

Takeaway Messages

The Matrix Profile (introduced a year ago) is a domain independent approach to make most time series tasks trivial.

It allows motif discovery, density estimation, anomaly detection, rule discovery, joins, segmentation, clustering, visualization etc.

However, sometimes you may wish to impose domain dependent constraints from your particular domain. The Annotation Vector is a simple principled way to do so.

Top-1 motif pair Top motif location Top motif location

A ran random walk time series *T* with two sine waves embedded and its selfjoin matrix profile **P**. The matrix profile at the *i*th location records the distance of the subsequence in T, at the i^{th} location, to its nearest neighbor.

Matrix Profile and Time Series **Motifs Discovery**

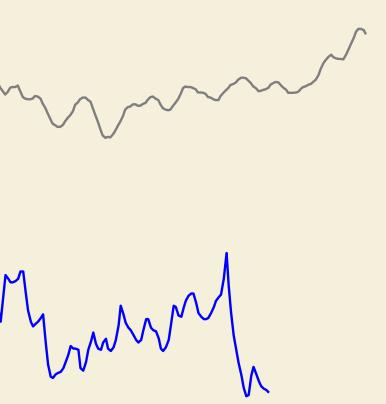
If you know the nearest neighbors of every subsequence in a time series, you can solve many time series data mining tasks trivially. For example, to find time series motifs, you locate the subsequence pairs with the smallest mutual distance.

The Matrix Profile is a data structure that gives you that information. The Matrix Profile can be computed fast thanks to [1].

References

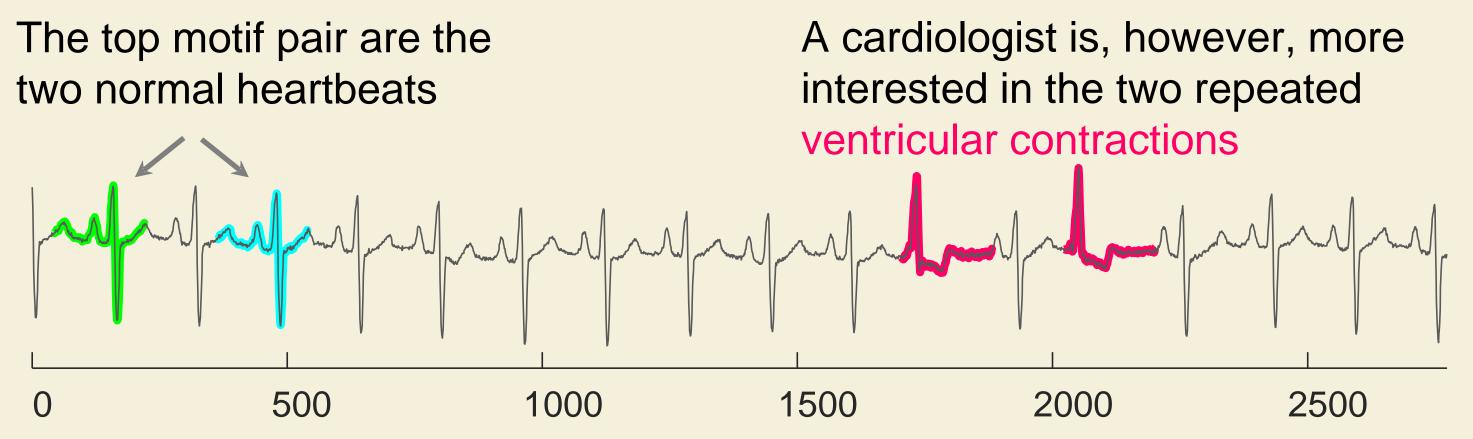
To learn more about the Matrix Profile and the wonderful things it has to offer: [1] <u>http://www.cs.ucr.edu/~eamonn/MatrixProfile.html</u> To learn more about the Annotation Vector and download code and datasets: http://www.cs.ucr.edu/~hdau001/guided_motif_search/

Introducing the Annotation Vector



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Classic Motif Search: What you see may not be what you want



A snippet of ECG data from BIDMC Congestive Heart Failure Database

Annotation Vector Framework

Main idea: combines the Matrix Profile (MP) with the Annotation Vector to produce a new Matrix Profile, which incorporates the contextual bias for the problem at hand.

The Annotation Vector is a time series consisting of real-valued numbers between [0 – 1].

A lower value indicates the subsequence starting at that index is less desirable, and therefore should be biased against.

The Math behind

 $CMP_i = MP_i + (1 - AV_i) * \max(MP)$ where

- *CMP_i* is the corrected Matrix **Profile value at index** *i*
- *MP_i* is the original Matrix Profile value at index *i*
- AV_i is the Annotation Vector value at index *i*
- max(*MP*) is the maximum value of the original Matrix Profile

Case Study: Suppressing Hardlimited Artifacts

