

Mixed-transform based codec for 2D compression of ECG signals

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Abstract—A method for ECG compression, by imaging the record as a 2D array and implementing a transform lossy compression strategy, is advanced. The particularity of the proposed transformation consists in applying a Discrete Wavelet Transform along one of the dimensions and the Discrete Cosine Transform along the other dimension. The performance of the method is demonstrated on the MIT-BIH Arrhythmia database. Significant improvements upon the 1D version of the codec, and on benchmarks for 2D ECG compression, are achieved.

I. INTRODUCTION

Cardiovascular diseases (CVDs) are the number one cause of global death. The World Health Organization has estimated that 17.9 million people died from CVDs in 2016. Over three quarters of these deaths take place in low and middle income countries. A major goal in the Sustainable Development Agenda of the United Nations is to reduce these figures one third by 2030. Within this agenda, prevention and routine controls play a central role. The electrocardiogram (ECG) is one of the most common tests in the diagnosis of CVDs. It goes without saying that techniques for safely compressing these types of data are essential to the development and support of clinical health care.

In a recent publication [1] a method for effective high compression of ECG signals has been proposed. That method, which is applied on a 1D record, was shown to significantly improve upon benchmarks on the same database [2]–[4]. In this Communication we extend the compression technique in [1] to allow for its application on a 2D array constructed out of 1D ECG signal. It is demonstrated that, for the same level of distortion, the average compression performance on the MIT-BIH Arrhythmia database considerably improves in relation to the 1D processing. The method is also shown to improve upon previous state of the art benchmarks concerning 2D ECG compression [5]. MATLAB software for reproducing results and facilitating future comparisons has been made available on a dedicated webpage [6].

II. PROPOSED CODING STRATEGY

A digital ECG signal represents a sequence of heartbeats, each of which is characterized by a combination of

three graphical deflections, known as QRS complex, and the so called P and T waves. 2D ECG compression relies on this feature. Our approach operates on raw data and consists of the following steps.

- A) 1D to 2D conversion by segmentation and alignment of heartbeats.
- B) Application of a Discrete Wavelet Transform (DWT) along the direction of the segmented beats and the Discrete Cosine Transform (DCT) along the perpendicular direction.
- C) Quantization, organization, and entropy coding of the information needed to recover the ECG record from the compressed file.

A. 1D to 2D conversion

The conversion of the 1D ECG record into a 2D array requires segmentation and alignment of heartbeats. We implement this step as done in [5]. Firstly a QRS detection algorithm is applied to locate the R peaks. Each of these peaks is aligned with the previous one. Since the length of the heartbeats are not uniform, a regular array \mathbf{A} is obtained by padding rows with zeros. The duration of the heartbeats are stored as components of a vector, say \mathbf{h} , which has to be passed on to the decoder. Fig.1 illustrates a 2D array of size 86×359 produced from a short 1D ECG record consisting of 25,000 samples.

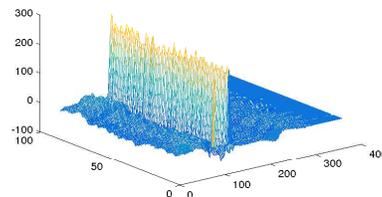


Fig. 1. 2D array produced by segmentation and alignment of heartbeats.

B. Transformation of the 2D array

This step introduces the distinctive feature of the proposed codec. Instead of applying a 2D wavelet transform

on the array \mathbf{A} , as it is done in other 2D ECG compression methods, e. g. [5], we apply a different transform in each dimension. More precisely, we apply the 1D cdf97 DWT on the rows of \mathbf{A} and the 1D DCT transform on the columns of \mathbf{A} , i.e., we create the transformed array \mathbf{B} as follow:

$$\mathbf{B} = \widehat{\mathcal{W}}_{1r} \widehat{\mathcal{C}}_{1c} \mathbf{A}, \quad (1)$$

where $\widehat{\mathcal{W}}_{1r}$ indicates the 1D cdf97 DWT operating on the rows of the array $\widehat{\mathcal{C}}_{1c} \mathbf{A}$ and $\widehat{\mathcal{C}}_{1c}$ indicates the DCT transform operating on the columns of the array \mathbf{A} . The convenience of performing this mixed transformation for encoding purposes becomes clear from the graphs of Fig. 2. The upper graph represents the absolute value of the 2D cdf97 DWT of \mathbf{A} and the lower graph the absolute value of the array \mathbf{B} as given in (1). The distribution of most significant elements in \mathbf{B} (lightest regions in the lower graph) benefits the coding strategy described below.

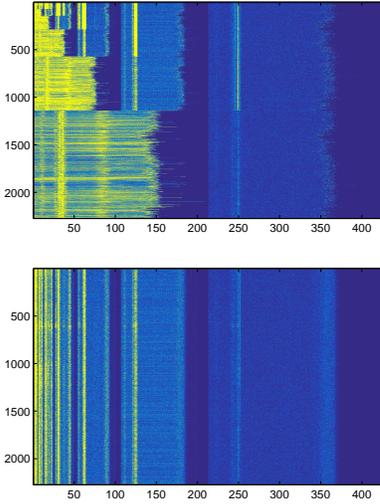


Fig. 2. Magnitude of the 2D cdf97 DWT (upper graph) and magnitude of mixed transform given in (1) (lower graph).

C. Encoding

The encoding process begins by adopting a column-major order to express the $N \times M$ array \mathbf{B} as a 1D vector $\mathbf{b} = (b(1), \dots, b(NM))$. Hereafter the encoding proceeds as in [1]. The components of \mathbf{b} are converted to integer numbers by a mid-tread uniform quantizer as follows:

$$b^\Delta(i) = \lfloor \frac{b(i)}{\Delta} + \frac{1}{2} \rfloor, \quad i = 1, \dots, NM. \quad (2)$$

where $\lfloor x \rfloor$ indicates the largest integer number smaller or equal to x and Δ is the quantization parameter.

The absolute value of the elements (2) are placed in a smaller vector, say $\mathbf{c} = (c(1), \dots, c(K))$, after the elimination of zeros. The signs are encoded separately in a vector $\mathbf{s} = (s(1), \dots, s(K))$ using a binary alphabet (1 for + and 0 for -).

Assuming that the nonzero values in (2) occur at the positions ℓ_1, \dots, ℓ_K , these indices are re-ordered in ascending order $\ell_i \rightarrow \tilde{\ell}_i, i = 1, \dots, K$, which guarantees that $\tilde{\ell}_i < \tilde{\ell}_{i+1}, i = 1, \dots, K$. This induces a re-order in the coefficients, $\mathbf{c} \rightarrow \tilde{\mathbf{c}}$ and in the corresponding signs $\mathbf{s} \rightarrow \tilde{\mathbf{s}}$. Defining $\delta(i) = \tilde{\ell}_i - \tilde{\ell}_{i-1}, i = 2, \dots, K$ the array $\boldsymbol{\delta} = (\tilde{\ell}_1, \delta(2), \dots, \delta(K))$ stores the indices $\tilde{\ell}_1, \dots, \tilde{\ell}_K$ with unique recovery.

Finally the vectors $\tilde{\mathbf{c}}, \tilde{\mathbf{s}}, \boldsymbol{\delta}$, as well as the length of the heartbeats \mathbf{h} , are compressed using Huffman coding. The additional numbers which have to be passed to the decoder are: i) the quantization parameter Δ ii) the mean value of the 1D ECG record and iii) the size of the 2D array \mathbf{A} .

III. 1D ECG SIGNAL RECOVERY

At the decoding stage, after reverting Huffman coding, the locations $\tilde{\ell}_1, \dots, \tilde{\ell}_K$ of the nonzero entries in the transformed array, after quantization, are readily obtained. This allows the recovery of the array as follows. i) Set $b^r(i) = 0, i = 1, \dots, NM$ and $b^r(\tilde{\ell}_i) = (2\tilde{s}(i) - 1)\tilde{c}(i)\Delta, i = 1, \dots, K$. ii) Reshape the vector \mathbf{b}^r as a 2D array \mathbf{B}^r of size $N \times M$. The array \mathbf{A}^r is recovered from \mathbf{B}^r inverting the $\widehat{\mathcal{W}}_{1r}$ and $\widehat{\mathcal{C}}_{1c}$ transformations (c.f.(1)). The re-conversion to the 1D signal say, \mathbf{f}^r , from the 2D array \mathbf{A}^r is straightforward using the heartbeat lengths in \mathbf{h} and the mean value signal.

The achieved compression ratio CR, which is defined as

$$\text{CR} = \frac{\text{Size of the uncompressed file.}}{\text{Size of the compressed file}} \quad (3)$$

depends on the required quality of the recovered signal. This is assessed with respect to the standard PRD metric as given by

$$\text{PRD} = \frac{\|\mathbf{f} - \mathbf{f}^r\|}{\|\mathbf{f}\|} \times 100\%, \quad (4)$$

where, \mathbf{f} is the original signal, \mathbf{f}^r is the signal reconstructed from the compressed file and $\|\cdot\|$ indicates the 2-norm.

IV. NUMERICAL RESULTS

For all the tests the full MIT-BIH Arrhythmia database [7], which contains 48 ECG records, is used. Each of these records consists of $N = 650,000$ 11-bit samples at a frequency of 360 Hz. At the QRS detection step a MATLAB implementation [8] of the Pan Tompkins algorithm was applied [9].

The comparison with 1D compression is realized with respect to the 1D version of the strategy adopted here, which has been shown in [1] to over-perform previously reported results [2]–[4]. Table I produces comparisons for PRD in the range [0.4 1]. The range [0.4 0.7] corresponds to very low level distortion of the recovered signal. For $\text{PRD} < 0.4$ the proposed coding strategy is not effective. Nonetheless, it is worth noting that, because the approach is applied on raw data, requiring $\text{PRD} < 0.4$ implies to force the reproduction of the small high frequency

noise present in all the records. As discussed in [1], the decomposition of the $\text{cdf}97$ DWT in 4 levels produces the best 1D compression results on the MIT-BIH Arrhythmia database. In 2D, however, results improve by decomposing into 6 levels. Table I shows the mean value CR and corresponding standard deviation (std) yielded by the 1D and 2D methods. In both cases the quantization parameter has a different value for each record so as to achieve, for every record in the database, the sharp values of PRD given in the first row of Table I. Since the compressibility of the records is not uniform, fixing the same PRD for all the records generates large dispersion in CR. This is reflected in the std values.

TABLE I
MEAN VALUE COMPRESSION RATIOS FOR PRD VALUES SHARPLY REPRODUCED BY EVERY RECORD IN THE DATABASE.

PRD	1.00	0.90	0.80	0.70	0.60	0.50	0.40
CR (1D)	42	39	35	32	28	24	19
std	12	11	10	9	8	7	5
CR (2D)	85	73	61	50	39	29	20
std	50	42	34	28	21	15	10

Table II produces comparison with results in Table VIII of [5], for the whole database with reconstruction quality in our range of interest. The method in [5] employs a modified set partitioning in hierarchical trees (SPIHT) algorithm, which is shown to produce superior results than other image compressions techniques, including JPEG2000. The reported values of PRD are said to have been calculated after subtraction of a baseline of 1024 to the original data. The corresponding values are indicated here as PRD_B . The notation PRD is kept to indicate the PRD with respect to raw data.

TABLE II
COMPARISON WITH THE RESULTS IN TABLE VII OF [5] FOR THE WHOLE DATABASE

Method	PRD_B	std	CR	std	PRD	std
[5]	6.82	–	30	–	–	–
1D	6.82	0.01	31	14	0.77	0.41
2D	6.82	0.01	58	63	0.77	0.41
[5]	3.81	–	20	–	–	–
1D	3.81	0.01	19	10	0.43	0.23
2D	3.81	0.01	26	30	0.43	0.23

V. REMARKS AND CONCLUSIONS

The numerical tests demonstrate that the extension to operate in 2D of the 1D compression strategy proposed in [1] yields, on the whole, very significant improvement in compression power. A distinctive feature of the 2D approach is that, fixing quality, there is very large dispersion in the values of CR. This is due to the fact that compressing in 2D is greatly beneficial for records of very regular morphology. Only some of the records

in the MIT-BIH Arrhythmia database possess this trait. Fig. 3 shows the histogram of CR for the 2D approach and $\text{PRD}_B = 6.82$.

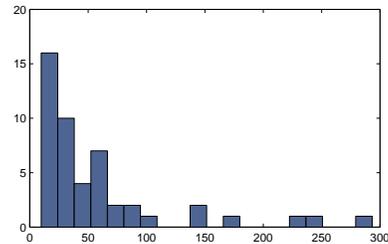


Fig. 3. Histogram of the CR obtained with the 2D approach corresponding to $\text{PRD}_B = 6.82$ for every record in the database.

We are aware that the calculation of PRD subtracting a baseline of 1024 adopted in [5] has generated confusion leading to propagation of unfair comparison with values of PRD without subtraction of baseline. Table II gives the two metrics. The quantization parameter Δ , which controls quality, has been set differently for each record in order to reproduce the sharp values of PRD_B as those reported in [5]. The values of std are not reported in that publication.

The benefit of 2D compression comes at the expense of some additional computation. With respect to the 1D implementation there is an extra time for QRS detection and for converting the 1D array into a 2D one. Furthermore, the Huffman coding step becomes more relevant in 2D compression than it is in 1D. However, as shown in Tables I and II, the improvements in compression results justify the computational overhead.

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