Similarity Measurement of Biological Signals Using Dynamic Time Warping Algorithm

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Abstract—The problem of similarity measurement of biological signals is considered on this article. The dynamic time warping algorithm is used as a possible solution. A short overview of this algorithm and its modifications are given. Testing procedure for different modifications of DTW, which are based on artificial test signals, are presented.

Keywords: biological signal, dynamic time warping, ECG, artificial signals, testing methods.

I. INTRODUCTION

Modern methods of functional diagnostics of human body provide wide range of opportunities for leading and recording large amount of biological signals. These signals are indirect indices of human body changes. Sometimes, estimation of changes in these signals are only way of making diagnosis. Thereby, the task of fast and correct interpretation of biological signals becomes actual. For a long time, analysis of biological signals was carried out with the help of human experts. The correctness of results interpretation in this approach depends on experience and qualification of an expert. Expert also can make a mistake during analysis, which may cause wrong interpretation of analysis results.

Nowadays, using modern mathematical methods and high performed computers, statistical data about changes of biological signals and their aftermaths for human body based on multiple measures were obtained [1][2]. This data help experts with interpreting of biological signals but the task of precise analysis of biological signals is still actual.

One approach to the analysis of biological signals is a similarity measurement between tested signal and some reference signal, which parameters are known [3]. For solving this task dynamic time warping algorithm (DTW) are widely used. This method works well in many different fields, e.g. in tasks of speech recognition, and analysis of complex time series. [4]-[10]. However, algorithm has high sensitivity to input signals and their changes. Therefore, there are many different modifications of DTW, allowing getting additional advantages when analyzing real data. Besides that, if input signals are very complex, the task of interpreting of algorithm results becomes complicated.

Due to problems described above, it is necessary to test this method and its modifications using simple signals with known parameters. Experiments with different signals will give information about sensitivity of algorithm to concrete changes in concrete types of signals.

The main goal of the research is to find an optimal modification of DTW algorithm, which is the most appropriate for analyzing specific changes in biological signals. Testing procedure of DTW algorithm based on artificial testing signals is described in this article. The questions of extracting and interpreting information from output parameters of the algorithm are considered.

In the second part of the article a comparison analysis of classical DTW algorithm and one of its modifications are presented.

II. FEATURES OF BIOLOGICAL SIGNALS

Most biological signals are quasiperiodic. This term has strict mathematical definition for deterministic systems. However, for biological signals this means that they can change their period in time due to stretching, shrinking and shifting of single patterns relative to each other's. Besides that, biological signals have variable amplitude, which can changes from one pattern to another within certain limits.

One of the examples of biological signals is electrocardiographic (ECG) signal. In general, ECG signal consists of sequence of three-dimensional cycles of electric vector of the heart (heart vector). Analysis of these cycles are complicated task. To simplify it ECG signal is divided into three projections on coordinate axes. Fragment of X-projection of ECG signal is shown on Fig. 1.
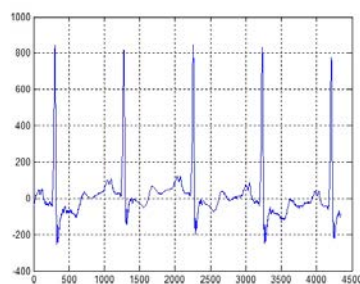

Fig. 1. Fragment of X-projection of ECG signal.

This signal is a continuous sequence of heartbeat cycles. For similarity analysis, separation of these beats is needed. This separation might be done, for instance, by standard algorithms, which are based on determining fiducial points of every heartbeat [1],[11]. Fig. 2 shows a single beat, separated using the described technology.
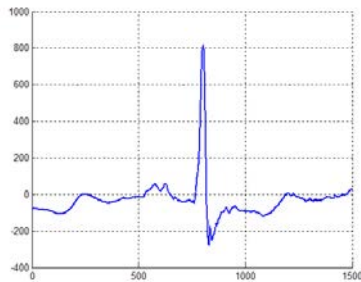

Fig. 2. Single heartbeat extracted from the ECG signal.

In practice biological signals are often divided into different segments and complexes. Regularities described above are typical for both a whole signal and its segments. As an example a part of a special segment of single heartbeat is considered (Fig. 3). This signal is obtained with the help of high pass filtering because the most interesting changes of this segment waveform appears in high-frequency component and these changes are invisible in standard ECG.
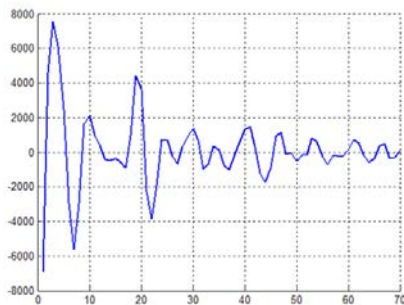

Fig. 3. Part of ST-segment of single heartbeat.

III.   TEST SIGNALS DEVELOPMENT

As described above, before analyzing real biological signals it is needed to find the most appropriate algorithm for this task. To do this, it is necessary to understand relationship between output parameters of algorithm and features of input signals. For solving this task special testing procedure based on artificial test signals are developed.

Test signals must have the same features as real signals. In ideal case, test signals must precisely repeat behavior of real signals and have known parameters available for changing. One of the examples of such test signals for simulating ST-segment shown above are signals based on sequences of impulses filtered with second-order band pass Butterworth filter (Fig. 4).
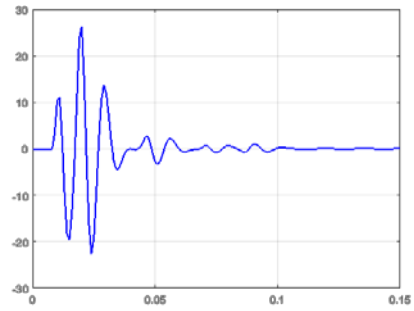

Fig. 4. Example of test signal based on sequence of impulses.

Such test signals are described in [12].

This approach allows precisely simulate different complexes of single heartbeats but the correct interpretation of testing results becomes very difficult due to complexity of a signal.

In this case, at the first step it is necessary to use signals with simple waveform (e.g., segments of sine wave and their combinations). Such signals can have the following changeable parameters:
- width of segment
- amplitude of segment
- initial displacement
- length of final interval.

Examples of such testing signals are described in [13].

In this study single segments of sine function are used as test signals.

DTW algorithm needs two signals: reference and test. Signal shown on Fig. 5 are used as a reference signal. This signal is not changeable during testing.
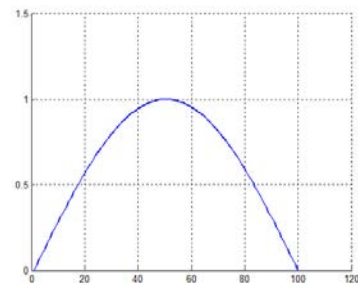

Fig. 5. Reference signal.

As a testing signal arbitrarily changeable signal is used (Fig. 6).
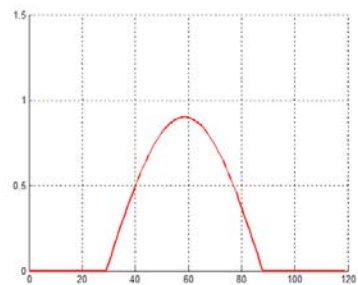

Fig. 6. Testing signal.

All test signals are a combination of the initial displacement, half-wave segment of sine function with variable amplitude and width and the end part of zero-values.

Changing parameters of test signal is made with respect of reference signal parameters.

Both test and reference signals are shown on Fig. 7 (reference signal is blue; test signal is red).
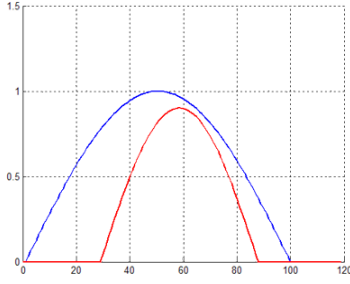

Fig. 7. Both reference and test signals.

IV. CLASSICAL DTW ALGORITHM

General description of DTW is given in [3]. As input parameters, two signals: reference and test are used. Both signals are sampled at equidistant moments t_i, e.g. $\Delta t = t_{i+1} - t_i$. The aim of algorithm is a warping of time axis using stretching and shrinking in such way that the test signal matches the reference one as good as possible.

We will denote the reference signal by $R = (R(t_1)...R(t_M))$ and the test signal by $T = (T(t_1)...T(t_N))$.

At the first step of DTW so called local distance matrix d are calculated. Matrix has the following form:

$$d = \begin{pmatrix} d(1,1) & \cdots & d(1,N) \\ \vdots & \ddots & \vdots \\ d(M,1) & \cdots & d(M,N) \end{pmatrix}$$

We denote the distance between $R(t_m)$ and $T(t_n)$ by $d(m,n)$, where $m \in [1...M]$ and $n \in [1...N]$ are indices of reference and test signal respectively. Shortly we say that d is the local distance matrix includes of pairwise distances between each pair of points (m,n).

At the second step accumulated distance matrix D is calculated based on matrix d. Matrix D has the following form:

$$D = \begin{pmatrix} D(1,1) & \cdots & D(1,N) \\ \vdots & \ddots & \vdots \\ D(M,1) & \cdots & D(M,N) \end{pmatrix}$$

In general, the element $D(m,n)$ of the accumulated distance matrix defines the minimal total distance of the two signal segments $R_m = (R(t_1)...R(t_m))$ and $T_n = (T(t_1)...T(t_n))$.

The calculation of D needs the initial steps:

$$D(1,1) = d(1,1) \tag{1}$$

and

$$D(m,1) = d(m,1) + D(m-1,1), \tag{2}$$
$$D(1,n) = d(1,n) + D(1,n-1), \tag{3}$$

which give the elements of the first row and the first column of D. Then the other elements can be calculated iteratively by

$$D(m,n) = d(m,n) + \\ + \min(D(m-1,n), D(m,n-1),$$

$$D(m-1,n-1), \tag{4}$$

here $m \in [2...M]$, $n \in [2...N]$ are indices of points of reference and test signals respectively.

Formula (4) allows finding minimal transition to the next point from all admissible ones. Admissible transitions are defined with the help of so-called weighting matrix, which includes all possible ways of transition from one point to another. This matrix is sometimes also called step-pattern [14].

It should be noted, that this formula is used only in algorithms without modifications of weighting matrix.

At the third step, the optimal warping path w are calculated based on accumulated distances matrix. This path is the shortest admissible way from the first element of D to its last element. Calculation of w starts from $D(M,N)$ and goes backward until finding element $D(1,1)$. In this way we get the connection of both time series with the shortest total length. This is only a short explanation of mathematical background of DTW. Detailed mathematical description of this is given in [3].

There are two types of constraints of classical DTW algorithm: global constraints and local constraints.

Global constraints mean that both first and end points of reference signal must match starting and ending points of warped test signal, i.e. the following conditions are satisfied

$$M1 = w(N1); \tag{5}$$
$$M2 = w(N2), \tag{6}$$

where $M1, M2$ are starting and ending points of reference signal respectively and $N1, N2$ are starting and ending points of test one [9].

Local constraints mean that warping path is able to go only from current point to its closest neighbors and is not able to go backward. In this case weighting matrix has the following form

$$((m, n-1); (m-1, n-1); (m-1; n)), \tag{7}$$

where $m \in [1...M]$ and $n \in [1...N]$ are numbers of points of reference and test signals respectively. Visual representation of classical weighting matrix is shown in Fig. 8. More detailed information about local constraints is given in [3].
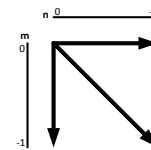

Fig. 8. Weighting matrix for classical DTW algorithm.

V. MODIFICATIONS OF DTW ALGORITHM

The idea of DTW modification is in relaxing or even eliminating global or/and local constraints.

Local constraints modification is realized with changing of classical weighting matrix. There are two ways of this changing. First is including weighting coefficients to all admissible ways of transition in classical weighting matrix. Second way is adding new admissible ways of transition or modifying existing ones [10][15].

Global constraints modifications are realized with use of open-beginning and open-end approaches [15]. Open

beginning approach assume that condition (5) presented in section IV not to be satisfied and open-end approach allows condition (6) not to be satisfied.

In this work modification with relaxing of local constraints using approach of adding new admissible transitions to the weighting matrix are described.

The modified weighting matrix has the following form:

$$((m-1,n); (m,n-1); (m-1,n-1); (m-2,n-1); (m-1,n-2)) \quad (8)$$

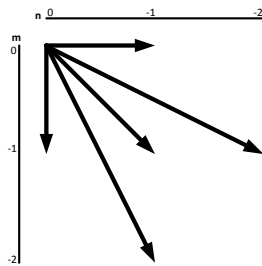Visual representation of the matrix is shown on Fig. 9.

Fig. 9. Weighting matrix for modified DTW algorithm.

VI. TESTING PROCEDURE AND FUNCTIONS, CREATED DURING TESTING

The first goal of testing is sensitivity estimation of classical DTW algorithm and its modifications to changes of input signals and differences between reference and test signals.

The second goal is comparison of classical and modified algorithm to find the most appropriate variant for solving the research task.

In the testing process so-called subsequent matching of test and reference signal are used. In this case, reference signal is a template, imposed on the test signal to find fragments of reference signal in test one. This approach is suitable for testing both simple signals and ones that are more complex.

Testing procedure includes two steps: testing of classical DTW algorithm and testing of its modification with changed weighting matrix.

The same signals are used for testing both DTW variations.

Length of reference and test signals are used in this work is not the same.

Reference signal has constant parameters during testing and parameters of test signal are changed with respect to parameters of reference one.

During testing the following diagrams and graphs are created:
- Diagram of local distances matrix
- Diagram of accumulated distances matrix with the graph of an optimal warping path
- Graphs of signals before and after time warping procedure
- Graph of matching function, which illustrated matching between single points of signals.

VII. TESTING CLASSICAL AND MODIFIED DTW ALGORITHM

Series of experiments with different test signals was carried out on the research. The most significant results are presented in this article. In this section testing of signals with the following parameters are presented.

Reference signal parameters:
- amplitude – 1

- width of impulse – 100
- no initial displacement
- final zero-valued segment is not existent.

Parameters of test signal corresponding to parameters of reference signal:
- signal amplitude – 0.8 of amplitude of reference signal
- signal width – 0.7 of reference signal width
- initial displacement – 0.4 of reference signal width (starts with the starting point of reference signal)
- length of final zero-valued segment – 0.45 of reference signal width.

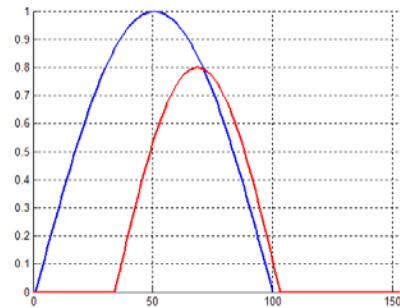Both reference and test signals are shown on Fig. 10.

Fig. 10. Both test and reference signals (reference are blue, test are red).

Diagrams and graphs obtained during testing this pair of signals are described below.

At the first step, classical DTW algorithm was tested.

Local distance matrix (Fig. 11) is shown just for visualization of relationships between reference and test signals. This matrix does not contain any significant information except pairwise distances between each points of reference and test signals. At the diagram, lighter regions correspond to shorter distances between points; darker regions correspond to longer distances.
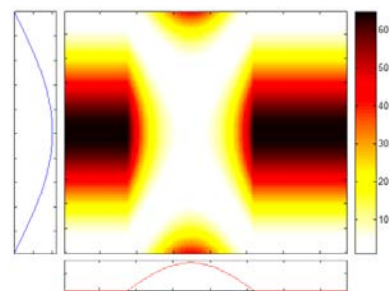

Fig. 11 Local distances matrix.

Accumulated distances matrix with the optimal warping path is shown in Fig. 12. As in diagram above, lighter regions correspond to shorter distances between points; darker regions correspond to longer distances. Optimal warping path (black line) always lies in the region of the shortest accumulated distances.
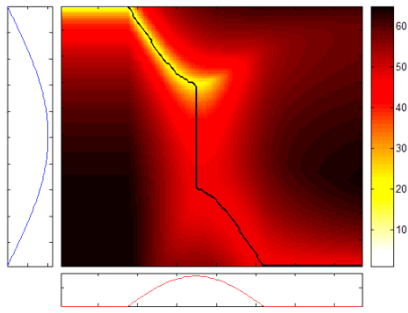
Fig. 12. Accumulated distances matrix and optimal warping path (black line) for classical algorithm.

Experiments showed that decreasing of test signal amplitude with respect to amplitude of reference signal caused appearing of vertical linear segment in the optimal warping path. Length of this segment corresponds to amount of points of reference signal, which are placed above test signal. This length increases linearly with linear increasing the difference between amplitudes of reference and test signals.

Segments of simultaneous increasing and decreasing both reference and test signals corresponds to polygonal lines placed close to diagonal before and after linear segment. When shrinking test signal with respect to base signal, these segments go left with increasing of width difference between test and reference signals; when stretching test signal, segments go right.

Initial displacement and final zero-valued segment correspond to horizontal lines in optimal warping path. Length of these lines depends on length of corresponding parts of test signal.

Signals before (left graph) and after (right graph) time warping are shown in Fig. 13.
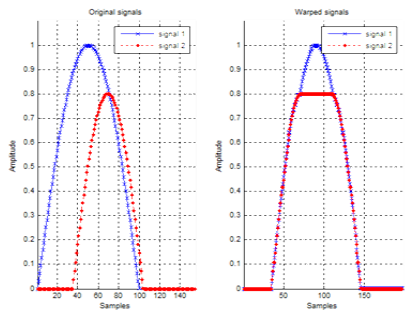

Fig. 13. Both reference and test signals before (left graph) and after (right graph) warping for classical algorithm.

Experiments showed that classical DTW algorithm well compensates differences of width between reference and test signals. The algorithm is also good for compensating the time shifts because it compensates both initial displacement and final zero-valued segment. However, this algorithm is not able to compensate differences in amplitude. The upper horizontal segment corresponding to this difference appears on the graph after time warping.

Matching function (Fig. 14) shows matching of single points of reference and test signals with blue lines. In addition, this function contains information about matching distances for each single point of signals, i.e. length of points shifting during time warping.
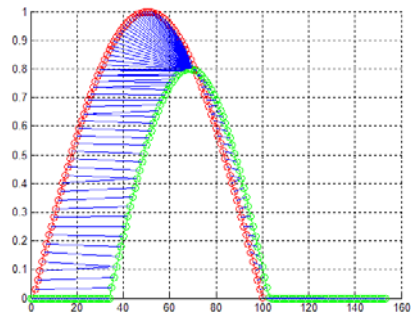

Fig. 14. Matching function for classical algorithm (reference signal is red, test signal is green, blue lines show matching of each point of reference and test signals).

One can see that points are matching irregularly. So-called multiple matching problem appears. This means that after warping of time axis, matching between multiple points of one signal and a single point of another signal appears. Multiple matching problem causes vertical or horizontal segments in the graph of optimal warping path.

On the graph showed above at segments of increasing and decreasing both reference and test signals this problem is not significant because amount of multiple points connected to a single one is not big. However, in the segment corresponding to amplitude difference this problem is very significant because all points of reference signal above test signal are matched with a maximum point of test signal that causes long vertical line in the middle of warping path. Points of the test signal corresponding to initial displacement and final zero-valued segment are matched sequentially to each other.

At the second step, modified DTW algorithm described in the section 5 was tested.

The same signals as at previous step were used for testing.

When testing any modifications of DTW there was no changes in the local distances matrix.

However, accumulated distance matrix (Fig. 15) for modified DTW algorithm is modified.
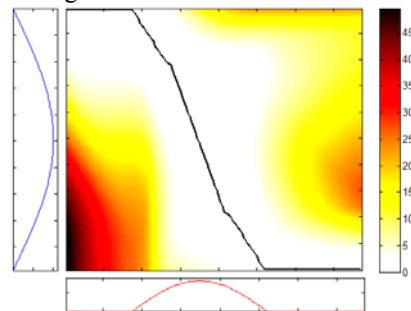

Fig. 15. Accumulated distances matrix and optimal warping path (black line) for modified algorithm.

Since the weighting matrix is changed from (7) to (8), the corresponding formula to (4) gives in general smaller values of $D(m,n)$.

Weighting matrix of this modification has more admissible transitions then in classical one, thus vertical segment of optimal warping path is absent. Instead of this, a linear segment corresponding to amplitude difference appears. As in previous case, "step segments" of optimal path correspond to segments of simultaneous increasing and decreasing both reference and test signals. Horizontal lines of optimal path correspond to initial displacement segment and final zero-valued segment of testing signal.
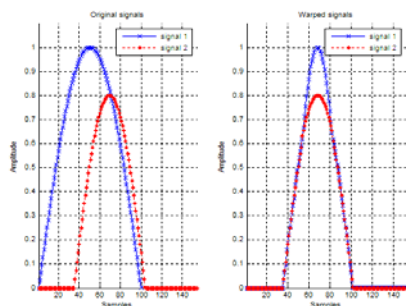
Fig. 16. Signals before (left graph) and after warping (right graph) for modified algorithm.

Studying of warped signal (Fig. 16) shows that when using modified algorithm, it better deals with differences between amplitudes of reference and test signals even if this difference is very big (instead of linear segment in previous case, here the segment, which repeats waveform of signal with lower amplitude). However, this modification is not able to compensate completely the amplitude difference between signals. Algorithm also well enough deals with width differences and shifting of signals between each other.
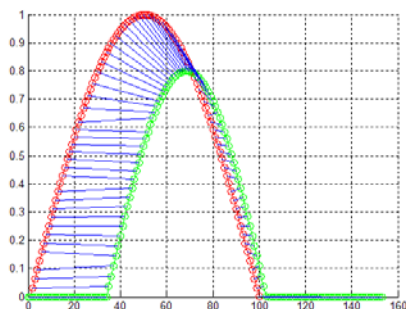

Fig. 17. Matching function for modified algorithm.

Analysis of matching function (Fig. 17) shows that modified algorithm could better match points of reference and test signals. Besides that, multiple matching situations is completely absent. As in classical algorithm, points of the parts with zero-valued signal are sequentially connected to each other.

VIII. SUMMARIZING OF TEST RESULTS

Comparative analysis of two DTW algorithms showed that classical and modified algorithm well enough compensate the difference in width between reference and test signals if this difference is big (this is normal for real biological signals). Both algorithms also can completely compensate shifting of signals relative to each other.

Modified DTW algorithm better deals with amplitude differences of signals then classical one. It should be noted however, that neither classical algorithm nor modified one is able to completely compensate difference in amplitudes. To solve this problem so-called two-dimensional DTW might be used [16]. This algorithm allows warping both time and amplitude axes.

During testing, problem of multiple matching was studied as well because it can have make significant changes in optimal warping path causing horizontal or vertical segments in the optimal warping path. There are different ways of dealing with this problem: one of them is trying to completely

avoid such situations, another way is to avoid these situations but restrict the maximal number of points connected to a single one. The question about amount of points connected to a single point decides based on information about input signals and research task. It should be noted, that maximal amount of multiple points connected to a single one needs to be small because large amounts of points connected to one point do not allow warped function completely match to reference one.

When studying this problem during testing it was found that amount of points matched to a single one depends on two factors: density distribution of signal's points, and amplitude difference between signals.

Experiments showed that influence of amplitude difference might be eliminated using modifications of DTW algorithm. In particular, modification of DTW considered in this article minimizes amount of multiple matching situations and amount of points, which are able to match single point.

For eliminating second factor it is necessary to provide the same density distribution of points along reference and test signals. Besides that, the difference between densities of reference and test signals has to be not very big.

In practice, it is often impossible to provide these conditions because density of points in real biological signals depends on their length, waveform and other factors. In this case, it is necessary to make additional experiments to find the optimal amount of points, which are able to match a single one.

IX. CONCLUSION

The problem of using DTW algorithm for similarity measurement of biological signals was considered in this work. A short description of classical approach for DTW and some of its possible modifications was given.

Procedure for testing different modifications of DTW algorithm based on artificial signals with changeable parameters was presented. Main requirements for artificial signals, which simulated real biological signals, were described. To present abilities of testing procedure comparative analysis of classical DTW approach and one of its modifications was carried out.

Results of analysis showed some advantages of considered modification in contrast to classical DTW procedure. However, for more detailed study of DTW algorithms features and their behavior when testing real biological signals more tests with more complex signals is needed.

At the next steps of research comparing of large amount of different modifications of DTW procedure will be carried out based on presented testing procedure. It is planned to increase amount and complexity of test signals and then use different examples of real data to check the results of experiments with artificial data.

Another direction of further work is developing of methods of effective extraction of information from the output parameters of DTW algorithm. During studying of output data of classical DTW algorithm it was found that some of them are not informative for analyzing of input signals waveform changes. For this reason, it is necessary to develop additional methods of retrieving information from output parameters of DTW algorithm.

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