Identification of *R*-peak occurrences in compressed ECG signals

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***Abstract*—Heart Rate (HR) is one of the mostly used electrocardiogram (ECG) feature in many automatic detectors of anomalies. This paper deals with a preliminary study on a novel approach which, through the combination of Machine Learning (ML) and Compressed Sensing (CS), aims at retrieving vital information from a digital compressed single-lead electrocardiogram (ECG) signal. As a potential key information to estimate the heart rate, this study focuses on the identification of R-peak occurrences. The study has been conducted on two different types of signal both obtained from the compressed samples provided by a CS algorithm, already available in literature. The results demonstrate that the use of CS in combination with a ML technique can find high competitiveness when compared to a state of the art method working on the uncompressed ECG signal.**

***Index Terms*—Internet-of-Medical-Things, Machine Learning, ECG Signal, Heart Rate, Compressed Sensing, Feature extraction, Wearable devices.**

I. Introduction

Thanks to the Internet-of-Medical Things (IoMT), there has been a huge spread of wearable devices for healthcare applications. Machine Learning (ML) and Compressed Sensing (CS) are some of the tools involved in this kind of systems. Indeed, at the end of the first decade of 2000, Compressed Sensing has been investigated for healthcare applications [1]–[3]. The theory behind the Compressed Sensing basically states that when dealing with specific signals, satisfying the condition to be sparse in some domain, they can be reconstructed from a smaller number of samples, than that the actually needed by Nyquist rate sampling. The reconstruction phase from the compressed samples usually involves complex algorithms with a relatively high computational cost that should be able to guarantee the signal integrity by keeping clinical relevant features [5], [6]. This cost is balanced by the very small payload of the wirellesly transmitted data provided by the wearable device that performs data compression. In general, the CS methods require low computational effort for the compression, which is performed on the wearable device, and high computational effort for the reconstruction, which is usually performed on a more powerful device (e.g laptop), [13], [14]. However, not all the ECG features are relevant for some clinical evaluation, thus in such applications it is not needed to reconstruct the entire ECG signal [15], [16]. For example, in case of the most well-known cardiac arrhythmia, the Atrial Fibrillation, there is a huge literature dedicated to the process of automatic detection. For this purpose, there are works which take in consideration both the morphological and rhythmic aspects of the ECG, such as the one proposed in [15], [16] but there are also many works which implement a very accurate detector of Atrial Fibrillation [8], [17], where the base feature is only the Heart Rate. The work presented in [5] represents one of the first and best approaches of Information Retrieval in compressed signals. The authors considered a framework where the ECG signals are represented under the form of CS linear measurements. The QRS locations have been estimated from the compressed signal by computing the correlation of the compressed ECG and a known QRS template. The results show that this solution is competitive with methods applied to the reconstructed signal.

The detector proposed in this paper aims at identifying the number of R-peaks, by means of Machine Learning, in a signal obtained from a compressed version of a windowed portion of a raw single-lead ECG. The study has been conducted on two types of signal, both outputs of the CS method described in [7]: (i) the first one obtained from a 1-bit quantization process, and (ii) the second one obtained from the multiplication of a sensing matrix with the original signal.

The proposed detector presents the advantage of not requiring the reconstruction of the signal. In addition, this approach aims at identifying the R-peaks occurrences with a high Compression Ratio, by keeping comparable accuracy in the classification process, with respect to the state of the art. Furthermore, in case the reconstruction of the entire ECG would be needed, the domain of the CS method in [7] allows to obtain a better reconstructed signal. Finally, the detector involves the use of Machine Learning predictive models. This represents another advantage because such models may have a very small computational cost. In this paper, the key detection is focused on the identification of R-peaks. The R-peak occurrences can represent a crucial information of an ECG, which can lead to a highly precise estimation of the heart-rate.

The rest of the paper is structured as follows. Section II

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describes the dynamic sensing scheme proposed in [7], which has been adopted for providing the compressed data to the proposed R-peak occurrences detector. Section III presents the novel approach for R-peak occurrences identification. Section IV reports the design and the results of the empirical study conducted to evaluate the different versions of the proposed approach. Finally, Section V concludes the paper and provides suggestions for possible future research directions.

II. Brief description of the dynamic sensing scheme

The R-peak occurrences detector proposed in this paper has been tested on two types of compressed data provided by the CS dynamic sensing scheme proposed in [7]. This CS method is based on a sensing matrix, which depends on the power of each frame of the ECG signal. In particular, it provides a vector $\mathbf{y}$ of M samples that is a compressed version of the vector $\mathbf{x}$ of N ECG samples. In the following, a brief description of the CS-based method [7] is reported. Let us consider the vector $\mathbf{x}$, a frame of N samples of the ECG signal. The value x_{avg} is obtained as the average of $\mathbf{x}$. Then, the vector $\mathbf{x}_a$ is evaluated as follows:

$$\mathbf{x}_a \;=\; |\,\mathbf{x} - x_{avg}\,| \tag{1}$$

According to a threshold x_{th}, which is chosen experimentally, the Power Information Vector (PIV) $\mathbf{p}$ is constructed. This vector contains the values of one at the indices where the vector $\mathbf{x}_a$ exhibits values higher than x_{th}, and zeros, otherwise. The sensing matrix $\mathbf{\Phi}$ is defined as a circulant matrix, where the first row is the vector $\mathbf{p}$:

$$\mathbf{\Phi} = \begin{bmatrix} p(1) & p(2) & \dots & p(N) \\ p(N-CR+1) & p(N-CR+2) & \dots & p(N-CR) \\ \vdots & \vdots & \ddots & \vdots \\ p(CR+1) & p(CR+2) & \dots & p(CR) \end{bmatrix} \tag{2}$$

where, $CR = \frac{N}{M}$ is the compression ratio. The vector $\mathbf{y}$, containing the compressed data, is given by the multiplication between the sensing matrix $\mathbf{\Phi}$ and $\mathbf{x}$. All those processing steps are intended to be performed by a wearable device, battery powered and wirelessly connected to Internet. Thus, it sends the vectors $\mathbf{p}$ and $\mathbf{y}$ to another device, having much more processing capabilities (e.g. a laptop), for performing the signal reconstruction of $\mathbf{x}$. In particular, $\mathbf{p}$ contains information related to the power of the acquired N samples and has a size of $N/8$ bytes, and $\mathbf{y}$ contains the M compressed samples and has a size of $b \cdot M/8$ bytes, where b is the number of bits used for representing an ECG sample. From those two vectors, the reconstruction of the signal $\mathbf{x}$ is performed as follows. At the beginning, from the vector $\mathbf{p}$, the sensing matrix $\mathbf{\Phi}$ is constructed (2). The dictionary matrix $\mathbf{\Psi}$ is defined according to the Mexican hat wavelet kernel, which has been considered to define the domain where the signal $\mathbf{x}$ is sparse;

$$\mathbf{\Psi} = \left[\mathbf{\Psi_{base}}, \boldsymbol{u}\right] \tag{3}$$

where, $\boldsymbol{u}$ is a vector of N ones, and $\mathbf{\Psi_{base}}$ is given by:

$$\mathbf{\Psi_{base}} = \Bigg[\boldsymbol{\psi}(2,0), \boldsymbol{\psi}(2,2), \boldsymbol{\psi}(2,4), \dots, \boldsymbol{\psi}\left(2, 2\left\lfloor\frac{N-1}{2}\right\rfloor\right), \boldsymbol{\psi}(4,0), \boldsymbol{\psi}(4,4), \boldsymbol{\psi}(4,8), \dots, \boldsymbol{\psi}\left(4, 4\left\lfloor\frac{N-1}{4}\right\rfloor\right), \dots, \boldsymbol{\psi}(N,0)\Bigg] \tag{4}$$

with:

$$\boldsymbol{\psi}(a,b) = \frac{2}{\sqrt{3a}\cdot\pi^{1/4}} \cdot \left[1 - \left(\frac{\mathbf{n}-b}{a}\right)^2\right] \cdot e^{-\frac{1}{2}\left(\frac{\mathbf{n}-b}{a}\right)^2} \tag{5}$$

with $\mathbf{n} = [0, \dots, N-1]^T$. By knowing the matrices $\mathbf{\Phi}$ and $\mathbf{\Psi}$, the Orthogonal Matching Pursuit (OMP) algorithm is performed to estimate the $\boldsymbol{\alpha}$ coefficients vector, which represent the sparse coefficient of the signal in the Mexican hat domain. Finally, once the $\boldsymbol{\alpha}$ is available, the reconstructed signal $\hat{\mathbf{x}}$ is obtained as follows:

$$\hat{\mathbf{x}} = \mathbf{\Psi} \cdot \boldsymbol{\alpha} \tag{6}$$

In order to detect the R-peaks occurrences, it would be needed to perform the reconstruction and then to apply any kind of detector. The reconstruction is performed by OMP, which exhibits a computational complexity of $O((N+M)S)$, where, S is the number of iterations of the OMP algorithm, which is in any case lower than N. The idea underlying this paper is not performing the OMP reconstruction, but executing the R-peak detector algorithm directly on the compressed vector $\mathbf{y}$ or the PIV, $\mathbf{p}$.

III. The proposed approach

For identifying R-peak occurrences, the proposed ML-based method has been implemented by considering separately as input the two signals provided by the CS method previously described: in the ***PIV*** version of the proposed tool, the input of the classifier is the signal resulting from the process of 1-bit quantization, the PIV, $\mathbf{p}$; while, in the ***CS*** version, the input is the signal resulting from the CS process, $\mathbf{y}$.

The *PIV* and the *CS* detectors basically differ in the technique of Digital Signal Processing expected in the workflow. This is depicted in Fig. 1. The final stage of classification is handled by a Machine Learning classifier which provides the number of R-peaks in the windowed segment of the signal.

A. The Machine Learning Classifier

The Machine Learning classifier chosen in this preliminary phase of the study is the *Random Forest*, first proposed by Breiman [10]. A random forest basically represents a combination of tree predictors. In this context, a tree is defined as a function of a randomly initialized vector. This vector follows these properties: (i) it is sampled independently and

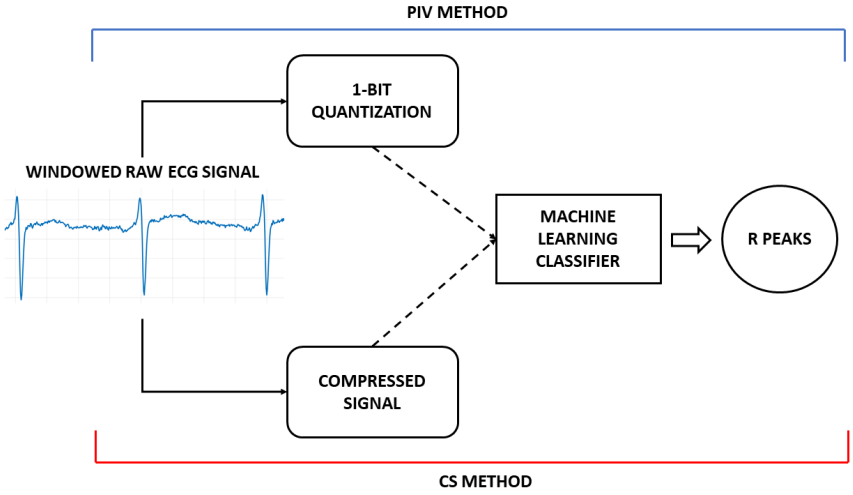

Fig. 1. The different workflows for the two proposed versions of the R-peak occurrences detector.

(ii) with the same distribution as all the other trees in the forest. In other words, a random forest integrates trees and each of them provides a class prediction, as outcome.

The class with the highest number of votes represents the prediction of the entire model. Breiman in [10] defines the algorithm as follows:
"a random forest is a classifier consisting of a collection of tree-structured classifiers $\boldsymbol{h}(\boldsymbol{x}, \boldsymbol{\Theta_j}), \boldsymbol{j} = \mathbf{1}, ...$ *where the* $\boldsymbol{\Theta_j}$ *are independent identically distributed random vectors and each tree casts a unit vote for the most popular class at input* $\mathbf{x}$*"*.
Thus a Random Forest represents a tree-based ensemble with each tree depending on a collection of random variables. More formally, suppose given a k-dimensional random vector:

$$\mathbf{A} = (\mathbf{A_1}, ..., \mathbf{A_k})^{\mathbf{T}} \tag{7}$$

representing the input, and a random variable $\mathbf{Y}$, representing the output. In this case, assuming an unknown joint distribution $\mathbf{T_{AB}}(\mathbf{A}, \mathbf{B})$, the goal – as expected by the algorithm – is to find a prediction function $\mathbf{f}(\mathbf{A})$ for predicting $\mathbf{B}$. The function $\mathbf{f}(\mathbf{A})$ is determined by a loss function $\mathbf{L}(\mathbf{B}, \mathbf{f}(\mathbf{A}))$ and defined to minimize the expected value of the loss:

$$\mathbf{E_{AB}}(\mathbf{L}(\mathbf{B}, \mathbf{f}(\mathbf{A}))) \tag{8}$$

where the subscripts denote expectation with respect to the joint distribution of A and B. In the classification scenario, if the set of possible values of $\mathbf{B}$ is denoted by $\mathbf{B}'$, minimizing $\mathbf{E_{AB}}(\mathbf{L}(\mathbf{B}, \mathbf{f}(\mathbf{A})))$ for zero-one loss gives:

$$\mathbf{f}(\mathbf{a}) = \underset{\mathbf{b} \in \mathbf{B}'}{\operatorname{argmax}} [\mathbf{T}(\mathbf{B} = \mathbf{b} | \mathbf{A} = \mathbf{a})] \tag{9}$$

otherwise known as the Bayes rule [18].

Thus intuitively, the Random Forest algorithm expects to divide the source data in a random number of subsamples. For each of these – based on a random set of features – a decision tree is built. The final prediction is taken depending on the individual votes, which fall into leaves. The results, from each individual tree, are gathered and avareged. An example of such a procedure, is depicted in Fig. 2. In the classical Breiman implementation, the training dataset covers around the 63 % of the total data while the remaining (approximately the 37 %) is used to validate the ensemble of the decision trees, in other words the model.

IV. Experimental Assessment

In this Section, details about the experiments conducted to compare and validate the two versions of the proposed tool, are given. The dataset used for the assessment is the Physionet [9] MIT-BIH Normal Sinus Rhythm Database[1]. This database includes 18 long-term ECG recordings of subjects referred to the Arrhythmia Laboratory at Boston's Beth Israel Hospital. The ECG recordings belonging to this database do not present significant arrhythmia episodes; they include 5 men (aged 26 to 45) and 13 women (aged 20 to 50).

To compare the results of the presented approach (working on the compressed data), the Pan-Tompkins method [11] (working on the original signal) has been used as state of the art. Indeed, it is largely considered as the QRS detector of reference in the literature. The setup phase for the training and testing of the model has consisted of the following choices:

- *Feature Alignment*: an observation window with a fixed length of 2 s, has been chosen. Thus, considering a sampling frequency of 128 Hz, a portion of 256 samples is obtained from a raw ECG signal.
- *Class labels*: for a supervised experiment, a 3-class classification model has been considered. More specifically, each class contains the information related to the R-peak occurrences in each of the 2 s ECG segments. The 3 classes chosen in this part of the study are: (1) for 1 single R peak, (2) for 2 R-peaks and (3) for 3 R-peaks.

[1] https://physionet.org/content/nsrdb/1.0.0/

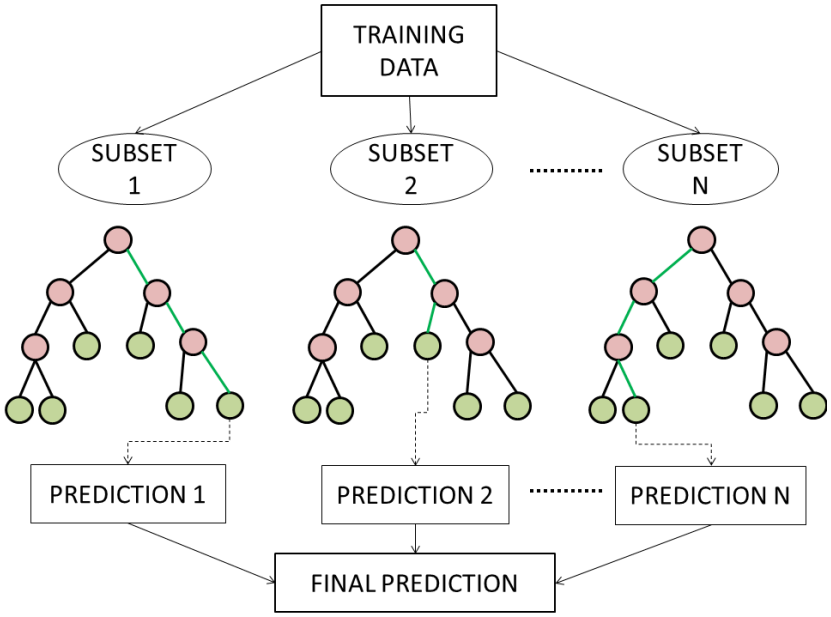

Fig. 2. Example of a Random Forest workflow.

- *Validation of the model*: to evaluate the accuracy of the presented approach, a classical Leave-1-Person Out (L1PO) cross-validation has been used. The data has been decomposed in n folds, one for each subject. Then, each of such folds has been used as test set and the union of the remaining folds as training set. This type of validation process has the effect that the data related to a single patient were embedded once in the test dataset and *n-1* times in the training dataset. This technique allows to build a classifier which is not trained and tested on the data belonging to the same patient. It has been chosen to evaluate the model in the most challenging scenario: a patient-independent detection tool.
- *Number of instances*: due to the long-lasting records in the NSR database and the costly validation, the proposed choice was to work with a sample size having $95\,\%$ of confidence level and $5\,\%$ of confidence interval, with respect to the population. In this case, the population is a long-term ECG record. Considering that each record lasts 24 hours, there is a population of around $43\,200$ $2\,\mathrm{s}$ segments. Thus, for the specific purpose of this study, around 380 instances have been randomly selected for each of the records belonging to the dataset. The selection of the instances respected the representativeness of the class label for each population.

To evaluate the classifier, the metrics 11-14 have been considered for class-specific analysis (where each of the possible classifications is evaluated, e.g. class for occurrence equal to 1, 2 and 3), while metrics 15-16 for global analysis:

$$PRECISION = \frac{TP}{TP + FP} \tag{10}$$

$$RECALL = \frac{TP}{TP + FN} \tag{11}$$

$$MCC = \frac{(TP * TN) - (FP * FN)}{\sqrt{((S_P) * (TP + FN) * (TN + FP) * (S_N)}} \tag{12}$$

$$F1_{score} = \frac{2 * TP}{(2 * TP) + FP + FN} \tag{13}$$

$$ACCURACY = \frac{TP + TN}{TP + TN + FP + FN} \tag{14}$$

$$ICI = \frac{FP + FN}{TP + TN + FP + FN} \tag{15}$$

where TP, FP, TN, FN indicates "correctly classified", "incorrectly classified", "correctly rejected" and "incorrectly rejected", respectively; *ICI* is the "Incorrectly Classified Instances" parameter, S_P is the sum of positives and S_N is the sum of negatives.

A. Proposed method with PIV

For the evaluation of this detector, a fixed threshold of $0.3\,\mathrm{mV}$ in the process of 1-bit quantization has been used, see Fig. 3. This is the x_{th} defined and presented between equations 1 and 2. In Tab. I the class-specific metrics are reported. The main outcome from Tab. I is that the classification is more accurate when dealing with ECG windows containing 2 or 3 R-peaks. Class 1 presents a high loss in terms of precision. As indicated, the Pan-Tompkins method, applied to the original raw signal, was the reference to the state of the art. For such a purpose, the work presented in [12] has been used. The

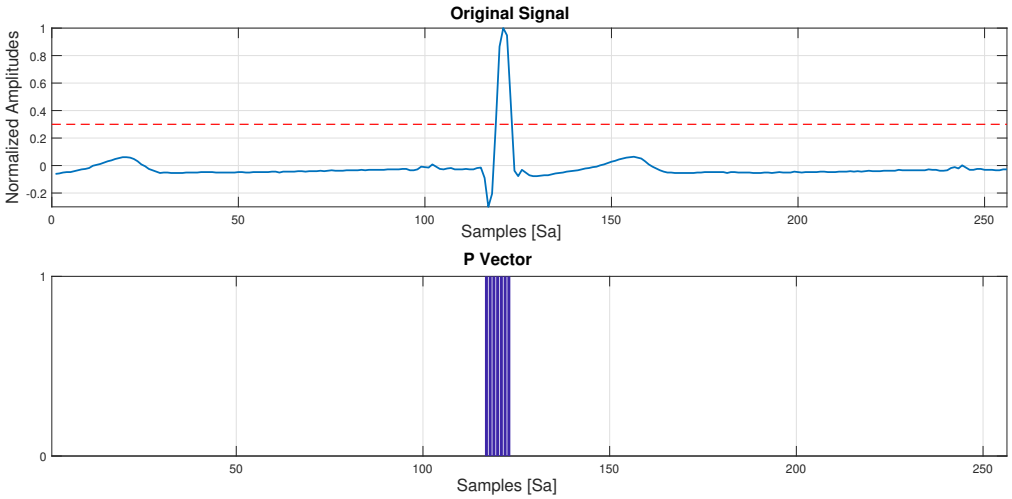

Fig. 3. Example of a signal submitted to the process of 1-bit quantization.

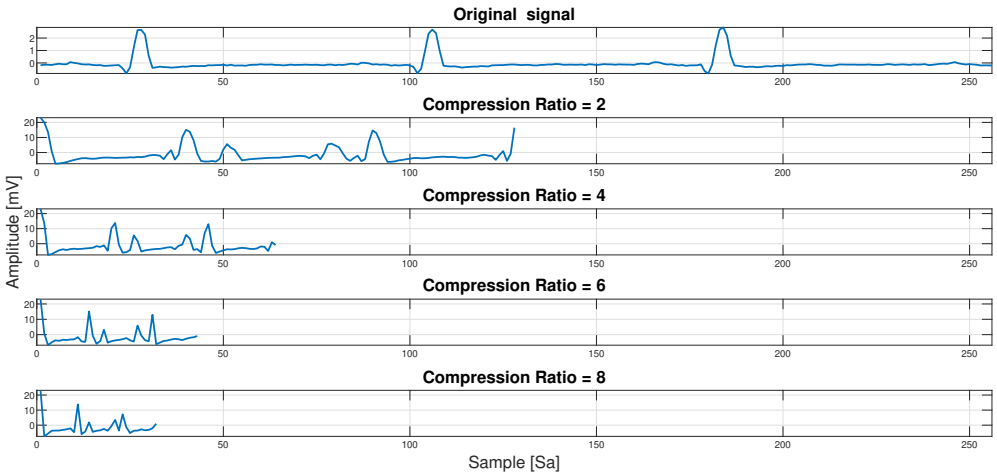

Fig. 4. An example of the compressed samples contained in $\mathbf{y}$ for several values of CR.

TABLE I
DETAILED GLOBAL METRICS EVALUATED FOR EACH CLASS.

Metrics by class	Precision	Recall	MCC	F_1 score
R-peaks = 1	0.361	0.898	0.564	0.515
R-peaks = 2	0.919	0.906	0.826	0.912
R-peaks = 3	0.913	0.904	0.818	0.908

TABLE II
PERFORMANCE COMPARISON IN TERMS OF GLOBAL METRICS OF THE METHOD BASED ON PIV AND PAN-TOMPKINS.

Method	Accuracy	ICI
PIV	0.905	0.095
Pan-Tompkins	0.928	0.072

comparison between the performances obtained by the *PIV* method and the Pan-Tompkins approach are reported in Tab. II.

The outcome of this experiment mainly reveals that the detection in the *PIV* stage is highly comparable with a milestone in the state of the art.

B. Proposed method with compressed samples

For this version of the proposed approach, the performance at 4 different CR have been investigated. The highest ratio evaluated is 8, which means a 32 samples input to the classifier. An example of compressed signals at several CR is shown in Fig. 4.

The results obtained in this study are reported in Tab. III.

The loss in terms of global accuracy with respect to the state of the art becomes significant in this study. What emerges here is that the accuracy in the identification of R-peaks does not highly depend on the compression ratio, considering the subset $2, 4, 6, 8$. This experiment has shown that, when dealing with applications of R-peak occurrences detection,

TABLE III
PERFORMANCES COMPARISON IN TERMS OF GLOBAL METRICS AT DIFFERENT CR.

CS Method	Accuracy	ICI
CR = 2	0.743	0.257
CR = 4	0.741	0.259
CR = 6	0.727	0.273
CR = 8	0.726	0.274

the Power Information Vector embeds much more information with respect to the compressed signal. Thus, for this specific type of detection, the quantization stage provides better results than the Compressed Sensing full algorithm. However, the compressed signal does not have any knowledge of the $\mathbf{\Phi}$ matrix. In other words, this result can be due to the fact that the compressed signal does not embed the information on how it has been obtained from the original signal.

V. CONCLUSIONS AND FUTURE WORKS

In this work, a study about the possibility to perform information retrieval in signals derived from an ECG, is reported. Specifically, the aim of the work was the identification of the number of R-peaks (as important feature in the process of precise estimation of heart rate) in a windowed signal. For this purpose, two types of signals have been taken in consideration: (i) the *PIV*, which is obtained after a stage of 1-bit quantization and (ii) the *CS*, which results after the entire process of Compressed Sensing. The classification stage has been assigned to a very well known classifier – the Random Forest – which provides a final model's classification based on the individual trees' classifications.

The results show that the *PIV* detector is highly comparable with the most used method in the state of the art, the Pan-Tompkins approach, with a loss of approximately $2\,\%$ on the global accuracy. The *PIV* detector shows comparable results even when compared with a similar approach in the state of the art, the one by Da Poian *et al.* [5]. In this work, the authors report a sensitivity of around $91\,\%$ when dealing with a signal compressed with a CR approximately equal to 6.67. The *PIV* detector also shows similar values (approximately $90\,\%$ but with the possibility to reach values of CR equal to 12. On the other hand, by using the detector with the compressed signal as input, the global loss – in terms of accuracy – assumes a significant amount. The huge advantage in building a detector, such as the one proposed in this work, relies on (i) the very low-cost elaboration to obtain the *Power Information Vector* in the CS domain and (ii) on the benefit that – even if there is a specific need to work with the full ECG signal – with a single *PIV* it is possible to reconstruct up to 12 ECG signals. As future works, many studies can be further conducted, such as (i) trying to use different categories of classifiers – specifically, the LSTM Recurrent Neural Network, highly suited in case of time-series – and (ii) trying to detect cardiac pathologies directly in the CS domain.

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