# A Novel Approach in Testing the Accuracy of ECG Compression using Partial Percentage RMS Difference and Dynamic Time Warping

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*Abstract:* - Compression of recorded ECG data has been a topic of interest since the introduction of computer storage and later Holter monitor applications of ECG recording technology. Compression is typically performed using an approximation algorithm belonging to one of three classes; direct data compression; transformation and parameter extraction. Some debate exists as to how the accuracy of each implementation should be measured and despite obvious limitations of a percentage RMS difference (PRD) calculation it has been used as a metric for comparing different compression techniques in terms of PRD versus compression ratio. This article questions the use of a percentage RMS difference (PRD) function as a sole measure of the fidelity of the compressed signal by demonstrating the possible error in the compressed signal that a total PRD fails to detect. A novel accuracy test procedure is presented which demonstrates how partial PRD calculations and more importantly dynamic time warping can be used to compare an annotated ECG signal and its reconstructed approximation identifying distortion of clinically significant information.

*Key-Words:* - ECG Compression, Dynamic Time Warping, Approximation Error, Dynamic Programming, Direct Data Compression, Pattern Recognition.

## 1 Introduction

Despite the rapid increase in storage capability and data transmission speeds, growth in the use of Holter monitors and remote ECG monitoring 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 sorted 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 [1], the SAPA algorithms [2] and piece-wise approximation algorithms [3,4]. There are a range of transformation and parameter extraction methods also with varying levels of complexity utilizing Fourier and wavelet techniques such as [5,6].

In general direct methods are considered superior to transforms in terms of system simplicity and approximation error [7], although transform methods typically provide a higher compression ratio and are not as sensitive to original recording sampling frequency [8].

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 [9]. However the PRD provides very limited insight into the ability of a compression algorithm to preserve diagnostically significant information contained within the recording [8]. Indeed the final decision on the clinical acceptability of the approximation usually depends on the reconstructed signals being visually inspected by a cardiologist [10].

This article 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 was applied. 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.

The benefit of using partial PRD calculations and applying DTW as opposed to the commonly used total PRD calculation as a measure of accuracy shall be

demonstrated by comparing the results of two different approximation algorithms, although the same principle applies for any compression method. Approximations yielding the same total PRD value from each algorithm will be tested and results compared using partial PRD's and DTW to demonstrate the limitations of the PRD and the benefits of the new approach.

# 2 Background

The piecewise linear approximation algorithm (PLA) as proposed by Koski et al [3] and the second scan along polygonal algorithm (SAPA2-Centre Line Criterion) as suggested by Ishijima et al [2] are both direct data compression algorithms.

## 2.1 Piecewise Linear Approximation (PLA)

The PLA algorithm as reported by Koski et al [3] presents a method of segmenting 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 [11] 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 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.

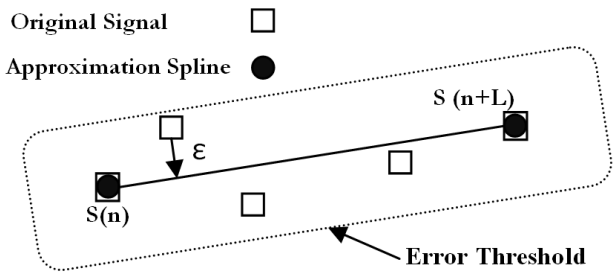


Fig. 1 The PLA Algorithm

The overall result is that the approximated signal shall always pass to 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.

## 2.2 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 originally presented by Ishijima et al [2]. It is based on calculating a number of slopes from a selected vertex (start point of a segment S(n) in Fig 2.) 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. 2) 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 saved as M1 and the largest slope value from the vertex to the endpoint minus Vth is saved as M2 as shown in Fig. 2.

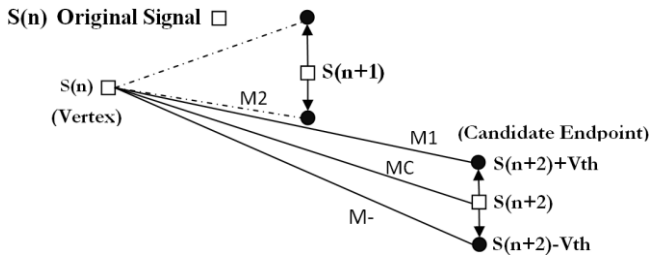


Fig. 2 The SAPA-2 Algorithm

As the endpoint is incremented and the segment length increases the following criteria must always apply:

$$Mc \leq M1 \text{ and } Mc \geq M2 \quad (1)$$

If it does not the segment is terminated, at the previous sample (S(n+1) in Fig.2) forming the end of the current segment and the vertex for the next.

## 2.3 Percentage RMS Difference Calculation

The error introduced by compression of ECG data is frequently measured using the percentage root-mean-square difference [12]. Even though it is acknowledged by most of the authors who use it as not guaranteeing the preservation of clinical information [8], it is still used as a measure of accuracy in most of the compression articles referenced here.

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

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

## 2.4 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 [11] or by calculating a distance matrix between the two signals. By matching the unknown ECG signal to the signal with known characteristics it is then possible to identify similar characteristics in the unknown signal [13]-[15].

The implementation of the algorithm used by the authors was most similar to that suggested by Theodoridis [16] and Huang et al [13]. 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 by single dimension Euclidean distance:

$$D(a,b)=[S1(a,b)-S2(a,b)]^2 \quad (3)$$

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:

$$c(a,b) = d(a,b)+\min \begin{cases} d(a,b-1) \\ d(a-1,b-1) \\ d(a-1,b) \end{cases} \quad (4)$$

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. 3 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 3.) to optimally match a corresponding point in the other signal during the warping process.

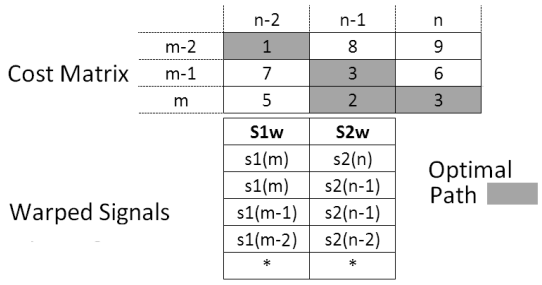


Fig. 3 Warping Process

Fig. 4 demonstrates the results of dynamic time warping of two ECG recordings of differing shape and profile.

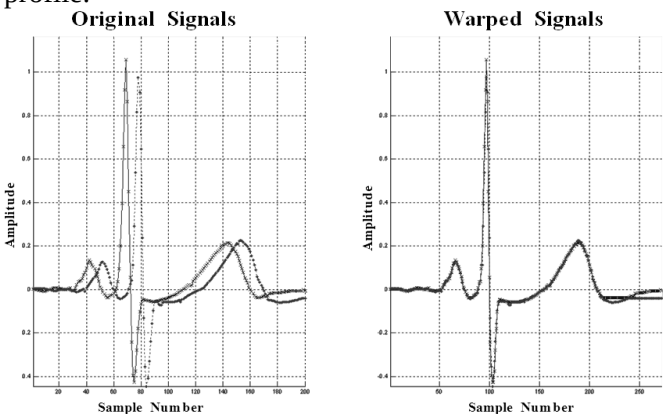


Fig. 4 Results of dynamic time warping process

If the same signal is used as both inputs to the warping algorithm there will be no padding 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.

## 3 Compression Accuracy using Partial PRD

Despite the frequent use of PRD calculations as a means of comparing the accuracy of different compression algorithms, its ability to reflect preservation of the timing of the ECG components (P-wave, QRS complex etc) is questionable. As a rule of thumb it can be validly stated that 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) could hence be regarded as the more accurate.

Two test signals were chosen from the QT Database of fully annotated ECG recordings available on the MIT-Physiobank website [17]. The two signals were originally contained in the Normal Sinus Rhythm Database as detailed by Laguna et al [18]. 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 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. 5 are created by connecting the signals at annotated points.

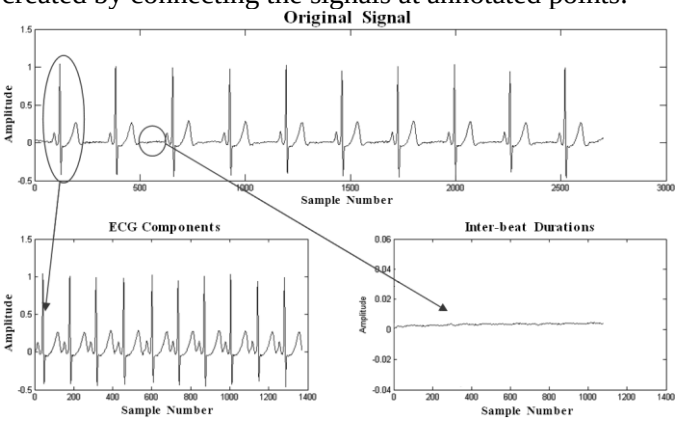


Fig. 5 Partial ECG signals

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.

**Table 1: Test Signal # 16272**

| Total PRD % | PLA Beat PRD % | SAPA-2 Beat PRD% | PLA Inter Beat PRD % | SAPA-2 Inter Beat PRD % |
|---|---|---|---|---|
| 0.5 | 0.3 | 0.1 | 4.6 | 5.1 |
| 1.0 | 0.7 | 0.5 | 10.5 | 13.6 |
| 5.0 | 3.5 | 4.3 | 55.0 | 40.0 |
| 7.0 | 4.4 | 6.3 | 83.4 | 45.0 |
| 10.0 | 6.3 | 9.3 | 98.0 | 58.0 |

**Table 2: Test Signal # 16539**

| Total PRD % | PLA Beat PRD % | SAPA-2 Beat PRD% | PLA Inter Beat PRD % | SAPA-2 Inter Beat PRD % |
|---|---|---|---|---|
| 0.5 | 0.4 | 0.3 | 5.6 | 8.2 |
| 1.0 | 0.9 | 0.7 | 11.2 | 12.5 |
| 5.0 | 3.9 | 4.6 | 49.8 | 40.6 |
| 7.0 | 5.3 | 6.4 | 73.8 | 50.2 |
| 10.0 | 8.3 | 9.1 | 87.3 | 67.8 |

As can be seen from Tables 1 and 2 despite each algorithm producing the same total PRD, they actually preserve the ECG beats and compress outlying inter-beat noise to quite different extents. Take the total PRD value of 10% in Table 1, the inter-beat PRD values of 98% and 58% for PLA and SAPA-2 respectively demonstrating they have had a significantly different effect on inter-beat variations in the signal. A partial PRD calculation offers some insight into the difference between both algorithms. However, in truth partial PRD's, just as total PRD figures still do not offer any insight into the preservation of diagnostically important information in the original signal as shall become apparent.

## 4 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 recoding 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 both the PLA and SAPA-2 algorithms. 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 compared with the number of sample points retained for reconstruction after approximation.

Table 3: Mean ± standard deviation of fiducial error due to approximation and mean compression ratio (CR)

| (a) P-onset | | |
|---|---|---|
| Total PRD % | SAPA-2 (ms) | PLA (ms) |
| 0.01 | 0.0±0.0 | 0.0±0.0 |
| 0.5 | 0.9±1.6 | 2.5±2.2 |
| 1.5 | 2.7±3.6 | 4.1±2.3 |
| 2.5 | 7.8±5.0 | 12.0±7.5 |
| 3.5 | 10.8±6.0 | 21.2±16.2 |

| (b) P-termination | | |
|---|---|---|
| Total PRD % | SAPA-2 (ms) | PLA (ms) |
| 0.01 | 0.0±0.0 | 0.0±0.0 |
| 0.5 | 0.0±0.1 | 0.2±0.2 |
| 1.5 | 0.5±0.9 | 0.7±0.5 |
| 2.5 | 1.4±1.4 | 1.4±1.5 |
| 3.5 | 1.8±1.6 | 3.1±2.8 |

| (c) QRS-onset | | |
|---|---|---|
| Total PRD % | SAPA-2 (ms) | PLA (ms) |
| 0.01 | 0.0±0.0 | 0.0±0.0 |
| 0.5 | 0.0±0.1 | 0.8±1.6 |
| 1.5 | 0.4±0.6 | 1.8±1.9 |
| 2.5 | 0.9±1.1 | 4.1±2.6 |
| 3.5 | 2.5±1.7 | 8.4±5.7 |

| (d) QRS-termination | | |
|---|---|---|
| Total PRD % | SAPA-2 (ms) | PLA (ms) |
| 0.01 | 0.0±0.0 | 0.0±0.0 |
| 0.5 | 0.0±0.0 | 0.0±0.1 |
| 1.5 | 0.0±0.0 | 0.1±0.3 |
| 2.5 | 0.1±0.2 | 0.5±1.1 |
| 3.5 | 0.7±1.7 | 0.6±1.1 |

| (e) T-termination | | |
|---|---|---|
| Total PRD % | SAPA-2 (ms) | PLA (ms) |
| 0.01 | 0.0±0.0 | 0.0±0.0 |
| 0.5 | 0.4±0.9 | 0.2±0.3 |
| 1.5 | 0.4±0.6 | 0.5±0.6 |
| 2.5 | 1.6±2.6 | 1.7±2.3 |
| 3.5 | 3.9±3.9 | 3.2±3.4 |

| (f) Standard Deviation in Cardiologist Annotation | |
|---|---|
| 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 % | 0.01 | 0.5 | 1.5 | 2.5 | 3.5 |
| PLA C.R. | 1.2 | 2.6 | 4.9 | 6.7 | 7.9 |
| SAPA2 C.R. | 1.0 | 1.2 | 1.8 | 2.3 | 2.9 |

The results in Table 3 demonstrate that the two algorithms have different mean error figures with regard to each fiducial point despite both 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 standard deviation in the annotation of the same ECG recording by different cardiologists as reported by Zywietz [19].

Using the PRD versus compression ratio decision method both 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 7.9 and the SAPA2 just 2.9 (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 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 variation that applies to its annotation by different cardiologists, altering the clinically significant information. The PRD algorithm fails to detect this.

# 5 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. 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 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 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 the other, SAPA-2 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 on measurement of the duration of ECG components [20].

The dynamic time warping results are in contradiction with both the total PRD calculation which would indicate that both approximations to be 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. This novel method of testing approximation accuracy is a powerful alternative to PRD calculation and raises significant concerns over the use of PRD to determine approximation accuracy and as a metric of comparing approximation algorithms. Time warping essentially provides a similar test to having the approximations viewed by a cardiologist. The results indicate that direct data compression, transform and parameter compression algorithms should be compared using dynamic time warping and not PRD versus CR.

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