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Gaussian-based analysis for accurate compressed ECG trace streaming

Alessandra Galli[1], Giada Giorgi[1], Claudio Narduzzi[1]

[1]*Department of Information Engineering, University of Padua, via G. Gradenigo, 6/b, I-35131, Padova, Italy, e-mail:* {alessandra.galli, giada.giorgi, claudio.narduzzi}@unipd.it

***Abstract* – Wearable cardiac monitors can usefully contribute to early detection of potential cardiovascular pathologies, however ECG trace data streaming over wireless links creates some significant challenges. We propose a signal analysis approach based on a Gaussian dictionary to model and compress ECG traces. The algorithm operates on fixed-length segments, and achieves effective compression for wireless data transmission, associating just 10 bytes to each Gaussian feature. At the same time it enables accurate reconstruction of ECG traces from the reduced data set. We tested our method on a set of 46 ECG recordings taken from the Physionet MIT-BIH Arrythmia Database, obtaining 90% data compression rates, while percent relative deviation of reconstructed traces is always below 5%.**

I. INTRODUCTION

Recent years have witnessed an explosive growth in the availability of wearable cardiac monitoring devices, from fitness trackers to medical grade monitors analysing multiple-lead electrocardiogram (ECG) signals [1]. On account of their reduced impact on patient quality of life and mobility, these devices can contribute to heart profile evaluation and enhance diagnostics. In particular, continuous heart monitoring plays an important role in early detection of potential cardiovascular pathologies, that are a major cause of death worldwide.

In a mobile context, data acquisition and processing devices are tasked with delivering healthcare measurement information to a data collection and analysis centre, most likely a cloud-based one [2]. For instance, Bluetooth low-energy (BLE) is often employed for short-range data transmission from sensing units to a smartphone, the latter then providing the link to a cloud-based application [3]. The combination provides good throughput, while range is dependent on wireless network coverage and transmission endurance can be limited by energy consumption.

Unobtrusive long-term cardiac monitoring requires *guaranteed throughput* to reliably transfer an accurate continuous flow of measured data [4], hence endurance and transmission range need to be emphasized. It is also useful to remember, as a reference, that one ECG channel sampled at 500 Hz with 12-bit resolution produces 6000 bits per second. This yields over 500 Mb per lead in a single day [5], creating some significant challenges to mobile applications streaming data over wireless links.

Several papers have presented effective data compression algorithms for wireless applications [6, 7]. The focus is on the use of simple, low complexity algorithms to reduce the amount of transmitted data and prolong sensor battery life, while minimizing information loss [8]. However, compression is often treated as an independent problem, rather than by ECG-specific feature analysis [9].

Signals recorded during largely unrestricted daily life activities can be affected by acquisition noise, motion and electrode artifacts [10], placing greater emphasis on denoising. In this regard, compressive sensing (CS) exploits to advantage the underlying sparse-signal assumptions [11], [12]. Besides achieving useful compression ratios, CS allows detection of significant ECG features directly from compressed data, dispensing with the need to reconstruct waveforms first [5], [13]. On the contrary, traditional Holter recorders *preserve* information about whole traces, enabling trained clinicians to carry out detailed analyses of waveforms where the need arises. It might be impossible to do this from compressed data, unless full waveforms can be accurately reconstructed from them.

With these requirements in mind, we present a signal analysis approach that provides an effective compression scheme for wireless data transmission, at the same time enabling accurate reconstruction of ECG traces from the reduced data set. For this purpose we rely on signal modelling by Gaussian kernels and exploit the fact that a low number of suitable components suffices to accurately represent each cardiac cycle. This allows to meet different challenges at the same time:

1. achieve greater robustness against noise and artifacts in recorded traces;
2. support accurate and reliable trace interpretation for analysis and diagnosis;
3. provide compact representations of trace data for archiving, transmission and efficient analysis.

Advanced cardiac monitors can often run rather sophisticated signal analysis algorithms, suggesting that computing power is generally available within edge devices to support the monitoring framework we propose.

II. WAVEFORM MODEL

A cardiac cycle corresponds to a sequence of elementary waves representing different stages of activity (P wave, QRS complex formed by Q, R and S waves, and T wave). Each wave can be modelled by at least one Gaussian kernel, that is, a function $g_\sigma(t)$ defined as:

$$g_\sigma(t) = \frac{1}{\sqrt{2\pi}\sigma} e^{-\frac{t^2}{2\sigma^2}}. \quad (1)$$

To help describe asymmetries in P and T waves, the addition of a second kernel is suggested in the literature [14]. Therefore, in principle a QRS complex is modeled by three Gaussian kernels, P and T waves by two kernels each, totalling *seven*.

The ECG trace is usually partitioned into segments containing only a single heart beat, which requires preliminary detection of peaks associated with the R waves. Single-beat segmentation is critically dependent on the R-peak detection algorithm running on the monitoring device. In our approach we adopt instead *fixed* segmentation, that allows to dispense with R-peak detection. ECG traces are partitioned into segments represented by a sample vector $\underline{\mathbf{x}} = [x(n_1 T_s), \ldots, x(n_2 T_s)]^T$, where T_s is the sampling interval, $n_1 T_s < 0 < n_2 T_s$ with $n_2 - n_1 + 1 = N$, and superscript 'T' denotes transposition. Segment length is NT_s *regardless* of the number of heart beats within.

The location and number of ECG wave complexes can vary and is, in general, unpredictable, although an upper bound based on physiological limits can be set. The model then takes the form:

$$x(nT_s) = \sum_{i=1}^{I} a_i g_{\sigma_i}(nT_s - \tau_i), \quad (2)$$

where a_i is the magnitude of the i-th Gaussian component, σ_i is its shape (dispersion) parameter and τ_i the time position relative to the start of the segment. For greater flexibility, we just set a generic upper bound I on the total number of kernels within a segment.

The use of Gaussian mixture models was proposed in [15] for the generation of realistic synthetic ECG traces and in [14] for ECG compression and classification. Several authors have since considered Gaussian models in ECG-related works and adapted them to different purposes, but identification of model parameters in (2) is a non-linear estimation problem that is often associated with computationally-intensive algorithms, ill-suited to a wearable context [16], [17].

An effective alternative is represented by dictionary-based analysis. The basic idea is to provide a predefined pool of Gaussian kernels, called a *dictionary*, where each kernel is characterized by a different combination of parameters τ and σ. The analysis algorithm picks the ones that best match model (2) for the given segment $\underline{\mathbf{x}}$. The use

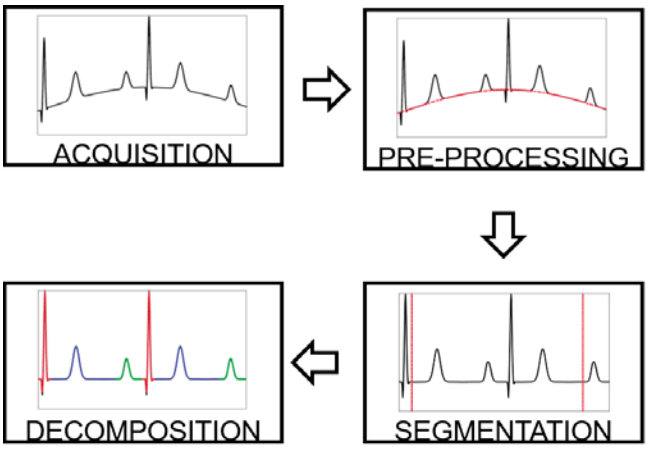

Fig. 1. Main steps of the proposed framework.

of a Gaussian dictionary was shown to provide promising results in the analysis of ECG traces [18].

Each dictionary element (*atom*) can be described as a column vector of N sampled values of a Gaussian kernel:

$$\underline{\mathbf{g}}_{(\tau_h,\sigma_k)} = [g_{\sigma_k}(n_1 T_s - \tau_h), \ldots, g_{\sigma_k}(n_2 T_s - \tau_h)]^T. \quad (3)$$

where τ_h is a specific time position in a set of H allowable values and σ_k is a specific dispersion taken from a set of K possible choices. As a dictionary only allows discrete sets of values for parameters σ and τ, correct design and a suitable trade-off between the size of the dictionary and waveform approximation accuracy are essential.

The generic dictionary matrix $\mathbf{D}$ has the form:

$$\mathbf{D} = [\mathbf{D}_{\sigma_1}\ \mathbf{D}_{\sigma_2}\ \ldots\ \mathbf{D}_{\sigma_K}] \quad (4)$$

where each $N \times H$ matrix block contains H column vectors $\underline{\mathbf{g}}_{(\tau_h,\sigma_k)}$ characterised by different time shifts, but with a common value of parameter σ_k. The size of the full dictionary $\mathbf{D}$ is $N \times M$, with $M = HK$. Because of the way $\mathbf{D}$ is built, the indication of column index m suffices to determine values of *both* τ and σ, that is: $\underline{\mathbf{g}}_{(\tau_h,\sigma_k)} = \underline{\mathbf{d}}_m$ for some m.

To find all the components of model (2) we apply an *orthogonal matching pursuit* (OMP) recursive greedy algorithm [19].

III. SEGMENTATION AND PROCESSING

Processing steps in the proposed approach follow the straightforward sequence shown in Fig. 1.

A. Pre-processing

The acquired ECG trace is first pre-processed to remove low frequency noise and baseline wander due to respiration and motion artifacts. These components are first extracted by applying two cascaded median filters. The first filter of

200-ms width removes QRS complexes and P waves, the resulting signal is then processed by a median filter of 600-ms width to remove T waves [20]. The resulting output contains baseline wander, that is then subtracted from the original ECG signal.

B. Segmentation

Although fixed segmentation may appear straightforward, it calls for great care in dealing with edge effects. In fact, it may happen that larger elementary waves are found close to either end of the analyzed segment, resulting in significant truncation of the relevant waveform.

Gaussian model (2) can adapt to a variety of waveforms which, unfortunately, means that it is easily affected by edge effects. The analysis algorithm attempts to replicate truncation by concentrating as many Gaussian kernels as needed close to the edge of the analyzed segment, resulting in local overfitting. Since a limited number of kernels is allotted for each segment, this may cause sub-optimal allocation and underfitting elsewhere in the segment.

The problem has been addressed as follows:

- head and tail edge extensions of the segment are introduced to minimize truncation in Gaussian kernel vectors within the dictionary;
- overlap is introduced between consecutive segments. As a consequence, elementary waveforms subjected to truncation are considered for both segments, but only the better fitting is kept;
- the upper bound I is increased to account for overlaps and discarded estimates.

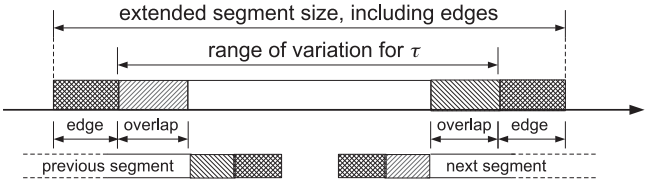

Fig. 2. Segment structure, with edges and overlap areas.

The segment structure assumed for the algorithm is shown in Fig. 2, where the cross-hatched parts at the two ends represent the edge allowance for Gaussian atoms. Edge width is equal to the maximum value assigned to the dispersion parameter σ within the dictionary. Single-hatched rectangles represent the overlap areas, that are the same width as the edges.

Figure 3 refers to one of the ECG traces analyzed for this work. For a 30-minute recording time, a trace is partitioned into 1042 segments, that are all superposed in this figure. Estimated Gaussian kernel amplitudes α_i are plotted versus time position τ_i. This parameter was allowed to

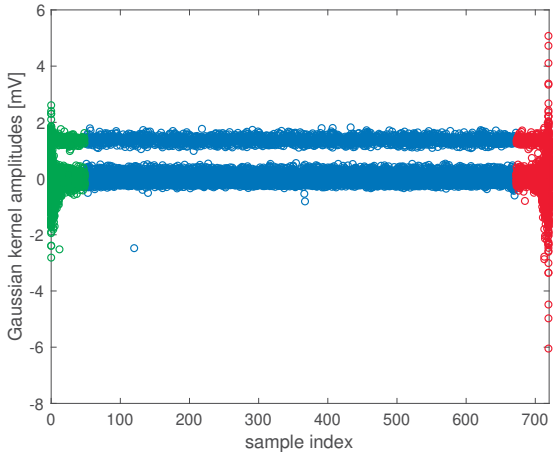

Fig. 3. Plot of Gaussian kernel amplitudes versus delays. All segments of a single ECG trace are overlapped. Green and red show overlap areas where estimated coefficients are discarded.

vary over a range of 2 s, that is the full segment length, corresponding to 720 samples as shown, since the sampling rate is 360 Hz. Edges are 48 samples long (approximately 130 ms), which is the same length as the overlap areas.

Analyzed segment length is actually 624 samples (1.73 s), that is, the blue part of the plot in Fig. 3. Estimates from this part of the segment can be streamed out for wireless transmission. The halves of the leading and trailing overlap areas, where coefficient estimates are discarded, are shown respectively in green and red. Some coefficients in those areas are significantly larger, as a result of the algorithm attempt to overfit truncated waveforms.

For the trace of Fig. 3 overlap areas where estimates are discarded are little more than 14% of the range of delay variation. On the other hand, discarded estimates are about 25% of the total provided by the algorithm. This confirms the clustering effect caused by overfitting at the segment ends and suggests that the overlap-and-discard approach described above can deal with edge effects effectively.

C. Decomposition

Dictionary-based signal analysis centers on finding a sparse solution to a matrix-vector equation, formally:

$$\hat{\underline{\mathbf{a}}} = \arg\min_{\underline{\mathbf{a}}} ||\underline{\mathbf{a}}||_0 \quad \text{subject to:} \quad ||\underline{\mathbf{x}} - \mathbf{D}\underline{\mathbf{a}}||_2 < \epsilon \qquad (5)$$

where $\underline{\mathbf{a}}$ is the vector of Gaussian kernel coefficients a_i and ϵ is a threshold value associated to the energy of the residual $\underline{\mathbf{r}} = \underline{\mathbf{x}} - \mathbf{D}\hat{\underline{\mathbf{a}}}$.

The OMP iterative approximation algorithm can be summarized as follows. After initializing the set of selected dictionary column indexes to the empty set, $\mathcal{S} = \varnothing$ and the signal estimate to $\hat{\underline{\mathbf{x}}} = \underline{\mathbf{0}}$, the algorithm is the itera-

tive application of the following steps:

1. compute $\underline{\mathbf{r}} = \underline{\mathbf{x}} - \underline{\hat{\mathbf{x}}}$, then select dictionary index: $m^* = \arg\max_m |\underline{\mathbf{d}}_m^T \underline{\mathbf{r}}|^2$
2. accordingly update the selected index set: $\mathcal{S} = \mathcal{S} \cup m^*$ and the dictionary submatrix $\mathbf{D}_\mathcal{S}$;
3. compute a new amplitude estimate: $\underline{\hat{\mathbf{a}}}_\mathcal{S} = \left(\mathbf{D}_\mathcal{S}^T \mathbf{D}_\mathcal{S}\right)^{-1} \mathbf{D}_\mathcal{S}^T \underline{\mathbf{x}}$;
4. calculate the new signal estimate: $\underline{\hat{\mathbf{x}}} = \mathbf{D}_\mathcal{S} \underline{\hat{\mathbf{a}}}_\mathcal{S}$.

Iterations are stopped either when the maximum allocated number of Gaussian kernels I_{max} has been reached, or when percent relative deviation (PRD) of $\underline{\hat{\mathbf{x}}}$ from the analyzed segment $\underline{\mathbf{x}}$ drops to 1% or lower.

Each OMP iteration step involves matrix-vector products, the computation of a pseudo-inverse of progressively larger size and, above all, the search for a peak value over a vector the same size as the dictionary column. Computational cost increases with the number of components modelled by (2). Shorter segments can be processed faster, but the number of segments gets larger and, with fixed overlap length, efficiency decreases. The selected 2-s segment length appears to be a reasonably effective compromise.

For our trials MatLab running on a 2,6 GHz Intel Core i7 quad-core processor took about 240 ms for the analysis of a 2-s segment, which suggests real-time analysis is achievable also with less-performing processors.

IV. MAIN RESULTS

To characterise the proposed approach we considered the set of 30-minute ECG recordings provided by the MIT-BIH Arrythmia Database, hosted at *https://physionet.org* [21]. Specifically, we selected only traces from modified limb lead II, as they were available for 46 records. Results thus refer to the analysis of nearly 48,000 segments and over 100,000 heart beats, some of which are labelled as anomalies.

A. Compression

For each Gaussian kernel modelling the trace, the algorithm provides amplitude, dictionary column index and absolute position index within the trace. The latter is the sum of the segment start index and relative position τ_i within the segment. Since amplitude accuracy is important we use for this a 32-bit floating point format. Dictionary column indexes are represented by unsigned 16-bit values, while 32 bits are needed for the position index. This means exactly 10 bytes are needed for each Gaussian component.

Since heart rate and ECG trace shape can vary, it is easier to assess compression by comparing the size of acquired traces with the corresponding sequence of parameter estimates. This shows that a 30-minute ECG trace taking about 1 Mbyte is converted into a data sequence of approximately 100 kbytes. The resulting compression ratio is around 90% and corresponds to less than 500 bits per second, which is compatible with typical low-power wide-area network data rates.

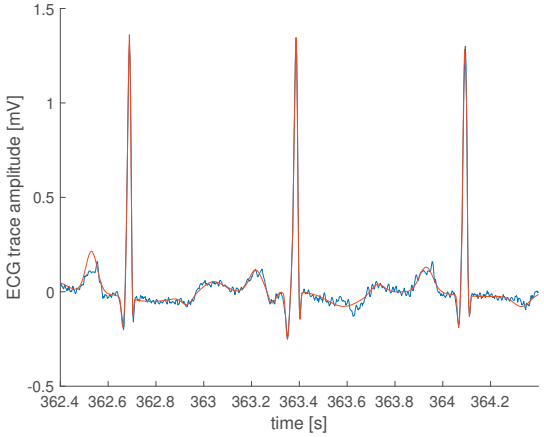

Fig. 4. Comparison between original (blue) and reconstructed (red) trace for a representative ECG segment.

B. Waveform reconstruction accuracy

If the Gaussian model that describes the ECG signal is accurate enough, the proposed algorithm enables to reconstruct a trace without introducing artifacts. An example of reconstruction for one of the ECG trace segments is shown in Fig. 4, where it can be seen that some mild smoothing has been introduced in the reconstructed trace.

Percent Root mean square Difference (PRD) is an index of distortion caused by model approximation, defined as:

$$\mathrm{PRD} = 100 \cdot \sqrt{\frac{\sum \left[\hat{x}(nT_s) - x(nT_s)\right]^2}{\sum x^2(nT_s)}} \qquad (6)$$

where $\hat{x}(nT_s)$ is the signal reconstructed by the proposed Gaussian model and summations extend over a whole trace.

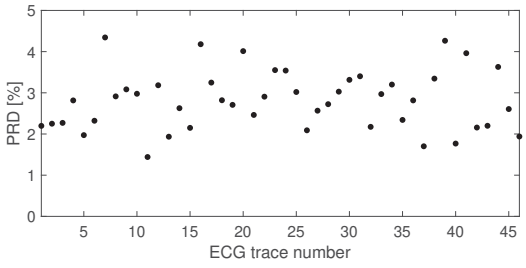

Fig. 5. Percent relative deviation (PRD) for 46 analysed traces from MIT-BIH Arrythmia Database (for trace interpretation, usually 0-2% = very good, 2-9% = good) [22].

PRD values are plotted in Fig. 5 for each of the reconstructed traces. Even for the pathological traces contained in the database they are always below 5%, which is considered to correspond to good trace quality [22].

V. CONCLUSIONS

Our model-based approach makes use of an algorithm where accuracy and computational complexity can be tuned to meet the needs of long-term ECG monitoring, overcoming issues about acquisition and wireless transmission of signals by wearable devices.

The proposed signal analysis approach achieves significant data compression, allowing to send ECG trace data as a stream at around 500 bit/s, which is sustainable by low-power wide-area network devices in mobile applications. Gaussian kernels achieve accurate morphological modelling of ECG traces, allowing accurate waveform reconstruction.

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