Detection of Bundle Branch Block using Higher Order Statistics and Temporal Features

Yasin Kaya
Department of Computer Engineering, Adana Alparslan Türkeş Science and Technology University, Turkey

Abstract: *Bundle Branch Block (BBB) beats are the most common Electrocardiogram (ECG) arrhythmias and can be indicators of significant heart disease. This study aimed to provide an effective machine-learning method for the detection of BBB beats. To this purpose, statistical and temporal features were calculated and the more valuable ones searched using feature selection algorithms. Forward search, backward elimination and genetic algorithms were used for feature selection. Three different classifiers, K-Nearest Neighbors (KNN), neural networks, and support vector machines, were used comparatively in this study. Accuracy, specificity, and sensitivity performance metrics were calculated in order to compare the results. Normal sinus rhythm (N), Right Bundle Branch Block (RBBB), and Left Bundle Branch Block (LBBB) ECG beat types were used in the study. All beats containing these three beat types in the MIT-BIH arrhythmia database were used in the experiments. All of the feature sets were obtained at a promising classification accuracy for BBB classification. The KNN classifier using backward elimination-selected features achieved the highest classification accuracy results in the study with 99.82%. The results showed the proposed approach to be successful in the detection of BBB beats.*

Keywords: *ECG, arrhythmia detection, bundle branch block, genetic algorithms, neural networks, k-nearest neighbors, support vector machines, backward elimination, forward selection.*

Received August 20, 2019; accepted October 5, 2020
https://doi.org/10.34028/iajit/18/3/3

---

1. Introduction

The Electrocardiogram (ECG) is an indication of the electrical activity of the heart. It can be recorded non-invasively from points on the patient's body. The ECG is a widely used biological signal and an essential tool in assessing the state of the heart [5, 19]. The heart's electrical conduction system allows it to work properly. It's tracing in ECG consists of several deflections named P wave, QRS complex, and T wave. R is the most prominent point of that shape and it used to calculate heart rate using the R-R measure. The most important part of this system, the bundle branches, provide ventricular contraction. The Bundle Branch Block (BBB) is an obstruction in the bundle of His of the lower heart. A complete heart block occurs as a junction of blocks in both bundles. A more common event is the isolated right or left BBB. These usually coexist with a normal sinus rhythm and are distinct from any disorder with Atrioventricular (AV) conduction. The ECG patterns have a characteristic that makes the QRS complex wider, but very diverse [2, 8]. There are two types of BBB: Right Bundle Branch Block (RBBB) and Left Bundle Branch Block (LBBB). In the RBBB, there is a R-S-R complex in the V1 lead, while a QRS complex is in the V6 lead. In the LBBB, there are "M" and "W" patterns in the V6 and V1 derivations, respectively. The LBBB and RBBB are found within the normal population and are possible signs of increased cardiovascular disease risk. If a LBBB can be clearly associated with an acute chest pain episode, it most likely indicates myocardial infarction, one of the deadliest heart conditions [2]. Thus, the classification of ECG beats is extremely important in detecting arrhythmias in patients hospitalized in the intensive care unit [5]. Automatic splitting of the heart beats into sub-categories using Computer Aided Diagnosis (CAD) reduces the ECG examination time for cardiologists [18].

Various approaches have been proposed for the detection of BBB beats in particular. These methods include Neural Network (NN) based and hybrid approaches [1, 4, 5, 20, 21, 22, 23, 26], the basic decision rule [6, 9], deep learning methods [12, 14, 15], random forests [11], and the Support Vector Machine (SVM) [7]. A review of the literature reveals that detection of BBB arrhythmias via hybrid approaches is carried out in three stages. The first stage is feature extraction using mathematical and statistical models, morphological measures, and frequency-based features. The second stage consists of a feature reduction technique such as the Genetic Algorithm (GA) [1, 17, 21], bat algorithm [22], firefly algorithm [20], particle swarm optimization [3], principal component analysis [11] or the bacteria foraging algorithm [23]. In the third stage, a classifier scheme is designed to classify the BBB beats.

It can be seen from the recent studies; researchers have done a lot of work to classify heart arrhythmias. Ceylan and Özbay [5] used a wavelet NN for classification of BBB beats. They implemented a hybrid NN using Morlet and Mexican hat wavelet functions as the activation function in the hidden layer. Isin and Ozdalili [15] proposed a method using a deep convolutional NN and achieved a correct recognition rate of 98.51%. In another work, Goeirmanto *et al*. [9] detected BBB by calculating the QRS angle that indicates the state of the blood circulation in the heart. Davydov and Khramov [6] proposed a simple mathematical analysis-based method for perceiving BBB. They used 39 test samples and achieved a sensitivity value of 73%. Huang *et al*. [13] implemented a heartbeat classification approach using three different classifiers: the linear SVM, the weighted linear discriminant classifier and the minimum distance classifier. They used matching features with each classifier to achieve better performance and a majority voting strategy to calculate the final types of beats. In their study, Allami *et al*. [1] proposed a GA and NN-based hybrid method. They used temporal and morphological features extracted from standard ECG recordings and achieved a classification accuracy of 98%.

Nature-inspired algorithms have been widely used in machine learning and engineering fields in recent years. Kora and Krishna [20] used most of these algorithms to detect BBB beats and performed different studies on the same data set. They implemented a hybrid firefly algorithm, a GA [21], an adaptive bacterial foraging algorithm [23] and a bat algorithm [22] and achieved classification accuracy of 99.1, 98.9, 98.74, and 98.9%, respectively. Kaya *et al*. [16] proposed a GA-based approach to classify BBB. They used signal amplitude values as features and the GA to select the best features to represent one heartbeat.

In this study, we proposed an approach for the classification of BBB beats. Normal sinus rhythm (N), RBBB and LBBB ECG beat types were used in the study. All beats in the MIT-BIH arrhythmia database [24] containing these three beat types were used in the experiments. We calculated the statistical and temporal attributes for a heartbeat and used them for BBB detection. The proposed approach achieved promising classification performance.

2. Methods

A block diagram of the approach proposed in this study is shown in Figure 1. The system includes pre-processing and beat parsing, feature extraction, feature selection, and classification steps. In the pre-processing and beat parsing steps, the fluctuations in the signal were removed using filters and the signal was split into beats. The window width centering on the R peak was set at 200 samples to represent a heartbeat [18].

The statistical and temporal features of the beat were calculated in the feature extraction step. The most valuable features were determined in the feature selection step and the classification results werecalculated in the classification step.

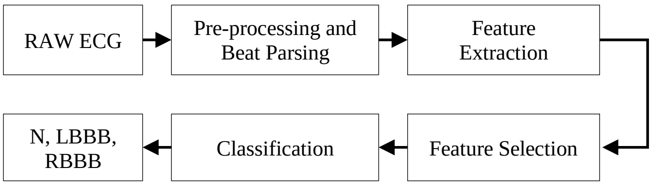

Figure 1. Block diagram of the proposed BBB classification approach.

2.1. Database

We used the signal files from the MIT-BIH arrhythmia database [24], which consists of 48 two-channel recordings of approximately 30 min each at a 360-Hz sampling rate. All of these files were obtained from 47 patients examined at the BIH Arrhythmia Laboratory between 1975 and 1979.

In the study, 45 ECG recordings were used. Three files were not used in the tests because they did not contain the MLII derivation and the related beat types. Table 1 presents the file numbers and beat counts for each beat type used in the study. Figure 2 shows the N, LBBB, and RBBB beats taken from files numbered 100, 109, and 118, respectively.

Table 1. File numbers and beat counts for each beat type used in the study.

Beat Type	File Number	Beat Count
N	100, 101, 103, 105, 106, 108, 112, 113, 114, 115, 116, 117, 119, 121, 122, 123, 200, 201, 202, 203, 205, 208, 209, 210, 212, 213, 215, 217, 219, 220, 221, 222, 223, 228, 230, 231, 233, 234	74722
LBBB	109, 111, 207, 214	8069
RBBB	118, 124, 207, 212, 231, 232	7250
Total	**45 Signal Files**	**90041**

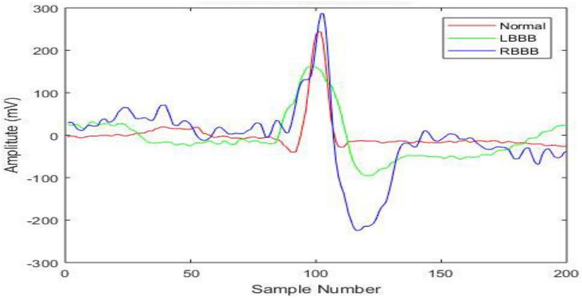

Figure 2. Normal beat taken from File No. 100, LBBB beat from file no. 109 and RBBB beat from file no. 118.

2.2. Pre-Processing and Beat Parsing

The ECG data obtained from the MIT-BIH arrhythmia database contained some noise that required attention to improve the next step of the model. As noise in the ECG signal negatively affects the calculated features, the noise in the signal had to be removed before the feature extraction step. First, the mean of the signal was subtracted from the signal to obtain a zero averaged signal. The frequency components below 2

Hz were then removed using filters to eliminate the baseline wander in the signal [19]. At the last stage, the noise-canceled signal was segmented into vectors to represent the beat. The vector length was set as 200 samples and the R peak was at the 100th point. Annotations from the database were used to locate the R point.

2.3. Feature Extraction

Features commonly used for BBB classification include wavelet transform [5], signal amplitude values [16, 20, 21, 22, 23], deep learning systems [15], mathematical QRS angle values [9], morphological QRS values [6], Independent Component Analysis (ICA) [13] and Principal Component Analysis (PCA) [11]. In this study, we used the arithmetic mean, standard deviation, distribution range, interquartile range, skewness, and kurtosis statistical features for BBB classification [19]. These statistics were first calculated from the whole beat of all 200 samples. The same values were calculated from four equal sub-segments of 50 samples in order to increase the capacity to represent the beat. These statistical features were calculated by the formulas in Equations (1)-(6).

$$Aritmetic\,mean\ \bar{x} = \frac{\sum_{i=1}^{n} x_i}{n} \tag{1}$$

$$Standard\ deviation = \sqrt{\frac{\sum_{i=1}^{n}(x_i - \bar{x})^2}{n}} \tag{2}$$

$$Range = \max(x) - \min(x)\,, i = 1..n \tag{3}$$

$$Interquartile\ range = Q3 - Q1 \tag{4}$$

$$Skewness = \frac{\sum_{i=1}^{n}(x_i - \bar{x})^3}{\left(\sum_{i=1}^{n}(x_i - \bar{x})\right)^3} \tag{5}$$

$$Kurtosis = \frac{\sum_{i=1}^{n}(x_i - \bar{x})^4}{\left(\sum_{i=1}^{n}(x_i - \bar{x})\right)^4} \tag{6}$$

Where $\bar{x}$ is the arithmetic mean of the samples, n is the sample count and x_i is the i^{th} sample value.

The standard deviation is equal to the square root of the variance and is an indicator of the statistical dispersion of the data. The range is defined as the difference between the highest and lowest number in the given range. The interquartile range is equal to the sample distance between the lower (Q1) and upper (Q3) quartiles; Q1 and Q3 equal the median value of the first and second half of the sorted data, respectively. Skewness refers to the amount and direction of movement of the horizontal symmetry. For a normal distribution, the skewness is zero and any symmetric data must have a skewness close to zero. Negative values for skewness indicate a slope to the left, and positive values for skewness indicate a slope to the right. Kurtosis is an indicator of the sharpness of the central peak according to the standard distribution curve [10]. In addition, the previous and following R-R intervals were used as features. The previous R-R and following RR features were calculated as the temporal difference between the previous beat and the following beat of the active beat. There is no time signature in these computed statistical features, thus the order of these features does not affect feature selection and classification stages, but the number of selected features affects the classification rates.

2.4. Feature Selection

In this step, the most relevant features were selected from the calculated features using feature selection methods. Three feature selection methods were used in this study: forward selection, backward elimination, and genetic feature selection.

2.4.1. Forward Selection and Backward Elimination

Forward Selection (FS) and Backward Elimination (BE) are two deterministic greedy feature selection algorithms. Greedy algorithms follow an intuitive solution to select the most appropriate feature locally at each stage, hoping to find a global optimum.

The FS starts with an empty set of features. A new population is created by adding unused features and evaluated by a classifier. The feature that provides the highest accuracy is passed to the next generation. The new round begins with a subset of the modified features. The search is terminated when the specified finishing criterion is reached. The following pseudo code denotes the FS procedure:

Algorithm 1: Forward Selection

```
1. Create an initial population with n individuals.
2. Evaluate each feature subset with a classifier
3. Select best k feature.
4. For each of k feature sets do
    • If there are only t unused feature.
    • Make t duplicates of the feature set and add one of the formerly unemployed features to the feature set.
5. if the performance improves, go to step 2
```

The BE starts with all of the features. A new population is created by subtracting a feature at a time. A classifier evaluates the new population. The feature that minimizes the performance in the population is removed last. The search is terminated when the specified finishing criterion is reached. Algorithm 2 demonstrates the BE procedure.

Algorithm 2: Backward Elimination

```
1. Create a feature set which uses all features.
2. Evaluate the population with a classifier
3. Select best k feature.
4. For each of k feature set do
    • If there are j features used
    • Make t duplicates of feature set and erase one of the formerly employed features from the feature set.
5. If the performance improves, go to step 2
```

2.4.2. Genetic Feature Selection

GA was developed in the 1970s. The GA is a proposed model for population evolution in a particular environment [25]. Each member of the population is represented as a chromosome of a gene sequence. Each gene has two possible values (to select or not to select a corresponding feature) and each gene is transformed into a parameter of the problem space. An evaluation function calculates the performance value by evaluating each individual.

The algorithm begins by working with random solutions (chromosomes) called the "population". Chromosomes are taken from the starting population and used to generate new populations. When creating a new population, selection, crossover, and mutation genetic operators are applied. The fitness value is calculated for each individual in the population. These actions are repeated until the predetermined finishing criterion is reached, such as the best result, population count or duration of the process. The new population is better than the previous population because at least one of the best chromosomes is copied to the new population unchanged. This is called the "elitism strategy" [16].

Figure 3 shows the implementation of the GA in feature selection. Each chromosome in the population consists of binary genes, and each gene represents a feature. A classifier evaluates each chromosome and calculates the fitness value. The fitness value indicates the accuracy of the classifier. The GA aims to find a subset of features maximizing classification accuracy.

A standard GA using a tournament-based selection strategy was used in the experimental test in this study. The size of the tournament parameter that specifies the fraction of the current population which should be used as tournament members was set as 0.25. The population size parameter was set as 5 and the maximum number of generation parameters was set as 30. These parameters were selected based on experimental observations and we didn't use any fine-tuning or parameter optimization method.

2.4.3. Classification of BBB

Three different classifiers were used comparatively in this study: K-Nearest Neighbors (KNN), NN, and SVM. A feed-forward NN trained by a back-propagation algorithm was used. The NN had one hidden layer, which had 10 nodes and used the following parameters for training:

Training cycles: 500
Momentum: 0.2
Learning rate: 0.3
Error epsilon: 0.00001

In the KNN classification experiments, the k parameter was set as 1 and the distance function parameter was set as the Euclidian distance. Another classifier used in the experiments was SVM. A kernel-type parameter was taken as the Radial Basis Function (RBF) and the gamma and C parameters were set as zero in the SVM classifier. A 10-fold cross-validation method was used to validate the classifier results. In the 10-fold cross-validation, the dataset was divided into 10 equal sections. One section was used for testing and the other sections were used for the training of the system in each step. After 10 repetitions, the classification performance was calculated by taking the average of the calculated values.

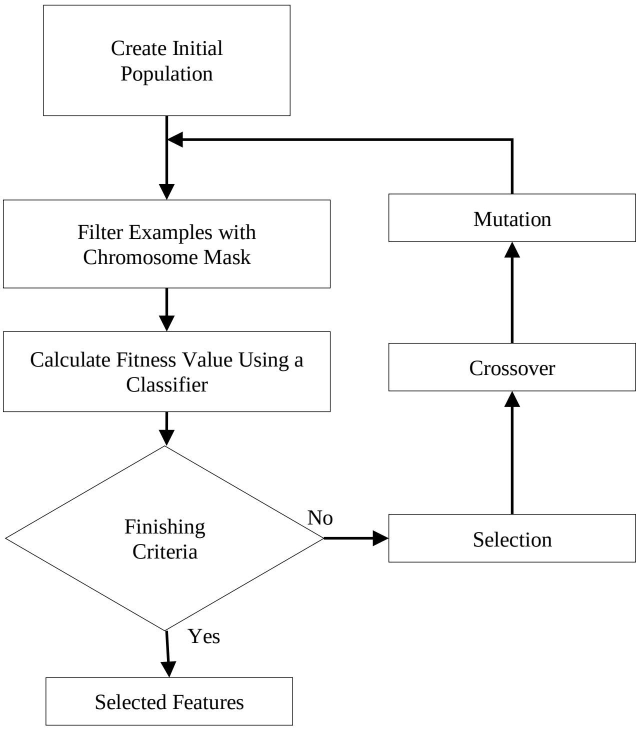

Figure 3. Genetic feature selection flow diagram.

The parameters used in these algorithms were obtained from empirical observations. No fine-tuning method was used for parameter optimization. Generally, algorithms were implemented with the specified standard parameters.

3. Experimental Results

There are many factors for the success of a heartbeat classification system. The most notable of these are the quality of the ECG signal, the ability of the calculated features to represent the heartbeat, the classification algorithms applied, and the data set used for the training of these algorithms. The heartbeats used in the experimental tests in this study were taken from the MIT-BIH arrhythmia dataset. The proposed BBB classification approach was tested by a total number of 90041 beats gathered from 45 signal files in the database. These beats comprised 74722 N samples, 8069 LBBB samples, and 7250 RBBB samples. In this work, a 10-fold cross-validation technique was used for testing and training the system.

In the feature extraction step, we calculated 32 features, including 30 statistical and 2 temporal features for a beat. Table 2 shows the entire list of features.

Table 2. Calculated statistical and temporal features.

Statistical Features						
Feature	**Mean**	**Std. Dev.**	**Range**	**IQR**	**SKEW**	**KURT**
Entire beat	MEA0	STD0	RANG0	IQR0	SKEW0	KURT0
Segment 1	MEA1	STD1	RANG1	IQR1	SKEW1	KURT1
Segment 2	MEA2	STD2	RANG2	IQR2	SKEW2	KURT2
Segment 3	MEA3	STD3	RANG3	IQR3	SKEW3	KURT3
Segment 4	MEA4	STD4	RANG4	IQR4	SKEW4	KURT4
Temporal Features						
Previous R-R				Following R-R		

Three feature selection algorithms were used in this study to determine valuable features for representing the data. A KNN classifier trained with 15000 beats was used as an evaluation function in the feature selection step. Table 3 presents the obtained features at the feature selection step.

Table 3. Selected feature with feature selection algorithms.

Feature	**GA**	**BE**	**FS**
SKEW0	0	1	0
KURT0	0	1	0
RANG0	0	0	0
IQR0	0	1	1
STD0	1	1	0
MEA0	0	1	1
SKEW1	0	1	1
KURT1	1	1	0
RANG1	1	1	1
IQR1	1	1	1
STD1	0	1	0
MEA1	0	1	1
SKEW2	1	1	1
KURT2	1	1	1
RANG2	1	1	1
IQR2	1	1	1
STD2	1	1	0
MEA2	1	1	1
SKEW3	1	1	0
KURT3	0	1	0
RANG3	1	1	1
IQR3	1	1	1
STD3	0	0	1
MEA3	1	1	1
SKEW4	0	1	1
KURT4	1	1	0
RANG4	1	1	1
IQR4	0	1	1
STD4	0	1	1
MEA4	1	1	1
Previous RR	1	1	1
Next RR	0	1	1
Total	**18**	**30**	**22**

Using the GA, BE, and FS methods, 18, 30, and 22 features were selected, respectively. The selected features are indicated as one in the table. The three performance metrics of accuracy, specificity and sensitivity were calculated using Equations (7), (8) and (9):

$$Accuracy = \frac{\sum_{i=1}^{3} TP_i}{Total\,Beats} \quad (7)$$

$$Specificity_i = \frac{TP_i}{TP_i + \sum FP_i} \quad (8)$$

$$Sensitivity_i = \frac{TP_i}{TP_i + \sum FN_i} \quad (9)$$

Where *i* symbolizes the class number, TP_i represents the true positive for class *i*, FP_i represents the false positive for class *i*, and FN_i represents the false negative for class *i*. Specificity and sensitivity values were calculated for each class, and the calculated accuracy value indicated the accuracy of the whole system. Thus, the average of the specificity and sensitivity values were used in the results.

We used SVM, NN, and KNN classifiers to obtain the experimental results in this study. These algorithms were tested using 32 computed features and three of their selected subsets. Table 4 shows the experimental results.

Table 4. BBB classification results.

Classifier	**Features**	**Accuracy**	**Sensitivity**	**Specificity**
NN	GA	99.13%	96.94%	98.86%
	BE	99.69%	99.08%	99.55%
	FS	99.11%	96.90%	99.12%
	32 Features	99.69%	99.10%	99.54%
SVM	GA	99.58%	98.86%	99.29%
	BE	99.71%	99.18%	99.53%
	FS	99.69%	99.15%	99.50%
	32 Features	99.74%	99.25%	99.58%
KNN	GA	99.80%	99.63%	99.49%
	BE	**99.82%**	**99.65%**	**99.54%**
	FS	99.81%	99.64%	99.53%
	32 Features	99.81%	99.65%	99.53%

4. Discussions

In this study, we used MATLAB 2017a software for the pre-processing, beat parsing, and feature calculation steps and RAPIDMINER STUDIO Academic Edition for the feature selection and classification steps. All classifiers used in the experiments obtained similar results. The KNN classifier using BE-selected features achieved the highest performance in the experiments and attained an accuracy value of 99.82%. Table 5 shows the confusion matrix of the results. It can be seen from the table that 8040, 74627, and 7210 samples were correctly classified for LBBB, normal, and RBBB, respectively.

Table 5. Classification confusion matrix of three classes using KNN classifiers feeding BE-selected features.

		Reference Label			
		LBBB	**Normal**	**RBBB**	**Class Precision**
Classifier Prediction	**LBBB**	8040	64	2	99.19%
	Normal	25	74627	38	99.92%
	RBBB	4	31	7210	99.52%
	Class Recall	99.64%	99.87%	99.45%	

The distinction between the LBBB and N class is particularly difficult because these beats overlap significantly [13]. Nevertheless, the proposed approach made it possible to distinguish between the three classes with high classification accuracy. Table 6 demonstrates the performance of the proposed approach in comparison with other works.

Table 6. Performance comparison with other studies on BBB detection.

Studies	Method for BBB detection	Accuracy
Ceylan and Özbay [5]	Wavelet NN	99.2%
Isin and Ozdalili [15]	Deep Learning	98.51%
Bhattacharyya and Snekhalatha [4]	Neural Network	~
Goeirmanto *et al.* [9]	QRS angle	~
Kora and Krishna [20]	Hybrid Firefly and Particle Swarm Optimization	99.1%
Kora and Krishna [21]	Genetic Neural Network	98.9%
Yang *et al*. [26]	Neural Network	88.7%
Hao *et al.* [11]	Random Forest	98.4%
Kora and Kalva [23]	Adaptive Bacterial Foraging Optimization and Neural Network	98.74%
Davydov and Özbay [6]	Basic Threshold Method	74%spe.
Huang *et al*. [13]	Linear SVM	83.31%
Allami *et al*. [1]	GA and BB	98.71%
Kora and Krishna [22]	Bat Algorithm and NN	98.9%
Proposed approach	FS and KNN	99.81%
	GA and KNN	99.80%
	Statistical-temporal features and KNN	99.81%
	BE and KNN	99.82%

Ceylan and Özbay [5] used a wavelet-based feature extraction method and NN-based classifier to classify BBB beats. They performed their experiments on 1231 beats in three classes and obtained 99.2% classification accuracy. Although they achieved an acceptable performance, the number of beats used in the experiments was limited. Kora and Krishna [20, 21, 22], Kora and Kalva [23] used nature inspired algorithm and NN-based hybrid approaches in their latest studies. They used amplitude values of the signal as features. The nature inspired algorithm was used to select the best features and the NN was implemented to classify BBB beats. The authors classified a total of 19039 beats with three classes from the MIT-BIH arrhythmia database and obtained similar classification rates (~99%). Two studies [6, 9] used nonconventional techniques to detect the BBB beats and failed to report the numerical classification accuracy performance. Huang *et al*. [13], using linear SVM, obtained the worst results in the comparison table. Hao *et al*. [11] used PCA, magnitude squared coherence and wavelet transform for feature extraction and a random forest classifier for classification. Their methods achieved a classification accuracy of 98.9% for LBBB detection and 98.4% for RBBB detection. This shows that the differences in the datasets used in the experiments and the diversity in the verification methods of the tests make it impossible to directly compare the studies. However, in the present study, the use of large data sets, the selection of data from different patients, and the high classification accuracy better highlight the proposed approach compared to the others.

5. Conclusions

This study presented an approach with high performance BBB detection using the entire collection of N, LBBB, and RBBB beats in the MIT-BIH arrhythmia database. We calculated temporal and statistical features from amplitude values of one heartbeat to achieve this classification process. A window width of 200 samples was used to represent a beat and was divided into four equal segments for feature calculation. The whole beat and the four equal sub-segments were used to calculate 30 statistical features. Two temporal features were added to this attribute set. We used three feature selection algorithms, namely GA, FS, and BE, to reduce the feature size. Three classification algorithms, namely NN, SVM, and KNN, were used to classify BBB heartbeats and normal beats. Promising classification accuracy rates for BBB detection was obtained with all feature sets. The KNN classifier using BE-selected features achieved the highest result in the study with a classification accuracy of 99.82%. The results show the proposed feature set and classification scheme can be adapted to the CAD system for use in the detection of BBB heartbeats.

References

[1] Allami R., Stranieri A., Jelinek H., and Balasubramanian V., “A Genetic Algorithm: Neural Network Wrapper Approach for Bundle Branch Block Detection,” *in Proceedings of Computing in Cardiology Conference (CinC)*, Vancouver, pp. 461-464, 2016.

[2] Ashley E. and Niebauer J., *Cardiology Explained*, Remedica, 2004.

[3] Belkadi M. and Daamouche A., “Swarm Intelligence Approach to QRS Detection,” *The International Arab Journal of Information Technology*, vol. 17, no. 4, pp. 480-487, 2020.

[4] Bhattacharyya S. and Snekhalatha U., “Classification of Right Bundle Branch Block and Left Bundle Branch Block Cardiac Arrhythmias Based on ECG Analysis,” *in Proceedings of Artificial Intelligence and Evolutionary Algorithms in Engineering Systems*, Kumaracoil, pp. 331-341, 2015.

[5] Ceylan R. and Özbay Y., “Wavelet Neural Network for Classification of Bundle Branch Blocks,” *in Proceedings of the World Congress on Engineering*, London, pp. 1-5, 2011.

[6] Davydov N. and Khramov A., “Bundle branch Block Detection based on QRS Analysis of Digital ECG Signal,” *Journal of Biomedical Photonics and Engineering*, vol. 2, no. 3, pp. 030401, 2016.

[7] Fu K., Qu J., Chai Y., and Dong Y., “Classification of Seizure Based on The Time-

Frequency Image of EEG Signals Using HHT and SVM," *Biomedical Signal Processing and Control*, vol. 13, pp. 15-22, 2014.

[8] Geiter H., "Understanding Bundle-Branch Blocks," *Nursing Critical Care*, vol. 5, no. 6, pp. 5-8, 2010.

[9] Goeirmanto L., Mengko R., and Rajab T., "Comparison of The Calculation Qrs Angle for Bundle Branch Block Detection," *IOP Conference Series Materials Science and Engineering*, vol. 128, no. 1, pp. 012037, 2016.

[10] Groeneveld R. and Meeden G., "Measuring Skewness and Kurtosis," *Journal of the Royal Statistical Society*, vol. 33, no. 4, pp. 391-399, 1984.

[11] Hao C., Sivanesan S., Majmudar M., and Rajput K., "Combinational Feature Based Random Forest Classification for Enhanced Bundle Branch Block Beat Detection," *in Proceedings of IEEE EMBS International Conference on Biomedical and Health Informatics*, Las Vegas, pp. 319-322, 2018.

[12] Hou B., Yang J., Wang P., and Yan R., "LSTM-Based Auto-Encoder Model for ECG Arrhythmias Classification," *IEEE Transactions on Instrumentation and Measurement*, vol. 69, no. 4, pp. 1232-1240, 2020.

[13] Huang H., Liu J., Zhu Q., Wang R., and Hu G., "Detection of Inter-Patient Left and Right Bundle Branch Block Heartbeats in ECG Using Ensemble Classifiers," *BioMedical Engineering OnLine*, vol. 13, pp. 72, 2014.

[14] Huang J., Chen B., Yao B., and He W., "ECG Arrhythmia Classification Using STFT-Based Spectrogram and Convolutional Neural Network," *IEEE Access*, vol. 7, pp. 92871-92880, 2019.

[15] Isin A. and Ozdalili S., "Cardiac Arrhythmia Detection Using Deep Learning," *Procedia Computer Science*, vol. 120, pp. 268-275, 2017.

[16] Kaya Y., Gürcan F., and Pehlivan H., "Genetic Feature Selection for Detection Bundle Branch Block Beats of ECG," *in Proceedings of 1nd International Turkish World Enginering and Science Congress*, Antalya, pp. 87-95, 2017.

[17] Kaya Y. and Pehlivan H., "Feature Selection Using Genetic Algorithms for Premature Ventricular Contraction Classification," *in Proceedings of 9th International Conference on Electrical and Electronics Engineering*, Bursa, pp. 1229-1232, 2015.

[18] Kaya Y. and Pehlivan H., "Classification of Premature Ventricular Contraction in ECG," *International Journal of Advanced Computer Science and Applications*, vol. 6, no. 7, pp. 34-40, 2015.

[19] Kaya Y., Pehlivan H., and Tenekeci M., "Effective ECG Beat Classification Using Higher Order Statistic Features and Genetic Feature Selection," *Biomedical Research*, vol. 28, no. 17, pp. 7594-7603, 2017.

[20] Kora P. and Krishna K., "Hybrid Firefly and Particle Swarm Optimization Algorithm for the Detection of Bundle Branch Block," *International Journal of the Cardiovascular Academy*, vol. 2, no. 1, pp. 44-48, 2016.

[21] Kora P. and Krishna K., "Bundle Block Detection Using Genetic Neural Network," *in Proceedings of Information Systems Design and Intelligent Applications*, Visakhapatnam, pp. 309-317, 2016.

[22] Kora P. and Krishna K., "Detection of Bundle Branch Block Using Bat Algorithm and Levenberg Marquardt Neural Network," *in Proceedings of 1st International Conference on Information and Communication Technology for Intelligent Systems: Volume 1. Smart Innovation, Systems and Technologies*, Ahmedabad, pp. 553-561, 2016.

[23] Kora P. and Kalva S., "Detection of Bundle Branch Block using Adaptive Bacterial Foraging Optimization and Neural Network," *Egyptian Informatics Journal*, vol. 18, no. 1, pp. 67-74, 2017.

[24] Moody G. and Mark R., "The Impact of the MIT-BIH Arrhythmia Database," *IEEE Engineering in Medicine and Biology Magazine*, vol. 20, no. 3, pp. 45-50, 2001.

[25] Yang J. and Honavar V., "Feature Subset Selection Using A Genetic Algorithm," *IEEE Intelligent Systems and their Applications*, vol. 13, no. 2, pp. 44-49, 1998.

[26] Yang, T., Gregg R., and Babaeizadeh S., "Detection of Strict Left Bundle Branch Block by Neural Network and A Method to Test Detection Consistency," *Physiological Measurement*, vol. 41, no. 2, 2020.

Yasin Kaya received the B.S. degree in Statistics and Computer Science in 1999 and his M.S. and Ph.D. degrees in Computer Engineering in 2006 and 2017, respectively, from the Karadeniz Technical University, Trabzon, Turkey. Since 2018 he has been an assistant professor at the Computer Engineering Department of Adana Alparslan Türkeş Science and Technology University, Turkey. He has published several journal and conference articles in his areas. His research interests include biomedical signal processing, arrhythmia detection and classification, biomedical image processing, pattern recognition, and nature inspired algorithms.