Compressing ECG signals by piecewise polynomial approximation

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COMPRESSING ECG SIGNALS BY PIECEWISE POLYNOMIAL APPROXIMATION

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ABSTRACT

Compression of digital ElectroCardioGram (ECG) signals has traditionally been tackled by heuristical approaches. Recently, it has been demonstrated [1] that exact optimization algorithms outclass these heuristical approaches by a wide margin with respect to reconstruction error. As opposed to traditional time-domain algorithms, where some heuristic is used to extract representative signal samples from the original signal, the exact optimization algorithm in [1] formulates the sample selection problem as a graph theory problem. Thus well known optimization theory can be applied in order to yield optimal compression. In [1], linear interpolation is applied in reconstruction of the signal. This paper generalizes the optimization algorithm such that reconstruction can be made by second order polynomial interpolation in the extracted signal samples. The polynomials are fitted in a way that guarantees minimal reconstruction error, and the method proves good performance compared to the case where linear interpolation is used in reconstruction of the signal.

1. INTRODUCTION

The amount of data involved in storage and transmission of digital ElectroCardioGram (ECG) signals is large. It is therefore an apparent need to compress such signals in order to keep the amount of data in manageable sizes. The compression must be done in a way that makes accurate reconstruction of the signal possible. Time-domain algorithms for signal compression is based on the idea of extracting a subset of signal samples from the original signal. Which signal samples to be extracted depend on the underlying criterion for the sample selection process. To get a high performance time-domain compression algorithm, much effort should be put in designing intelligent sample selection criteria.

Most of the well known time-domain compression algorithms for ECG signals today, are based on fast heuristics in the sample selection process. Examples of such algorithms is the popular FAN algorithm [2], the well known AZTEC [3] algorithm and recently attempts of improvements to time-domain algorithms, such as SLOPE [4] and AZTDIS [5]. The common stamp of these algorithms is that they are all based on some heuristic criterion and therefore they are all suboptimal. As opposed to these algorithms, the *Cardinality Constrained Shortest Path* (CCSP) algorithm presented in [1] is based on a rigorous mathematical model of the entire sample selection process. By modelling the signal samples as nodes in a graph, optimization theory may be applied in order to achieve the best compression possible under the given circumstances. Which compression that is "best" depends on the error measure that is considered. In [1] the goal is to minimize the reconstruction error given a bound on the number of samples to be extracted. The samples of the original signal are modeled as nodes in a directed graph. Any pair of nodes are connected with an arc, the direction of which is given from the sample order. Including a particular arc corresponds to letting the end nodes of the arc constituting consecutive samples in the extracted subset of signal samples.The length of each arc in the digraph can be defined in a variety of ways. In [1] the length of the arc connecting two samples i and j is defined as the contribution to reproduction error from eliminating all samples recorded between i and j. Defining the problem in this way, minimization of the reconstruction error can be recognized as solving the *cardinality constrained shortest path problem* defined on the graph.

Reconstruction of a signal compressed by any of the time-domain algorithm mentioned so far is done by linear interpolation between the elements of the extracted subset of signal samples. This is a simple, but computationally effective way of reconstructing the signal. However, an ECG signal is not linear in its nature, but rather more curvaceous. It would therefore be interesting to investigate if it is possible to get a better approximation to the original signal, under the same compression ratio, by using a polynomial of higher degree in reconstruction of the signal. In this paper we therefore demonstrate how the algorithm in [1] can

be further developed in order to reconstruct the signal by second order polynomials.

Applying linear interpolation in the reconstruction phase, the algorithm in [1] is proven to converge in cubic time. In [6] it is demonstrated how to cope with real time constraints of the algorithm. In this paper it is shown that the idea presented in [1], and roughly sketched here, can be applied to the case where polynomial approximation is used in reconstruction of the signal without increasing the computational complexity of the algorithm.

In the next section the problem is defined in strict mathematical terms. Section 3 is devoted to the solution method. Finally, computationally results are reported, and in the concluding section different aspects of the method along with future work are considered.

2. OPTIMIZATION MODEL

Denote the samples taken from an ECG signal at constant interval by $y(1), y(2), ..., y(N)$. Let M denote the bound on the number of extracted samples and S denote the *sample set* $S = \{y(1), y(2), ..., y(N)\}$. We seek an appropriate *compression set* $C = \{n_1, n_2, ..., n_M\} \subseteq \{1, 2, ..., N\}$ and the corresponding sample values. Assume $n_1 = 1$ and $n_M = N$. The approximation is then given by $\hat{y}(n) = y(n)$ if $n \in C$ and $\hat{y}(n) = f_{n_k,n_{k+1}}(n)$ where $n_k < n < n_{k+1}$ for all $n \notin C, n \in \{1, 2, ..., N\}$. Here $f_{n_k,n_{k+1}}(n)$ denotes a presumed reconstruction of $y(n)$ based on $y(n_k)$, $y(n_{k+1})$ and all the intermediate samples and will be given a precise definition in the next section. In this way we get a piecewise approximation to the original signal. Between two sample amplitudes corresponding to two succeeding elements of C, different functions are used in reconstruction of the signal. The choice of C will thus have a vital importance for the quality of our approximation of the signal.

Define the directed graph $G = (V, A)$ whose *vertex set* $V = \{1, 2, ..., N\}$ and *arc set* A contains node pairs (i, j) where $i, j \in V$ and $i < j$. If $n_1, n_M \in V$, the set $(n_1, n_2, ..., n_M)$ is said to be a *path* from n_1 to n_M in G if $n_1, ..., n_M \in V$ are distinct vertices and $n_1 < n_2 < \cdots < n_M$. Let P_n denote the path from node 1 up to node n. The length of each arc (i, j) in A is given as the contribution to the total reconstruction error by eliminating all nodes between i and j. This can be expressed as $c_{ij}^2 = \sum_{n=i+1}^{j-1} (\hat{y}(n) - y(n))^2$. The length of P_n will thus be the sum of the length of all arcs included in the path up to node n. Each arc (i, j) in A represents the possibility of letting i and j be consecutive members of C. Including an arc (i, j) in C has the effect of increasing the total path length by c_{ij}^2.

Hence we are faced with the following problem : Minimize the length of P_N under the constraint that P_N contains no more than M vertices. With the reconstruction method applied here, this is a a modified version of the problem presented in [1].

3. SOLUTION METHOD

We now go on to show that the algorithm in [1] can be modified such that it handles second order reconstruction polynomials and still preserves its computational complexity of $\mathcal{O}(MN^2)$.

To be able to extract samples from S in an optimal way, we need to know the contribution to reconstruction error introduced by including any two samples as consecutive members of C. The aim now is therefore to fit a function f_{ij} to the data set $\{(n, y(n)) : n = i, ..., j\}$ in such a way that the reconstruction error is minimized. We wish to use a second order polynomial in this context, that is we let $f_{ij}(n) = a_{0ij} + a_{1ij}n + a_{2ij}n^2, n \in [i, j]$. If we interpolate between two end points i and j, we have for each arc (i, j) :

$$c_{ij}^2 = \sum_{l=i+1}^{j-1} \left(a_{0ij} + a_{1ij}l + a_{2ij}l^2 - y(l)\right)^2 \quad (1)$$

$$a_{0ij} + a_{1ij}i + a_{2ij}i^2 = y(i) \quad (2)$$

$$a_{0ij} + a_{1ij}j + a_{2ij}j^2 = y(j) \quad (3)$$

The optimal parameters a_{0ij}, a_{1ij} and a_{2ij} are found by minimizing (1) under the constraints given in (2) and (3). By inserting these optimal parameters into (1), the minimal c_{ij}^2 is found for each arc.

The graph G consists of $\frac{N(N-1)}{2}$ arcs. The expression for c_{ij}^2 is a sum of $j - i + 1$ terms. Straightforward computation of all a_{0ij}'s, a_{1ij}'s, a_{2ij}'s and all c_{ij}^2's will thus result in an algorithm with a complexity of $\mathcal{O}(N^3)$. Fortunately, this can be avoided by careful computation of the arc lengths.

The arc lengths are given by (1). Assume that we express (1) in terms of a_{2ij} by the use of (2) and (3). By taking the derivative of this expression with respect to a_{2ij} we arrive at an expression of the following form :

$$a_{2ij} = \frac{\sum_{l=i+1}^{j-1} (\alpha_{0ij} + \alpha_{1ij}l + \alpha_{2ij}l^2)y(l) + \delta_{1ij}}{\delta_{2ij}} \quad (4)$$

where

$$\delta_{1ij} = \sum_{l=i+1}^{j-1} \beta_{0ij} + \beta_{1ij}l + \beta_{2ij}l^2 + \beta_{3ij}l^3 \quad (5)$$

$$\delta_{2ij} = \sum_{l=i+1}^{j-1} \gamma_{0ij} + \gamma_{1ij}l + \gamma_{2ij}l^2 + \gamma_{3ij}l^3 + \gamma_{4ij}l^4 \quad (6)$$

All α_{ij}'s, β_{ij}'s and γ_{ij}'s are simple expressions in i, j, $y(i)$ and $y(j)$ and hence all these coefficients are computed in $\mathcal{O}(N^2)$ time. The sums of powers of l are evaluated by closed form formulas, and hence all δ_{1ij} and δ_{2ij} are computed in $\mathcal{O}(N^2)$ time. By defining $\Delta_{pj} = \sum_{l=1}^{j} l^p y(l)$, $p = 0, 1, 2$, we see that $\Delta_{p1}, \ldots, \Delta_{pN}$ are computed in $\mathcal{O}(N^2)$ time. Next, we compute

$$a_{2ij} = \frac{\sum_{p=0}^{2} \alpha_{pij}(\Delta_{p,j-1} - \Delta_{pi}) + \delta_{1ij}}{\delta_{2ij}} \qquad (7)$$

$1 < j < N$, involving $\mathcal{O}(N^2)$ operations.

When the optimal parameters are computed in the way described above, they are inserted into (1) in order to find the minimum arc lengths. This will lead to an expression of the form

$$c_{ij}^2 = \sum_{l=i+1}^{j-1} \left(a_{0ij}^2 + 2a_{0ij}a_{1ij}l + \left(2a_{0ij}a_{2ij} + a_{1ij}^2\right) l^2 + 2a_{1ij}a_{2ij}l^3 + a_{2ij}^2 l^4 - 2y(l)\left(a_{0ij} + a_{1ij}l + a_{2ij}l^2\right) + y^2(l)\right)$$

By applying the same technique as in computation of a_{2ij}, all arc lengths are available in $\mathcal{O}(N^2)$ time.

When all arc lengths are available, the actual sample extraction takes place. This is accomplished by a dynamic programming algorithm thoroughly described in [1].

4. NUMERICAL EXPERIMENTS

In order to analyze the performance of the algorithm described here, several ECG recordings taken from the MIT [7] database were applied in the coding experiments. Two of the test signals are presented in Figure 1.

As a measure of closeness between the original signal and the coded signal the *Percentage Root Mean Difference* is used. This is defined as

$$PRD = \sqrt{\frac{\sum_{l=1}^{N}[y(l) - \hat{y}(l)]^2}{\sum_{l=1}^{N}[y(l) - \bar{y}]^2}} \times 100\% \qquad (8)$$

where $\overline{y}$ is the mean value of the original signal y, and $\hat{y}$ is the reconstructed signal. As a measure of the data reduction obtained, the *Sample Reduction Ratio* is used. This is defined as

$$\frac{\text{Number of samples in original signal}}{\text{Number of retained samples}} \qquad (9)$$

Figure 2 show the PRD recorded for the two test signals at different sample reduction ratios. The FAN algorithm is outclassed by both versions of the CCSP algorithm

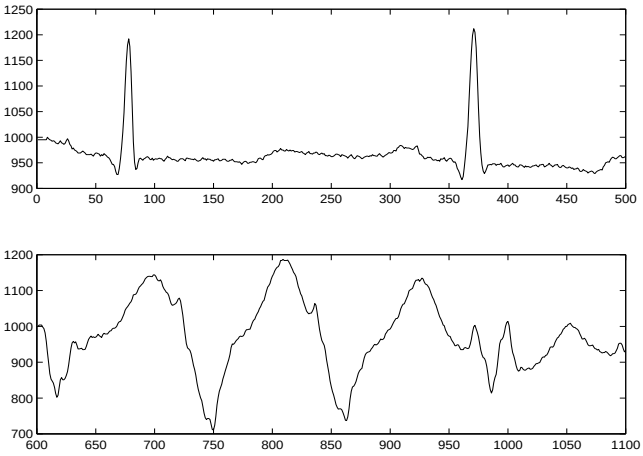

Figure 1: Test signals: 1) Normal sinus rhythm (MIT100, sample nr. 1 to 500) 2) Ventricular rhythm (MIT203, sample nr. 601 to 1100)

by a wide margin, especially at high sample reduction ratios. The version of the CCSP algorithm based on polynomial reconstruction have higher performance with respect to PRD than does the one based on linear interpolation for all sample reduction ratios considered in this case.

The gain of applying second order polynomial in reconstruction of the signal may seem very high by looking at Figure 2. However, the sample reduction ratios for the polynomial reconstruction case is not in accordance with the actual number of parameters that are needed in order to reconstruct each signal segment. This is due to the fact that in order to describe a second order polynomial, *three* parameters are generally needed while only two are necessary in the linear interpolation case.

As basis for reconstruction of the signal between two extracted samples we need one amplitude (the other is given as the previous end point) and the distance from the previous sample value, referred to as *run*, in the linear reconstruction case. In order to do second order polynomial reconstruction, we represent each polynomial $f_{n_k,n_{k+1}}$ by the amplitude $y(n_k)$, the run length, $n_{k+1} - n_k$, and the approximate sample value $\hat{y}\left(\frac{n_k+n_{k+1}}{2}\right)$. This data set determines the piecewise polynomial reconstruction uniquely. This way we get two amplitudes and one run as output from the compression algorithm in the polynomial case whereas the linear case required only one sample value and one run as output for each signal segment to be reconstructed.

In practice, entropy coding of the selected samples along with the corresponding runs take place. This is part of our future work with the existing algorithms. At this stage we are concerned with the compression method, which seems to have a high potential. However, it is clear that by applying entropy coding to the results it is possible to make a

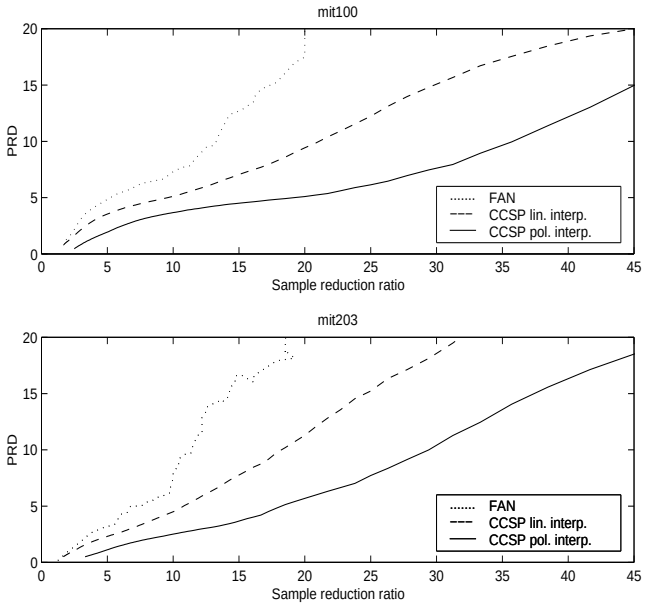

Figure 2: Sample reduction ration versus PRD for test signal 1: mit100 and test signal 2: mit203

more justified comparison of the methods. Encoding of the results will make it possible to evaluate a distortion measure as a function of *bit rate = average number of bits used to represent one signal sample* in the original signal. By doing this we also have a basis of comparing the results from the time-domain techniques to results from other types of techniques, such as transform domain techniques.

The algorithm presented in [1] compresses the given signal in an optimal way with respect to reconstruction error, given a bound on the number of signal samples to be extracted. The polynomial interpolation case is based on the same idea. The algorithm interpolates between two end points, but the third point used to represent $f_{n_k,n_{k+1}}$ is approximated on basis of the optimal polynomial coefficients. In a complete compression scheme, this approximated signal sample has to be quantized and this will cause the actual distortion to differ from the optimal distortion with some amount. In order to give a realistic picture, this approximated signal sample has been round off to the nearest integer in this context. In the case of test signal 1 with a sample reduction ratio of 20, the deviation from the optimal distortion amounts to 0.78 % of the optimal distortion. For the same compression ratio with test signal 2, the deviation amounts to 0.14 %. The deviation grows larger for lower sample reduction ratios, as more samples are retained and thus we get a higher contribution to the total quantization error. For test signal 1 with a sample reduction ratio of 10, the deviation amounts to 1.68 % of the optimal distortion.

The complexity of the algorithm for polynomial interpolation is of $\mathcal{O}(MN^2)$ as in the linear case, but the execution time is a bit longer in the polynomial interpolation case. This is probably due to the computations necessary to find the optimal polynomial coefficients. In order to cope with real time constraints, the techniques presented in [6] will be applied in future enhancements of the method.

5. CONCLUSIONS

This paper demonstrates how the optimal time-domain coder presented in [1] can be further developed in order to use second order polynomials in reconstruction of the signal. This is done without increase in the computational complexity of the algorithm. Compared to the algorithm in [1] where linear interpolation is applied in reconstruction of the signal, the algorithm presented here shows promising results. For reasonable sample reduction ratios, the algorithm based on polynomial interpolation gives significantly less reconstruction error than the one based on linear interpolation.

To be able to compare the algorithm developed here to other methods regarding compression of ECG signals in a fully justified way, the results have to be entropy coded. This will be part of our future work along with other possibilities of further development of the existing algorithms.

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