Automatic identification of characteristic points related to pathologies in electrocardiograms to design expert systems

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Abstract. Electrocardiograms (ECG) record the electrical activity of the heart through twelve main signals called shunts. Medical experts examine certain segments of these signals in where they believe the cardiovascular disease is manifested. This fact is an important determining factor for designing expert systems for cardiac diagnosis, as it requires the direct expert opinion in order to locate these specific segments in the ECG. The main contributions of this paper are: i) to propose a model that uses the full ECG signal to identify key characteristic points that define cardiac pathology without medical expert intervention, and ii) to present an expert system based on artificial neural networks capable of detecting bundle branch block disease using the previous approach. Cardiologists have validated the proposed model application and a comparative analysis is performed using the MIT-BIH arrhythmia database.

Keywords: ECG, cardiovascular disease, bundle branch blocks, medical diagnosis, multi-layer perceptron.

1. Introduction

Cardiovascular diseases are the leading cause of death in the Western world, causing about 4.3 million deaths a year in Europe with a great economic impact, amounting to more than 192 billion euros annually.

Heart diseases can be manifested as alterations in the electrical cardiac system path resulting in an altered distribution heartbeat sequence. The electrocardiogram (ECG) is an electrical cardiac signal representation, which is widely used by the medical community to determine the most physiological and structural changes affecting the cardiac system path.

Generally speaking, an ECG is a set of pulses where the electrical activity of the heart is recorded. An ECG is organized into two sections called leads**,** where each one reflects the differential voltage between two electrodes placed on the skin in different places. An ECG graphical

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representation with all the leads is shown in Fig. 1. The leads are divided into three groups: three bipolar limb leads (called I, II, III), three unipolar limb leads (called aVR, aVL and aVF) and six precordial or chest leads (called V1 to V6). In this case, it is important to note that leads III, aVR, aVL and aVF are lineal combinations from leads I and II (Bayés de Luna, 2006).

The heart pulses are produced by the cardiac diastole and systole, representing the depolarization and repolarization from the myocytes heart cells**,** which generate an electrical signal called pulse (see Fig. 2). A pulse begins in the P-wave, which is where the atrium systole begins; then, QRS-waves are presented, showing the ventricular activity; and finally**,** it ends in the T-wave, which is considered the ventricular systole end.

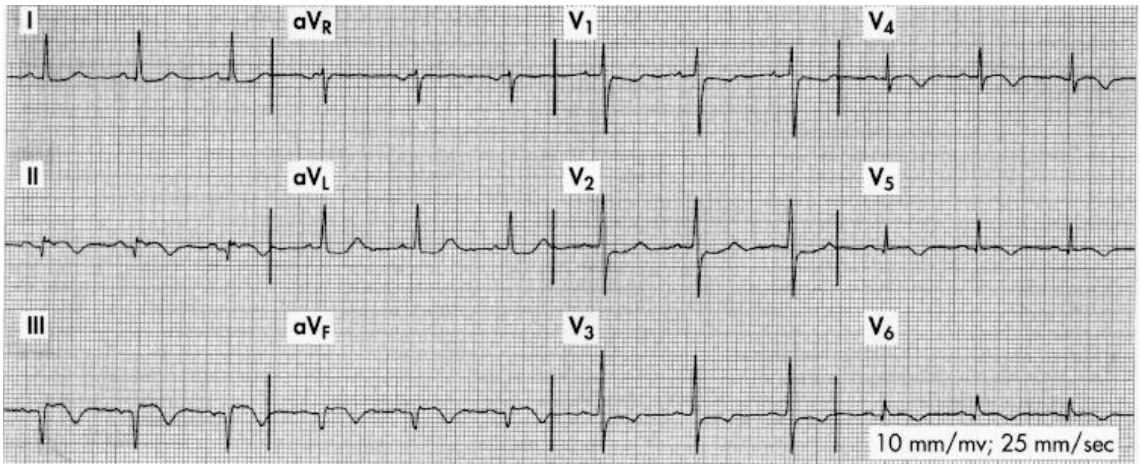


Fig. 1. ECG with theirs leads.

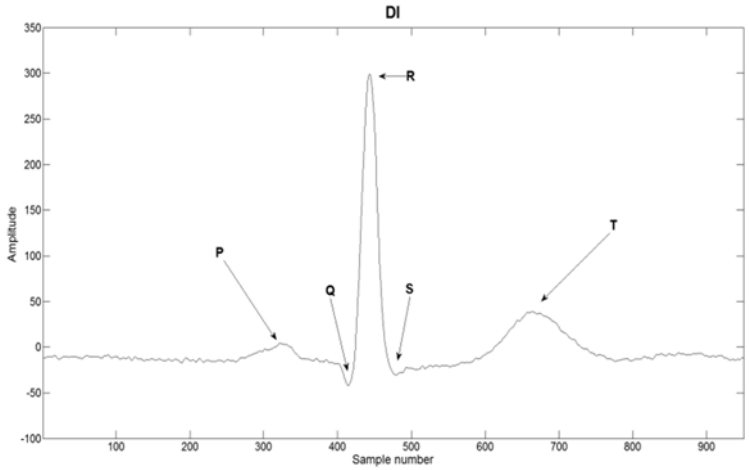


Fig. 2. Heart pulse showing atrium and ventricles depolarization and repolarization: P-wave, QRS-waves and T-wave.

The cardiovascular disease classification and diagnosis involves the evaluation of a large number of pulses that are represented in the ECG, with a high level of detail. This is a time consuming task, and requires professionals with hands-on experience. It is important to mention that, in general, the primary health care levels do not have specialists in cardiology. As regards this, studies have shown that a qualified professional reaches an average success rate of about 95%, while the rate decreases to 55% in the case of medical professionals that are not specialized on the ECG analysis. This being so, it is believed that having automatic ECG diagnostic tools will improve significantly the early diagnosis of cardiovascular diseases.

Traditionally, ECG assessment in clinical environments involves the heart pulse segments analysis by medical specialists to detect the pathology. In the case of automatic ECG evaluation in clinical environments, the process is similar, as the systems analyze pulse parts (segments) that are highlighted by specialists. To perform this analysis, different methods have been proposed in literature about features extraction for automatic ECGs classification systems. These methods can be classified into: (1) methods based on signal morphology consisting in obtaining different measures both of time and voltage (Benali *et al.* 2012; Chazal *et al.* 2004; Hosseini *et al.* 2006; Jekova *et al.* 2008; Korürek and Dogan 2010; Hadj Slimane and Bereksi Reguig 2005; So and Chan 1997; Pan and Tompkins 2007; Chazal and Reilly 2006); (2) statistical methods (Ceylan and Özbay 2007; Ge *et al.* 2002; Yu and Chou 2009; Hyvärinen and Oja 1997; Hyvärinen *et al*. 2001; Hyvärinen 1999) where techniques as the autoregressive analysis, correlation analysis and independent component analysis are applied (Dokur and Ölmez 2001; Khorrami and Moavenian 2010; Martis *et al.* 2012); (3) analysis of eigenvectors used to estimate frequency and signals power measurements from noise-corrupted data (Übeyli 2009; Akay *et al.* 1990; Übeyli et al. 2003); and finally (4), methods based on Hermite polynomial expressions (Osowski and Stodolski 2003; Lagerholm *et al.* 2000).

However, in the above processes, the support of specialists is needed to interpret the original signal where the pathology at issue shows, and thus, define the ECG segment where the pathology is detected, that is to say, the region where the selected feature extraction methods should be applied. This fact is a crucial factor for designing expert systems for cardiac diagnosis, as it requires the direct intervention of experts, their experience and training to establish these segments.

Due to this, the following questions arise: Is it possible to identify key characteristic points associated to a cardiac pathology analyzing the full ECG electrical signal without medical experts' intervention? And if this is the case, is it feasible to use these key points in automatic classification processes using expert systems to diagnose cardiac pathologies?

The main contributions of this paper are: i) to propose a model that uses the full ECG signal to identify key characteristic points that define cardiac pathologies, without medical experts intervention, and ii) to present an expert system based on artificial neural networks capable of detecting bundle branch block disease using the previous approach.

This paper is organized as follows: in Sect. 2 preliminaries are presented; in Sect. 3 a model for extraction of the key characteristic points related to pathologies in ECGs is presented; in Sect. 4 the model is tested using artificial neural networks trained with a database of ECGs with bundle branch block pathologies and also a comparative analysis is performed using the MIT-BIH arrhythmia database; finally, discussions and conclusions are presented in Sect. 5.

2. Preliminaries

2.1. Artificial Neural Networks

Artificial Neural Networks (ANNs) are computing systems, inspired by the biological neural networks, which are constituted by a collection of connected units called neurons. ANNs can be divided into two main groups: those that use supervised learning and those that use unsupervised learning. The Multi-Layer Perceptron (MLP) belongs to the first group and its training algorithm is called the backpropagation algorithm (Haykin 2008). An MLP is a feed-forward neural network in which all neurons of each layer are connected with all neurons of next layer, beginning at the input layer and ending at the output layer through one or several hidden layers. Learning patterns are pairs (input, desired output) used to train the MLP. In the learning process (training), the ANN adapts the connection weights, attempting to minimize the difference between the MLP output and the desired output. After training, the MLP is able to recognize (or classify) new patterns not used in the learning process.

ANNs are widely used in several tasks such as pattern recognition (Patel *et al.* 2017; Ikeda *et at.* 2017; Moon *et al.* 2017), prediction (Chang *et al.* 2017; Kang 2017; Rathore and Kumar 2017), decision support (Karanik *et al.* 2016), classification (Percy *et al.* 2017; de Jesús Rubio 2017; Plaza-Leiva *et al.* 2017) and medical diagnosis (Esmaeilpour and Mohammadi 2016; Abbasi and Esmaeilpour 2017). Particularly, ANNs have been widely adopted in cardiac disease diagnostic using ECG signals (Dokur and Ölmez 2001; Güler and Übeyli 2005; Gholam Hosseini 2006; Hosseini *et al.* 2006; Ceylan and Özbay 2007; Übeyli 2009; Korürek and Dogan 2010; Benali *et al.* 2012; Gacek and Pedrycz 2013; Figuereido Dalvi *et al.* 2016; Sadrawi *et al.* 2017; Park *et al.* 2017; Li *et al.* 2017; Pławiak 2018; Xia *et al.* 2018).

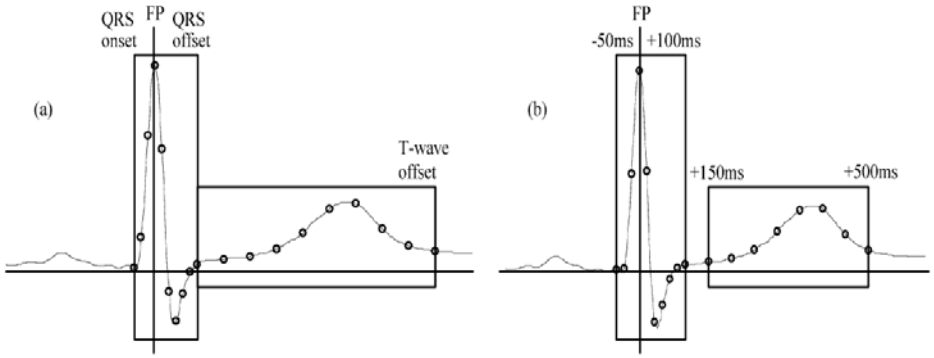


Fig. 3. Two-time sampling methods for extracting ECG morphology features.

2.2. Feature extraction approaches

This section shows different techniques found in the literature for feature extraction in ECG signals that are used for automatic classification of heartbeats. These techniques are designed to obtain a set of features that minimizes the structural complexity of the classifier, while maintaining the information contained in the ECG signal.

- Morphological features. These approaches get different measures of both time and voltage. Time measures include intervals between heartbeats and the duration of the segments. Voltage measures are obtained by sampling the signal at a certain frequency, as well as observing the values of fiducial points (see Fig. 3).

  We can highlight the works done by Chazal *et al.* (2004), Jekova *et al.* (2008), Benali *et al.* (2012), Korürek and Dogan (2010), He *et al.* (2006), Gholam Hosseini *et al.* (2006) and Melgani and Bazi (2008).
- Statistical methods. Several statistical techniques can be applied to extract features from the ECG signal: autoregressive analysis (Ge *et al.* 2002; Wang and Paliwal 2003 and Wei *et al.* 2002); independent component analysis (Yu and Chou 2009), and principal component analysis (Ceylan and Özbay 2007).
- Signal processing. Signal processing is an area of systems engineering, electrical engineering and applied mathematics (Marple 1987 and Ljung 1999) that deals with operations or analysis of signals, in either discrete or continuous time. The domain in which to process a signal is chosen by making an informed guess (or by trying different possibilities) as to which domain best represents the essential characteristics of the signal. Four different transforms have been found in literature: 1) discrete fourier transform (DFT) (Dokur *et al.* 1999) that transforms one function into another which is called the frequency domain representation, or simply the DFT of the original function (often a function in the time domain). The DFT requires an input function that is discrete and whose non-zero values have a limited (finite) duration. Such inputs are often created by sampling a continuous function (Dokur and Ölmez 2001); 2)

discrete cosine transform (DCT) that expresses a sequence of finitely data points in terms of a sum of cosine functions oscillating at different frequencies. A DCT is a Fourier-related transform similar to DFT, but using only real numbers (Khorrami and Moavenian 2010; GholamHosseini *et al.* 1998); 3) continuous wavelet transform (Mallet 1999; Strang and Nguyen 1996; Daubechies 1994, Kumar and Inbarani 2017) that was introduced as a windowing technique with variable-sized regions. Wavelet decomposition introduces the notion of scale as an alternative to frequency, and maps a signal into a time-scale plane. This is equivalent to the time-frequency plane used in the short time Fourier transform. Each scale in the time-scale plane corresponds to a certain range of frequencies in the time-frequency plane. Wavelets are localized waves that extend for a finite time duration compared to sine waves which extend from minus to plus infinity (Khorrami and Moavenian 2010); and 4) the discrete wavelet transform (DWT): is any wavelet transform for which the wavelets are discretely sampled. As with other wavelet transforms, a key advantage it has over Fourier transforms is temporal resolution: it captures both frequency and location information (location in time) (Martis *et al.* 2012; Ocak 2009).

- Eigenvector methods: are used for estimating frequencies and powers of signals from noise-corrupted measurements. These methods are based on an eigen-decomposition of the correlation matrix of the corrupted signal. Even when the signal-to-noise ratio is low, the eigenvector methods produce frequency spectra of high resolution (Übeyli 2009).
- Hermite polynomials: are a classical orthogonal polynomial sequence that arise in probability, in combinatory and in numerical analysis as Gaussian quadrature. They are also used in systems theory in connection with nonlinear operations on Gaussian noise (Linh and Osowsky 2003).

2.3. Bundle branch block disease

Bundle branch blocks are diseases related to defects in the electrical conduction system of the heart. This electrical system begins in the sinoatrial node, which acts as the natural pacemaker of the heart, situated on the upper right atrium. As shown in Fig. 4, the electrical impulse of the heart travels through the atria by several roads converging in the atrioventricular (AV) node. In the AV node**,** the electrical impulse is delayed in order to allow the full contraction of atria, and then, it travels down the Hiss bundle and splits into the left and right bundle branches.

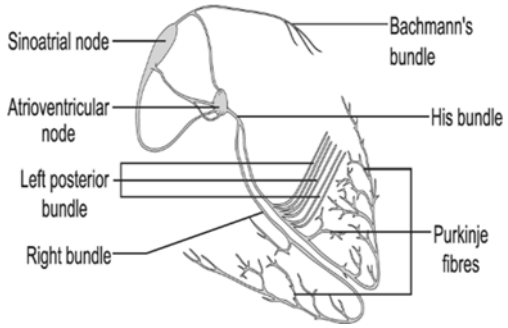


Fig. 4. The electrical systems of the heart.

The left bundle branch is subdivided into the left anterior fascicle, the left posterior fascicle and the septal fascicle, while the right bundle branch contains only one fascicle. All fascicles are composed of millions of Purkinje fibers, which in turn interdigitise with individual cardiac myocytes, allowing for rapid, coordinate, and synchronous physiologic depolarization of the ventricles.

Several reasons may cause damage to the bundle branches or fascicles that impair their ability to transmit electrical impulses appropriately, such as underlying heart disease, myocardial infarction and so on. When this happens, the electrical impulse may be delayed (first degree), intermittently stopped (second degree) or completely stopped (third degree), altering the pathways for ventricular depolarization. Whether the electrical impulses change their course, it can cause delays and changes in the directional propagation of the impulses. These disturbances cause a loss of ventricular synchrony and a drop in cardiac output. A pacemaker may be required to restore an optimal electrical supply to the heart.

Since electrocardiography expresses the electrical activity of the heart, then heart diseases could be diagnosed by morphological study of recorded data. For this purpose, Cardiologists commonly used this tool for diagnosis of cardiovascular diseases since it is effective, non-invasive, and inexpensive.

The most representative sign of bundle branch blocks and hemi blocks lies in the QRS complex. Left bundle branch blocks (LBBB) widen the entire QRS, and generally, shift the electrical axis of the heart to the left. Meanwhile, right bundle branch blocks (RBBB) widen only the last part of the QRS complex, and may shift the electrical axis of the heart slightly to the right.

Furthermore, first degree bundle branch blocks widen QRS complex in ECG due to the delay introduced in any point of the fascicle (Bayés de Luna 2006).

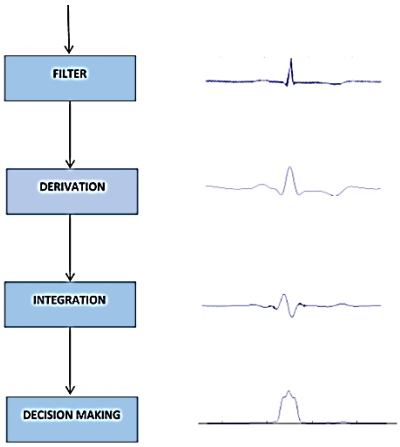


Fig. 5. R peak detection algorithm.

2.4. Algorithm for R peaks detection

In this section, we present the algorithm implemented to detect the R peaks in an ECG. The algorithm determines the QRS complex and RR interval of the signal (Fig. 2) in order to detect the R peaks. The algorithm consists of 4 stages (see Fig. 5): filtering, derivation, integration and decision making.

Stage 1: Filtering

According to Thakor et al. (1983), Pahlmand and Sörnmo (1984), the range of frequencies in which most of the energy density of the QRS complex is found is 10Hz. Considering this, the algorithm implements a FIR bandpass filter consisting of a high-pass and a low-pass filter with a cut off frequency of 5Hz and 15Hz respectively, both of order 90.

Stage 2: Derivation

The variation speed (or derivative) of a signal is, by definition, the variation of amplitude of the signal in a given interval of time. Considering this, the algorithm takes a small interval to obtain the instant speed of the signal.

Stage 3: Integration

Once the speed of the signal variation is determined, it is necessary to find the points with maximum slope, which indicate the approximate position of the QRS complex peak. An important characteristic of the sought signal is that not only it has an ascending slope**,** but also a high negative slope following it. This means that it generates not only a peak but two in the analysed signal, and the middle point between them (zero on the derivative of the original function) corresponds to the maximum of the QRS complex, which is the R peak.

In order to detect the QRS complex, the signal is integrated in a time window. This implies analysing qualitatively the energy of a given sector or window of the signal, and then moving that time window linearly, repeating the process. If an adequate time interval is chosen, with aforementioned peaks contained in the integration, a maximum would be obtained precisely in that point and that would be our guide to detect the R peak. In this way, the selection of an appropriate width for the integration time window is important, to avoid the capture of undesired phenomena. Normally, this is proportional to the average of the QRS complex. For this reason, this value should be in a range between 50 and 110 milliseconds (Thakor *et al.* 1983). We opted for a width value of 80 milliseconds which provides an ideal time window for the majority of the situations, being very useful for a qualitative analysis such as this one.

Stage 4: Decision Making

While the detection of the R peak would seem trivial with a signal similar to the one shown in Fig. 2, electrocardiograms can vary greatly from patient to patient, and the QRS complex area in particular is very unstable and it can present two peaks instead of one, overlapping with the T wave, peak inversions or intensification of the valleys indicated as Q and S in Fig. 2.

Because of these particularities, detecting the maximum value of the integration is not enough. An analysis of the surroundings of the peaks must be performed taking into account the slope of the signal and the amplitude (energy) of the wave in that interval and, afterwards, choosing the most appropriate point according to the definition of the R peak of a cardiac signal, that is the maximum value (in module with respect the continuous offset voltage of the signal) of the signal with a slope greater than that of the P and T waves, and which can be found within these complexes. The decision making is done in 4 steps:

(1) The peaks of the integration signal are found as those zones which exceed a certain threshold level, which is evaluated as a proportional value to the average of the signal (taking into account noise according to Singh and Tiwari (2006)). If a peak is not found, the procedure is repeated with a lower threshold, until a threshold level low enough is reached that can reassure that there is no peak whatsoever in the analysed signal.
(2) Once the peaks are found, the instant of time corresponding to the maximum values of the signals are detected (evaluated in module), in the lower and upper half of the nodule.
(3) Afterwards, the slopes of these peaks are compared in order to discern if it is a great amplitude peak corresponding to a T complex or signal noise.
(4) Once the position of the possible QRS complex is established, the difference between peaks with regards to time, and according to the average of heart beats per minute**,** which is updated on real time with each peak detected, then it is decided if the peak corresponds to a normal complex or an arrhythmia or noise in the bandpass filter.

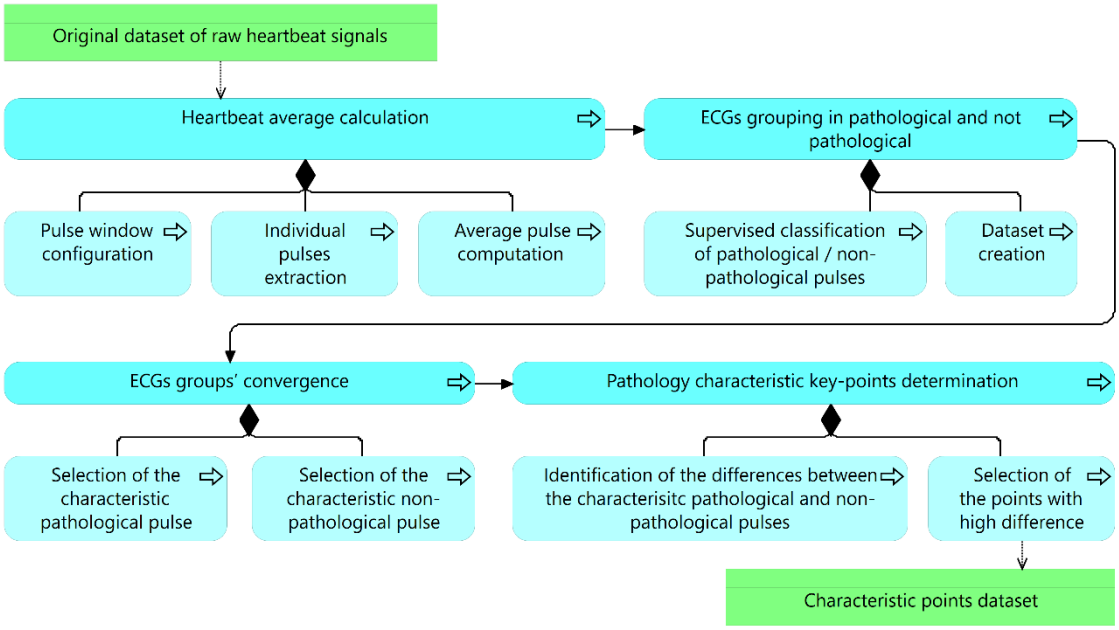


Fig. 6. Outline of the proposed model for the determination of key characteristic points in ECGs.

3. A model for the determination of key characteristic points related to pathologies in ECGs

The proposed model has four sequential phases (see Fig. 6): (1) Heart beat average calculation; (2) ECGs grouping; (3) ECGs Groups' convergence; and (4) characteristic key-points determination.

Phase 1: Heartbeat average calculation.

The ECG records procurement process involves multiple environmental factors that influence the resulting signal. The distortion noise caused by external factors obstructs the characterization signal tasks; therefore, filtration is highly required. In this case**,** a signal homogenization process has been considered based on the beat average calculation of each ECG lead. This procedure consists of 3 steps:

(1) Pulse window configuration. For each branch D, consisting of a set points (x, y), where $y = f(x)$, that represents a heart electrical signal; it is considered a W ($W \subset D$) window composed of N cardiac pulses (Fig. 1). The number of pulses registered by each lead is variable, and depends on the physician and the equipment used. In this study, we have considered that the ideal window should have at least a size 11 pulses ($N \geq 11$). This value has been estimated

empirically. In this case, it is considered that the window should contain enough information about the behavior of the average electrical signal, required to perform the analysis.

(2) Individual pulses extraction. The beginning and end of a pulse is not defined in the signal, therefore**,** it is necessary to recognize the R peak of each heartbeat (which is the most prominent ECG wave). The R peaks identification (see Sect. 2.3), is performed to define the first N maxima or minima locals, using the absolute value. Then individual pulses are obtained through a set of sub-windows $\boldsymbol{w_i}$, $i = 1 \ldots N$, ($w_i \subset W$) of 950 points**,** centered in each R peak. Similarly, $\boldsymbol{w_i}$ size has been defined based on different empirical studies, considering that this definition includes a complete heart cycle. From this, the domain is unified for all sub-windows.

(3) Average pulse calculation. A characteristic pulse from lead B is computed as the sub-windows w_i average. So that each point b_j from B is calculated as

$$b_j = \frac{\sum_{i=1}^{N} \boldsymbol{w_i}[j]}{N} \tag{1}$$

where b_j is the j-th point from B ($j = 1 \ldots 950$).

Phase 2: ECGs grouping in pathological and not pathological.

This phase involves the characteristic pulses classification by cardiologists resulting in two datasets (G): G_P Pathological, where $G_P = \{B|B$ presents the selected pathology$\}$; and G_R Referential, where $G_R = \{B|B$ not presents the selected pathology$\}$. Therefore, $G_P \cap G_R = \emptyset$; and $G_P \cup G_R$ represents the characteristic pulses full database.

Phase 3: ECGs groups' convergence.

In this phase an H selected pulse is computed from each group considered: H_P for the pathological group and H_R for the reference group. To this end, each point forming the selected pulse is calculated from a convergence function that gathers all the characteristic pulses from the group:

$$H_G = K(G) \tag{2}$$

where K is a convergence function such as K: $G \rightarrow R^n$. Under this model, the convergence functions that could be applied are the arithmetic mean, median, mode, and principal components. The selection of K will be experimentally analyzed and discussed later in this paper.

Phase 4: Pathology characteristic key-point determination.

Characteristic points are considered where the absolute difference between the representatives of the group from H_R and H_P is greater than or equal to a difference threshold, such as:

$$C = \{c | c \in \mathbb{N} \wedge c \leq 950 \wedge |H_R[c] - H_P[c]| \geq u\} \quad (3)$$

where C is the set consisting of all the characteristic points, and u is the difference threshold: $u \in R^+$.

Fig. 7 shows the absolute difference from an ECG 8-lead and the difference activation threshold. The example shows slight differences in leads V1, V4, V5 and V6; strong differences in V2 and V3; and no difference in leads I and II.

An example obtained by applying the proposed model to a pathological ECG is shown in Fig. 8, where selected points appears in red over the ECG trace.

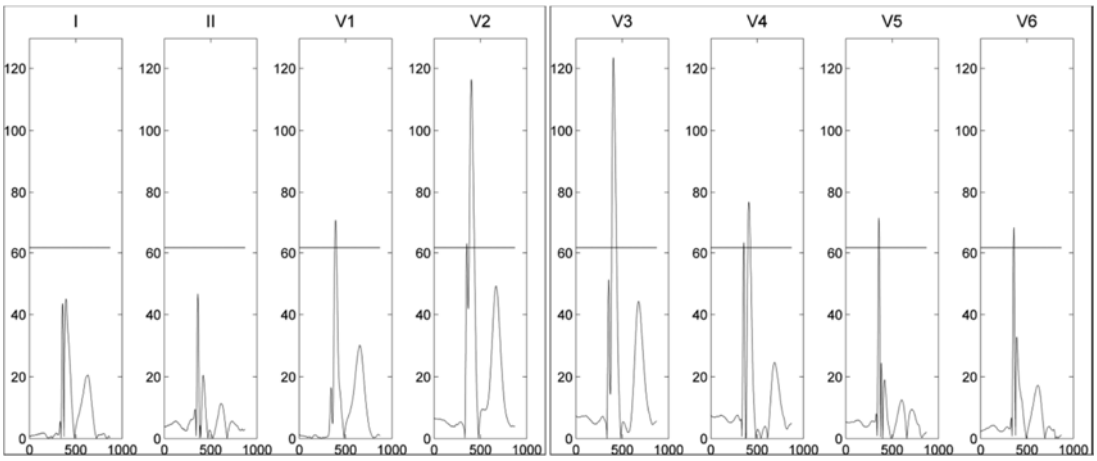
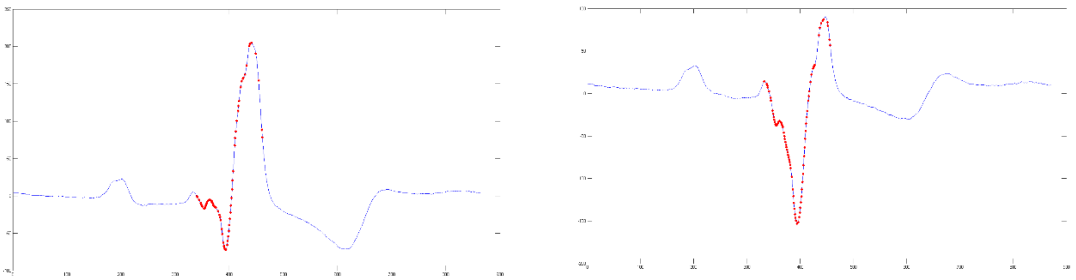


Fig. 7. Absolute difference from an ECG 8-lead.



Lead V2 Lead V3

Fig. 8. Example of a characteristic point from a pathological ECG after the application of the proposed model.

4. Experimental validation

4.1. ECG Database

For this work it is used the database developed at the Biomedical Research Institute of Malaga and the Company Gem-Med SL, extracting 821 records (576 men and 245 women), aged between 14 and 92 years (a median of 65 years), and a body mass index (BMI) between 14.19 and 61.60 kg / m^2. The database has eight ECG leads (I, II and V1 to V6), from which it is possible to recover the remaining four (III, aVR, aVL, aVF).

ECG signals were sampled at a frequency of 1 KHz and filtrated with a band-pass filter of 0.5 Hz and 45 Hz to correct the baseline and to suppress interferences (motion artefact, power line interference, wrong positioning of electrodes, etc.). The original data was saved in SCP-ECG format, which stands for Standard Communications Protocol for Computer Assisted Electrocardiography.

The database comprised both known healthy and pathological individuals. A group of cardiologists diagnosed each pathology with four possible results: sure, probable, discarding, or negative. Those ECGs showing unequivocal signs of the disease under study are marked as sure. If a marker is not clear, or does not appear, the ECG is marked as probable. When there is only an indication but cannot guarantee the diagnosis**,** it is marked as discarding. Finally, ECGs that do not show any indication associated with the pathology under study are marked as negative. Only the healthy individuals (447 ECGs) and those diagnosed with bundle branch blocks (RBBB and LBBB – 127 ECGs) were accounted for.

4.2. Validation using an automatic classifier based on ANNs

The proposed model was applied to a sub-set from the database of 127 ECGs with the pathology bundle branch block and 662 randomly selected with no pathologies. The mean, median, mode, and principal components have been considered as convergence functions. The characteristic points resulting from the model application in each case have been used as an input dataset to train an automatic classifier based on ANNs. The objective is to identify the best statistical method performance considered as convergence function for the representative pulse calculation.

Moreover, since there are various characteristic extraction methods widely used for ECG characterization oriented to the training of automatic classification systems, a comparison was made in the validation process between the proposed model versus the following features extraction methods: sampled signal, Fourier transform, and wavelet functions (Haar, db2, db4, cof1, coif2, sym2, and sim4).

4.2.1. Training sets conformation

The training datasets used by the ANN classifier system were configured as follows:

- Training set, used to optimize the network parameters to and minimize the error. It employs 60% from total dataset (475 elements: 77 pathological and 398 non-pathological).
- Validation set, used for overtraining detection. It employs 20% from total dataset (157 elements: 25 pathological and 132 non-pathological).
- Test Set, used to check the ANN performance. These set is not used in the training process. It employs 20% from the total dataset (157 elements: 25 pathological and 132 non-pathological).

4.2.2. Number of neurons and differentiation threshold determination

The ANNs architecture used is the MLP. The optimal number of neurons at the hidden layer and the threshold value have been obtained using an empirical search. To this end, it has been executed a training iteration, starting at two neurons in the hidden layer, and increasing this number until one hundred. This process was repeated for each differentiation threshold *u*, starting at 99% from the maximum value of the output signal on phase 4 and decreasing 5% at each iteration, ending at 10% from the maximum value of the signal. The Matthews correlation coefficient (MCC) has been used to evaluate the classification performance:

$$MCC = \frac{TP \times TN - FP \times FN}{\sqrt{(TP + FP) \times (TP + FN) \times (TN + FP) \times (TN + FN)}} \quad (4)$$

where *TP* represents the number of true positives, *TN* the number of true negative, *FP* the number of false positives, and *FN* the number of false negatives.

4.2.3. Computation results

For each feature extraction method, the trained ANNs were sorted according to the obtained MCC values, from highest to lowest, selecting the one that showed the highest MCC value in each case.

In Table 1**,** values achieved of sensitivity and specificity are shown. The best ANN presents a sensitivity value of 100%, a specificity value of 99.24% and the value 97.69 for MCC, using 30 neurons in the hidden layer, applying the mode and with a threshold of 30%. This configuration will be used in order to compare the proposed model with recent works (see Sect. 4.4). Fig. 9 show**s** the confusion matrix for the best ANN described.

Table 1. Sensitivity (S), Specificity (E), Number of neurons in Hidden Layer (N) and Differentiation Threshold (U).

	Average				*Median*				*Mode*				*PCA*			
	S	E	N	U	S	E	N	U	S	E	N	U	S	E	N	U
Original	96%	99.2%	44	50%	96%	99.2%	8	50%	100%	99.2%	30	30%	92%	100%	32	95%
Sampled	92%	99.2%	90	50%	100%	98.5%	58	40%	96%	98.5%	2	50%	96%	100%	34	75%
Fourier	88%	97.7%	80	20%	72%	100%	38	30%	88%	99.2%	52	10%	84%	97.7%	90	99%
Haar	84%	97.7%	10	30%	60%	100%	52	40%	64%	100%	58	30%	92%	97.7%	48	85%
db2	56%	98.5%	12	30%	52%	98.5%	94	30%	36%	98.5%	86	30%	40%	100%	98	75%
db4	84%	99.2%	40	30%	60%	100%	60	40%	12%	98.5%	46	70%	20%	99.2%	22	85%
coif1	60%	98.5%	70	30%	56%	94.7%	76	30%	28%	100%	56	30%	40%	98.5%	68	70%
coif2	92%	98.5%	30	30%	80%	97%	48	40%	8%	99.2%	74	40%	12%	100%	12	90%
sym2	60%	98.5%	22	30%	56%	97.7%	54	30%	40%	97%	76	30%	56%	97%	58	75%
sym4	80%	99.2%	2	30%	68%	98.5%	74	30%	4%	100%	54	90%	12%	100%	76	75%

Fig. 9. Confusion matrix associated with the best ANN.

4.3. Experts Validation

A group of eight cardiologists examined the characteristic points resulting from application of the proposed model using the differentiation threshold associated with the training that obtained the highest MCC value. A graphic set composed of three figures for each derivation was shown to the experts, containing an ECG with pathological characteristic points, an ECG with non-pathological characteristic points and an overlap of the first two. Fig. 10 shows an example set of ECGs, used by experts, where the characteristic points have been marked in red.

The assessment of the experts show that the graphic representation of the characteristic points is similar to the tests performed in clinical practice. Moreover, when comparing the graphical representation of the characteristic points from the ECG charted without pathologies to the ones in the ECGs with right bundle branch block, the points identified as characteristic from the proposed model are those that mark the main differences in the chart. This subjective assessment has been issued by all experts that took part of the survey, and it is considered highly important due to their commitment in the clinical practice routine.

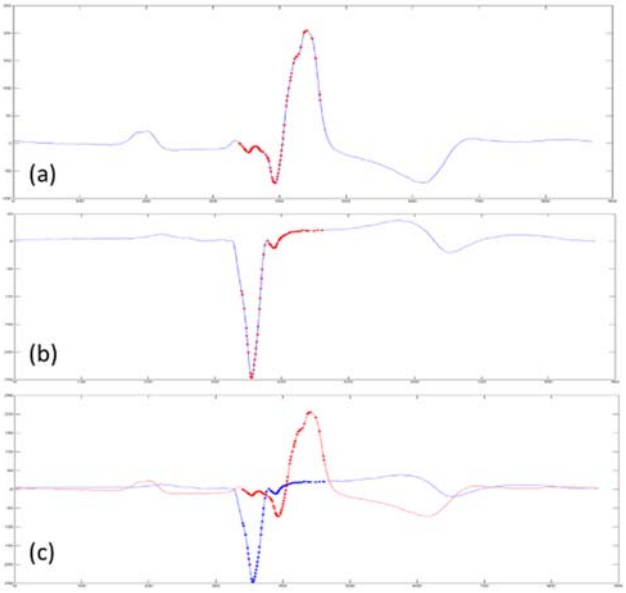


Fig. 10. Graph example shown to cardiologists for process validation. In this case, (a) represents the lead V2 from an ECG diagnosed with bundle branch block, (b) represents the lead V2 from a healthy ECG, and (c) represents the superposition of (a) and (b). Characteristic points have been marked in red for (a) and (b).

4.4. Performance with the MIT-BIH arrhythmia database

The MIT-BIH arrhythmia database (Goldberger *et al.* 2000) is a well-known database that contains 48 recordings of 30-min excerpts of two-lead ambulatory ECG signals from 47 patients. Each recording was band-pass filtered at 0.1–100 Hz and digitized at 360 Hz. The database contains approximately 109,000 heartbeats, each annotated with its types and the location of the QRS complex. In this study, the following record numbers from MIT-BIH database were considered: 109, 111, 207 and 207 for left bundle branch block (LBBB) and 118, 124, 212 and 231 for right bundle branch block (RBBB).

Some recent and related works that also use the MIT-BIH database have been revised and compared with the present proposal. Sharma and Chandra Ray (2016) proposed a classifier based on a multi-class support vector machine for electrocardiogram beat classification using a Hilbert–Huang transform (HHT) for feature selection which includes a set of essential features such as weighted mean frequency, Kolmogorov complexity and other statistical features (median, standard deviation, kurtosis, skewness and central moment). Figuereido Dalvi *et al.* (2016) proposed a heartbeat classification system based on ANNs in which a pre-processing step performed on the ECG was needed for baseline removal and, after, a set of features based on the RR interval were extracted and reduced by principal component analysis. Park *et al.* (2017)

proposed a cascaded random forest classifier for arrhythmia detection using an adaptive strategy for feature extraction that considers normalized beat morphology features when running in a resource-constrained environment, but taking account of a wider range of features in high-performance environments. Li *et al.* (2017) proposed a method based on genetic algorithm back propagation neural network (GA-BPNN) for classifying ECG signals with feature extraction using wavelet packet decomposition combined with statistical methods to extract the effective features of ECG signals. The genetic algorithm is employed to decrease the dimensions of the feature sets and to optimize the weights and biases of the back propagation neural network.

Comparison of performance classification using the MIT-BIH arrhythmia database is shown in Table 2. The performance of each method has been obtained directly from the published manuscript by their respective authors. From Table 2, it can be appreciated that the proposed model achieves similar good results but, in contrast to the other methods, no signal pre-processing is needed, the original ECG electrical signals have been used.

5. Conclusions

The objective of this study was to answer two questions that are fundamental to expert systems development in electrocardiography: Is it possible to identify key characteristic points that define cardiac pathologies analyzing the full ECG electrical signal without medical experts' intervention? And if this is true, is it feasible to use these key points in automatic classification processes using an expert system to diagnose cardiac pathologies?

The main contributions of this paper were: i) to propose a model that uses the full ECG signal to identify key characteristic points that define cardiac pathologies without medical experts' intervention, and ii) to present an expert system based on artificial neural networks capable of detecting bundle branch block disease using the previous approach.

Table 2. Comparison of performance classification using the MIT-BIH arrhythmia database (Goldberger et al., 2000)

Literature	LBBB			RBBB		
	Sensitivity	Specificity	Accuracy	Sensitivity	Specificity	Accuracy
Sharma and Chandra Ray (2016)	99.30	99.90	99.79	99.60	99.98	99.91
Figueiredo Dalvi *et al.* (2016)	82.62	99.38	98.49	76.56	99.96	99.23
Park *et al.* (2017)	97.46	99.96	99.78	98.15	99.99	99.87
Li *et al.* (2017)	100.00	99.31	100.00	96.67	99.32	96.67
Proposed model	99.54	99.84	99.81	99.27	99.97	99.90

A model for the determination of key characteristic points related to pathologies in ECGs has been presented. This model has been tested on the branch block pathology by an experimental validation using a classification system based on artificial neural networks, which has shown similar results to current systems using the MIT-BIH arrhythmia database.

Cardiologists have validated the proposed model application who recognized that the characteristic points selected are highly similar to the points that are manually analyzed in clinical practice. Also, these specialists have highlighted that as the manually ECG reading and assessment process is expensive in terms of time and training requirements, the proposed model can be used as a tool to quickly identify the characteristic points on the diagram, being this highly intuitive for both, experienced specialists and physicians in primary health care.

Finally, it is important to note that these results open a new way for the designing of expert systems design for cardiac pathologies identification, because it allows us to study other points from the signal that have not been considered until now because they were not included in the segments selected by experts.

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Conflicts of Interest

None

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