

JTimeWarp: A software for Aligning Biological Signals using Warping Methods

Burhanettin İrmikci Ahmet Elbir Fethullah Karabiber

Computer Engineering Department, Yildiz Technical University, Istanbul, 34220, TURKEY

Abstract—It is a very common problem to align signals upon time-axis for analysis of datasets obtained from biological experiments. Since biological or chemical signals may be measured differently due to some factors such as temperature, pressure and others laboratory conditions, the signals may have different time scales. In this study, three commonly used signal alignment methods are implemented in a software named JTimeWarp. First, Dynamic Time Warping (DTW), which is the most popular method, is implemented. DTW method takes a look for an optimal warping path between two time series. DTW method has three basic steps: (1) generates cost matrix using a distance function; (2) computes accumulated cost matrix from the values contained in cost matrix; (3) finds warping path through the use of accumulated cost matrix. While building a warping path, DTW uses the elements of the accumulated cost matrix whose values are the smallest along the way. [1]

Correlation Optimized Warping (COW) is another method derived from DTW to deliver better performance in finding an optimal alignment between two given time-dependent sequences under certain restrictions. COW applies piecewise linear stretching or compression of one signal, instead of pointwise warping like DTW. The dynamic programming optimization is used to determine the optimal positions of end points or nodes of the predetermined segments. [1]

Parametric Time Warping (PTW) is unique with its approach to signal warping. PTW tries to fit a polynomial function defining the misalignment of signals. The polynomial functions generated by PTW include many terms in the parametric time warping. For these reasons, PTW approach is different amongst others warping methods. [1] In this study, a user friendly and interactive software called JTimeWarp is developed to align signals automatically. The software is implemented using java programming language and java swing library. User can load data and select a warping method for alignment. Since there is no perfect alignment methods, the software gives the users option of the manual correction. User can apply one of the warping methods and then correct the errors manually using interactive options. User also can apply all three methods at the same time and the select the best one for the signal alignment.

REFERENCES

- [1] Tom G. Bloemberg, Jan Gerretzen, Anton Lunshof, Ron Wehrens, Lutgarde M.C. Buydens, Warping Methods for Spectroscopic and Chromatographic Signal Alignment: A Tutorial Review, *Analytica Chimica Acta* (2013)
- [2] Szymańska, Ewa, et al. "Evaluation of different warping methods for the analysis of CE profiles of urinary nucleosides." *Electrophoresis* 28.16 (2007)