The dtw package

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Dynamic time warping

Let

$$X = (x_1, ..., x_N)$$

and

$$Y = (y_1, ..., y_M)$$

be time series we want to compare. We also assume that a nonnegative, local dissimilarity function f is defined between any pair of elements x_i and y_j, with the sortcut:

$$d(i,j) = f(x_i, y_j) \geqslant 0$$

$d(\cdot,\cdot)$ is often L_p norm.

Dynamic time warping

The idea is the choice of warping curve $\phi(s), s = 1, ..., T$:

$$\phi(s) = (\phi_x(s), \phi_y(s))$$
$$\phi_x(s) \in \{1, ..., N\}$$
$$\phi_y(s) \in \{1, ..., M\}$$

The warping functions ϕ_x and ϕ_y remap the time indices of X and Y. Given ϕ we compute the average accumulated distortion between the warped time series X and Y.

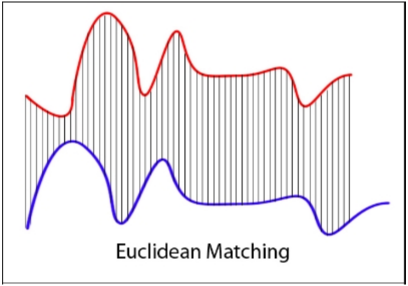
$$d_\phi(X, Y) = \sum_{s=1}^{T} d(\phi_x(s), \phi_y(s)) m_\phi(s) / M_\phi$$

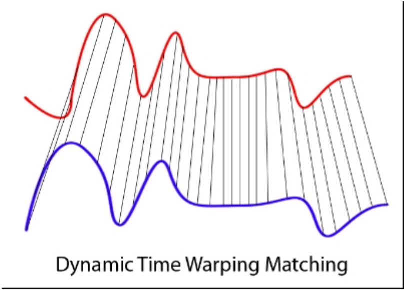
where $m_\phi(k)$ is a per-step weighting coeffcient and M_ϕ is the corresponding normalization constant, which ensures that the accumulated distortions are comparable along different paths.

Dynamic time warping

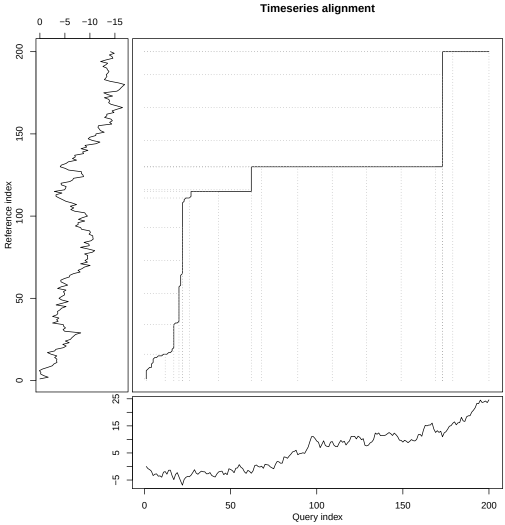
The goal of DTW is to find such a function ϕ which minimizes the DTW distance:

$$D(X,Y) = \min_{\phi} d_{\phi}(X,Y)$$





Algorithm


Timeseries alignment
0
−5
−10
−15
Reference index
0
50
100
150
200
25
15
5
−5
0
50
100
150
200
Query index

Algorithm

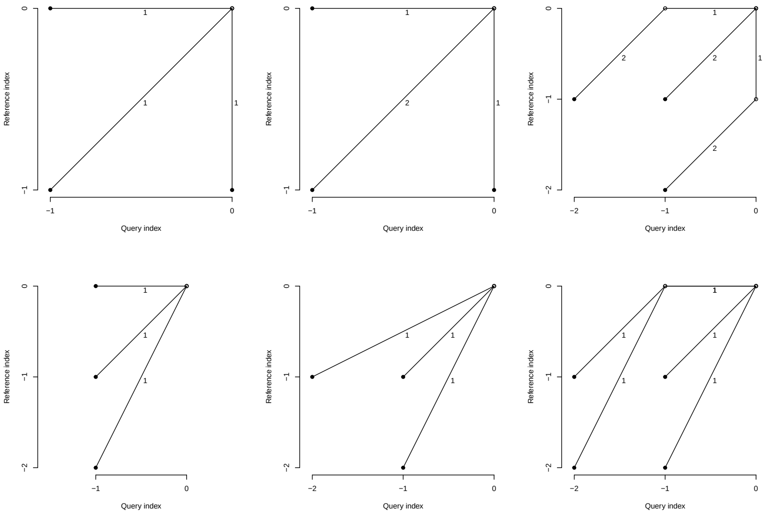
We build a cost matrix with formula:

1. $$g[1,1] = d(1,1)$$

2. $$g[i,j] = \min \begin{cases} g[i,j-1] + d(i,j) \\ g[i-1,j-1] + d(i,j) \\ g[i-1,j] + d(i,j) \end{cases}$$

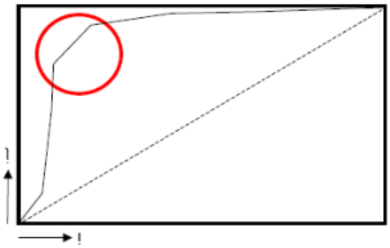
3. We obtain ϕ by finding an optimal path from $g[N,M]$ to $g[1,1]$.

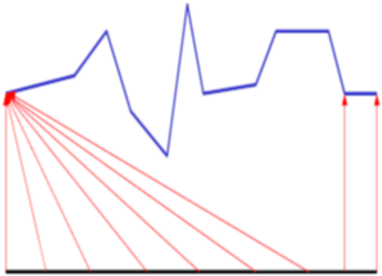
Step patterns



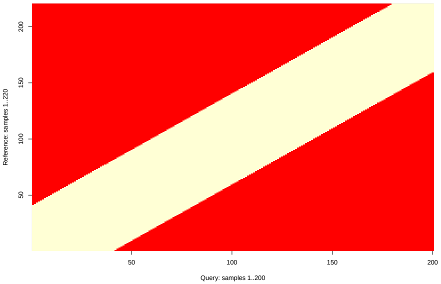
Warping window

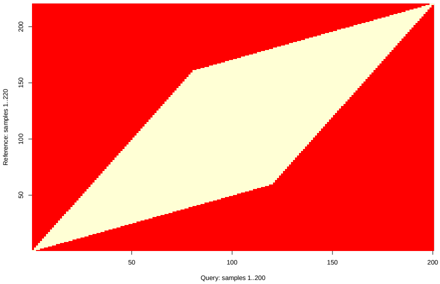
$$|i_s - j_s| \leqslant w, \quad w > 0$$





Types of window

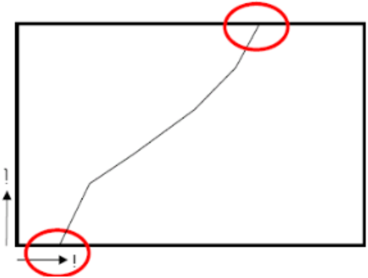


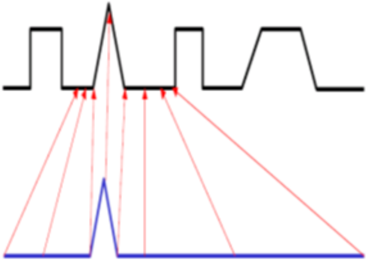


Restrictions on the Warping Function

Boundary conditions

$$i_1 = 1, i_T = N \quad and \quad j_1 = 1, j_T = M$$

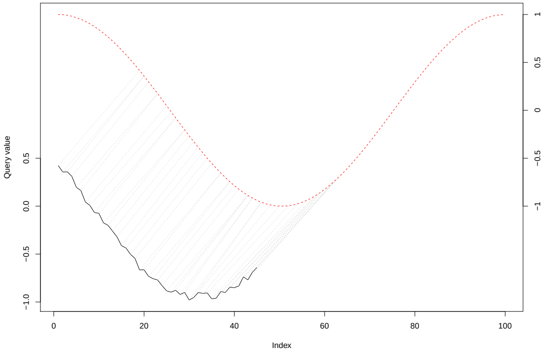




Open bounds

$$Y^{(p,q)} = (y_p, \dots, y_q)$$

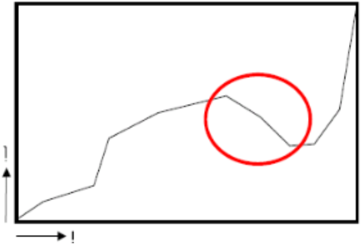
$$DTW_{OBE}(X, Y) = \min_{1 \leqslant p \leqslant q \leqslant M} DTW(X, Y^{(p,q)})$$

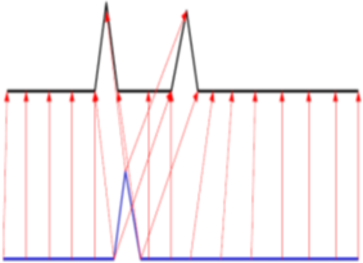


Restrictions on the Warping Function

Monotonicity

$$i_{s-1} \leqslant i_s \quad and \quad j_{s-1} \leqslant j_s$$

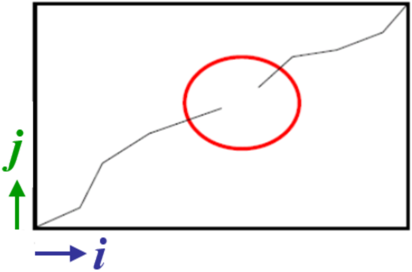


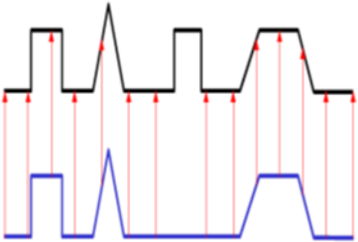


Restrictions on the Warping Function

Continuity

$$i_s - i_{s-1} \leqslant 1 \quad \textit{and} \quad j_s - j_{s-1} \leqslant 1$$

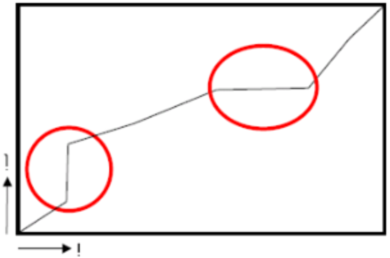


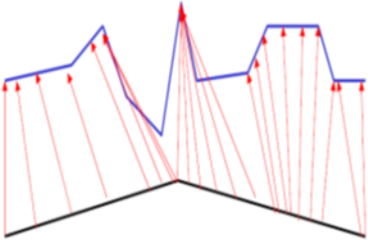


Restrictions on the Warping Function

Slope constraint

$$\frac{j_{s_p} - j_{s_0}}{i_{s_p} - i_{s_0}} \leqslant p \quad and \quad \frac{i_{s_q} - i_{s_0}}{j_{s_q} - j_{s_0}} \leqslant q$$

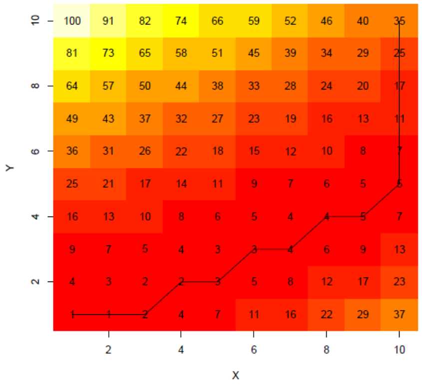




Example

Let:
$X = (1, 2, 3, 4, 5, 6, 7, 8, 9, 10)$,
$Y = (2, 4, 6, 8, 10, 12, 14, 16, 18, 20)$.

$D_{L1}(X, Y) = 55$
$D_{DTW}(X, Y) = 35$



The dtw package

- dtw() - computes DTW measure.
- dtwPlot() - plots matched time series in two way, three way or with density.
- step.pattern= - argument in dtw() allowing us to choose pattern from 28 possibilities.
- window.type= - argument in dtw() allowing us to choose type of window constraint.

Advantages

- Fast computation - dtw() function is written in C.
- Wide variety of step patterns (28).
- Many ways of visualization.
- Overloaded plot() method.
- dtwPlotTwoWay() provides argument offset, which allows to see time series in a way that they are not overlaying each other.

Disadvantages

- Hard to find Itakura step pattern.
- Does not support database with multivariate time series. You have to do this by loop.
- Does not support continuity, monotonicity and slope constraint in a direct way. You can cheat this by creating your own step pattern.
- It is easy to make a mistake with choosing query and a reference, because the DTW measure in general is not symmetric.
- Lack of a function which can plot cost matrix in easy way.

References

Toni Giorgino

Computing and Visualizing Dynamic Time Warping Alignments in R: The dtw Package

Journal of Statistical Software August 2009, Volume 31, Issue 7.

Paweł Teisseyre

Porównanie szeregów czasowych z wykorzystaniem algorytmu DTW

Zlot uzytkowników R 21 September 2010

Elena Tsiporkova

Dynamic Time Warping Algorithm for Gene Expression Time Series