ECG Data Coding Using Piecewise Fractal Interpolation

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ABSTRACT

In this paper, we describe an approach to ECG data coding based on a fractal theory of iterated contractive transformations defined piecewise. The main characteristic of this approach is that it relies on the assumption that signal redundancy can be efficiently captured and exploited through piecewise self-transformability on a block-wise basis.

The variable range size technique is employed to reduce the reconstruction error. Large ranges are used for encoding the smooth waveform to yield high compression efficiency, and the smaller ranges are used for encoding rapidly varying parts of the signal to preserve the signal quality.

The suggested algorithm was evaluated using MIT/BIH arrhythmia database. A high compression ratio is achieved with a relatively low reconstruction error.

INTRODUCTION

In recent years, many algorithms for ECG data compression have been suggested. The need for ECG data compression stems from two main reasons; effective storage and effective real time transmission [1].

ECG data compression methods have been divided into three groups; direct methods, transformation methods and parameter extraction methods [1],[2]. The direct methods base their detection of redundancies on the direct analysis of the actual signal samples. Most of the direct data compression techniques employ polynomial predictors and interpolators. In contrast, transformation methods mainly use spectral and energy distribution analysis for detecting redundancies. The parameter extraction method is an irreversible process with which a particular characteristic or parameter of the signal is extracted.

Traditional methods to represent the single-valued data include polynomial fits and autoregressive moving-average (ARMA) models. With a polynomial fit, a data sequence is represented by the value of a polynomial evaluated at each sample point. ARMA models represent data as the output of a filter that is excited by an input, such as an impulse or white noise, with filter coefficients determined by a least-squares fit of the filter output to the data. With iterated function systems (IFS), the model uses the data itself to represent the discrete sequence and, as a result, is very different from traditional approaches [3]. In this paper, we apply IFS theory to discrete sequences of ECG signal.

ITERATED FUNCTION SYSTEMS

IFS theory has recently received a great deal of attention [3]-[9]. A fractal may be seen as a compact description of the hierarchy of features in a given phenomenon. Some of the best examples of this is the so called self-similar or self-affine fractals. These can be generated by finite collections of mappings acting on a metric space where a different map is chosen at random at each time step. Such dynamic systems have been given the name Iterated Function Systems (IFSs) by Barnsley[4][5].

An IFS is defined as a complete metric space X with a distance function h and a finite set of contractive mappings, $\{w_i : X \rightarrow X \text{ for } i = 1,2,...,M\}$. Each map, w_i, is usually affine and has the contractivity factor s_i where s_i satisfies $h(w_i(x), w_i(y)) \leq s_i \cdot h(x, y)$ for all $x, y \in X$, $0 \leq s_i < 1$.

The signal is encoded in the form of an iterative system (a space and a map from the space to itself) $W: X \rightarrow X$. The space X is a complete metric space of discrete sequences, and the mapping W (or some iterate of W) is a contraction. The contractive mapping fixed point theorem ensures convergence to a fixed point upon iteration of W. The goal is to construct the mapping W with fixed point 'close'(based on a properly chosen metric $h(f, g)$) to a given discrete sequence that is to be encoded, and such that W can be stored compactly. The collage theorem provides motivation that a good mapping can be found [4]. The decoding procedure consists of iterating the mapping W from any initial discrete sequence until the iterates converge to the fixed point.

Fractal techniques have been used for some time to create amazingly realistic computer graphics, such as mountain ranges and tree foliage. They are based on algorithms that recursively or iteratively generate patterns based on local rule. One of these algorithms is based on affine transforms. A transformation $w_i : X \rightarrow X$ of the form

$$w_i\begin{pmatrix} x \\ y \end{pmatrix} = \begin{pmatrix} a_i & b_i \\ c_i & d_i \end{pmatrix}\begin{pmatrix} x \\ y \end{pmatrix} + \begin{pmatrix} e_i \\ f_i \end{pmatrix} \quad (1)$$

where a_i, b_i, c_i, d_i, e_i, and f_i are real numbers, is called a two-dimensional affine transformation. Each affine transformation w_i can skew, stretch, rotate, scale and translate an input data.

IFS are able to produce fractals that we may consider to be any set with non-integer dimension and details at all scales of magnification. IFS's can produce complicated functions with only a few maps.

BLOCK-BASED FRACTAL CODING

Recently fractal techniques have been applied to coding real data [6]-[9]. The following block-based fractal coding technique exploits similarities in different parts of a one-dimensional signal.

Similar patterns in different parts of the signal must be matched by using affine transforms. This affine transforms have to be contractive. A method of forcing a spatial contraction is the pattern matching between blocks with eight samples and blocks with a number greater than 8, for instance 16.

The blocks with eight samples must tile the signal and are called range blocks. The blocks with 16 samples are called domain blocks and can be taken from any part of the signal.

For each range block in turn a domain block must be found that has a similar pattern. Maximizing the number of different patterns that can be extracted from the signal, will improve the chance of finding a good pattern match.

In encoding a signal, the type and magnitude of these data manipulations must be known by both the encoder and decoder. Therefore in order to code a range block, the encoder must transmit codewords to the decoder that indicate the location of the domain block in the signal and what type of modifiers must be used in order to generate the correct pattern for the range block.

There are many possible domain blocks in a signal, and there are a multitude of modifiers that could be used in order to try to generate a suitable pattern match for each range block. However, all this information must be transmitted to the decoder, so it is prudent to use only the minimum number of domain blocks and modifiers as is necessary to produce a set of patterns rich enough that most range blocks can find a satisfactory match. This reduced set of modifiers is a subset of the affine transform.

The decoding process can be dealt with in a similar way. The decoder is initialized with an arbitrary signal, and parts of the signal corresponding to domain blocks are taken, modified, and used to reduce other parts of the signal corresponding to range blocks. The striking aspect of fractal transforms is that, as the above algorithm is iterated, the decoded signal becomes increasingly more like the encoded signal and less as the arbitrary signal used as a starting point.

If the starting signal at the decoder had been different, a sine wave for instance, the signal at the decoder would still have converged to the signal at the encoder, although it might take a different number of iterations. This is because only contractive transforms were allowed. That is, the area of the domain block is greater than the area of the range block. At the decoder, any error associated with the original starting signal is reduced by the sample-value scaling factor at each iteration until it becomes insignificant [10].

FRACTAL INTERPOLATION

Fractal interpolation functions provide a new means for fitting experimental data. The graph of the fractal interpolation function can be made close to the data. Moreover, one can ensure that the fractal dimension of the graph of the fractal interpolation function agrees with that of the data, over an appropriate range of scales.

Let a set of data $\{(x_i, y_i) : i = 0,1,2,\dots,M\}$ be given. The interpolation points are taken as a subset of the data points with (x_0, y_0) and (x_M, y_M). The space X is the $x \times y$ plane and the interpolation function is constructed with M-affine maps of the form

$$w_i\begin{pmatrix} x \\ y \end{pmatrix} = \begin{pmatrix} a_i & 0 \\ c_i & d_i \end{pmatrix}\begin{pmatrix} x \\ y \end{pmatrix} + \begin{pmatrix} e_i \\ f_i \end{pmatrix}. \tag{2}$$

Affine maps such as (2) are often called shear transformations [4]: vertical lines are mapped to vertical lines contracted by the factor d_i. In equation (2), the parameter d_i is called the contraction factor for map i and is constrained to be real and lie in the interval (-1,1). Its value is independent of the interpolation points and it helps control the shape of the interpolation function between interpolation points.

Each affine map is constrained to map the endpoints of the set of interpolation points to two consecutive interpolation points. That is,

$$w_i\begin{pmatrix} x_0 \\ y_0 \end{pmatrix} = \begin{pmatrix} x_{i-1} \\ y_{i-1} \end{pmatrix} \text{ and } w_i\begin{pmatrix} x_M \\ y_M \end{pmatrix} = \begin{pmatrix} x_i \\ y_i \end{pmatrix} \text{ for } i = 1,2,\dots,M. \tag{3}$$

Thus, once the contraction factor d_i for each map has been chosen, the remaining parameters may be found using the endpoint constraints equation (3) and are given by

$$a_i = \frac{x_i - x_{i-1}}{x_M - x_0} \tag{4}$$

$$e_i = \frac{x_M x_{i-1} - x_0 x_i}{x_M - x_0} \tag{5}$$

$$c_i = \frac{y_i - y_{i-1}}{x_M - x_0} - d_i \frac{y_M - y_0}{x_M - x_0} \tag{6}$$

$$f_i = \frac{x_M y_{i-1} - x_0 y_i}{x_M - x_0} - d_i \frac{x_M y_0 - x_0 y_M}{x_M - x_0} \tag{7}$$

After the map parameters have been determined, the fractal interpolation function may be constructed with one of two algorithms: the deterministic algorithm or the random iteration algorithm [3].

The piecewise self-affine fractal model is a generalization of the linear fractal interpolation model and has its mathematical roots embedded in recurrent IFS theory [6],[7].

While the description of these models may be succinctly expressed, the fractal functions may be very complicated. In addition, since the number of degrees of freedom associated with these models is very large, it is important to find an efficient solution to the inverse problem.

One method for finding the best set of interpolation points for a given data set would be to exhaustively search all possible combinations of interpolation points and for each set, search for a set of contraction factors. However, this method is not computationally feasible and a more efficient procedure is required. We used the contraction factor calculation method suggested by Mazel and Hayes [3]. In this algorithm, the number of maps that one uses is variable and an error tolerance is set a priori.

INVERSE ALGORITHM

The encoding process of the AFI method proceeded as follows. Initially, the range block size s_R was chosen. A search was then performed for the domain block with size twice that of the range block which best minimized the distance between the original function H and the interpolation function $w(H)$. If this best domain block and its corresponding w resulted in an error less than a predetermined tolerance e_c, w was stored and the process was repeated for the next range block. If the predetermined tolerance was not satisfied, the range block was subdivided into two equal size blocks. This process was repeated until the tolerance condition was satisfied, or a range block of a predetermined minimum size r_{min} was reached. For range blocks of size r_{min}, the best w was stored whether or not e_c was satisfied. The process was continued until the entire signal was encoded.

The following steps are details of an iterative algorithm protocol for finding both the interpolation points and the contraction factors for a practical data set.

1) Choose the tolerance level e_c and the minimum range size r_{min}.
2) Choose the range block size s_R and the domain block size s_D with $s_D > s_R$.
3) Choose the domain block.
4) Compute the contraction factor d_i for the map associated with the range block defined by the pair of interpolation points.
5) If $|d_i| \geq 1$, choose the next domain block and then go to step 4.
6) Compute the map parameters and form the map w_i associated with the pair of interpolation points. Apply the map to each point of the function to yield $w_i(H)$.
7) Compute and temporarily store the distance between the original function H_i and the interpolation function $w_i(H)$.
8) Repeat steps 3-7 until the end of the function is reached.
9) If the distance $h(H_i, w_i(H)) \geq e_c$, then subdivide the range size and repeat steps 3-8 until the distance $< e_c$ or a range block of a predetermined minimum size was reached.
10) Store the pair of interpolation points and contraction factor that yield the minimum value of $h(H_i, w_i(H))$ from step 6 and 7.
11) Choose the next range block and repeat steps 3-10 until the entire function has been searched.

The above algorithm finds an IFS with a self-affine attractor that approximates the given function. The maps of the IFS found will be such that map w_i, when applied to H, will yield a function w_i(H) that is within a minimum distance of H_i. There is flexibility in the choice of the distance measure.

RESULTS

The amount of compression was represented in terms of compression ratio (CR) defined as the ratio between the number of bits needed to represent the signal and the number of bits in the compressed data.

As a quantitative measure of distortion, we have used the percent rms difference (PRD) defined as

$$PRD = \sqrt{\frac{\sum_{n=0}^{N-1}[x_{org}(n) - x_{rec}(n)]^2}{\sum_{n=0}^{N-1} x_{org}^2(n)}} \times 100 \qquad (8)$$

where $x_{org}(n)$ and $x_{rec}(n)$ are the original sampled ECG signal and the reconstructed signal, respectively, and N is the total number of samples in the data set. The PRD is easy to calculate, and thus is extensively used in the ECG compression literature [2].

The described AFI method with variable range size was tested using one channel of data from each of the MIT/BIH arrhythmia databases sampled at 400 samples/s with a 12-bit resolution.

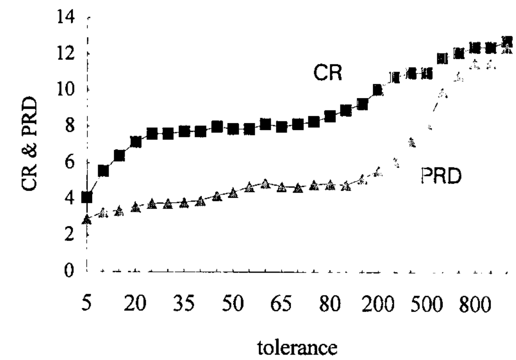

Fig. 1. Compression ratio and PRD with partitioning tolerance.

The coding-decoding system is based on the construction of a fractal code—a contractive data transformation for which the original data is an approximate fixed point—that produces a sequence of signals which converges to a fractal approximation of the original when applied iteratively on any initial data at the decoder.

For the MIT/BIH data we used $r_{min} = 8$ and the Euclidean distance measure. The variable range size technique is employed to reduce the reconstruction error and increase the compression ratio. Large ranges are used for encoding slowly varying parts of ECG to yield high compression efficiency, and pulse-like QRS complexes are divided into smaller ranges to preserve the range detail.

The values of the domain block size s_D and the range block size s_R are varied while the quotient s_D/s_R was held constant at two. As the range block size and domain block size are increased, we increase the compression ratio since we model larger pieces of given data with each map and, consequently, fewer maps are used.

For each map, the fractal interpolation requires the following parameters to represent a given data sequence: interpolation points, domain endpoints, contraction factors, range size, domain size and position.

Affine mapping coefficients are found for each range having the size of 64, 32, 16 or 8. The average storage requirement for a single w_i was 52 bits. The contraction factor d_i is quantized 6 bits. The position of R_i was inferred from the ordering. Only 10 bits were required to identify the size of R_i and the location of D_i, this number being dependent on both the choices of the number of possible domains and the level in the partitioning.

Fig. 1 is a plot of the compression ratio and PRD versus the tolerance for the range partitioning. The performance of the algorithm is demonstrated in Fig. 2. An ECG record with abnormal complex is shown.

Using the same database, the algorithm was compared with the fixed range fractal interpolation compression method [11]. The reconstructed and error signal using the FI algorithm are shown in Fig. 3, respectively. The comparison of the FI and AFI is summarized in Table I. In the new scheme, the reconstruction errors are distributed more uniformly and the peak error is usually lower at any compression ratio.

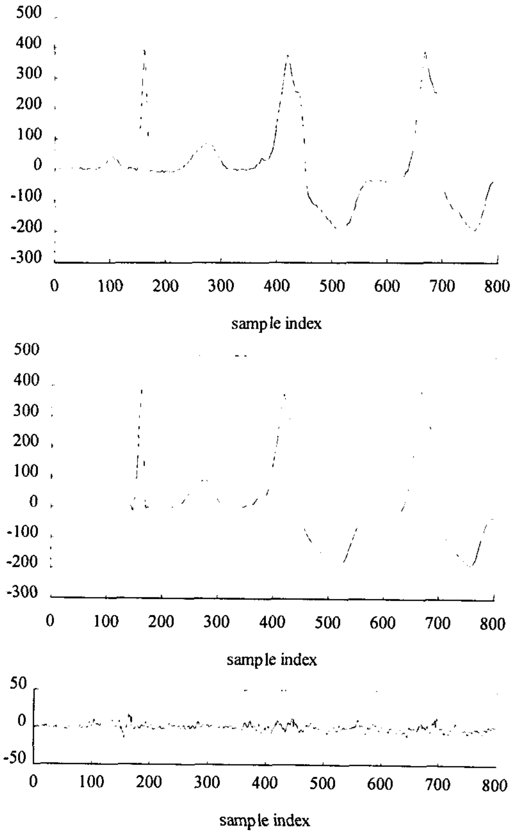

Fig. 2. Original ECG signal, its reconstruction using the AFI algorithm and the error signal.

In applications where a PRD of about 5% is acceptable, the AFI method yields CR as high as 9.09, without any entropy coding of the parameters of the fractal code. Note that a low PRD of 3.59% was achieved at CR of 7.16.

CONCLUSION

This paper presented an ECG data coding systems referred *Adaptive Fractal Interpolation* method that is based on a theory of iterated contractive data transformations. The AFI design issue is to select an adaptive data sequence partition made of nonoverlapping range blocks. The piecewise self-affine fractal interpolation is used where a discrete data set is viewed as being composed of contractive affine transformation of pieces of itself.

The AFI method using variable range size is found to yield a significantly lower reconstruction error for a given compression ratio than the fixed range size fractal interpolation method.

The attempt of fractal interpolation coding on ECG waveforms shows acceptable results. We believe that it is an interesting area that is worth further investigation.

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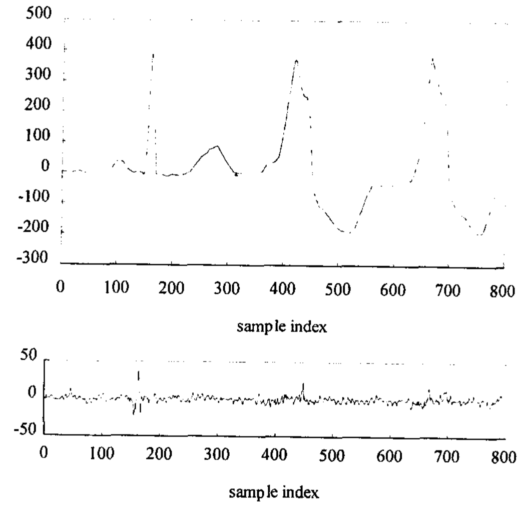

Fig. 3. Reconstructed and error signal using the FI algorithm.

Table I. The comparison of the FI and AFI algorithms.

FI			AFI		
range size	**CR**	**PRD**	tolerance	**CR**	**PRD**
7	3.22	2.32	5	4.07	2.91
8	3.68	3.25	10	5.56	3.29
9	4.14	3.41	20	7.16	3.59
10	4.60	3.80	30	7.62	3.77
12	5.52	4.24	50	7.88	4.39
16	7.36	5.76	100	8.92	4.81
20	9.19	6.73	200	10.06	5.62
24	11.03	10.52	500	10.99	8.19

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