A Beat-to-Beat P Wave Analysis in Healthy Population

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Abstract

Aim of this study is to explore and quantify possible beat-to-beat variations in P wave characteristics. Two-minute X-lead ECG recordings were analyzed. Data were obtained from Physionet database. Each P wave was fitted by a Gaussian function whose parameter variations were investigated over two minutes window. The normalized root mean squared error (NRMSE) between each P wave and its fitting was computed. To evaluate the variability of the estimated parameters, the coefficient of variation (CV) was computed. The proposed model well fitted the P waves, being the mean NRMSE 0.047 $\pm$ 0.030 mV (range 0.012 - 0.140 mV). A variability was found in all patients for both the parameters A and σ, reflecting P waves amplitude and duration, respectively, being CV_A 0.087 $\pm$ 0.050 mV (range 0.032 - 0.253 mV) and CV_σ 0.093 $\pm$ 0.053 (range 0.028 - 0.27). These preliminary results could be used as a starting point for future beat-to-beat P wave analysis in patients with atrial conduction pathologies.

1. Introduction

Changes in P wave morphology have been documented between patients with and without paroxysmal atrial fibrillation [1] and in healthy subjects of different age [2]. The morphology of P wave can be informative about various pathologies of the atria and the duration of the P wave has drawn much attention in health and pathology. This feature has been studied in different leads and has been associated with atrial fibrillation and other pathologies [3].

Besides elongation of P wave, the presence of multiple deflections is also believed to be an important morphological property associated with an altered substrate, and potentially, a modified and even fragmented propagation pathway in the atria. For this reason, modern signal decomposition methods have been used to enhance P wave patterns from the background noise and derive robust measurements of wave properties, with approaches based on Gaussian decomposition [4], Wavelets decomposition [5].

Traditionally, the analysis of P waves has been based on signal averaging techniques, that efficiently suppress gaussian noise. However, these techniques presume the superposition of a stationary component and unwanted interference, theoretically of gaussian nature. Following this assumption, P-wave triggered averaging [6] has been proposed for optimal delineation of atrial activity, and several studies have been performed, based on the average P waves [7].

Although the signal stationarity assumption, and consequently the averaging approach, has lead to valuable findings, the information embedded in P-wave can be revisited from another perspective that is not based on the same assumptions, i.e. in terms of the possible information embedded in the variability of P waves, in either normal or pathologic conditions. There is only a previous attempt to examine P wave changes on a beat to beat basis [8], where the authors clustered P waves into one/two clusters, to classify individuals into two groups: those who have a constant P wave morphology and those that suffer of beat-to-beat morphology changes. However, beat-to-beat changes have never been deeply investigated or quantified.

Aim of the present work is to assess the variability of P waves in normal subjects of both sexes, spanning over different ages. Moving beyond the P-wave measures depending on fiducial point detectors [9], a model based approach is proposed here, that fits the shape of P wave. Model parameters are then used to evaluate beat-to-beat P wave changes.

2. Methods

2.1. Data and preprocessing

The dataset used was extracted from the PTB Diagnostic ECG Database including 50 recordings from health volunteers of both sexes and various ages (mean age 40 $\pm$ 14 years, range 17-69 years). Two-minute recordings of X-Frank lead (sampled at 1000Hz) were used. For each recording, the fiducial points were extracted. Ecgpuwave tool was used [9],which is based on the an enhancement of the algorithm of Pan and Tompkins [10]. The result is

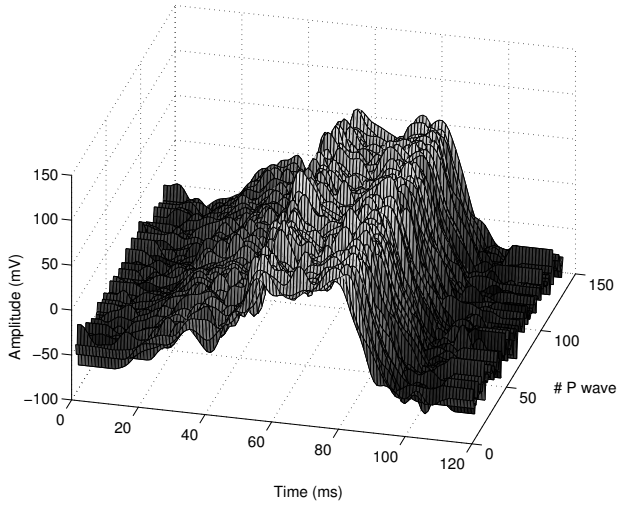

Figure 1. Example of aligned and detrended P waves over two minutes: a certain degree of variability in the waves can be appreciated even by visual inspection.

a list of annotations, marking in each beat the beginning-peak and end of P wave, QRS complex and T wave. The P wave segments were then isolated for further processing. After a basic preprocessing, which included 0.5-160 Hz bandpass filtering (for removing baseline wandering and high frequency noise), 50 Hz notch filtering and detrending, a quality check was performed, to exclude unreliable P wave segments, by looking at P wave morphology. In details, all P waves were aligned against a reference P wave, here defined as the first normal P wave of the ECG; waves poorly cross-correlated with the other beats were rejected. After this procedure, on average 126 $\pm$ 24 (range 75-195) good quality beats were available for each subject.

2.2. Gaussian model

Each valid P wave was fitted by a Gaussian function, defined by three parameters: mean μ, standard deviation σ and amplitude A:

$$\varphi(x) = Ae^{-\frac{(x-\mu)^2}{2\sigma^2}} \quad (1)$$

The physical analogue of these three parameters is: the P wave amplitude for A, the P wave duration for σ and the location of the P wave (center) for μ . While this is a natural mapping, directly deriving from the wave's morphology, it does not imply that the method focuses on the detection of P wave's limits.

The estimation of model parameters is accomplished by an optimization procedure based on a non-linear minimization algorithm, such as the Levenberg-Marquardt algorithm [11]. This algorithm is capable of alternating between a slow descent approach while being far from the minimum and a fast, quadratic convergence while being close to the minimum.

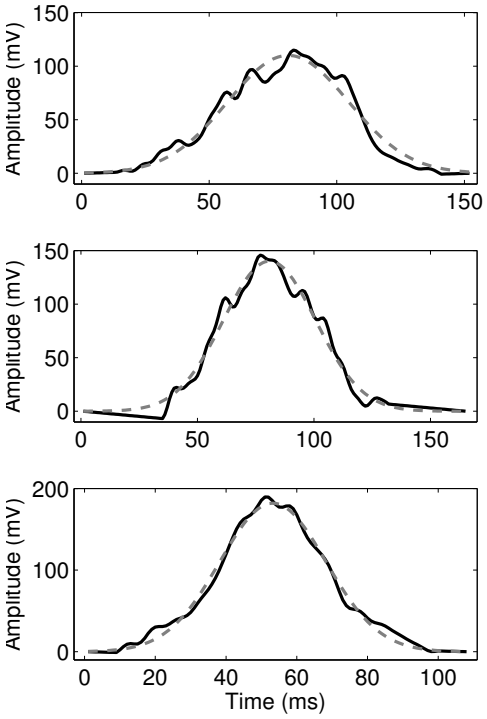

Figure 2. P waves (solid black line) with superimposed the Gaussian models (dotted gray line) fitting the wave for three different subjects.

The variation in model parameters was investigated over two minutes window. To assess the method reliability, the normalized root mean squared error (NRMSE) between each P wave and its fitting was computed. To evaluate the variability of the estimated parameters, the coefficient of variation (CV), defined as the ratio of the standard deviation to the mean, was computed.

3. Results

Despite its simplicity, the model could well represent the P waves, an example from three different subjects is shown in Fig. 2. Accordingly, the normalized root mean squared error (NRMSE) averaged on the whole population is very low, being 0.047 $\pm$ 0.030 mV (range 0.012 $\pm$ 0.140 mV).

Table 1 shows the mean, the standard deviation and the coefficient of variation averaged for the whole population for the amplitude A and the standard deviation σ of the Gaussian model.

Figure 3 shows the trends of Gaussian amplitude and

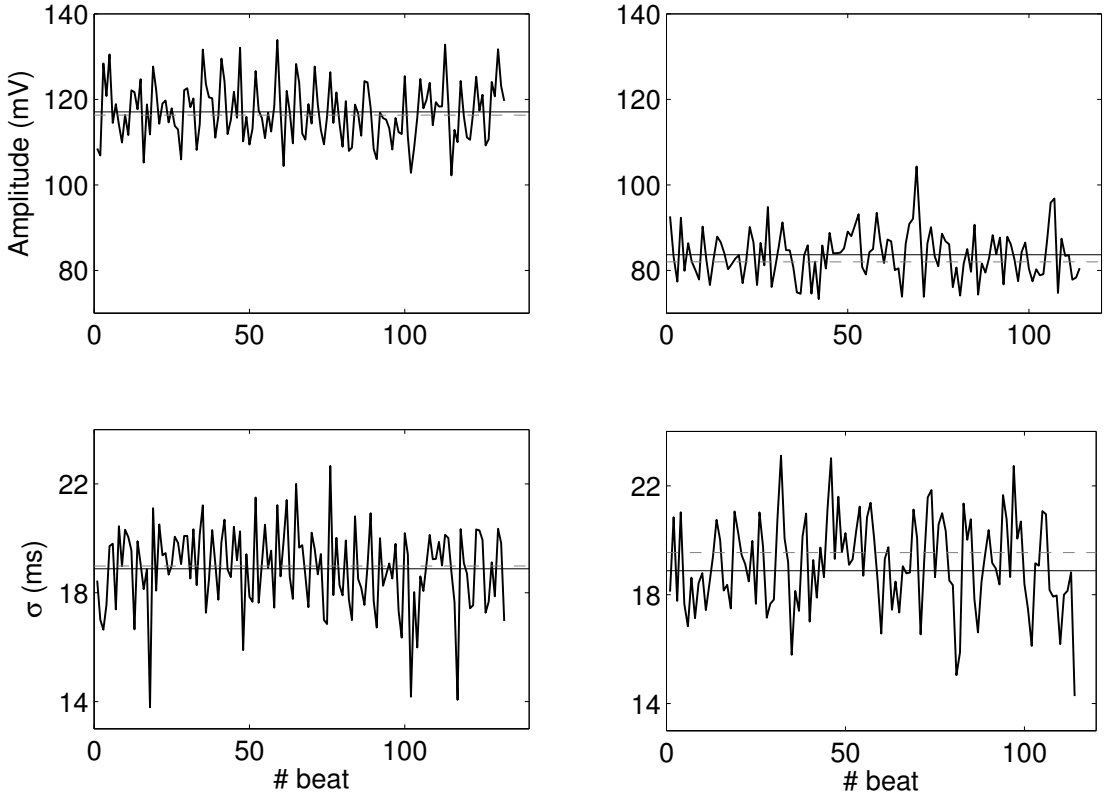

Figure 3. Trends of Gaussian amplitude and standard deviation σ for a 17-year old (left column) and a 69-year old (right column) subject, with superimposed the mean value of the beat-to-beat parameter (solid black line) and the parameter obtained modeling the average P wave (dashed gray line).

Table 1. Model parameters (mean $\pm$ one SD for the whole population.

	A	σ
$mean$	120 ± 32 mV	20 ± 3 ms
SD	10 ± 6 mV	1.87 ± 1.06 ms
CV	0.087 ± 0.050	0.093 ± 0.053

A = amplitude, σ = standard deviation of the Gaussian model

standard deviation for a young and an old subject. A slight degree of variability can be observed in both subjects, being their coefficient of variability $CV_A = 0.057$, $CV_\sigma = 0.079$ and $CV_A = 0.067$, $CV_\sigma = 0.088$, respectively. The variability seems to be not significantly related to the subjects' age, as shown in Figure 4, where the CV of both the amplitude and the standard deviation of the Gaussian model is plotted against subjects' age. In addition, even if not shown, no age-dependency was found in both the amplitude and the standard deviation of the Gaussian model.

Finally, a comparison between the beat-to-beat analysis and the analysis of the average P wave has been performed. The Gaussian model was applied to the average P wave and its parameters were compared to the mean of the parameter values obtained from the beat-to-beat analysis. In Figure 3, it can be observed that the mean value of the beat-to-beat parameters (solid black line) is different from the parameter obtained modeling the average P wave (dashed gray line). This result has been confirmed when analyzing the whole population, as shown in Table 2, thus, as expected, it can be stated that some components are eliminated during the averaging. In all subjects but one, the mean amplitude obtained by the beat-to-beat analysis is always higher than that obtained modeling the average P wave; on the contrary, the standard deviation σ is always smaller.

4. Conclusion

Even if slight, some beat-to-beat variations can be found in P waves morphology in healthy subjects. Thus, it

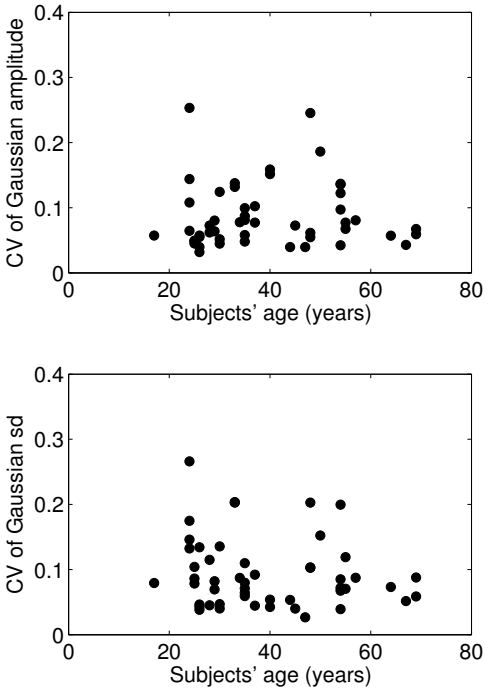

Figure 4. Coefficient of variation (CV) for the amplitude and standard deviation of the Gaussian model for each subject, plotted against subject's age.

Table 2. Comparison of beat-to-beat parameters vs. average P wave parameters.

	Beat-to-beat mean	mean P	p-value
A	120 ± 32 mV	118 ± 32 mV	< 0.0001
σ	20 ± 3 ms	21 ± 3 ms	< 0.0001

A = amplitude, σ = standard deviation of the Gaussian model, paired t-test used for comparison.

seems a reasonable hypothesis that these variations exist and could even be more pronounced in patients for example with atrial arrhythmia. These preliminary results lay the foundation for future beat-to-beat P wave analysis in patients with atrial conduction pathologies. The Gaussian model, despite it simplicity, could be further applied to investigate beat-to-beat variability. Finally, the existence of variability will need to be assessed in other leads too, to evaluate how the beat-to-beat variability in P wave covaries, for example in the three orthogonal leads.

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