extracted features. After extracting the required features, the EEG signal classification is applied, using the SVM method to categorize the EEG signal. The main conclusion was that the level of decomposition is the main factor of accuracy. This process is irrespective of the selection process of the frequency bands and the required features. The results also indicated that 40% of redundancies were deleted from the extracted features.

Salem et al. [12] discussed the diagnosis of epileptic seizures from EEG signals, mainly in obtaining signal statistical properties rather than directly dealing with the signal itself. The researchers utilized DWT to partition the EEG signal into several sub-bands, then they calculated the statistical function for each sub-band. The authors extracted various statistical features from signal sub-bands, then used Ant Colony (AC) classifier with these statistical properties as parameters to categorize the EEG signal into normal or abnormal signals. In this classification step, rules were applied in the categorization process to define epileptic seizures in EEG. The results proved the effectiveness of the approach (DR = 100%, FAR = 9%).

The authors in [7] suggested an efficient approach for epilepsy and epileptic seizure detection, producing and applying three algorithms: Quick prop, Rprop, and Spike prop. Three performance measures were used: classification accuracy, computational efficiency, and convergence epochs. Extensive parametric analysis is applied to identify the parameter values, which improves efficiency and accuracy. EEGs are collected from three groups: healthy people, epileptic people in a seizure-free interval, and epileptic people in a seizure. The results show that the R prop algorithm is the best training algorithm for the large training dataset, and the model yields a high classification accuracy reach of 92.5%

Acharya et al. [8] employed a new model depending on neural network NNS analysis, classifying normal and abnormal signals to diagnose epileptic seizure activity from EEG signals. Two kinds of EEG signals were selected for analysis: epileptic and normal signals. The signals were reprocessed and split using DWT. Many properties such as mean, standard deviation, entropy, median, skewness, and kurtosis were computed and utilized for the Classification. The results showed good classification accuracy of nearly 100%. The primary purpose of the study was to use less NNA computation time to provide better accuracy.

Kaya et al. In [13], the authors introduced a hybrid method for the Classification of the EEG signals to identify epileptic seizures. The proposed method consists of Multi-DWT and an artificial neural network (ANN). The author enhanced the entropy algorithm with a variant they dubbed "improved approximate entropy" to calculate abnormalities in EEG signals. The proposed method was tested accurately and was implemented and compared with other systems. The authors utilized the sensitivity and accuracy parameters to measure the efficiency of the new system. Finally, EEG signals were classified as normal and epileptic seizures with accuracy reaching 90%.

Torse et al. [4] proposed a new seizure diagnosis method implemented in hardware devices to help epileptic patients.

The authors processed the EEG signals in both the time and frequency domains using the Chebyshev filter for preprocessing the EEG signals, after which they split the signals into five sub-bands, for each of which they calculated the required features. DWT is used for feature extraction, after which the thresholding process is implemented to remove noise from the signals. After that, the classifiers are executed to categorize the signal. The results were compared with other works, and they achieved an accuracy of 96% using SVM and 98% using ANN.

Sarma et al. [14] suggested an application for automated seizure diagnosis. In this model, the EEG signals were split using db2 DWT. Eight statistical properties, four gray-level co-occurrence matrices, and Renyi entropy were obtained from the EEG signals and sub-bands. After that, genetic algorithms were utilized to select the relevant features and minimize the dimensions of the features. The authors learned and tested the model using an SVM classifier. Two databases were used in the experiments, and the performance of the classifier was evaluated for both. The results showed that the relevant features using a genetic algorithm produce better accuracy for seizure detection[15].

Alfahoumi et al. [16] proposed a new method for collecting the features from the required technique and selecting the properties of EEG signals. The proposed method is based on the selection method applied by order statistic HOS for DWT details. After that, the genetic algorithm was utilized to select the features and minimize the dimensions of the properties. The new model gives more accurate results than other algorithms, depending on discrete Fourier transform (DFT).



Figure 1. Block Diagram of The Proposed Methodology

A hybrid technique system was proposed to categorize EEG signals based on a multiwavelet transform as a feature extractor and ANN classifier. In [17], multiwavelet transforms were applied to split the signals into high- and low-frequency coefficients, utilizing different wavelets and scaling functions. The decomposed signals were implemented to improve approximate entropy to compute the irregularities and disturbance in the signals. The results of the approximate entropy are used to train the feed-forward neural network (FFNN). FFNN is an artificial intelligence algorithm used to

International Journal of Communication Networks and Information Security (IJCNIS)

create the training dataset. According to these datasets, the signals were categorized as epileptic seizure or normal. In order to assess the efficiency of the proposed model, a set of metrics, such as sensitivity, specificity, and accuracy, were calculated. The results showed that the new model gave better accuracy compared to existing ones.

In [18], the authors used SVM for spectrum sensing in order to detect signals presence in a particular frequency band. The results show that the SVM classifier achieves the highest detection performance compared to the other classifiers (ED and ANN). Thus SVM will be a main part of our investigation.

3. Methodology

Most of the automated systems for epileptic detection pass through four main steps; the first step is EEG signal preprocessing, then EEG signal decomposition using EEG signal analysis methods[19]. Features extraction, then Features dimension reduction, finally EEG signals Classification. Figure 1 depicts the methodology used in the proposed mode. We use the Matlab environment to achieve the following steps:

- Read the EEG data and filter it out to eliminate noises using the Bandpass filter and smoothing method.
- Apply 54 DWT mother wavelets type to decompose the signal into sub-bands and extract various features (MAV, AVP, STD, SD, Skewness, Entropy, Mean, Max, Min, Kurtosis, Energy, and Normalized SD) for each band.
- Divide the 54 types into seven families (Biorthogo-nal, Coiflets, Daubechies, Reverse Biorthogonal, Symlets, Discrete Meyer, and Haar).
- Calculate the accuracy for each feature using the Euclidean distance equation 1.

3.1 Data Acquisition

The datasets were publicly collected from the University of Bonn, where the data comprises five collections (groups A– E). Each group contains 100 single EEG segments. The sampling rate for each collection is 173.6 HZ [20].

3.2 Data Preprocessing

Most studies start the epilepsy seizure detection process with the EEG signal preprocessing stage to remove noise from the EEG data. This stage is essential as it renders the initial EEG data and makes the later stages more accurate. The EEG data is filtered to remove noise carrying erroneous and redundant information. Internal or external resources can cause EEG data noises. The signal itself usually produces internal noises. The external noises are caused by the external resources surrounding the EEG signals, like the random movement of the patient. In Figure 2, we present the EEG signal before and after preprocessing.

3.3 Feature Extraction

After the signals have been preprocessed, the features extraction process is implemented. In this stage, the EEG signals are analyzed using different methods to decompose the EEG signals, such as STFT, FT, DWT, DFT, FFT, IDFT, CWT, and others [8]. The main goal of this stage is to split the EEG data into several segments and extract the required features from each. These features later form a massive matrix of features. In our work, we use Multi DWTs to decompose the signals. The features used in our work are:

- 1. Mean
- 2. Absolute Value (MAV)
- 3. Average Power (AVP)
- 4. Standard Deviation (SD)
- 5. Variance
- 6. Skewness
- Shannon Entropy
- 8. Max
 9. Min
- 9. Min
 10. Normalized SD
- 10. Normalized S
- 12. Energy



Figure 2. The Signals Before and After Preprocessing

Many methods can be utilized to analyze the EEG signals, which can be categorized into two types, Continuous (CWT) and discrete (DWT). As shown in Figure3, in the DWT methodology:

- 1. The low and high pass filters are used (passing signals through them).
- 2. The approximation coefficient and detailed coefficients are extracted.
- 3. The frequency of the subsequent signals from the previous phase is minimized to half using the Nyquist rule.
- 4. The coefficients of the low pass filter are transferred to the filters at the next step.
- 5. The same procedure is replicated to obtain the detailed and approximation coefficients.
- 6. Frequency resolution is improved with each phase, and time resolution is reduced.

The results of the features extraction stage are shown in table 1, where we have 16 dataset combinations. Each combination displays seven families. Each family displays: the best feature that achieves the highest accuracy, the best level of decomposition that resulted from the wavelet, and the max level of decomposition for each wavelet. The feature's accuracy is calculated according to the number of TP, TN, FP, and FN that appeared from applying Euclidean distance [21].



Figure 3. Signal Decomposition into Sub-bands

3.4 Features Selection and Reduction

The goal of feature selection or reduction is to reduce the data size (and thus accelerate computations). The selection process relies on choosing the best combination of features from a large number of initial features[22]. This step aims to reduce the features number by minimizing the properties or features that carry erroneous and redundant information. In this research, the feature selection is performed using similarity measures such as Euclidean, Manhattan, and Similarity distance.

3.4.1. Similarity Measures

Only forms of metrics are used to find the quantity of similarity between vectors, such as Euclidean, Manhattan, and Similarity distances. Similarity or distance may be used to signify the degree of convergence between vectors. Knowing that there is no single measure for all kinds of problems enables the obtainment of optimum results. The kind of problem and the form of data are the underlying factors in data processing and decision-making[23][24]. It is necessary to find suitable metrics to measure similarities.

In this work, we applied the Euclidean distance. Equation (1) represents the Euclidian distance formula:

$$Ecu(x, y) = \sqrt{\sum_{i=0}^{n-i} (xi - yi)^2}$$
(1)

Where: X and Y:

The selected features in the training and testing of EEG. E: The Euclidian distance.

3.5 EEG signals Classification

EEG signal classification plays a vital role in biomedical research to diagnose brain diseases. Effective classification technology helps distinguish between EEG segments to decide on the subject's health status [25][26]. Many methods are used to apply the classification step, the most common (as deployed in this study.

3.5.1. Decision Tree(DT)

DT algorithm belongs to the family of algorithms for supervised learning. Both regression and classification problem solving can be used. The general aim of using DT is to build a training model that can be used to predict the class or meaning of target variables by studying decision rules derived from previous results. DT algorithm attempts to solve problems by using tree representation. Each internal node corresponds to the attribute, and each leaf node corresponds to the class label. To forecast a record label class, we start from the root of the tree. We equate the meaning of the root attribute to the record attribute. Based on contrast, we obey the branch referring to that value and leap to the next node [27].



Figure 4. The advantages of DT

We begin to equate our record attribute value with other internal nodes of the tree until we reach the leaf node with the expected class value. The CART algorithm is used to create a tree, whereby the DT poses a query, and based on the response (Yes / No), it divides the tree into branches. In the decision tree, to predict the type of the specified dataset, the algorithm begins operating from the root node of the tree, then compares the value contained in the root attribute to the value of the actual dataset attribute, and, depending on the relation, follows the branch and jumps to the next node. On the next node, the algorithm again compares the importance of the attribute to the other sub-nodes and progresses further, repeating the method until it hits the node of the tree [28]. Figure 4 shows the advantages of the DT algorithm.

3.5.2. Random Forest(RF)

RF supervised learning algorithm is used for classification and regression problems, although it is primarily used for categorizing problems. It comprises trees, with more trees indicating a more durable forest. Similarly, RF renders decision trees on data samples and then gets predictions from all of them, eventually picking the best answer by voting [29]. A fixed approach is more apparent than a single DT since it eliminates over-fitting by averaging outcomes [18]. Figure 5 shows the operational principles of the RF algorithm [24].

Table 1. Results of Features Extraction using 54 DWT

members

Cases	Feature name	DWT name	Best level	Max	Accuracy
			number	level	
	AVP	Haar	6	12	99%
(AC)	Max	demy	5	5	98.5%
	Minimum	sym2	5	10	100%
	AVP	rbio1.1	6	12	99%
	AVP	db1	6	12	99%

International Journal of Communication Networks and Information Security (IJCNIS)

	AVP	coif1	5	9	99.5%
	AVP	bior1.1	6	12	99%
	MAV	Haar	5	12	100%
(AD)	MAV	demy	5	5	100%
	MAV	sym2	5	10	100%
	MAV	rbio1.1	5	12	100%
	MAV	db1	5	12	100%
	MAV	coif1	5	9	100%
	MAV	bior1.1	5	12	100%
	AVP	haar	1	12	96%
	MAV	demy	3	5	95.5%
	MAV	sym2	2	10	97%
	MAV	rbio1.1	1	12	96.5%
AE	MAV	db1	1	12	96.5%
	MAV	coif1	1	9	%96
	MAV	bior1.1	1	12	96.5%
BC	std	haar	7	12	98%
	Minimum	demy	3	5	96.5%
	AVP	sym2	3	10	98%
	Std	rbio1.1	7	12	98%
	Std	db1	7	12	98%
	Max	coif1	4	9	99%
	Std	bior1.1	7	12	98%
BE	AVP	haar	6	12	99.3%
	Max	demy	5	5	99%
	Minimum	sym2	5	10	100%
	AVP	rbio1.1	6	12	99.3%
	MAV	db1	6	12	99.3%
	MAV	coif1	5	9	99.6%
	AVP	bior1.1	6	12	99.3%
BD	std	haar	7	12	98.6%
	Max	demy	5	5	97.6%
	AVP	sym2	5	10	98.3%
	Std	rbio1.1	7	12	98.6%
	Std	db1	7	12	98.6%
	Minimum	coif1	5	9	%98.6
	Std	bior1.1	1	12	98.6%
1.01	4 7 7 7		0	10	0 = 0 (
ACE	AVP	haar	8	12	95%
ACE	AVP MAV	haar demy	8	12 5	95% 94%
ACE	AVP MAV AVP	haar demy sym2	8 5 5	12 5 10	95% 94% 94%
ACE	AVP MAV AVP AVP	haar demy sym2 rbio1.1	8 5 5 8	12 5 10 12	95% 94% 95% 95%
ACE	AVP MAV AVP AVP AVP	haar demy sym2 rbio1.1 db1	8 5 5 8 8 8	12 5 10 12 12 9	95% 94% 95% 95%
ACE	AVP MAV AVP AVP AVP MAV	haar demy sym2 rbio1.1 db1 coif1 bior1.1	8 5 8 8 5 8	12 5 10 12 12 9 12	95% 94% 95% 95% 94.3%
ACE	AVP MAV AVP AVP MAV AVP	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar	8 5 8 8 5 8 2	12 5 10 12 12 9 12 12	95% 94% 95% 95% 95% 94.3% 95% 97%
ACE	AVP MAV AVP AVP MAV AVP AVP AVP MAV	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy	8 5 5 8 8 5 8 2 3	$ \begin{array}{r} 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 12 \\ 12 \\ 10 \\ $	95% 94% 95% 95% 94.3% 95% 97% 97%
ACE	AVP MAV AVP AVP MAV AVP AVP MAV AVP	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2	8 5 5 8 8 5 8 2 3 3	12 5 10 12 9 12 12 12 5 10 5	95% 94% 95% 95% 95% 94.3% 95% 97% 97% 97%
ACE	AVP MAV AVP AVP MAV AVP AVP MAV AVP AVP AVP	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1	8 5 8 8 5 8 2 3 3 2	$ \begin{array}{r} 12 \\ 5 \\ 10 \\ 12 \\ 9 \\ 12 \\ 12 \\ 10 \\ 5 \\ 12 \\ \end{array} $	95% 94% 95% 95% 95% 94.3% 95% 97% 97% 97%
ACE	AVP MAV AVP AVP MAV AVP AVP MAV AVP AVP AVP AVP	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1	8 5 8 8 5 8 2 3 3 2 2 2	$ \begin{array}{r} 12\\ 5\\ 10\\ 12\\ 9\\ 12\\ 12\\ 12\\ 10\\ 5\\ 12\\ 12\\ 12\\ 12\\ 12\\ 12\\ 12\\ 12\\ 12\\ 12$	95% 94% 95% 95% 95% 95% 97% 97% 97% 97% 97%
ACE	AVP MAV AVP AVP MAV AVP MAV AVP MAV AVP AVP AVP AVP AVP	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1	8 5 8 8 5 8 2 3 3 2 2 2 2	$ \begin{array}{r} 12\\ 5\\ 10\\ 12\\ 9\\ 12\\ 12\\ 12\\ 10\\ 5\\ 12\\ 12\\ 9\\ 9\\ \end{array} $	95% 94% 95% 95% 95% 97% 97% 97% 97% 97% 97% 97%
ACE	AVP MAV AVP AVP MAV AVP MAV AVP MAV AVP AVP AVP AVP AVP AVP MAV	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1	8 5 8 8 5 8 2 3 3 2 2 2 2 2 2	$ \begin{array}{r} 12\\ 5\\ 10\\ 12\\ 9\\ 12\\ 12\\ 10\\ 5\\ 12\\ 12\\ 9\\ 12\\ 12\\ 9\\ 12\\ 12\\ 12\\ 12\\ 12\\ 12\\ 12\\ 12\\ 12\\ 12$	95% 94% 95% 95% 95% 95% 97% 97% 97% 97% 97% 97% 97% 97%
ACE	AVP MAV AVP AVP MAV AVP MAV AVP AVP AVP AVP AVP MAV AVP Std	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar	8 5 8 8 5 8 2 3 3 2 2 2 2 2 2 7	$ \begin{array}{r} 12 \\ 5 \\ 10 \\ 12 \\ 9 \\ 12 \\ 12 \\ 10 \\ 5 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12$	95% 94% 95% 95% 95% 97% 97% 97% 97% 97% 97% 97% 97% 96% 97% 98.6%
ACE ACD BCD	AVP MAV AVP AVP MAV AVP MAV AVP AVP AVP AVP AVP MAV AVP Std SD	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy	8 5 8 8 5 8 2 3 3 2 2 2 2 2 2 7 4	$ \begin{array}{r} 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 10 \\ 5 \\ 12 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 5 \\ 5 \\ \end{array} $	95% 94% 95% 95% 95% 95% 97% 97% 97% 97% 97% 97% 96% 97% 96% 97% 98.6%
ACE ACD BCD	AVP MAV AVP AVP MAV AVP MAV AVP AVP AVP AVP MAV AVP Std SD SD	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2	8 5 8 8 2 3 3 2 2 2 2 2 2 7 4 3	$ \begin{array}{r} 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 10 \\ 5 \\ 12 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 5 \\ 10 \\ \end{array} $	95% 94% 95% 95% 95% 97% 97% 97% 97% 97% 97% 97% 96% 97% 96% 97% 98.6%
ACE ACD BCD	AVP MAV AVP AVP MAV AVP AVP AVP AVP AVP MAV AVP Std SD SD Std	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 bior1.1 haar demy sym2 rbio1.1	8 5 8 5 8 2 3 2 2 2 2 7 4 3 7	$ \begin{array}{r} 12 \\ 5 \\ 10 \\ 12 \\ 9 \\ 12 \\ 12 \\ 10 \\ 5 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 5 \\ 10 \\ 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12$	95% 94% 95% 95% 95% 95% 97% 97% 97% 97% 97% 97% 96% 97% 96% 97% 98.6% 98.6%
ACE ACD BCD	AVP MAV AVP AVP MAV AVP AVP AVP AVP AVP AVP Std SD SD Std Std	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 bior1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar	8 5 8 5 8 2 3 2 2 2 7 4 3 7	$ \begin{array}{r} 12 \\ 5 \\ 10 \\ 12 \\ 9 \\ 12 \\ 12 \\ 10 \\ 5 \\ 12 \\ 12 \\ 12 \\ 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12$	95% 94% 95% 95% 95% 95% 97% 97% 97% 97% 97% 97% 97% 97% 97% 97
ACE ACD BCD	AVP MAV AVP AVP MAV AVP AVP MAV AVP AVP MAV AVP Std SD SD Std Std Std Max	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 bior1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar	8 5 8 5 8 2 3 2 2 2 2 7 4 3 7 4	$ \begin{array}{r} 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12$	95% 94% 95% 95% 95% 97% 97% 97% 97% 97% 97% 97% 96% 97% 98.6% 98.6% 98.6% 98.6% 99.3%
ACE ACD BCD	AVP MAV AVP AVP MAV AVP AVP MAV AVP AVP AVP Std SD SD Std Std Std Std Std	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar	8 5 8 5 8 2 3 2 2 2 7 4 7 4 7 4 7 4 7	$\begin{array}{c} 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 10 \\ 5 \\ 12 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\$	95% 94% 95% 95% 95% 97% 97% 97% 97% 97% 97% 96% 97% 98.6% 98.6% 98.6% 99.3%
ACE ACD BCD BDE	AVP MAV AVP AVP MAV AVP AVP AVP AVP AVP AVP Std SD SD Std Std Std Std AVP	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar	8 5 8 5 8 2 3 2 2 2 2 2 7 4 7 4 7 4 7 1	$\begin{array}{c} 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 $	95% 94% 95% 95% 95% 95% 97% 97% 97% 97% 97% 97% 96% 97% 98.6% 98.6% 98.6% 98.6% 99.3% 99.3%
ACE ACD BCD BDE	AVP MAV AVP AVP MAV AVP AVP AVP AVP AVP AVP Std SD SD Std Std Std Std Std AVP	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar db1 coif1	8 5 8 5 8 2 3 2 2 2 2 2 2 7 4 7 1 3	$\begin{array}{c} 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 10 \\ 5 \\ 12 \\ 12 \\ 12 \\ 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 5 \\ 5 \\ 5 \\ 5 \\ 5 \\ 5 \\ 5 \\ 5 \\ 5 \\ $	95% 94% 94% 95% 95% 95% 97% 97% 97% 97% 97% 97% 97% 97% 97% 98.6% 98.6% 98.6% 98.6% 99.3% 98.6% 99.3%
ACE ACD BCD BDE	AVP MAV AVP AVP MAV AVP AVP MAV AVP AVP AVP Std SD SD SD Std Std Std AVP Std AVP	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2	8 5 8 5 8 2 3 2 2 2 2 2 2 2 7 4 7 1 3 3 3	$\begin{array}{c} 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 10 \\ 5 \\ 12 \\ 12 \\ 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 12 \\ 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 5 \\ 10 \\ 10 \\ 10 \\ 10 \\ 10 \\ 10 \\ 10 $	95% 94% 94% 95% 95% 95% 97% 97% 97% 97% 97% 97% 97% 96% 97% 98.6% 98.6% 98.6% 98.6% 99.3% 98.6% 99.3% 96.6% 97%
ACE ACD BCD BDE	AVP MAV AVP AVP MAV AVP AVP MAV AVP AVP MAV AVP Std SD SD Std Std Std Std AVP MAV AVP AVP	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1	8 5 8 5 8 2 3 2 2 2 2 2 2 2 7 4 7 4 3 3 1 3 1 3 1	$\begin{array}{c} 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 10 \\ 5 \\ 12 \\ 12 \\ 12 \\ 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12$	95% 94% 94% 95% 95% 95% 97% 97% 97% 97% 97% 97% 96% 97% 98.6% 98.6% 98.6% 98.6% 98.6% 99.3% 98.6% 99.3% 96.6%
ACE ACD BCD BDE	AVP MAV AVP AVP AVP MAV AVP MAV AVP AVP MAV AVP Std SD SD SD Std SD Std SD Std AVP MAV AVP	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1	8 5 8 5 8 2 3 2 2 2 2 2 2 2 7 4 7 4 3 1 3 1 1 1 1 1	$\begin{array}{c} 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 10 \\ 5 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 $	95% 94% 94% 95% 95% 95% 97% 97% 97% 97% 97% 97% 96% 97% 98.6% 98.6% 98.6% 98.6% 98.6% 98.6% 99.3% 98.6% 99.3% 96.6% 97.%
ACE ACD BCD BDE	AVP MAV AVP AVP AVP MAV AVP AVP AVP AVP MAV AVP Std SD SD Std SD Std SD Std SD Std AVP AVP AVP	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar db1 coif1 bior1.1 haar db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar db1 coif1 bior1.1 haar db1 coif1 bior1.1 haar db1 coif1 bio1.1 bio1.1 haar db1 coif1 bio1.1 db1 coif1 db1 coif1 db1 coif1 db1 coif1 db1 coif1 db1 coif1 db1 coif1 db1 coif1 db1 coif1 db1 coif1 db1 coif1 bio1.1 db1 coif1 coif1 bio1.1 db1 coif1 bio1.1 db1 coif1 bio1.1 db1 coif1 bio1.1 db1 coif1	$ \begin{array}{r} 8 \\ 8 \\ 5 \\ 8 \\ 5 \\ 8 \\ 2 \\ 2 \\ 2 \\ 2 \\ 2 \\ 2 \\ 2 \\ 7 \\ 4 \\ 7 \\ 7 \\ 4 \\ 7 \\ 1 \\ 3 \\ 3 \\ 1 \\ 2 \\ 7 \\ 4 \\ 7 \\ 1 \\ 3 \\ 3 \\ 1 \\ 2 \\ 2 \\ 2 \\ 2 \\ 2 \\ 2 \\ 2 \\ 2 \\ 2 \\ 2 \\ 2 \\ 7 \\ 4 \\ 3 \\ 1 \\ 2 \\ $	$\begin{array}{c} 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 10 \\ 5 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 $	95% 94% 94% 95% 95% 95% 97% 97% 97% 97% 97% 97% 96% 98.6% 98.6% 98.6% 98.6% 98.6% 98.6% 98.6% 98.6% 99.3% 96.6% 97.6%
ACE ACD BCD BDE	AVP MAV AVP AVP AVP MAV AVP MAV AVP AVP MAV AVP Std SD SD Std SD Std SD Std SD Std AVP MAV AVP AVP	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 bior1.1 haar demy sym2 rbio1.1 bior1.1 haar demy sym2 rbio1.1 bior1.1 haar demy sym2 rbio1.1 bior1.1 haar demy sym2 rbio1.1 bior1.1 haar demy sym2 rbio1.1 bior1.1 haar demy sym2 rbio1.1 bior1.1 haar db1 coif1 bio1.1 bio1.1 bio	8 5 8 5 8 2 2 2 2 2 2 2 2 7 4 7 4 7 4 3 1 3 1 2 1 3 1 2 1 2 1 3 1 2 1 3 1 2 1 1 2 1 2 3 3 3 3 3 3 3 3 3 3 3	$\begin{array}{c} 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 10 \\ 5 \\ 12 \\ 12 \\ 12 \\ 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 12 \\ 12 $	95% 94% 94% 95% 95% 95% 97% 97% 97% 97% 97% 97% 96% 98.6% 98.6% 98.6% 98.6% 98.6% 98.6% 98.6% 98.6% 99.3% 96.6% 97% 96.6% 96.6%
ACE ACD BCD BDE	AVP MAV AVP AVP AVP MAV AVP MAV AVP MAV AVP Std SD SD Std SD Std SD Std SD Std SD Std AVP AVP AVP AVP MAV AVP AVP MAV AVP MAV	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar db1 coif1 bior1.1 haar db1 coif1 bior1.1 haar db1 coif1 bior1.1 haar db1 coif1 bior1.1 haar sym2 rbio1.1 bior1.	8 5 8 5 8 2 2 2 2 2 2 2 2 7 4 7 4 7 1 3 1 2 1 3 1 2 1 3 1 2 1 3 1 2 1 3 1 2 1 3 1 2 1 3 5 6 7 1 3 3 1 3 1 3	$\begin{array}{c} 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 10 \\ 5 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 $	95% 94% 94% 95% 95% 95% 97% 97% 97% 97% 97% 97% 97% 98.6% 98.6% 98.6% 98.6% 98.6% 98.6% 98.6% 99.3% 98.6% 99.3% 96.6% 96.6% 96.6% 96.6%
ACE ACD BCD BDE ABC	AVP MAV AVP AVP AVP MAV AVP AVP AVP AVP MAV AVP Std SD SD Std SD Std SD Std Std AVP MAV AVP AVP MAV AVP AVP MAV AVP	haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 db1 coif1 bior1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar demy sym2 rbio1.1 haar coif1 bior1.1 haar coif1 bior1.1 haar coif1 bior1.1	$ \begin{array}{r} 8 \\ 8 \\ 5 \\ 8 \\ 5 \\ 8 \\ 2 \\ 2 \\ 2 \\ 2 \\ 2 \\ 2 \\ 7 \\ 4 \\ 7 \\ 7 \\ 4 \\ 7 \\ 1 \\ 3 \\ 3 \\ 1 \\ 1 \\ 2 \\ 1 \\ 8 \\ 5 \\ $	$\begin{array}{c} 12 \\ 5 \\ 10 \\ 12 \\ 12 \\ 9 \\ 12 \\ 12 \\ 10 \\ 5 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 \\ 12 $	95% 94% 94% 95% 95% 95% 97% 97% 97% 97% 97% 97% 97% 97% 98.6% 97% 98.6% 98.6% 98.6% 98.6% 98.6% 99.3% 98.6% 99.3% 96.6% 95.3% 96.6% 96.6% 96.6% 96.2% 96.2%

	ATTO	1	0	10	06.00/
	AVP	rbio1.1	8	12	96.2%
	AVP	db1	8	12	96.2%
	MAV	coif1	5	9	95.5%
	AVP	bior1.1	8	12	96.2%
ABD	AVP	haar	8	12	96.2%
	MAV	demy	5	5	95.5%
	MAV	sym2	5	10	95.5%
	AVP	rbio1.1	8	12	96.2%
	AVP	db1	8	12	96.2%
	MAV	coif1	5	9	95.7%
	AVP	bior1.1	8	12	96.2%
ABE	AVP	haar	1	12	%97.2
	MAV	demy	3	5	97%
	SD	sym2	3	10	97.5%
	AVP	rbio1.1	1	12	97.2%
	AVP	db1	1	12	97.2%
	MAV	coif1	3	9	96%
	AVP	bior1.1	1	12	%97.2
ABCD	AVP	haar	8	5	96.2%
	MAV	demy	5	10	96.2%
	MAV	sym2	5	12	95.5%
	AVP	rbio1.1	8	12	95.5%
	AVP	db1	8	9	96.2%
	MAV	coif1	5	12	96.2%
	AVP	bior1.1	8	5	95.7%
ABDE	AVP	haar	8	5	96.2%
	MAV	demy	5	10	95.2%
	SD	sym2	5	12	95.2%
	AVP	rbio1.1	8	12	96.2%
	AVP	db1	8	9	96.2%
	MAV	coif1	5	12	95.5%
	AVP	bior1.1	8	5	96.2%
ABCDE	AVP	haar	8	12	%.97
	MAV	demy	5	5	96.2%
	AVP	sym2	5	10	96.2%
	AVP	rbio1.1	8	12	97%
	AVP	db1	8	12	97%
	MAV	coif1	5	9	96%
	AVP	bior1.1	8	12	96.4%



Figure 5. Random Forest Function Adaboost

The adaptive boosting algorithm is a boosting technique used as an ensemble method in machine learning. Its name derives from the weight reassigned to each instance, with higher weights for incorrectly classified instances. Boosting is used to reduce biased as well as variance for supervised learning. It works on the principle that learners are grown sequentially; except for the first, each subsequent learner is grown from previously grown learners. In simple words, weak learners are converted into strong ones. The Adaboost algorithm also works on the same principles as boosting, but there is a slight difference in execution[30].

3.5.4. Bagging

3.5.3.

This algorithm often considers homogenous weak learners,

where they learn independently from each other in parallel and combines them following a deterministic average process.

4. Evaluation

The evaluation process is conducted to measure the efficiency of the proposed approach. Multiple models were used, such as 10-fold cross-validation and hold-out test models. Various measurement criteria were calculated to determine the efficiency of our proposed model[31].

The assessment metrics are Recall (R), Accuracy (ACC), Precision (P), and F-measure (F). The evaluation parameters are evaluated using cross-validation (k-fold=10) and hold-out test model [12]. Figure 6 shows the confusion matrix followed in the evaluation process.



Accuracy

Classification accuracy is the total amount of accurate predictions (TP+TN) divided by the total number of predictions made for the dataset (TP+TN+FP+FN):

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$
(2)

Precision

The following equation quantifies the number of positive class projections that currently belong to the positive class.

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

Recall •

The following equation quantifies the number of positive class predictions produced out of all the positive examples in the dataset.

$$\operatorname{Re} call = \frac{TP}{TP + FN}$$
(4)

• F-measure (F1)

F-measure offers a single score that balances both the accuracy issues and the Recall in one number.

$$F1 = \frac{2*\operatorname{Re}\,call*Precision}{\operatorname{Re}\,call+Precision} \tag{5}$$

5. Experimental Results

This paper uses 16 combinations to distinguish the epileptic signal from the regular signal. In this analysis, a distinction was made between classifiers for 16 data combinations. This section presents and discusses the results of the described steps. Figure 7 shows the results of the proposed model with support vector machine (SVM) classifier; Figure 8 with a Decision tree (DT); Figure 9 with Random forest (RF) classifier; Figure 10 with K-nearest neighbor (KNN); Figure

11 with Artificial neural network (ANN); Figure 12 with Naïve Bayes classifier; Figure 13 with Adaboost classifier; and finally Figure 14 with Bagging classifier.



Figure 7. SVM classifier

Figure 7 shows the values of different metrics for SVM, where the values range between 98.4 and 99.6. As shown from the presented Figure, the precision metric is the highest one with an average equal to 99.6, while the recall metric is the lowest one with 98.4.



Figure 8. DT classifier

Figure 8 presents the metrics' values for DT, where the values range between 97.1 and 98.2. As presented from the Figure, the Recall metric achieves the highest value with an average equal to 98.2, while the precision metric is the lowest one with an average equal to 97.1.



Figure 9 lustrates the values of four metrics for the classifier (RF); the values lie between 98.9 and 99. as shown from the below Figure, the Recall metric achieves the highest one while the other three metrics are the lowest have the same values with range 98.9.

Figure 10 introduces the values of critical metrics for the classifier KNN. The values range between 97.2 and 99.2. As shown from the following Figure, the precision metric is the highest value with an average equal to 99.2, while the recall metric is the lowest, with a rate equal to 97.2.

F-measure





Precision

Recall

ACC

Figure 11. ANN classifier

Figure 11 shows the average values for four different criteria for ANN classifier, where the values range between 97.8 and 98.9 as shown from the presented Figure the recall metric is the highest one while the precision metric is the lowest one.



Figure 12. Naïve Bayes classifier

Figure 12 shows the Naïve Bayes 'different metrics values, where the values lie between 92.1 and 97.4. As shown from the following Figure, the recall metric is the highest with an average rate of 97.4, while the precision metric is the lowest with an average rate equal to 92.1.



Figure 13 shows the values of different metrics for Adaboost. The values lie between 97.8 and 98.8. As shown from the presented Figure, the F-measure metric achieves the lowest value with an average rate equal to 97.8, while

other metrics are equals in their values with an average rate equal to 98.8.



Figure 14 shows the key four metrics for the Bagging classifier, where the values equal 98.9, and all values are equal in average rate.



Figure 15. Average Accuracy of all classifiers

Figure 15 shows the average accuracy of all classifiers (SVM, DT, RF, KNN, ANN, Naïve Bayes, Adaboost, and Bagging); it presents values ranges between 94.8 and 98.9. The classifiers SVM, RF, Adaboost, and Bagging have nearly similar values reaching 98.9, while Naïve Bayes achieve the lowest value reach to 94.8.



Figure 16. Average Recall of all classifiers

Figure. 16 presents the average Recall of all previous classifiers, it presents values between 97.2 to 98.9, and the classifiers ANN, RF, Adaboost, and Bagging have nearly similar values reaching 98.9 while KNN achieves the lowest value reach to 97.2.



Figure 17. Average precision of all classifiers

Figure 16 illustrates the average precision of eight classifiers, it introduces values range between 92.1to 99.6, and the classifiers SVM, KNN, Adaboost, and Bagging achieve nearly similar values reach to 99, while Naïve Bayes achieve the lowest value reach to 92.1.



Figure 18. Average F-measure of all classifiers

Figure 18 shows information about the average accuracy of all tested classifiers; it presents values ranges between 94.5 and 99. In this case, the classifiers SVM, RF, and Bagging have nearly similar values reach 98.9, while Naïve Bayes achieve the lowest value reaches 94.5. Table 2 shows the performance of all classifiers for the selected features.

Table 2. Results of accuracy, sensitivity, and specificity for the different cases (all values percentages).

Cases	Measure/	ACC	Recall	Precision	F1
	/classifier				
	SVM	1	1 000	1.000	1.000
10	SVM	1	1.000	1.000	1.000
AC	DT	0.96	1.000	0.926	0.962
	RF	.0985	1.000	0.971	0.985
	KNN	0.995	1.000	0.990	0.995
	ANN	1.00	1.000	1.000	1.000
	Naïve	0.985	0.980	0.990	0.985
	Adaboost	1.00	1.000	1.000	1.000
	Bagging	0.995	0.995	0.995	0.995
	SVM	0.99	0.990	0.990	0.990
AD	DT	0.94	0.940	0.940	0.940
	RF	0.97	0.970	0.970	0.970
	KNN	0.995	1.000	0.990	0.995
	ANN	0.99	0.980	1.000	0.990
	Naïve	0.905	0.870	0.935	0.902
	Adaboost	0.99	0.990	0.990	0.990
	Bagging	0.99	0.990	0.990	0.990
	SVM	1.00	1.000	1.000	1.000
	DT	0.995	1.000	0.990	0.995
	RF	1.00	1.000	1.000	1.000
	KNN	1.00	1.000	1.000	1.000
AE	ANN	0.99	0.980	1.000	0.990
	Naïve	1.00	1.000	1.000	1.000
	Adaboost	1.00	1.000	1.000	1.000
	Bagging	1.00	1.000	1.000	1.000
BC	SVM	0.99	0.980	1.000	0.990
	DT	0.985	0.980	0.990	0.985
	RF	0.99	0.980	1.000	0.990
	KNN	0.98	0.960	1.000	0.980
	ANN	0.99	1.000	0.980	0.990
	Naïve	0.985	1.000	0.971	0.985
	Adaboost	0.99	0.990	0.990	0.990
	Bagging	0.985	0.985	0.985	0.985
BD	SVM	0.995	0.990	1.000	0.995
	DT	0.985	0.990	0.980	0.985
	RF	0.99	1.000	0.980	0.990
	KNN	0.99	0.980	1.000	0.990
	ANN	0.99	1.000	0.980	0.990

	Naïve	0.97	95.000	0.990	0.969
	Adaboost	0.995	0.995	0.995	0.995
	Bagging	0.995	0.995	0.995	0.995
BE	SVM	1.00	1,000	1,000	1.000
DL	DT	0.995	1.000	0.990	0.995
	RF	1.00	1.000	1,000	1,000
	KNN	1.00	1.000	1.000	1.000
	ANN	1.00	1.000	1.000	1.000
	Naïve	1.00	1.000	1.000	1.000
	Adaboost	1.00	1.000	1.000	1.000
	Bagging	1.00	1.000	1.000	1.000
ACD	SVM	0.993	0.990	1.000	0.995
neb	DT	0.973	0.995	0.975	0.990
	RF	0.987	0.995	0.985	0.990
	KADI	0.901	0.075	0.965	0.995
		0.98	0.975	0.995	0.985
	AININ	0.99	0.980	0.990	0.985
	Naive	0.966	0.970	0.933	0.951
	Adaboost	0.993	0.993	0.993	0.993
	Bagging	0.993	0.993	0.993	0.993
ADE	SVM	0.993	0.980	0.995	0.987
	DT	0.977	0.985	0.980	0.983
	RF	0.993	0.995	0.995	0.995
	KNN	0.987	0.985	0.995	0.980
	ANN	0.99	1.000	0.971	0.985
	Naïve	0.833	1.000	0.667	0.800
	Adaboost	0.987	0.987	0.987	0.970
	Bagging	0.987	0.987	0.987	0.987
BCD	SVM	0.983	0.975	1.000	0.987
	DT	0.99	0.995	0.990	0.993
	RF	0.99	0.990	0.995	0.992
	KNN	0.95	0.945	0.979	0.962
	ANN	0.99	1.000	0.980	0.990
	Naïve	0.983	1.000	0.952	0.976
	Adaboost	0.987	0.987	0.987	0.970
	Bagging	0.98	0.980	0.980	0.980
BDE	SVM	0.983	0.975	1.000	0.987
	DT	0.987	1.000	0.980	0.990
	RF	0.993	0.995	0.995	0.995
	KNN	0.977	0.970	0.995	0.982
	ANN	0.973	0.990	0.934	0.961
	Naïve	0.863	0.990	0.712	0.828
	Adaboost	0.983	0.984	0.984	0.984
120	Bagging	0.983	0.983	0.984	0.983
ABC	SVM	0.99	0.980	0.990	0.985
	DT	0.96	0.940	0.940	0.940
	KF	0.987	0.970	0.990	0.980
	KININ	0.973	0.940	0.975	0.950
	AININ	0.97	0.975	0.980	0.980
	Adobaat	0.98/	0.995	0.985	0.990
	AuaDOOSt	0.98/	0.90/	0.90/	0.970
ARD	SVM	0.99	0.990	0.990	0.990
and a	DT	0.977	0.980	0.951	0.966
	RF	0.983	0.980	0.970	0.975
	KNN	0.987	0.970	0.990	0.980
	ANN	0.976	0.995	0.971	0.983
	Naïve	0.893	0.850	0.988	0.914
	Adaboost	0.987	0.987	0.987	0.970
	Bagging	0.99	0.990	0.990	0.990
ABE	SVM	0.997	0.990	1.000	0.995
	DT	0.997	1.000	0.990	0.995
	RF	1.00	1.000	1.000	1.000
	KNN	0.997	0.990	1.000	0.995
	ANN	0.993	1.000	0.990	0.995
	Naïve	1.00	1.000	1.000	1.000
	Adaboost	0.987	0.987	0.987	0.970
	Bagging	0.997	0.997	0.997	0.997

International Journal of Communication Networks and Information Security (IJCNIS)

ABCD	SVM	0.985	0.975	0.995	0.985
	DT	0.963	0.950	0.974	0.962
	RF	0.985	0.980	0.990	0.985
	KNN	0.968	0.945	0.989	0.967
	ANN	0.98	0.985	0.975	0.980
	Naïve	0.983	0.985	0.980	0.983
	Adaboost	0.978	0.978	0.978	0.978
	Bagging	0.983	0.983	0.983	0.983
ABDE	SVM	0.98	0.970	0.990	0.980
	DT	0.975	0.980	0.970	0.975
	RF	0.99	0.995	0.985	0.990
	KNN	0.955	0.935	0.974	0.954
	ANN	0.97	0.975	0.970	0.973
	Naïve	0.868	0.995	0.794	0.883
	Adaboost	0.983	0.983	0.983	0.98.2
	Bagging	0.98	0.980	0.980	0.980
ABCDE	SVM	0.976	0.967	0.993	0.980
	DT	0.976	0.987	0.974	0.980
	RF	0.984	0.983	0.990	0.987
	KNN	0.97	0.957	0.993	0.974
	ANN	0.974	0.980	0.956	0.968
	Naïve	0.956	1.000	0.901	0.948
	Adaboost	0.978	0.978	0.978	0.978
	Bagging	0.98	0.980	0.980	0.980

6. Conclusion

There is an urgent need for improved and accurate epilepsy detection to increase patient care quality. Some automated systems have been proposed to detect epileptic seizures with sufficient accuracy for effective diagnostic purposes. This study presents a suitable method to increase accuracy in epileptic seizure detection, using the features extraction step, then choosing the best selection method to select suitable features. After that, we test eight classifiers for categorizing EEG signals as seizures or not. In this study, we use 54 DWTs to extract features, then our similarity metric selected suitable features, and we use eight classifiers to classify the signals. The results indicate that the SVM and Bagging classifiers outperform the other classifiers in most cases, achieving 98.8 in all metrics.

References

- R. Moshrefi, M. G. Mahjani, and M. Jafarian. "Application of wavelet entropy in analysis of electrochemical noise for corrosion type identification." Journal of Electrochemistry Communications Vol. 48, pp. 49-51, 2014.
- [2] A. Hamad, et al. "Hybrid grasshopper optimization algorithm and support vector machines for automatic seizure detection in EEG signals." International conference on advanced machine learning technologies and applications. Springer, Cham, 2018.
- [3] U. R. Acharya, et al. "Automatic identification of epileptic EEG signals using nonlinear parameters." Journal of Mechanics in Medicine and Biology Vol. 9, No. 04, pp. 539-553, 2009.
- [4] D. Torse, V. Desai, and R. Khanai. "A review on seizure detection systems with emphasis on multi-domain feature extraction and classification using machine learning." BRAIN. Broad Research in Artificial Intelligence and Neuroscience Vol. 8, No. 4, pp. 109-129, 2017.
- [5] E. Abdulhay, et al. "Classification of normal, ictal and inter-ictal EEG via direct quadrature and random forest tree." Journal of medical and biological engineering Vol. 37, No. 6, pp. 843-857, 2017.
- [6] F. Lotte, "A tutorial on EEG signal-processing techniques for mentalstate recognition in brain–computer interfaces." Guide to braincomputer music interfacing, pp.133-161, 2014.
- [7] A. Hamad, et al. "Feature extraction of epilepsy EEG using discrete wavelet transform." IEEE 12th international computer engineering conference (ICENCO). 2016.
- [8] U. R. Acharya, et al. "Automated EEG analysis of epilepsy: a review." Knowledge-Based Systems, Vol. 45, pp. 147-165, 2013.
- [9] D. Chen, et al. "A high-performance seizure detection algorithm based

on Discrete Wavelet Transform (DWT) and EEG." PloS one, Vol. 12, No. 3, pp. e0173138, 2017.

- [10] R. Ramos, et al. "The discrete wavelet transform and its application for noise removal in localized corrosion measurements." International Journal of Corrosion, Vol. 2017, 2017.
- [11] A. Hamad, et al. "A hybrid EEG signals classification approach based on grey wolf optimizer enhanced SVMs for epileptic detection." International Conference on Advanced Intelligent Systems and Informatics. Springer, Cham, 2017.
- [12] O. Salem, A. Naseem, and A. Mehaoua. "Epileptic seizure detection from EEG signal using Discrete Wavelet Transform and Ant Colony classifier." 2014 IEEE International Conference on Communications (ICC), 2014.
- [13] Y. Kaya, et al. "1D-local binary pattern based feature extraction for classification of epileptic EEG signals." Applied Mathematics and Computation, Vol. 243, pp. 209-219, 2014.
- [14] P. Sarma, et al. "Pre-processing and feature extraction techniques for EEGBCI applications-a review of recent research." ADBU Journal of Engineering Technology, Vol. 5, No. 1, 2016.
- [15] A. Baldominos, and C. Ramón-Lozano. "Optimizing EEG energybased seizure detection using genetic algorithms.", IEEE Congress on Evolutionary Computation (CEC). IEEE, 2017.
- [16] A. Grant, J. A. Hinojosa, and M. S. Oliveira. "Methods of eeg signal features extraction using linear analysis in frequency and time– Frequency Domains.", Vol. 2014, pp.1-7., 2014.
- [17] P. Sharanreddy, and P. K. Kulkarni. "EEG signal classification for epilepsy seizure detection using improved approximate entropy." Int J Public Health Sci, Vol. 2, No. 1, pp. 23-32, 2013.
- [18] M. Saber, et al. "Spectrum sensing for smart embedded devices in cognitive networks using machine learning algorithms." Procedia Computer Science, Vol. 176, pp. 2404-2413, 2020.
- [19] S. Madan, et al. "A case study on Discrete Wavelet Transform based Hurst exponent for epilepsy detection." Journal of medical engineering & technology, Vol. 42, No. 1, pp. 9-17, 2018.
- [20] M. Saber, et al. "Artificial neural networks, support vector machine and energy detection for spectrum sensing based on real signals." International Journal of Communication Networks and Information Security, Vol. 11, No. 1, pp. 52-60, 2019.
- [21] J. A. Nasiri, et al. "Intelligent arrhythmia detection using genetic algorithm and emphatic SVM (ESVM)." 2009 Third UKSim European Symposium on Computer Modeling and Simulation. IEEE, 2009.
- [22] Z. Zakeri, et al. "Influence of signal preprocessing on ICA-based EEG decomposition." XIII Mediterranean Conference on Medical and Biological Engineering and Computing 2013. Springer, Cham, 2014.
- [23] W. Mardini, et al. "Enhanced detection of epileptic seizure using EEG signals in combination with machine learning classifiers." IEEE Access, Vol. 8, pp. 24046-24055, 2020.
- [24] M. Al-Fawa'reh, and M. Al-Fayoumi. "Detecting stealth-based attacks in large campus networks." International Journal of Advanced Trends in Computer Science and Engineering, Vol. 9, No. 4, pp. 4262-4277, 2020.
- [25] C. A. Umale, et al., "Feature Extraction Techniques and Classification Algorithms for EEG Signals to detect Human Stress - A Review", Int. J. Comput. Appl. Technol. Res., Vol. 5, 8–14, 2016.
- [26] L. Hussain, et al. "Classification of electroencephlography (EEG) alcoholic and control subjects using machine learning ensemble methods." J Multidiscip Eng Sci Technol, Vol. 2, No. 1, pp. 126-131, 2015.
- [27] M. M. Jafar, et al., "Analysis and Investigation of Malicious DNS Queries Using CIRA-CIC-DoHBrw-2020 Dataset", Manchester J. Artif. Intell. Appl. Sci., Vol. 2, pp. 65–70, 2021.
- [28] M. Alshira'h, and M. Al-Fawa'reh. "Detecting phishing urls using machine learning lexical feature-based analysis." Int. J. Adv. Trends Comput. Sci. Eng., Vol. 9, No. 4, pp. 5828-5837, 2020.
- [29] R. Mousavi, M. Eftekhari, and F. Rahdari. "Omni-ensemble learning (OEL): utilizing over-bagging, static and dynamic ensemble selection approaches for software defect prediction." International Journal on Artificial Intelligence Tools, Vol. 27, No. 06, pp. 1850024, 2018.
- [30] N. Williams, S. Zander, and G. Armitage. "A preliminary performance comparison of five machine learning algorithms for practical IP traffic flow classification." ACM SIGCOMM Computer Communication Review, Vol. 36, No. 5, pp. 5-16, 2006.
- [31] A. Sharmila, and P. J. I. A. Geethanjali. "DWT based detection of epileptic seizure from EEG signals using naive Bayes and k-NN classifiers." Ieee Access, Vol. 4, pp. 7716-7727, 2016.