Pre-Processing for Value Based Dynamic Time Warping of the ECG Signal

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Abstract— **Dynamic time warping (DTW) has been used to characterise the ECG signal in many different applications with differing objectives. Multiple variations of the DTW algorithm including derivative, value and feature based dynamic time warping algorithms have been proposed. Each has its own associated strengths such as the reduced processing time of the derivative based method and the increased accuracy of feature based methods but each also has associated weaknesses such as reduced accuracy and greatly increased processing time respectively. The method of DTW chosen by a user is hence usually application specific. The objective in each case, however, is to generate a time, and as much as is possible, amplitude aligned comparison between an unknown query ECG recording and a known reference ECG signal. The ECG signal can be pre-processed in different ways to optimise this time alignment or normalisation of the two independent signals and generate the most efficient match between the two. This article examines a composite method of pre-processing amplitude normalisation of both the query and reference signals in order to reduce the errors most commonly associated with value based DTW. The improved accuracy of the composite normalisation procedure over standard normalisation is demonstrated and its results compared to the standard deviation evaluated in expert cardiologist annotations.**

Keywords –**Biomedical Signal Processing, Electrocardiogram, Dynamic Time Warping.**

I INTRODUCTION

Dynamic time warping (DTW) is a method of pattern recognition used in many different applications such as speech recognition [1], biometric identification [2] and ECG signal analysis [3]-[8]. The different variations of the algorithm can be sorted into three classes: value based DTW [2]-[5], derivative based DTW [6], [7] and feature based DTW [8]. One of the issues surrounding ECG pattern recognition is that the ECG itself is a non-stationary signal. As such a direct comparison between two different signals cannot be done directly using a Euclidean distance measurement between them. Linear time warping (LTW) is hence not applicable to ECG classification or comparison.

DTW offers a solution to this issue in that it uses a set of specified parameters for non-linear time-normalisation to minimise the difference between the two ECG recordings. The choice of DTW method is very much application and environment specific. For the purposes of this article the algorithms shall be discussed on the assumption that the objective is to identify the fiducial points for the P, QRS and T wave onset and termination since the duration of these waves are frequently used in the diagnosis of various cardiac conditions.

The authors will show how the limitations of value based dynamic time warping can be improved upon using a composite normalisation pre-processing technique. The resulting increase in accuracy improves the algorithms suitability for ECG wave classification and segmentation applications.

II BACKGROUND

a.) The Fiducial Points

A typical lead II ECG recording, its constituent P, QRS and T-waves and the approximate location of their onset and termination fiducial points are shown for each in Figure 1.

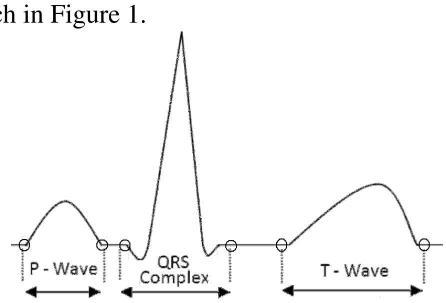

Figure 1: A lead II ECG beat and its constituent waves.

b.) Derivative Based DTW

Derivative based DTW involves creating a linearised version of the two signals and matching the slopes of the resulting splines of the linearization. The intention is to overcome the limitation of value based DTW (explained later) by using the slope of the region around the fiducial point to characterise the signal pre-DTW rather than the just one specific point itself. The assumption is that the fiducial point lies “near” to the endpoint of one of the splines following the approximation of the signal [6]. An approximation or linearization technique will end an approximated segment where variations in the signal cause the difference between the approximation and the original signal to exceed the defined threshold. The T-wave shown in Figure 2 was annotated by an expert cardiologist [9] and demonstrates how a fiducial point may not be near a significant variation in the signal and hence will not necessarily be located near to the beginning or end of a spline.

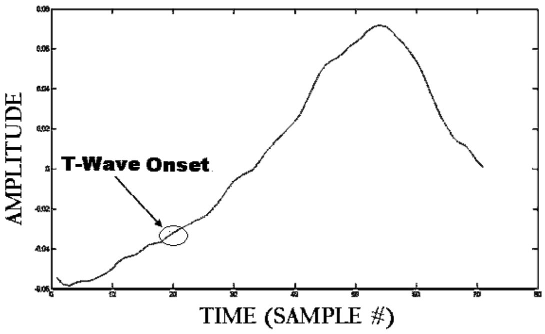

Figure 2: T-onset Annotation

The only way in which this T-wave onset would be located close to the beginning or end of an approximation spline is if the error threshold is extremely small, resulting in a larger number of approximation splines and hence defeating the purpose of using derivative DTW in the first place. If the true T-wave onset is not located near the end of a spline but is assumed to be [6], then the reference signal has been distorted and the original T-onset location and hence annotation is no longer relevant. The effect that approximation or linearization has on the location of the fiducial points in an ECG signal was investigated in [10] and would suggest that any significant linearization of the test signals could introduce a significant displacement of the fiducial points before DTW has even been applied.

c.) Feature Based DTW

Feature based DTW is an attempt to overcome the limitations of the other methods. During the comparison of samples in each of the two signals in the process of dynamic time warping, feature based DTW takes into consideration both the local and global features of the two signals. In doing so, it increases consideration of not only the overall shapes of the signals but also the local trend around the samples. The main issue with the use of feature based DTW is that it is very specific to the application and the signals under test. As such it must be adapted to suit the relevant conditions by the user and is computationally expensive. The trade off in the use of DTW remains between accuracy and computational speed. Feature based DTW is not yet suited to applications where the user is performing a significant amount of analysis i.e. evaluation of an ECG database or requires near real time results [2] although research is under way into increasing the speed of the process as reported by Xie et al [8].

For the purposes of this article it is assumed that the application of DTW in establishing the onset and termination of the fiducial points would be in either a near real-time scenario (i.e. the GP surgery or hospital setting) or in the analysis of the timing information found in a significant volume of ECG recordings, hence feature based DTW is not suitable. Combined with the results from examination of ECG compression [10] by linearization (as in derivative DTW), it would suggest that an improved method of value based dynamic time warping is the most suitable variation of the algorithm for the proposed applications.

d.) The Value Based DTW Algorithm

This article will show how the pre-processing normalisation method found in [2]-[5] can be improved upon using a composite normalisation method to increase value based DTW’s suitability to the applications discussed thus far.

Value based DTW, sometimes referred to as classical dynamic time warping takes each sample of the two recordings, and calculates the minimum Euclidean distance between each specific sample in one recording (the query) and every sample in the opposite signal (the reference). One criticism of value based DTW is that it does not take into account the position of each sample in the global signal but rather the Euclidean distance between just that point in the query and the other points in the reference signal. One way to minimise this source of error is to normalise both signals before the warping process has taken place [8]. Despite this limitation, value-based DTW is still one of the most commonly used methods of DTW [2]-[5].

Consider the two test signals, the reference signal s1 of length n and query signal s2 of length m. From the input signals two matrices of the same size are created, S1 an m x n matrix which contains the reference signal repeated on each row and S2 an m x n matrix which contains the query signal repeated in each column. A distance matrix D can now be calculated as a single dimension Euclidean distance:

$$D(a,b)=[S1(a,b)-S2(a,b)]^2 \qquad (1)$$

Where $1 \leq a \leq m$ and $1 \leq b \leq n$.

The next step calculates a cumulative distance or matrix C, which measures the minimum cost of matching each sample in the reference and query signals. The cost matrix C is created by starting at location (1,1) of matrix D and calculating the cumulative distance (or difference) of the first row and column of the matrix D and then storing the results in the corresponding location of a new cumulative distance matrix C (an m x n matrix also). The remaining cumulative values to be stored in the matrix C are calculated by following the recursive equation described by (2):

$$C(a,b) = D(a,b)+\min \begin{cases} D(a,b-1) \\ D(a-1,b-1) \\ D(a-1,b) \end{cases} \quad (2)$$

Where $1 \leq a \leq m$ and $1 \leq b \leq a$.

The final stage in the process involves starting at the last location C(m,n) of the cumulative distance matrix and moving to the lowest "cost" value stored in any one of the adjoining locations. By tracing all the way back to location (1,1) of the matrix C, and recording the path used that resulted in the minimum accumulated difference two new sample sets are then created called S1w and S2w. The x co-ordinates of the path are used to create S1w and the y co-ordinates for S2w.

e.) Composite Amplitude Normalisation pre- DTW

In most of the value based DTW articles referenced here both the query and reference are amplitude normalised such that the "R-peak" of each signal have the same value as shown in Figure 3.

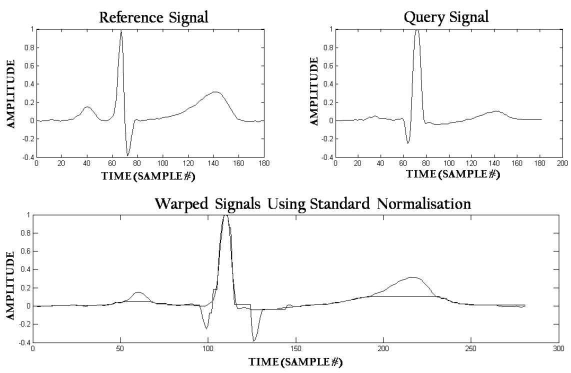

Figure 3: Standard Normalisation

It is a linear amplitude normalisation given by equation (3) and does not distort the morphology but merely increases the similarities between the two QRS complex amplitude profiles pre-DTW. For the single beat query and reference signals q(t) and r(t) in Figure 3 the amplitude normalisation is given by:

$$q_{\text{Normalized}}(t) = \left| \frac{\max\left[r(t)\right]}{\max\left[q(t)\right]} \right| \left[q(t)\right] \quad (3)$$

Where $q_{\text{Normalized}}$ is the resulting query signal.

This is intended to reduce the overall Euclidean distance between the two signals, and as suggested by Xie [8] et al normalisation will reduce the possible errors a value based DTW process is susceptible to. In this case we have normalized the query to the reference signal although both could be normalised such that their R-peaks are aligned to the same predefined voltage.

This standard normalisation will not however, serve to minimise the difference between the P and T waves of both the reference and query signals. So even if their shape and profile in the two signals are similar, the alignment process could in fact change their amplitudes in such a way as to increase the Euclidean distance between them pre-DTW process.

By the same token one can argue that the normalisation process should normalise the P, QRS and T-waves and warp the resulting query and references signals separately for each. The ECG signal can be segmented into regions around each of its constituent components using a segmentation technique such as those suggested by [11] or [12], and the value of the extrema of the P and T waves used to amplitude align the signals for composite normalisation. One cannot necessarily use the maximum value of the waves for normalisation, so we also allow for signals with inverted components such as the T-wave inversion shown in Figure 4. It is important to note that the segmentation into windows is only required to find the extrema for composite normalisation. The signals are not segmented before DTW i.e. complete ECG beats are warped to each other as shown in Figures 3, 5 and 6.

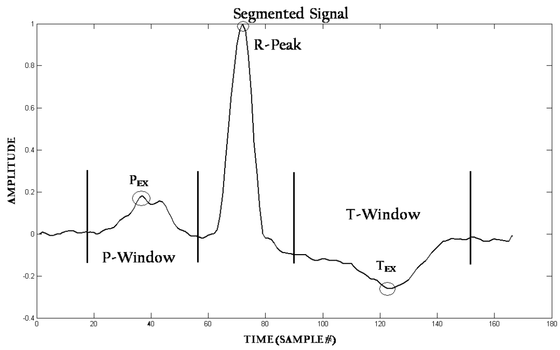

Figure 4: Composite normalisation

Composite normalisation is accomplished using three different amplitude aligned query signals:

$$q_{\text{Pnorm}}(t) = \left| \frac{r(p_{EX})}{q(p_{EX})} \right| \left[q(t)\right] \quad (4)$$

$$q_{\text{Rnorm}}(t) = \left| \frac{r(R_{pk})}{q(R_{pk})} \right| \left[q(t)\right] \quad (5)$$

$$q_{\text{Tnorm}}(t) = \left| \frac{r(T_{EX})}{q(T_{EX})} \right| \left[q(t)\right] \quad (6)$$

Figure 5 is an example of the same two signals having been warped together as in Figure 3 but with the P-waves of the query and references normalised together using equation (4).

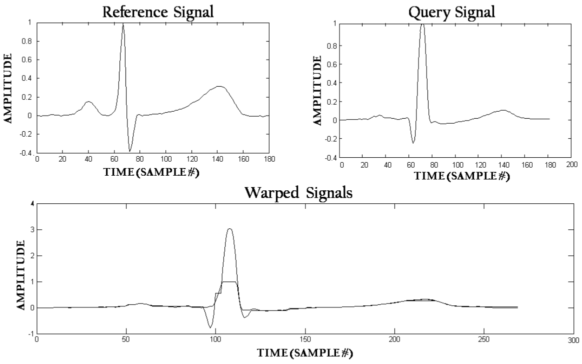

Figure 5: Warping of q_{Pnorm} with Reference.

It is clearly visible from Figure 5 that normalising the P-waves has resulted in a better warping of the query and reference P-waves. R-peak normalisation (5) is identical to standard normalisation so its resulting output is the same as in Figure 3.

Figure 6 shows the result of warping query and reference signals with normalised T-waves using equation (6), again it is clear that normalising the T-waves has improved the accuracy of the warping.

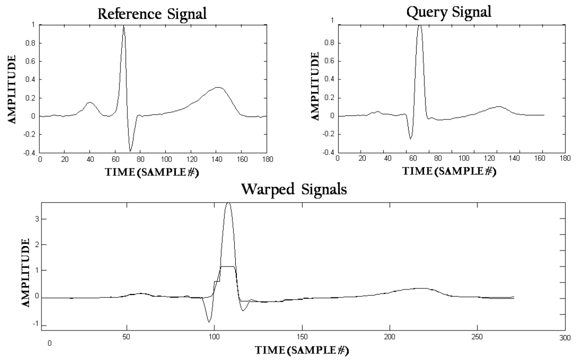

Figure 6: Warping of q_{Tnorm} to reference.

This composite method of amplitude normalising the signals pre-DTW should increase the accuracy of the resulting match between the two signals.

III THE TEST DATA

To establish the benefit of the new composite normalisation technique for value based DTW a large database of test signals was required. The test data was taken from the Physionet MIT QT Database available for download at [9]. A set of 719 beats were chosen from the manually annotated beats described as normal Lead II ECG recordings originally belonging to subsets of the Normal Sinus Rhythm and MIT-BIH-Arrhythmia databases as detailed in Table 1. The original data from the QT database had a 250Hz sampling frequency and hence a sampling period of 4ms. Unfortunately, many of the annotated beats available in the database are fragmented across each selection, and some annotations are incomplete in that they do not possess manually annotated T-onsets. An algorithm was written to read each of the manual annotations and create 719 records each with a full ECG single beat recording, and a full set of P, QRS and T-wave onsets, peaks and terminations. Where manually assigned annotations were incomplete the algorithm generated annotations also available for each selection were used to complete the records.

MIT-BIH-Arrhythmia		Normal Sinus Rhythm	
Sel 103:	30 beats	Sel 16265:	30 beats
Sel 114:	50 beats	Sel 16272:	50 beats
Sel 116:	50 beats	Sel 16273:	50 beats
Sel 117:	30 beats	Sel 16420:	30 beats
Sel 123:	30 beats	Sel 16483:	30 beats
Sel 213:	71 beats	Sel 16539:	30 beats
Sel 223:	31 beats	Sel 16773:	30 beats
Sel 230:	50 beats	Sel 16786:	30 beats
Sel 231:	47 beats	Sel 16795:	30 beats
Sel 233:	30 beats	Sel 17453:	30 beats

Table 1: The Test Data.

The compiled reference database used for test contained records from twenty different ECG recordings and a total of 719 fully annotated beats. The QT database was deliberately compiled so as to include as many different variations of ECG morphologies as possible so our test database should provide a rich variation of ECG Lead II morphologies.

IV RESULTS

The benefit of the composite normalisation technique being applied pre-DTW was investigated by taking each of the reference beats and comparing them to the other beats available in the same selection from the reference database and then all other signals in the database. The two test signals were normalised pre-DTW first using standard R-peak normalisation and then using the composite normalisation technique. For each type of pre-processing method the query and reference signals were then warped together using value based DTW.

a.) Warping Similar Signals

In this case the true fiducial points as annotated by the expert cardiologists are known for both the reference and query signals so the error between the true fiducial points and the fiducial points identified by the DTW algorithm in the query signal can be measured. Each reference beat can be assumed to be most similar to the other beats in the same selection as opposed to the beats in other selections.

In order to observe the effects of the alternative pre-processing techniques we approach it in two steps. The mean and root-mean-square-error (RMSE) in the estimated location of each fiducial point resulting firstly, from comparisons with each signal in the same selection recording and secondly, with every other beat in the reference database were calculated separately. This examines the proposed benefit of composite normalisation for constituent waves with similar and significantly different constituent wave amplitudes.

The signals from the arrhythmia and normal sinus rhythm databases are morphologically quite different. To avoid excessive averaging of results they are divided into P, QRS, T-wave onset and termination points for each database. Accuracy is expressed as the mean ± RMSE estimate error.

Mean Estimate Error ± RMSE (ms)		
Fiducial Point	Standard Normalisation	Composite Normalisation
P-Onset(ms)	-4.35±44.8	2.00±41.35
P-Termination(ms)	2.37±51.7	-1.09±42.63
QRS-Onset(ms)	-16.55±51.83	-16.55±51.83
QRS-Termination(ms)	-16.21±53.37	-16.21±53.37
T-Onset(ms)	1.23±67.80	5.13±56.58
T-Termination(ms)	0.53±45.74	-1.61±41.86

Table 2: Results for “like” Arrhythmia

Mean Estimate Error ± RMSE (ms)		
Fiducial Point	Standard Normalisation	Composite Normalisation
P-Onset(ms)	7.01±28.43	6.92±27.74
P-Termination(ms)	-3.33±23.20	-3.57±22.94
QRS-Onset(ms)	5.98±23.72	5.98±23.72
QRS-Termination(ms)	-4.48±22.18	-4.48±22.18
T-Onset(ms)	4.04±37.43	4.82±37.21
T-Termination(ms)	-6.50±28.50	-6.18±28.01

Table 3: Results for “like” Normal Sinus Rhythm

When analysing the data one must take into consideration that the sampling period of the signals is 4ms. With this in mind the mean estimate errors shown in Tables 2 and 3 have very little difference (less than one sample in each case) using either pre-processing technique. One can however, see that the composite normalisation technique does yield a lower RMSE for each fiducial point, significantly so (>9ms) in the case of the arrhythmia P-termination and T-onsets which would indicate increased stability of the algorithm. The benefits of composite normalisation should become more clear when signals with significantly different P and T-wave amplitudes are warped to each other.

b.) Warping all reference signals

The results in Tables 4 and 5 are again divided into signals taken from the Arrhythmia and Normal Sinus Rhythm databases to enable a more specific view of the effects of pre-processing techniques.

Mean Estimate Error ± RMSE (ms)		
Fiducial Point	Standard Normalisation	Composite Normalisation
P-Onset(ms)	-8.23±58.00	-2.25±46.00
P-Termination(ms)	9.66±58.83	1.13±53.50
QRS-Onset(ms)	26.17±62.84	26.17±62.84
QRS-Termination(ms)	-61.10±118.54	-61.10±118.54
T-Onset(ms)	-19.65±120.17	13.23±108.20
T-Termination(ms)	10.45±89.15	6.44±75.32

Table 4: Arrhythmia results for warping to all signals

Mean Estimate Error ± RMSE (ms)		
Fiducial Point	Standard Normalisation	Composite Normalisation
P-Onset(ms)	13.44±56.68	6.52±41.68
P-Termination(ms)	-18.45±48.81	-16.92±46.46
QRS-Onset(ms)	2.79±41.46	2.79±41.46
QRS-Termination(ms)	-16.34±67.66	-16.34±67.66
T-Onset(ms)	23.79±95.80	10.79±84.60
T-Termination(ms)	20.53±83.35	5.21±63.91

Table 5: Normal Sinus Rhythm results warping to all signals

As predicted the composite normalisation technique has produced mean estimate and RMSE values significantly lower than standard normalisation in Tables 4 and 5. It allows reference and queries of similar morphology but significantly different amplitudes to be warped more accurately by amplitude aligning the individual constituent wave’s pre-DTW.

c.) Measuring the accuracy of the algorithm

It has been demonstrated that pre-processing the query and reference signals using the composite normalisation method increases the accuracy of the value based dynamic time warping algorithm. In order to quantify the accuracy of the composite normalisation and value based DTW algorithm we can compare its ability to identify the fiducial points with the acceptable deviation in expert cardiologist annotations of the same signals as presented by [13].

Mean ± Standard deviation Error (ms)			
Fiducial Point	Deviation in Cardiologist Annotations	Normal Sinus Rhythm	MIT-BIH ARRHYTHMIA
P-Onset	±10.2	-1.17±6.07	-0.51±5.98
P-Termination	±12.7	0.24±6.00	0.99±7.39
QRS-Onset	±6.5	-0.03±4.05	0.91±9.52
QRS-Termination	±11.6	0.13±5.88	1.34±6.76
T-Onset	N/A	0.67±8.77	-0.26±15.26
T-Termination	±30.6	1.89±7.53	0.41±10.99

Table 6: Accuracy of the algorithm

The results in Table 6 are the mean and standard deviation of the error between the query and best reference match for each constituent wave. The standard deviation of cardiologist annotations in Table 6 is used as a minimum criterion for testing the stability of an automatic detection algorithm [13]. One can clearly see that the suggested algorithm provides results comparable with, and in most cases a standard deviation that is significantly less than the deviation associated with expert opinion. The composite normalisation technique reduces the error associated with value based DTW, increasing its usefulness.

VI CONCLUSION

There are many different ways to pre-process data and of applying the DTW algorithm. For each of the three different types of DTW; derivative, feature and value based DTW this article identified some of the strengths and weaknesses associated with each method. The choice of the most suitable form of DTW is dependent on different factors and is very much application specific.

One of the most commonly reported limitations of the value based DTW method is that it matches each point in both the query and reference signals on a sample by sample Euclidean distance measurement, regardless of the position of points locally or globally within the ECG beat. Normalising the query and reference signals such that their R peaks are aligned before DTW is commonly used to help limit shortcomings of value based DTW. A method of pre-processing the signals using composite normalisation was investigated where by the extrema of the P, QRS and T-waves are amplitude aligned pre-DTW as a method of further increasing the algorithms accuracy.

A large reference signal database of fully annotated real ECG recordings with significant morphological variation was compiled to test the composite normalisation method. Pre-processing the signal using standard and composite normalisation was compared when warping signals of similar morphologies and signals with significantly different P and T-wave amplitudes. For signals of similar amplitude and morphology the mean estimate errors were very similar (<1 sample error difference for each onset/termination using either method) with a significantly lower RMSE for the composite normalisation method found for the P and T-wave termination and onset respectively. The true benefit of the composite method of normalisation became apparent when warping signals of different amplitude levels, where improved mean estimate and significantly lower root-mean-square errors were recorded.

The accuracy of the composite normalisation method coupled with the value based DTW algorithm was tested over the reference database and its results compared with the deviation in expert annotations. Its results were shown to be highly comparable and within the acceptable standard deviation of expert cardiologist annotation deviation. We suggest that when using the value-based DTW for ECG classification, segmentation or other ECG analysis applications, the composite normalisation pre-processing technique should be used to reduce resulting error.

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