The Application of Dynamic Time Warping to Measure the Accuracy of ECG Compression

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***Abstract*—** many different methods of ECG compression have been suggested over the last number of decades. They are typically classed into to three distinct groups – Direct Data, Parameter Extraction and Transform methods. The metric most frequently used to differentiate between the accuracy of the different types of compression is a percentage root-mean-square difference (PRD) calculation versus compression ratio, despite the accuracy of such a method having been acknowledged as greatly limited. In this article PRD calculation and an improved partial PRD difference method are investigated and their significant shortcomings highlighted. Dynamic time warping is presented as a method of quantifying the approximation error which may be present but goes undetected by the percentage PRD calculation due to approximation of the ECG. Dynamic time warping provides a significantly more accurate metric for comparing compression algorithms and their respective accuracies. It allows for detailed comparison of differing approximation methods and variations of the same approximation method, not possible using the RMS difference versus compression ratio. Its usefulness is fully investigated by comparing several direct data compression algorithms, including a novel threshold variation of the scan along polygonal approximation technique. Results provided demonstrate possible misdiagnosis of cardiac conditions resulting from the limitation of the RMS difference versus compression ratio metric and the benefits of the application of dynamic time warping in examining the accuracy of different compression techniques.

***Keywords*—** ECG Compression, Dynamic Time Warping, Approximation Error, Scan Along Polygonal Approximation, Error Threshold, Pattern Recognition, Signal Processing.

I. Introduction

DESPITE the rapid increase in storage capability and data transmission speeds, growth in the use of Holter monitors and remote ECG transmission [1]-[3] makes the requirement of ECG compression as prevalent today as it was during the 1960's when research into ECG compression techniques began. ECG compression methods are classed into three distinct groups - direct data compression, transforms and parameter extraction. Direct data compression algorithms detect redundancies in the data by analyzing the actual samples of the signal. Numerous direct data compression techniques have been developed with increasing complexity including the AZTEC algorithm [4], [5] the SAPA algorithms [6] and piece-wise approximation algorithms [7], [8]. There is a range of transformation and parameter extraction methods also having varying levels of complexity utilizing Fourier, Wavelet and Principal Component Analysis techniques such as [9]-[13].

In general, direct methods are considered superior to transforms in terms of system simplicity and approximation error [11], although transform methods typically provide a higher compression ratio and are not as sensitive to original recording sampling frequency [14].

Many comparative studies of these methods and algorithms use a percentage root-mean-square difference (PRD) between the original input signal and the reconstructed version as a test of accuracy [15]. However the PRD provides very limited insight into the ability of a compression algorithm to preserve diagnostically significant information contained within the recording [14]. Indeed the final decision on the clinical acceptability of the approximation usually depends on the reconstructed signals being visually inspected by a cardiologist [16].

This article, is an extension of the early stage work reported in [17] and proposes that the accuracy of a reconstructed approximation in terms of preservation of the original signal morphology and the location of its fiducial points (p-wave onset and termination etc) can be better measured using a two pronged method. First of all the original and approximated signals are divided into ECG components and inter-beat durations with partial PRD's calculated over the two groups separately. In theory one would wish to maximize the PRD of inter-beat durations and limit the PRD over the actual ECG components and this test gives an insight into where the resulting compression is obtained. Secondly, a signal processing pattern recognition method known as dynamic time warping (DTW) can be used to warp the original and reconstructed signals to each other and ensure the patterns around the fiducial points of the original signal have remained intact.

For the purposes of this article the accuracy of six direct data compression methods shall be compared, although

dynamic time warping could also be applied to any reconstructed approximation from the transform compression methods. Three of the approximation algorithms suggested by the authors here are novel in that they combine existing fixed error threshold algorithms with variable error threshold calculation techniques. The results will demonstrate that DTW can be used to identify accuracy differences not only between completely different algorithms but also subtle variations of the same algorithm e.g. with fixed and variable error thresholds. Indeed, when selecting an approximation technique, the user needs to find a balance between compression ratio and accuracy, a process that simple PRD calculation makes extremely difficult. Approximations yielding the same total PRD value from each algorithm will be tested and the results compared using partial PRD's and DTW to demonstrate the limitations of the PRD and the benefits of the new DTW approach.

II. Background

To demonstrate the advantages of DTW as a measure of compression accuracy several compression algorithms shall be used to approximate the ECG recordings. The algorithms include the piecewise linear approximation algorithm (PLA) as proposed by Koski et al [7] and the scan along polygonal algorithm as suggested by Ishijima et al [6]. Three novel techniques based on a combination of the scan along polygonal algorithm and Furhts amplitude zone time epoc coding [4] algorithm with variable threshold shall also be used.

A. The Piecewise Linear Approximation

The PLA algorithm as reported by Koski et al [7] presents a method of dividing the ECG into segments without the necessity of defining a large number of parameters to control the segmentation process. Segmentation methods such as this are used in pulse wave recognition, signal compression and pre-processing for pattern recognition applications [18] as the fundamental principle is the same in each case.

The algorithm starts with the first sample S(n) in the signal to be approximated and windows to a higher sample number in the signal S(n+L) where L is the widow length in terms of samples. It connects the two points with a line to form the new approximated segment of the signal and then calculates the error voltage ε as the Euclidean distance between the approximated line and each sample of the original signal segment. If the error exceeds a predefined error threshold at a particular sample the segment is now terminated

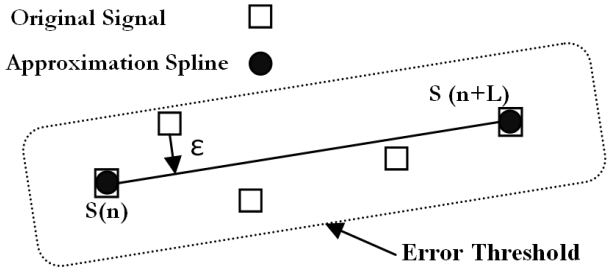

Fig. 1 The PLA Algorithm

at this point and the process repeats. If not, as in Fig. 1, the algorithm would then extend the endpoint to S(n+2L) and the process is repeated.

The overall result is that the approximated signal shall always be maintained within a predefined error threshold of the original signal. The sample number of the beginning, end and length of the segment can be recorded and used to reconstruct the approximation.

B. Scan along Polygonal Approximation (SAPA)

Presented by Ishijima et al [6], the SAPA technique is based on calculating the slope from one data point (the current vertex) to another the current end point of the spline ± the threshold error. The slopes from the vertex S(n) to the next point S(n+1)±Vth are recorded as M1 and M2. As the end point of the spline is extended from one point to the next, the smallest slope value from the vertex to the endpoint plus Vth is saved as M1 and the largest slope value from the vertex to the endpoint minus Vth is saved as M2. At all times the following slope criteria must hold:

$$M1>M2 \quad (1)$$

If for any candidate end point of the spline the criteria defined in (1) does not hold, as in Fig 2, the spline is terminated at the previous endpoint which will then act as the vertex of the next spline. The process is repeated on a sample by sample basis for the entire recording with the vertices and length of each spline recorded for reconstruction.

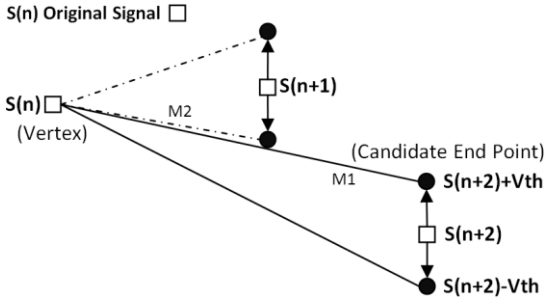

Fig. 2 The SAPA Algorithm

C. Scan along Polygonal Approximation with Centre Line Criterion (SAPA-2)

An extension of the first scan along polygonal compression method SAPA, the SAPA-2 algorithm is an ECG compression technique also presented by Ishijima et al [6]. It is based on calculating a number of slopes from a selected vertex (start point of a segment S(n) in Fig 3.) to a candidate end point of the segment. The algorithm initially selects the next data point S(n+1) as the candidate endpoint and calculates a slope to points at a predefined threshold above and below the sample. It then calculates a slope from the selected vertex to the candidate end point forming a centre line. The next point in the data, S(n+2) in Fig. 3, is now selected as the new candidate end point and the slopes are again calculated.

The smallest slope value from the vertex to the endpoint plus Vth is again saved as M1 and the largest slope value from the vertex to the endpoint minus Vth is saved as M2 as shown in Fig. 3. As the endpoint is incremented and the segment

length increases the following criteria must always apply:

$$MC \leq M1 \text{ and } MC \geq M2 \quad (2)$$

If they do not the segment is terminated, at the previous sample (S(n+1) in Fig.3) forming the end of the current segment and the vertex for the next.

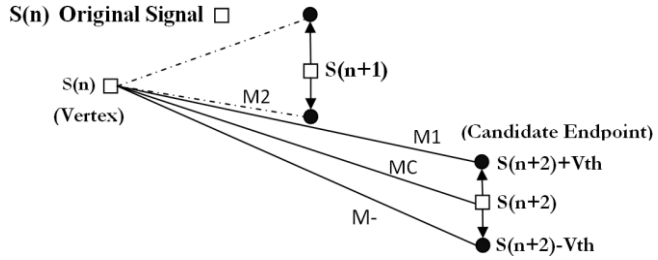

Fig. 3 The SAPA-2 Algorithm

D. Variable Error Threshold Approximation – The Amplitude Time Epoc Coding Algorithm (AZTEC)

The AZTEC algorithm [4] is intended for real time ECG data compression and typically offers a less accurate representation of the ECG signal than the other algorithms discussed. It effectively uses a sample and hold process to linearise the ECG by holding a sample until the approximation error exceeds the acceptable threshold error voltage. It generates a high compression ratio, low accuracy linearised signal as demonstrated in Fig 4 (pre-filtered).

Fig. 4 The AZTEC Algorithm

Since the AZTEC algorithm typically provides a low accuracy approximation, it shall not be included in the analysis here. AZTEC does however provide a variable error threshold not found in the other processing techniques discussed thus far. For approximation one would like to use a low error threshold for the ECG components themselves but a larger error threshold for the inter-beat durations in order to remove high frequency random spikes and noise which possess no clinically significant information. The AZTEC algorithm uses a statistical measurement known as the third moment along with the signal mean and standard deviation to vary the acceptable error threshold whilst the input signal is being processed. The error threshold is calculated recursively for a signal X with n samples as follows:

$$\text{Mean Value:} \quad \bar{X}_k = \frac{(k-1)\,\bar{X}_{k-1} + X_k}{k} \quad (3)$$

$$\text{Standard Deviation:} \quad \sigma_k = \sqrt{\frac{(k-1)\,\sigma^2_{k-1} + (X_k - \bar{X}_k)^2}{k}} \quad (4)$$

$$\text{Third Moment:} \quad M_k = \left[\frac{(k-1)\,M^3_{k-1} + (X_k - \bar{X}_k)^3}{k} \right]^{1/3} \quad (5)$$

$$CF_k = C_1\,(\sigma_k + M_k) \quad (6)$$

$$V_{th} = V_{th-1} - C_2 (CF_k - CF_{k-1}) V_{th-1} \quad (7)$$

Where $1 \leq k \leq n$, CF_k is the criterion function, C_1 and C_2 are pre-defined constants which can be varied to alter the variation of the error threshold as desired and V_{th} is the resulting error threshold. Although the AZTEC algorithm itself is intended for real time low accuracy applications its method of calculating a variable error threshold could be applied to more accurate algorithms that analyze the input signal on a sample by sample basis such as the SAPA algorithms.

E. Variable Threshold SAPA Algorithms – VTH-SAPA

If the variable threshold calculation originating from the AZTEC algorithm is applied to the SAPA and SAPA-2 compression techniques it may increase the usefulness of the SAPA algorithms by taking advantage of the AZTEC variable threshold calculation and combining it with the increased accuracy of the SAPA method of compression. These new variations of the SAPA algorithms shall be known as VTH-SAPA and VTH-SAPA-2. Fig. 5 demonstrates how the threshold dynamically varies with the variation of the ECG input signal.

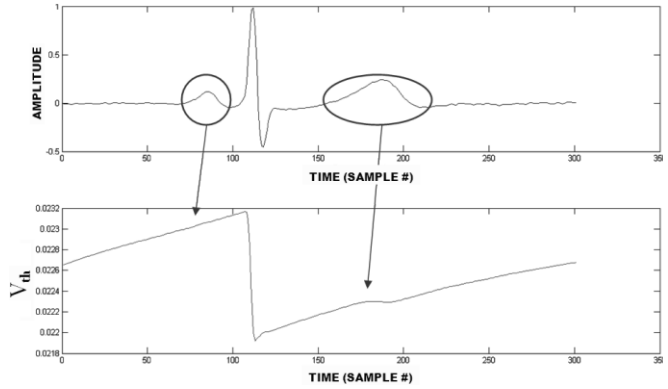

Fig. 5 Variable Voltage Threshold (C_1 =1 and C_2 = 4)

The constants C_1 and C_2 control the effect that CF_k has on the error threshold V_{th} but not the variation of CF_k itself i.e. its sensitivity to picks in the signal. Although some variation of the voltage error threshold is visible in Fig 5 the authors believe a more significant variation of the threshold due to the P and T-wave is desirable since the goal is for the error threshold to be sensitive to significant variations in the signal i.e. the P, QRS and T-waves. To achieve this, a new constant C_3 is introduced to the third moment equation (5) to accentuate the effect that the difference between the current sample X_k and the cumulative mean $\bar{X}_k$ has on the third moment. Now the third moment is calculated as

$$M_k = \left[\frac{C_3(k-1)\,M^3_{k-1} + (X_k - \bar{X}_k)^3}{k} \right]^{1/3} \quad (8)$$

With C_3=0.02 the increased sensitivity of the variable threshold to the presence of the P, QRS and T-waves is demonstrated in Fig. 6.

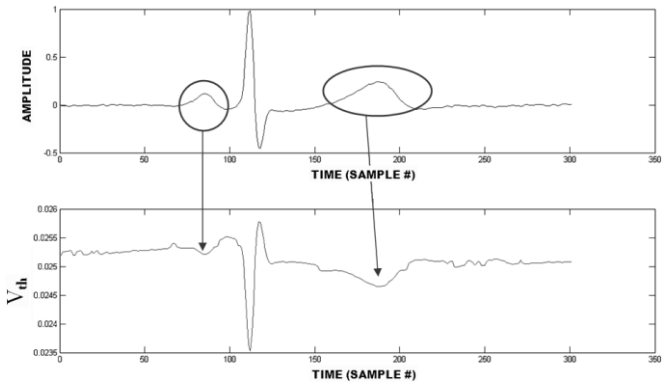

Fig. 6 Modified Variable Voltage Threshold

This final modified variable threshold calculation shall be applied to the SAPA-2 algorithm, and shall be known as the MOD-VTH-SAPA-2 algorithm.

F. Percentage RMS Difference Calculation

The error introduced by compression of ECG data is frequently measured using the percentage root-mean-square difference [19]. Even though it is acknowledged by most of the authors who use it as not guaranteeing the preservation of clinical information [14], it is still used as a measure of accuracy in most of the compression articles referenced here.

$$PRD=\sqrt{\frac{\sum_{i=1}^{n}\left[X(i)-A(i)\right]^2}{\sum_{i=1}^{n}X(i)^2}}\,x100 \tag{9}$$

Where X(i) and A(i) are samples of the original and approximated signals respectively.

G. Dynamic Time Warping

Dynamic Time warping is a process whereby two signals are time aligned with one another through expansion or compression of sample points. Dynamic time warping comes in many forms where the criteria for matching the two signals optimally may involve matching the slopes of the underlying segments as in [18] or calculating a distance matrix between each point in the two signals. By matching an unknown ECG signal to a signal with known characteristics it is possible to identify similar characteristics in the unknown signal [20]-[22].

The implementation of the algorithm used by the authors is most similar to that suggested by Theodoridis [23] and Huang et al [20]. Consider the two input signals, the known signal s1 of length n and unknown signal s2 of length m. From the input signals two matrices are created, S1 an mxn matrix which contains the known signal repeated on each row and S2 an mxn matrix which contains the unknown signal repeated in each column. A distance matrix D can now be calculated as a single dimension Euclidean distance:

$$D(a,b)=[S1(a,b)-S2(a,b)]^2 \tag{10}$$

Were $1\le a \le m$ and $1\le b\le n$.

The next step calculates a cumulative distance or "cost" matrix C, which measures the minimum cost of matching each sample in the two signals. The cost matrix C is created by starting at location (1,1) of matrix D and calculating the cumulative distance of row one and column one of the matrix D storing the results in the corresponding location of a new cumulative distance matrix C (an mxn matrix also). The remaining cumulative values to be stored in the cost matrix are calculated by following the recursive equation:

$$C(a,b) = d(a,b)+\min\begin{cases} d(a,b-1) \\ d(a-1,b-1) \\ d(a-1,b) \end{cases} \tag{11}$$

Were $1\le a\le m$ and $1\le b\le a$.

The final stage in the process involves starting at location C(m,n) of the cumulative distance matrix and moving to the smallest "cost" value stored in any one of the adjoining locations. One can traverse all the way back to (1,1) of the matrix C, recording the path used which results in the minimum accumulated difference. Two new sample sets are then created called S1W and S2W representing the x co-ordinates of the path for S1W and y co-ordinates for S2W. Fig. 7 demonstrates the optimal path calculation process. These two new signals are called the warped signals and are the same length as each other. The optimal path traced through the minimum cost of adjoining cells may dictate that certain samples of each signal may be repeated ("padding" as in Fig 7.) to optimally match a corresponding point in the other signal during the warping process.

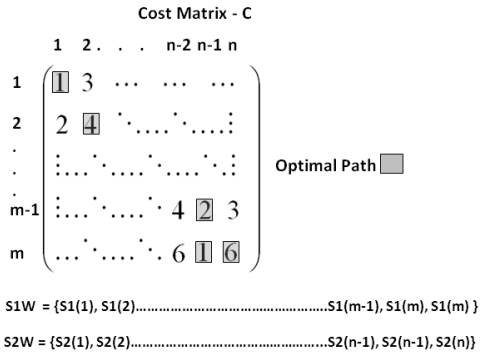

Fig. 7 Warping Process

Fig. 8 demonstrates the results of dynamic time warping of an ECG signal and its approximation.

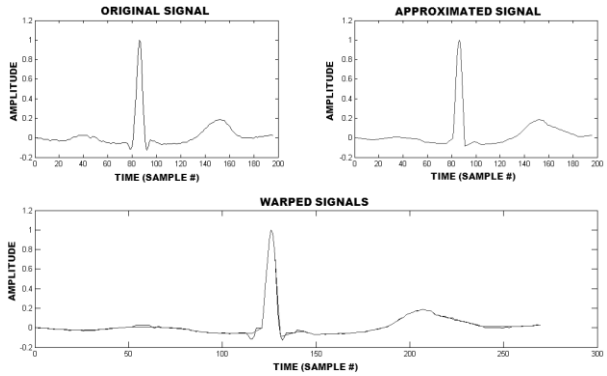

Fig. 8 Warped Original and Approximated Signals

Table 1: Test Signal # 16272								
Total PRD %	PLA Beat PRD %	PLA Inter-Beat PRD %	SAPA-2 Beat PRD%	SAPA-2 Inter-Beat PRD %	VTH-SAPA-2 Beat PRD %	VTH-SAPA-2 Inter-Beat PRD%	MOD-VTH-SAPA-2 Beat PRD %	MOD-VTH-SAPA-2 Inter- Beat PRD %
0.5	0.30	4.60	0.14	5.10	0.18	5.6	0.16	5.7
1.0	0.70	10.5	0.47	13.6	0.47	13.5	0.49	13.1
5.0	3.50	55.0	4.28	40.0	4.19	40.4	4.21	40.1
7.0	4.39	83.4	6.30	45.0	6.42	45.7	6.22	44.3
10.0	6.25	98.0	9.30	58.0	9.23	58.6	9.38	53.8

Table 2: Test Signal # 16539								
Total PRD %	PLA Beat PRD %	PLA Inter-Beat PRD %	SAPA-2 Beat PRD%	SAPA-2 Inter-Beat PRD %	VTH-SAPA-2 Beat PRD %	VTH-SAPA-2 Inter-Beat PRD%	MOD-VTH-SAPA-2 Beat PRD %	MOD-VTH-SAPA-2 Inter- Beat PRD %
0.5	0.40	5.56	0.28	8.19	0.28	7.65	0.28	7.68
1.0	0.85	11.2	0.74	12.5	0.76	12.7	0.69	12.7
5.0	3.91	49.8	4.57	40.6	4.81	41.4	4.55	45.3
7.0	5.32	73.8	6.44	50.2	6.33	49.9	6.18	53.6
10.0	8.32	87.3	9.10	67.8	9.06	71.1	9.09	65.9

If the same signal is used as both inputs to the warping algorithm no padding is required as the two signals will match perfectly. Similarly, if a high-accuracy, low-compression-ratio approximation of an ECG signal is matched to the original signal the warping algorithm will match the fiducial points of the approximated signal to the corresponding points in the original signal. However if the accuracy of the approximation is reduced it will begin to distort or alter the profile of the original signal and the dynamic time warping algorithm will then match the fiducial points from the approximation to other points in the original signal. In other words, the shape of the signal has been significantly distorted to the point where the sample annotated as the fiducial point in the original signal now corresponds to another point in the approximation i.e. it has been moved and an error in location has been introduced.

III. Compression Accuracy Using Partial PRD

In simplistic terms a compression algorithm should remove as much inter-beat noise as possible since it provides no clinically significant information whilst preserving the actual waves of the ECG as accurately as possible. A method of measuring this would be to calculate PRD values across the wave components of the ECG and then the inter-beat durations separately using annotations to divide the signals appropriately. The algorithm which minimises the PRD for the ECG components (P-onset to T-termination), whilst providing a higher PRD for inter-beat durations (T-termination to next P-onset) can therefore be regarded as the more accurate. In the absence of a set of annotations the user can segment the signal by visual inspection. Although this does not guarantee that the "beat" and "inter-beat" durations are exactly as described it should still offer a good approximation for the segmentation of the signal under analysis.

The application of partial PRD calculation shall be demonstrated using two test signals chosen from the QT Database of fully annotated ECG recordings available on the MIT-Physiobank website [24]. The two signals were originally contained in the Normal Sinus Rhythm Database as detailed by Laguna et al [25]. It is intended to demonstrate how two approximations can yield the same total PRD value but significantly different partial PRD results. Approximations using the PLA and each variation of the SAPA-2 algorithms were generated for several signals that yielded the same total PRD value. Each original signal and its corresponding approximation were then segregated into accumulated ECG "beat" and "inter-beat" durations. The waveforms shown in Fig. 9 are created by connecting the signals at annotated points.

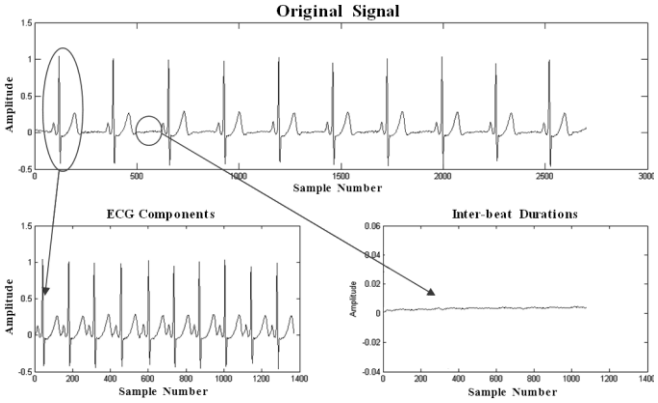

Fig. 9 Partial ECG signals

Partial PRD calculations are calculated between each "beat" component of the original and approximated signal and each "inter-beat" component of the original and approximated signals separately. The data shown in Tables 1 and 2 demonstrate how approximations which yield the same total PRD value can in fact provide significantly different partial PRD results.

As can be seen from Tables 1 and 2 above despite each algorithm producing the same total PRD, they actually preserve the ECG beats and compress outlying inter-beat noise to quite different extents. The partial PRD can be used to observe not only how different approximation methods i.e. the

PLA and SAPA algorithms preserve the signal but also to make observations with regard to variations of the same approximation technique (SAPA-2 in this case).

Observe from Table 1 that for low total PRD values of 0.5-1.0% the SAPA-2 algorithm results in a lower beat PRD and a higher inter-beat PRD value than the PLA algorithm as required. However as the total PRD increases beyond 1% the PLA algorithm results in lower beat PRD values than any of the SAPA-2 algorithms. The conclusion can be drawn that for the #16272 signal the algorithm chosen for approximation depends on the overall amount of compression required.

Partial PRD's can also identify the subtle performance changes introduced by adding the variable error threshold and its modified version to the SAPA-2 algorithm. From Table 2 for example, it can be seen that the VTH-SAPA-2 algorithm provides similar inter-beat PRD values and lower beat PRD values than its original SAPA-2 and MOD-VTH-SAPA-2 forms for most of the total PRD percentages.

Using just the total PRD calculation each of the approximations detailed in Tables 1 and 2 would have been regarded as having provided the same level of accuracy. It was shown how using partial PRD's further insight into approximation can be gained. The issue remains however that a low partial or total PRD value means that both of the signals had similar amplitude profiles overall but that does not ensure that the area around the fiducial points has not been distorted by the approximation. To identify that possible distortion DTW shall be applied.

IV. Dynamic Time Warping to Test Compression Accuracy

When annotating an ECG signal, a cardiologist will annotate the onset and termination of each component based on the shape and profile of the signal as observed simultaneously in one or many of the ECG recording leads. In order to achieve a genuine measure of what effect each algorithm has on the fiducial points and the ECG morphology around the fiducial points; dynamic time warping can be applied.

The dynamic time warping algorithm shall seek to match the two test signals and their approximations using the PLA, SAPA, SAPA-2 algorithms and variable error threshold algorithms VTH-SAPA, VTH-SAPA2 and MOD-VTH-SAPA2. After the two signals have been warped, the location of the fiducial points from the original signal should ideally match with the corresponding sample number in the approximated signal, provided no significant altering of the signal morphology has occurred. The warping algorithm by its very nature will match the fiducial point in the approximation and the profile surrounding it optimally to the same section within the original signal.

If the warping algorithm matches the approximated fiducial point to a different point in the original signal then the morphology has been altered by the approximation such that the locations of the fiducial points originally identified by the cardiologist have now been changed.

All ten of the Normal Sinus Rhythm signals available in the QT database were used to test the dynamic time warping algorithm. Five approximations yielding the same total PRD value for each algorithm and test signal were created and warped to the original signal. The mean error between the location of the original fiducial point and the optimum match in the approximated signal was calculated and along with the standard deviations of cardiologist annotation are shown in Table 3. Also provided in Table 3 is an estimate of the average compression ratio provided by each algorithm for each total PRD value. These compression ratios are calculated as the original number of sample points divided by the number of sample points retained for reconstruction after approximation.

A. Avoiding the Distortion of the Clinically Significant Fiducial Points

The results in Table 3 (next page) demonstrate that the algorithms have different mean error figures with regard to each fiducial point despite all approximation methods yielding the same total PRD calculation. To quantify the possible consequences of this section (f) in Table 3 is a measure of the acceptable standard deviation in the annotation of the same ECG recording by different cardiologists as reported by Jané et al [26].

Using the PRD versus compression ratio decision method all algorithms would have been classed as having maintained the same level of accuracy for a total PRD of 3.5% with the PLA providing a higher average CR of 7.92 than any of the other algorithms (see section (g)). The PLA algorithm would be chosen as the optimum algorithm as it yields a higher CR.

However it can be observed that for a total PRD of 3.5% the SAPA-2 algorithm preserves the P-onset with a mean and standard deviation error of 10.8±6.0ms from its original location while the PLA preserves it to within 21.2±16.2ms. The acceptable standard deviation (mean unattainable) between expert annotators in the location of a P-onset point in an ECG recording is ±10.2ms. The SAPA-2 algorithm preserves the location of the P-onset to within a lower mean than the PLA and also has a lower standard deviation than the cardiologists while the PLA algorithm does not. Due to its higher compression ratio the PLA algorithm has in fact altered the location of the fiducial point beyond the range of acceptability that applies to its annotation by different cardiologists, altering the clinically significant information. The PRD measure fails to detect this.

B. Establishing the effects of variable error threshold

As discussed in Section II the SAPA and SAPA-2 algorithms were altered by the authors to include a variable error threshold calculation. This variable error threshold dynamically changes as each sample of the signal is processed. During periods of low activity (i.e. between beats) the threshold will increase to attempt to remove as much inter-beat noise as possible and during high amplitude or sustained ECG activity (i.e. the QRS and T-waves) the threshold will reduce to attempt to preserve the morphologies as accurately as possible as demonstrated in Fig. 6. The differing behaviour of the fixed and variable versions of the algorithms is again impossible to identify from the total PRD calculation. Using the total PRD versus compression ratio selection criteria it would be concluded that the SAPA-2 algorithm is a better

Table 3: Mean± Standard Deviation of Fiducial Error Due to Approximation and Mean Compression Ratio (CR)

	(a) P-Onset						(b) P-Termination					
Total PRD %	PLA (ms)	SAPA (ms)	VTH-SAPA (ms)	SAPA-2 (ms)	VTH-SAPA-2 (ms)	MOD-VTH-SAPA-2 (ms)	PLA (ms)	SAPA (ms)	VTH-SAPA (ms)	SAPA-2 (ms)	VTH-SAPA-2 (ms)	MOD-VTH SAPA-2 (ms)
0.01	0.0±0.0	0.0±0.1	0.1±0.3	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0
0.5	2.5±2.2	1.6±1.7	1.7±1.7	0.9±1.6	0.9±1.8	1.2±2.1	0.2±0.2	0.4±0.3	0.3±0.3	0.0±0.1	0.0±0.1	0.0±0.1
1.5	4.1±2.3	3.4±2.4	3.2±2.3	2.7±3.6	2.8±3.8	3.0±3.8	0.7±0.5	0.4±0.4	0.4±0.4	0.5±0.9	0.5±0.9	0.4±0.8
2.5	12.0±7.5	15±9.8	15.8±10.6	7.8±5.0	7.6±4.6	7.4±4.3	1.4±1.5	1.5±1.3	1.6±1.6	1.4±1.4	1.4±1.4	1.3±1.4
3.5	21.2±16.2	34±18.4	39.0±24.9	10.8±6.0	12.0±6.6	10.7±6.3	3.1±2.8	4.0±3.1	4.1±3.1	1.8±1.6	1.8±1.7	1.9±1.9

	(c) QRS-Onset						(d) QRS-Termination					
Total PRD %	PLA (ms)	SAPA (ms)	VTH-SAPA (ms)	SAPA-2 (ms)	VTH-SAPA-2 (ms)	MOD-VTH-SAPA-2 (ms)	PLA (ms)	SAPA (ms)	VTH-SAPA (ms)	SAPA-2 (ms)	VTH-SAPA-2 (ms)	MOD-VTH-SAPA-2 (ms)
0.01	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0
0.5	0.8±1.6	0.9±1.2	1.0±1.3	0.0±0.1	0.0±0.1	0.0±0.1	0.0±0.1	0.0±0.1	0.0±0.1	0.0±0.0	0.0±0.0	0.0±0.0
1.5	1.8±1.9	2.1±1.4	2.0±1.3	0.4±0.6	0.4±0.7	0.4±0.7	0.1±0.3	0.1±0.2	0.2±0.5	0.0±0.0	0.0±0.0	0.0±0.0
2.5	4.1±2.6	4.5±3.0	4.4±2.8	0.9±1.1	1.2±1.0	1.3±1.1	0.5±1.1	0.2±0.3	0.2±0.3	0.1±0.2	0.1±0.2	0.1±0.2
3.5	8.4±5.7	7.1±6.2	6.3±4.3	2.5±1.7	2.3±1.7	2.8±1.7	0.6±1.1	0.7±1.4	0.7±1.4	0.7±1.7	0.8±1.8	0.7±1.5

	(e) T-Termination					
Total PRD %	PLA (ms)	SAPA (ms)	VTH-SAPA (ms)	SAPA-2 (ms)	VTH-SAPA-2 (ms)	MOD-VTH-SAPA-2 (ms)
0.01	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0
0.5	0.2±0.3	0.1±0.2	0.2±0.3	0.4±0.9	0.3±0.8	0.3±0.7
1.5	0.5±0.6	0.5±0.5	0.5±0.5	0.4±0.6	0.4±0.6	0.4±0.5
2.5	1.7±2.3	1.6.±1.5	1.5±1.3	1.6±2.6	1.6±2.6	1.6±2.4
3.5	3.2±3.4	4.4±3.4	4.2±3.2	3.9±3.9	3.8±3.1	3.8±3.7

(f) Standard Deviation in Cardiologist Annotations	
P-onset (ms)	±10.2
P-termination (ms)	±12.7
QRS-onset (ms)	±6.5
QRS-termination(ms)	±11.6
T-termination (ms)	±30.6

	(g) Mean Compression Ratio (C.R.)					
PRD %	PLA (ms)	SAPA (ms)	VTH-SAPA (ms)	SAPA-2 (ms)	VTH-SAPA-2 (ms)	MOD-VTH-SAPA-2 (ms)
0.01	1.193	1.195	1.172	1.002	1.002	1.003
0.5	2.629	2.351	2.354	1.204	1.204	1.200
1.5	4.863	4.287	4.231	1.806	1.803	1.798
2.5	6.657	5.778	5.741	2.347	2.340	2.317
3.5	7.920	6.911	6.928	2.853	2.868	2.851

choice of approximation than its variable threshold forms since it provides a higher C.R. for total PRD of 0.5-2.5%.

However when one examines the mean and standard deviation DTW error results it can be observed that the SAPA-2 algorithm typically preserves the P-wave more accurately whilst the MOD-VTH-SAPA-2 preserves the T-wave termination more accurately. Which algorithm the user would choose based on these results would be application specific but using DTW the user is now aware of the advantages and disadvantages of using the modified variable threshold version of the SAPA-2 algorithm.

V. Conclusion

Percentage RMS difference calculation has been used as a measure of approximation accuracy for decades primarily because it is a convenient calculation to perform. PRD versus compression ratios are typically used to differentiate between the accuracy of different compression algorithms.

A new method of applying the PRD algorithm is suggested which involves calculating PRD's over the constituent components of the ECG signal and inter-beat durations separately. Using partial PRD calculations it was possible to identify how approximations which yielded the same total PRD calculations can in fact have partial PRD results which differ significantly. Using partial PRD one can also observe the differences between the fixed and variable error threshold algorithms presented in this article. If a higher inter-beat PRD is observed it implies that more insignificant inter-beat noise was compressed. By the same token, a lower PRD value observed over the actual ECG components would imply that the algorithm preserves the morphology of the original signal more than one with a higher PRD value. However, neither the total or partial PRD values provide a very reliable test of the preservation of the original morphology as proven by the results of time warping.

Dynamic time warping is offered as a method of measuring distortion of the original signal due to approximation. By warping the original and approximated signals to each other the resulting alteration of the morphology and the fiducial points can be estimated. One would expect the approximation to preserve the location of the fiducial points to within the standard deviation of expert cardiologist's opinion in order to be acceptable. As an example a case is presented where two different approximation algorithms yielding the same total PRD values were compared in terms of CR and preservation of the fiducial points. It was shown how one algorithm, the PLA, distorted the P-onset location on average more than the standard deviation of cardiologist's annotations while all of the other five approximation algorithms did not. Yet with a higher

CR the PLA algorithm would have been chosen using the PRD versus CR selection criterion. The consequences of such error are significant since clinical diagnosis relies heavily on assessment of the duration of ECG components [27].

Three new variable error threshold versions of the SAPA and SAPA-2 algorithms were presented. Again using the total PRD versus CR selection criteria the subtle variations in accuracy that the different versions of the algorithms provide were not visible. However using DTW one could see what portions of the signal were best and least preserved using the various approximation algorithms. The selection of approximation method can then be made based on the application and what weight the user places on preservation of the various portions of the ECG.

The dynamic time warping results are in contradiction with both the total PRD calculation which would indicate that all approximations are as accurate as each other, and the partial PRD calculation which indicate the PLA algorithm provides similar or better preservation of the actual ECG or "beat" components of the original signal than the SAPA-2 algorithm. However the DTW results demonstrate that not only does the original SAPA-2 algorithm preserve the ECG morphology more accurately than the PLA, but that the novel variable threshold forms VTH-SAPA-2 and MOD-VTH-SAPA-2 can preserve the signal morphology in different ways also. With the plethora of new accuracy information an approximation method may be chosen depending on the user requirements rather than the crude PRD versus CR method.

This novel method of testing approximation accuracy which is a powerful alternative to PRD calculation, raises significant concerns over the use of PRD to determine approximation accuracy and is a useful method of comparing approximation algorithms. Time warping essentially provides a similar test to having the approximations viewed by a cardiologist. In this context the results indicate that direct data compression, transform and parameter compression algorithms should be compared using dynamic time warping and not PRD versus CR. The benefit of the approach is also that it does not require transformation of the signals to another domain to extract the significant features of the recording and the associated complexity and error associated with such transformations. In staying in the time domain the accuracy of the approximations are determined using the exact same time domain features of the signal used by the end user i.e. a cardiologist, during the analysis of the recordings and associated diagnosis.

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