Heart Beat Parametric Modeling Based on Monte Carlo Fitting Techniques

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***Abstract*— Synthesis of electrocardiogram (ECG) signals is closely linked to the modeling process since precise knowledge of the parameters of the heartbeat to be modeled is required. The knowledge of these parameters is achieved through methods of adjusting curves between simulated beats and real beats. These traditional optimization methods, such as nonlinear least squares or similar, suffer from the drawback of falling at local minima especially when the initial conditions are not given in an accurate fashion. In the present work, we have designed a novel method robust to deviations in the initial conditions based on Monte Carlo techniques derived from the ideas of the Particle Filtering. Our method allows to adjust the heart beat and to determine the parameters of a model already known in the literature that consists of the sum of five Gaussian curves. The method fits with errors very similar to the traditional method when the initial conditions are good, but better results are obtained in terms of squared error when the initial conditions are sufficiently degraded. Validation was carried out with real physiological and pathological ECG records from international databases.**

***Keywords*— ECG Modeling, Bayesian Filtering, Parameter Estimation.**

***Resumen*— La sintesis de señales de Electrocardiograma (ECG) está estrechamente vinculada al proceso de modelado ya que se requiere un conocimiento preciso de los parámetros de los latidos cardiacos que se pretende modelar. El conocimiento de dichos parámetros se consigue a través de métodos de ajuste de curvas entre latidos simulados y latidos reales. Estos métodos de optimización tradicionales como puede ser el método de ajuste por cuadrados mínimos no lineal o similares, sufren la dificultad de caer en mínimos locales sobretodo cuando no se les da condiciones iniciales precisas. En el presente trabajo diseñamos un método novedoso robusto a desvíos en las condiciones iniciales basado en técnicas de Monte Carlo derivado de las ideas del Filtrado Particular. Nuestro método permite ajustar el latido cardíaco y determinar los parámetros de un modelo ya conocido en la literatura que consiste en la suma de cinco gaussianas. El método ajusta con errores muy similares al método tradicional cuando las condiciones iniciales son muy buenas, pero se consiguen mejores resultados en términos de error cuadrático cuando las condiciones iniciales se degradan lo suficiente. Se llevó a cabo la validación con señales de ECG reales tanto fisiológicas como patológicas extraídas de bases de datos internacionales.**

***Palabras clave*— Modelado de ECG, Filtrado Bayesiano, Estimación de parámetros.**

I. Introduction

Cardiovascular diseases (CVD) are one of the leading causes of death in the world. According to data from the World Health Organization (WHO), just in Argentina, the 35% of all registered deaths were due to this type of disease in 2014 [1]. That is why the early detection and control of CVD has strong impact on the quality of life of thousands of people locally and worldwide. Biomedical research is built on two pillars: the collection of an enormous mass of clinical data from healthy or pathological patients, and the analysis of these data to determine patterns describing both physiological and pathological behaviors. Specific algorithms must be developed to perform the analysis and processing of the data and thus be

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able to obtain both useful and transferable information. This information will then allow the semi-automation of earlier and more accurate diagnoses, supported by specific devices designed for this purpose. The electrocardiogram (ECG) signal records the electric activity of the heart, showing the temporal variation of the electrical potential from electrodes arranged conveniently on the surface of the thorax. The morphology of this record and its interpretation from the detection of its characteristic waves (so-called fiducial points that comprise the P, Q, R, S, T waves) as well as various calculations that arise from the detection of such waves (ST segment, QT interval, PR interval and others) allow the diagnosis of different pathologies: various cardiac arrhythmias, ischemic heart disease or conduction abnormalities, as well as other types of CVD that affect ventricular repolarization (VR) of cardiac tissue and can be detected in advance by means of an appropriate analysis of the ECG signal [2]. In addition, this analysis may be useful in the diagnosis of other extracardiac diseases such as pulmonary thromboembolism or other electrolyte disturbances. Therefore this type of non-invasive and low-cost analysis continues being a fundamental tool for the cardiovascular evaluation of patients who arrive by spontaneous demand to the emergency rooms of any health center.

As mentioned, the study of the electrocardiogram, its wavelengths, its temporal intervals and patterns has been the object of intense research, since it provides substantial information of the heart function. Obtaining high resolution cardiac signals from a noisy electrocardiogram remains a problem of concern for the biomedical engineering community. Despite the rich literature in this field, there are still many clinical applications that lack reliable processing tools to extract the weak ECG components contaminated with background noise, which ultimately offer much information about the subtle characteristics of the ECG signal. Recent research in automated ECG processing focuses on wave delineation, pattern detection and / or data compression [3], [4]. ECG modeling and synthesis applies to classification of beats, compression, reconstruction and/or generation of synthetic ECG signals (for training professionals for example) [5].

Among the works that have dealt with the idea of modeling the wave sequence in an ECG, to extract and recognize patterns, we can mention the articles [6], [7] which proposes a model and classification method for the QRS complex using an orthonormal basis of Hermite functions. Baali [8] propose a parametric model based on orthogonal transformations, that involves the mapping of the ECG in the domain of singular values, whereas Philips and De Jonghe [9] apply a polynomial approximation for the compression of ECG data.

Suppappola et al. [10] focus on the modeling of ECG waves with Gaussian pulses. Thus, an ECG cycle results in a sum of such Gaussian pulses. Each Gaussian is characterized by its location, its amplitude and its width. The mentioned [10] work presents an iterative algorithm to approximate a given ECG by means of this model, estimating the necessary parameters. One of the parameters to be determined is the number of pulses that are needed to achieve a good representation for a given real ECG. In Clifford et al. [11] also arises the idea of modeling as the sum of Gaussian curves. In this case, they use 5 Gaussian functions, one for each characteristic wave. The work [5] proposes a dynamical model whose solution trajectories reproduce realistic synthetic ECG waves. The model generates a trajectory in the space of states (x, y, z). The approximate quasi-periodicity is reflected by the movement of the path around an attractive boundary cycle, a unit circumference in the (x, y) plane. Each beat is represented with a revolution around this limit cycle. Attending the asymmetry of the T wave, they propose as an alternative to use two Gaussian waves to represent it; and they may still consider the asymmetry of the inflection point Q, doubling the respective Gaussian. Thus, the model remains dependent on 3M morphological parameters, where M is the number of Gaussian functions involved. Clifford et al. [12] have proposed a method to find the parameters that best reproduce a beat of a given real ECG, thus achieving compression with loss. The parameter adjustment is carried out using non-linear optimization (gradient descendent method) to minimize the Euclidean distance between the data and the simulated model (least squared error). This would allow, according to the mentioned authors, to predict the performance of the model in a segment of an ECG and facilitate the rejection of beats for a specific study. The deviation of these parameters with respect to the physiological parameters would thus indicate a change in the morphology of the ECG constitutive waves, showing alterations that point out or suggest certain pathologies. The model then allows the 3M-dimensional representation of any ECG, physiological or pathological, which can then be used not only in filtering schemes that require a model but in compression, clustering and / or pattern classification applications to ECG signals in the mentioned space [11], [12].

The present work is part of a research about modeling normal and pathological ECG heartbeats in a parametric way fitting the heartbeat with a sum of Gaussian curves; in order to compress and classify ECG signals. We want to synthesize signals with certain pathologies and for that we first need to know how the parameters of the model for different morphologies vary. For this we need to read the parameters of a real signal segment with the least possible a priori knowledge. For all this we propose a new method for finding the parameters that better represent a given beat. This method is based on Monte Carlo simulation ideas. We explore the parameter space in a random but smart-oriented way, searching for the set that best adjusts the beat. The problem can be posed as an inverse problem stated as: Which parameters are most reliable for generating a given heartbeat. Our method is inspired on particle filtering ideas an adapts the method testing a high number of direct problems evaluating the reliability of each one with an appropriate fitness function.

II. Materials and Methods

A. Parameter estimation

The set of parameters that best represents a signal $s(k)$ may be obtained as those that minimize the squared error between the mentioned signal $s(k)$ and the parametric model $z(k)$.

$$\underset{a_i,b_i,\theta_i}{argmin} \|z(k) - s(k)\| \quad (1)$$

We use a heartbeat model proposed by Clifford and Mc Sharry [5] widely utilized in the literature composed by the sum of five Gaussians pulses

$$z(k) = \sum_{i=P,Q,R,S,T} a_i e^{\frac{-(k-\theta_i)^2}{2b_i^2}} \quad (2)$$

where θ_i is the position of the corresponding wave peak, a_i corresponds to the wave amplitudes and the b_i corresponds to wave widths.

The problem stated in Eq. 1 is nonlinear, and it is highly likely to have many suboptimal solutions. Usually, a local optimization algorithm is applied to find a solution. In local optimization, the search begins with a user-provided starting point, and iterates trying to improve a single current candidate point using local information, i.e, through linear or quadratic approximation of the nonlinear function. Therefore, the gradient and/or the hessian of the function should be numerically approximated by the algorithm or provided by the user. In this optimization scheme, the search for the optimum may get trapped in a suboptimal solution also known as local minimuns. In summary, to obtain a good solution, a good starting point should be supplied. In parameter estimation of EGC signals, a local optimization algorithm, (through the Matlab function lsqnonlin.m) is frequently used by the researchers in the area, obtaining heuristically the initial set of parameters.

For an automated online ECG parameter estimation implementation, it is no reasonable to know the initial set of parameters in an very accurate fashion to initiate the algorithm, even more in a pathological case. We want to be able to read heartbeat parameters with the least knowledge a priori posible. This is why we propose an optimization method that does not rely on the quality of the user-provided or precalculated parameters. Our proposed algorithm is a Monte Carlo search. This type of approach avoids the problem of getting stuck in local minimun, since it permits random exit of suboptimal neighborhood. We found that it is more independent of the starting point. It should be mentioned that the cost paid for this advantage may be higher memory usage and computational cost. But the method is highly parallelizable so with today's computers it is anyway an interesting technique to take into account.

The idea is to simulate a set of N particles in the search space. Initially, the search space is defined around an initial vector of parameters. Each particle is weighted with a fitness function, and the best ones (those with higher fitness or score) define the new search space. In each iteration, the search space moves towards the best particles and contracts as the optimum is reached. Convergence is attained when the objective function has almost no changes. In the following subsection we explain in detail the proposed algorithm.

B. Algorithm

Given the vector of initial parameters $X1$ in the parameter space, the algorithm generates N points called particles from certain random distribution. We use uniform distribution, so that the search space constitutes an hyperprism centered around the initial point $X1$ with a width of 33% of the mean for each side in each of the 15th dimensions. We have also proven with the Gaussian multivariate distribution, but we found that uniform distribution give better results. This is due to the fact that uniform distribution facilitates the particles to escape from suboptimal regions.

Each particle (set of possible parameters) generates a heart beat in the image space $z_{part_i}(k)$ that is contrasted to the real beat $s(k)$ computing the squared error between them in the usual form:

$$SqError_i = \sum_{k=1}^{L} (z_{part_i}(k) - s(k))^2, \quad (3)$$

where L is the lenght of the the real beat $s(k)$.

Then each particle is weighted with the fitness function defined by:

$$P_i = e^{-\frac{1}{2} SqError_i}, \quad (4)$$

which assigns a weight to each particle according to the error that occurs between the beat generated by the model (with the parameters that that particle indicates) and the actual beat $s(k)$. The weights are normalized to sum 1. Then the particle with greater weight is selected as the centroid of the next search space and in the following iteration the hyperprism is centered around this new particle and its sizes in all the dimensions are reduced according to the following law:

$$\sigma = \sigma * (1 - \log \frac{SqError_{selected-part}}{30}), \quad (5)$$

This law allows fast convergence when the error is large and slow contraction when the error is small. This is done until the error between the beat generated by the best particle and the actual beat changes in the last 10 iterations in an amount of less than 0.001 (it took about 70 iterations in our experimentation). Different tests were carried out with different numbers of particles, and in a compromise between precision and computation time we fixed N in 5000 particles.

Initialization

N : number of particles (default: 5000)

$X1$: vector of initial conditions

H = number of parameters to estimate (default: 15)

D : distribution (default: uniform)

I : improvement in last 10 iterations

$\mu = X1$ (centroid)

search space sizing parameter: $\sigma = \frac{|\mu|}{3}$

$W =$ weight function (default: Eq 4)

$E =$ error function (default: Eq 3)

Convergence=False

while not Convergence **do**

Define search space: $S = \Pi_{k=1}^{H} \mu_k \pm \sigma_k$

Sample $N - 1$ particles $part_i$, in the search space S with distribution D.

Add μ to the set of particles: $part_1 = \mu$

Weight particles: $P_i = W(part_i)$

Normalize weights: $P_i = \frac{P_i}{\sum_{i=1}^{N} P_i}$

Select the best solution: $index = \underset{i}{argMax}(P_i)$

Select the new centroid: $\mu = part_{index}$

Compute the Squared Error $SqError = E(part_{index})$

Search space update: $\sigma = \sigma * (1 - \log \frac{SqError}{30})$

if I < 0.001 **then**

convergence=True

end if

end while

C. Data Base

Real signals were taken from internationally validated databases such as the Physikalisch-Technische Bundesanstalt (PTB) ECG Database available in Physio-Bank [13]. The National Metrology Institute of Germany has provided this compilation of digitized ECGs for research, algorithmic benchmarking or teaching purposes to the users of PhysioNet. The ECGs were collected from healthy volunteers and patients with different heart diseases by Professor Michael Oeff, M.D., at the Department of Cardiology of University Clinic Benjamin Franklin in Berlin, Germany. It contains records of 52 healthy subjects and 148 patients with myocardial infarction and also provides some patients with other pathologies like Cardiomyopathy, Bundle branch block, Dysrhythmia, Myocardial hypertrophy and Valvular heart disease. The ECGs are digitized at 1Khz, with 16 bits resolution over a range of 16,384mV. Each record includes the 12 simultaneous leads and the orthogonal leads of Franz. The patient's medical history is available.

D. Validation

In order to validate our Monte Carlo parameter estimator, a series of simulations were performed, and compared with a local optimization algorithm. The objective is to show that our method is able to find the parameters that better fit an actual given signal, even if the search is started in a point far enough from the optimal zone. Also, we want to show that the good performance is reached both in normal ECG and pathological ECG signals.

Single lead ECG Data (Lead 2) was extracted from PTB Database from Physionet described in the previous section. We did our fitting tests for 6 different morphologies: 3 different Miocardical Infarction, lower side infarction (PTB-Patient N1), anterolateral Infarction (PTB-Patient N27), lowerposterolateral Infarction (PTB-Patient N65), an Hipertrophical with Atrial Fibrilation (Patient201), a Bundle Branch block (PTB-Patient171) and a Healthy Subject (PTB-Patient131).

This arrays were all preprocessed with 5th-order Butterworth highpass filter (Fc=0,5 Hz) for baseline wander rejection. From these signal, a representative beat is generated for each pathology. This is accomplished by a simple R-peak detection and time aligned averaging. The R-peaks were detected in the array with Pan-Tomkins algorithm for QRS detection [14]. Then the successive beats were separated in vectors and aligned w.r.t. the R-peaks. Point to point average was performed between different beats resulting in a single beat that modeled the general morphology of the ECG signal. The 15 beat parameters were manually measured in the representative beat to establish the $X0 = [a_p, ..., a_t, \theta_p, ..., \theta_t, b_p, ..., b_t]$ vector containing the most accurate parameters for that representative heartbeat.

The initial conditions vector for both optimization algorithms $X1$, is obtained by a perturbation performed to $X0$ with different levels of distortion δ.

For each δ level,

$X1_i = X0_i * W_i$

where W_i is a random number extracted from an uniform distribution with interval $[1 - \delta/2, 1 + \delta/2]$,

A measure of the distortion strength is defined by the euclidean distance between $X1$ and $X0$, $||X1 - X0||$. We have checked that this distance moves linearly with δ.

Iteratively we have varied δ from 0.1 to 1 in steps of 0.1. Then, for each step, we have tested 50 vectors $X1$ and compared the 2 methods: the traditional method used in the literature for nonlinear optimization (function "lsqnonlin" in matlab) (Method 1) versus our Monte Carlo method described previously (Method 2). The comparison is based on the SE averaged over the 50 attempts for each level of distortion δ.

III. Results and Discussion

In table I it can be observed that Method 2 (Monte Carlo method proposed) outperforms Method 1 showing a lower squared error between the model and the actual beat. The most important result is that it shows a considerable estability when the level of distorsion increases. Method 1 tends to increase the error when the level of distortion increases. This means that if we start Method 1 from a point far away from the set of optimun parameters it is harder for an optimization method of this kind to fit the curve. By last, this behaviour is almost independent of the ECG signal morphology we are trying to fit. Fig. 1 and Fig. 2 show a heartbeat of Miocardical Infarction (PTB-patient 1) fitted by both methods when the initial conditions are pseudo degraded ($\delta = 0.4$). We can observe that Method 1 can not reach a good performance when Method 2 adjust it with a much lower error. Fig. 3 shows optimum fitting with Method 2 in a Bundle Brunch Block signal, it can be observed very good performance in the fitting attempt. Finally Fig. 4 shows RMSE for both Methods while the level of distortion δ is varied from 0.1 to 1. We can observe that our approach gives the same error that gives the traditional approach when the initial conditions are good enough ($\delta = 0.1$), however when δ increases (i.e. initial conditions move away from ideal) our method gives better results in terms of RMSE. The data plotted in Fig. 4 corresponds to rows 9 and 10 in table I.

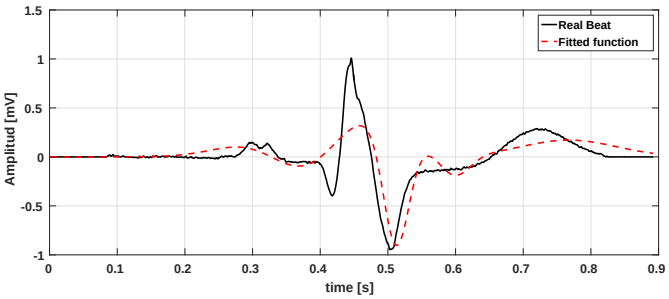

Fig. 1. Miocardical Infarction HeartBeat (PTB pat 1) fitted with Nonlinear Optimization method for suboptimal initial conditions (delta = 0.4)

IV. Conclusions

We have presented an alternative method for adjusting the parameters of a heartbeat that has the advantage of being more robust to initial conditions when they are far from the optimal. Non linear optimization methods require very accurate knowledge of the initial conditions to provide a good fit. A more robust method to degraded initial conditions is fundamental to know the parameters of any physiological or pathological beat that one wishes to model because in the real scenario we start from initial conditions totally uncertain. Knowledge of the parameters of a heart beat for phisiological or pathological modeling purposes is necessary for ECG synthesis, data compression and/or beat classification.

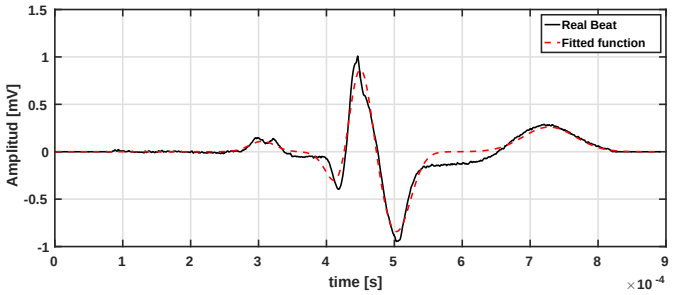

Fig. 2. Miocardical Infarction HeartBeat (PTB pat 1) fitted with Monte Carlo proposed method for suboptimal initial conditions (delta = 0.4)

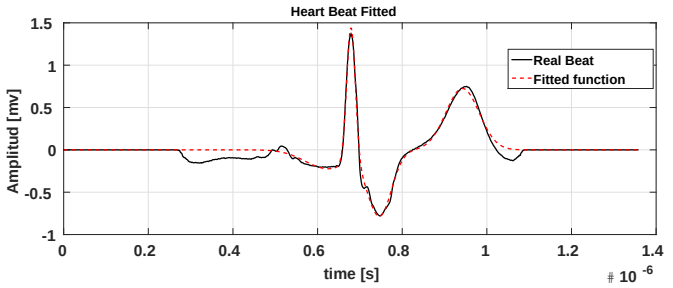

Fig. 3. Bundle Brunch Heartbeat (PTB pat 171) fitted with Monte Carlo proposed method

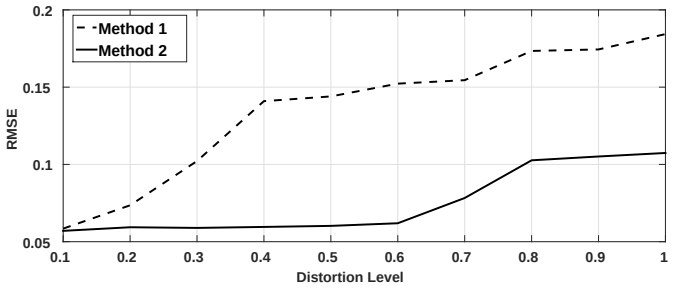

Fig. 4. RMSE for both methods in Bundle Brunch Heartbeat (PTB pat 171) for different levels of distortion

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References

[1] S. Mendis, T. Armstrong, D. Bettcher, F. Branca, J. Lauer, C. Mace, V. Poznyak, L. Riley, V. Silva, and G. Stevens, "Global status report on noncommunicable diseases 2014: World health organization," 2015.

TABLE I
SQUARED ERROR FOR BOTH METHODS FOR DIFFERENT ECG MORPHOLOGIES

Pathology	**Distortion level (delta)**									
	0.1	**0.2**	**0.3**	**0.4**	**0.5**	**0.6**	**0.7**	**0.8**	**0.9**	**1**
MI-IL (M1)	4.62	5.84	7.85	11.35	14.80	18.61	13.24	17.14	22.63	16.16
MI-IL (M2)	4.10	5.14	5.36	4.85	6.63	5.60	6.54	7.00	9.08	9.60
MI-AL (M1)	2.35	4.02	4.55	4.13	7.23	7.17	6.62	5.69	6.97	6.89
MI-AL (M2)	1.21	1.35	1.15	1.43	1.45	1.24	3.59	2.40	2.38	2.10
MI-IPL (M1)	1.99	2.93	5.81	9.84	11.74	16.93	13.07	14.26	18.34	18.11
MI-IPL (M2)	2.44	2.15	2.41	2.45	2.73	3.37	4.55	5.77	8.08	10.11
AF (M1)	3.08	4.12	9.56	10.22	10.53	12.63	10.57	12.69	11.14	10.97
AF (M2)	1.30	1.28	1.22	1.28	1.26	1.26	1.45	1.75	1.97	4.09
BB (M1)	4.63	7.34	14.17	26.95	28.13	31.46	32.39	40.81	41.27	46.11
BB (M2)	4.41	4.77	4.71	4.81	4.92	5.20	8.31	14.30	14.99	15.65
HS (M1)	1.96	6.51	20.76	22.94	22.79	24.88	23.88	23.98	18.64	30.91
HS (M2)	2.05	1.95	2.31	2.51	2.90	4.08	6.27	12.50	3.45	6.90

[2] R. J. Martis, U. R. Acharya, and H. Adeli, "Current methods in electrocardiogram characterization," *Computers in biology and medicine*, vol. 48, pp. 133–149, 2014.

[3] C. Li, C. Zheng, and C. Tai, "Detection of ecg characteristic points using wavelet transforms," *IEEE Transactions on biomedical Engineering*, vol. 42, no. 1, pp. 21–28, 1995.

[4] Y. Wu and L. Zhang, "Ecg classification using ica features and support vector machines," in *Neural Information Processing*. Springer, 2011, pp. 146–154.

[5] P. E. McSharry, G. D. Clifford, L. Tarassenko, and L. A. Smith, "A dynamical model for generating synthetic electrocardiogram signals," *IEEE Transactions on Biomedical Engineering*, vol. 50, no. 3, pp. 289–294, 2003.

[6] L. Sornmo, P. O. Borjesson, M.-E. Nygards, and O. Pahlm, "A method for evaluation of qrs shape features using a mathematical model for the ecg," *IEEE Transactions on Biomedical Engineering*, no. 10, pp. 713–717, 1981.

[7] M. Lagerholm, C. Peterson, G. Braccini, L. Edenbrandt, and L. Sornmo, "Clustering ecg complexes using hermite functions and self-organizing maps," *IEEE Transactions on Biomedical Engineering*, vol. 47, no. 7, pp. 838–848, 2000.

[8] H. Baali, R. Akmeliawati, M.-J. E. Salami, A. Khorshidtalab, and E. Lim, "Ecg parametric modeling based on signal dependent orthogonal transform," *IEEE Signal Processing Letters*, vol. 21, no. 10, pp. 1293–1297, 2014.

[9] W. Philips and G. De Jonghe, "Data compression of ecg's by high-degree polynomial approximation," *IEEE Transactions on Biomedical Engineering*, vol. 39, no. 4, pp. 330–337, 1992.

[10] S. Suppappola, Y. Sun, and S. A. Chiaramida, "Gaussian pulse decomposition: an intuitive model of electrocardiogram waveforms," *Annals of biomedical engineering*, vol. 25, no. 2, pp. 252–260, 1997.

[11] G. Clifford, A. Shoeb, P. McSharry, and B. Janz, "Model-based filtering, compression and classification of the ecg," *International Journal of Bioelectromagnetism*, vol. 7, no. 1, pp. 158–161, 2005.

[12] G. Clifford and P. McSharry, "Method to filter ecgs and evaluate clinical parameter distortion using realistic ecg model parameter fitting," in *Computers in Cardiology, 2005*. IEEE, 2005, pp. 715–718.

[13] Physionet. [Online]. Available: https://www.physionet.org/physiobank/database

[14] J. Pan and W. J. Tompkins, "A real-time qrs detection algorithm," *IEEE transactions on biomedical engineering*, no. 3, pp. 230–236, 1985.

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