Exact Indexing of Dynamic Time Warping

Eamonn Keogh

Computer Science & Engineering Department
University of California - Riverside
Riverside,CA 92521
eamonn@cs.ucr.edu

Fair Use Agreement

If you use these slides (or any part thereof) for any lecture or class, please send me an email, if possible with a pointer to the relevant web page or document.

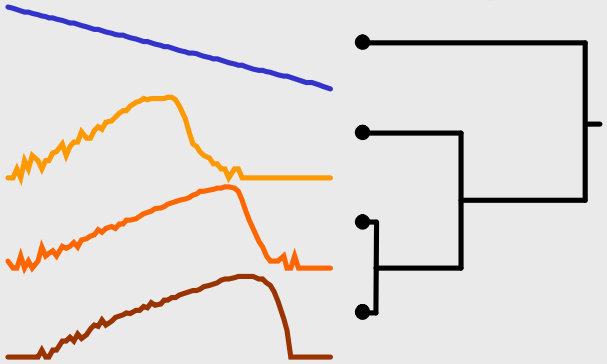
eamonn *eamonn@cs.ucr.edu*

Outline of Talk

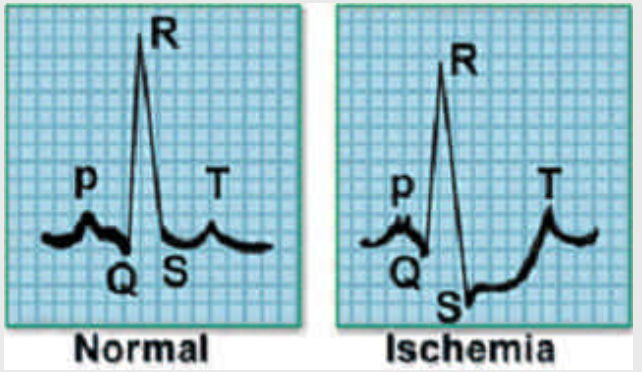
- Why do Time Series Similarity Matching?
- Limitations of Euclidean Distance
- Dynamic Time Warping
- Lower Bounding Dynamic Time Warping
- Indexing Dynamic Time Warping
- Experimental Evaluation
- Conclusions
- Questions

Why do Time Series Similarity Matching?

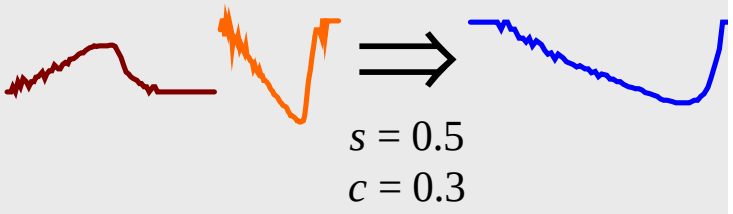
Clustering



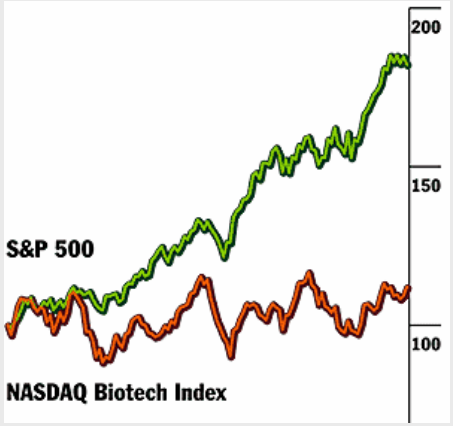
Classification



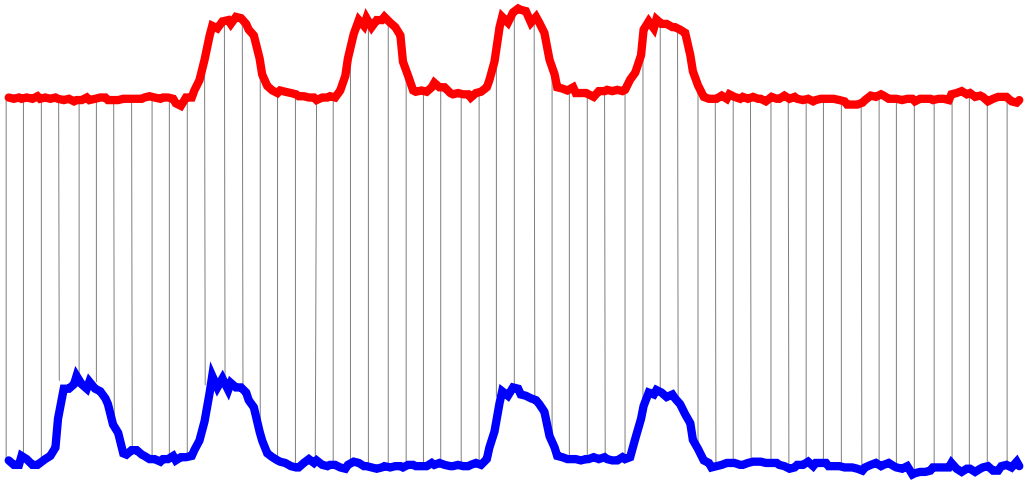
Rule Discovery



Query by Content

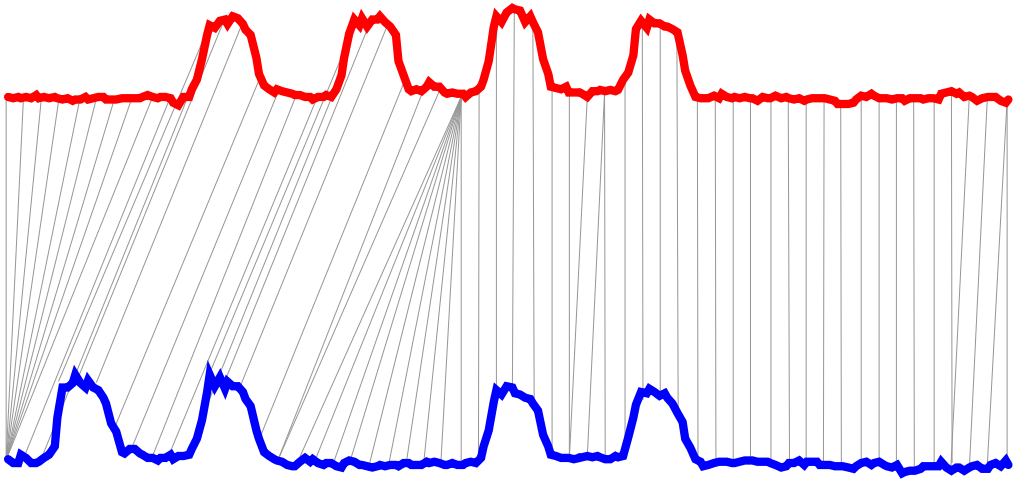


Euclidean Vs Dynamic Time Warping



Euclidean Distance

Sequences are aligned "one to one".



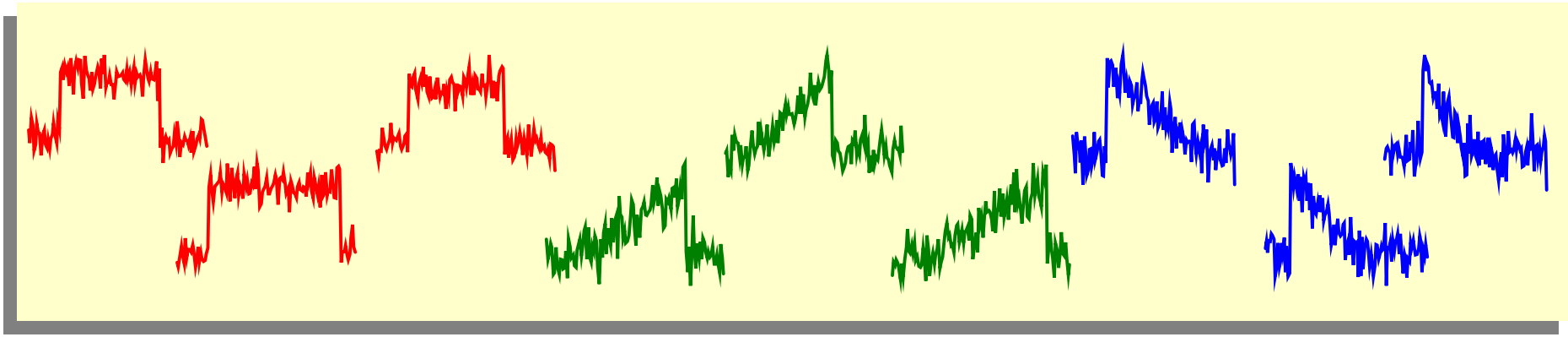
"Warped" Time Axis

Nonlinear alignments are possible.

Limitations of Euclidean Distance I

Classification

Classification Experiment on Cylinder-Bell-Funnel Dataset



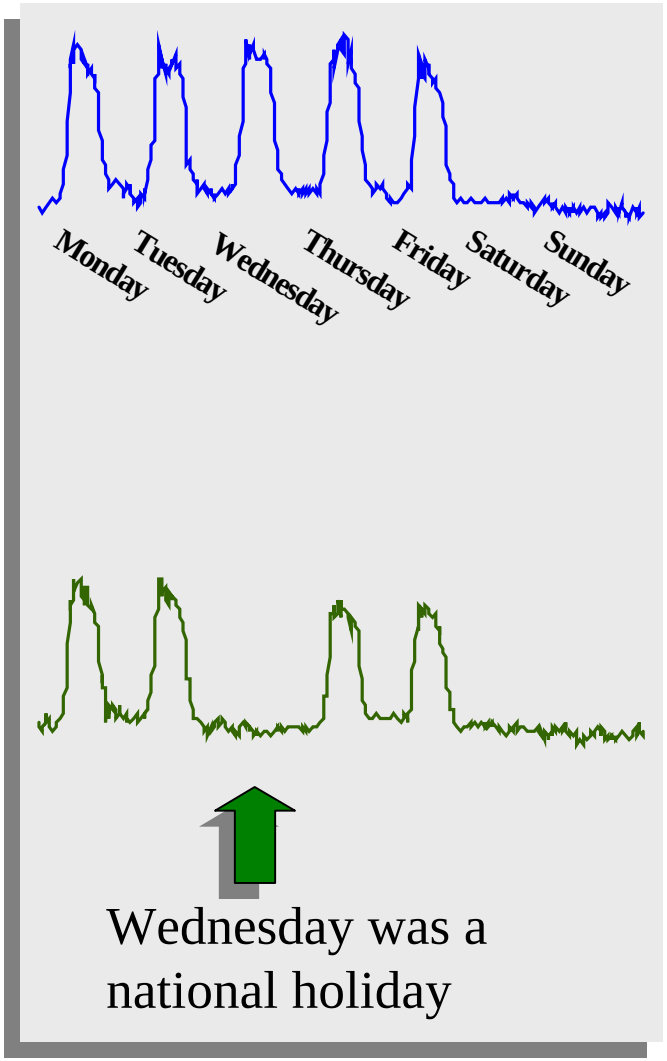
Training data consists of 10 exemplars from each class.

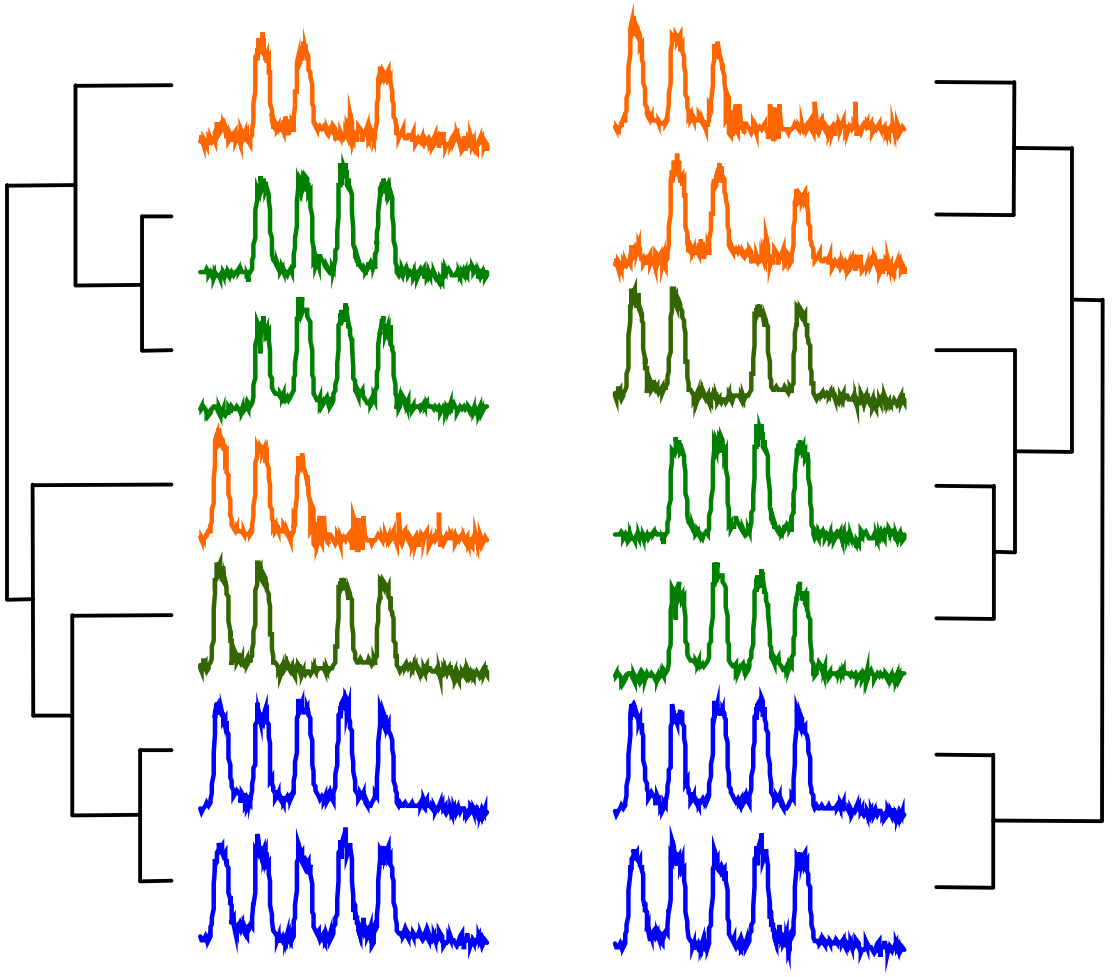
- (One) Nearest Neighbor Algorithm
- "Leaving-one-out" evaluation, averaged over 100 runs

• Euclidean Distance Error rate	**26.10%**
• Dynamic Time Warping Error rate	**2.87%**

Limitations of Euclidean Distance II

Clustering





Euclidean

Dynamic Time Warping

Because of the robustness of Dynamic Time Warping compared to Euclidean Distance, it is used in…

Bioinformatics: Aach, J. and Church, G. (2001). Aligning gene expression time series with time warping algorithms. Bioinformatics. Volume 17, pp 495-508.

Robotics: Schmill, M., Oates, T. & Cohen, P. (1999). Learned models for continuous planning. In *7th International Workshop on Artificial Intelligence and Statistics.*

Medicine: Caiani, E.G., et. al. (1998) Warped-average template technique to track on a cycle-by-cycle basis the cardiac filling phases on left ventricular volume. IEEE Computers in Cardiology.

Chemistry: Gollmer, K., & Posten, C. (1995) Detection of distorted pattern using dynamic time warping algorithm and application for supervision of bioprocesses. IFAC CHEMFAS-4

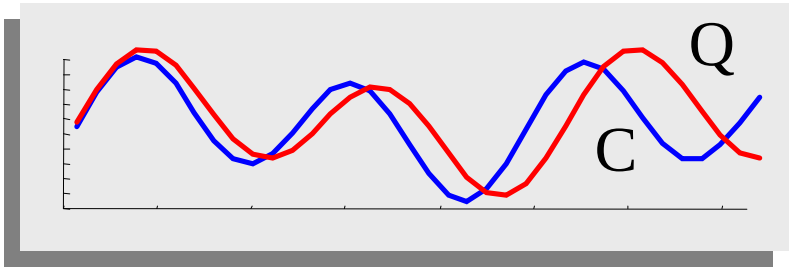
Gesture Recognition:
Gavrila, D. M. & Davis,L. S.(1995). Towards 3-d model-based tracking and recognition of human movement: a multi-view approach. In IEEE IWAFGR

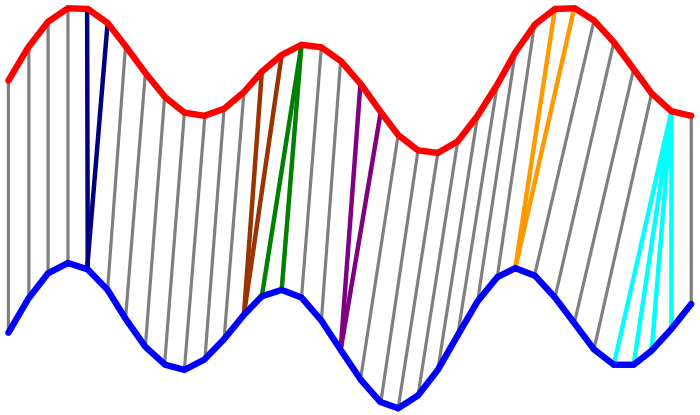
Meteorology/ Tracking/ Biometrics / Astronomy / Finance / Manufacturing …

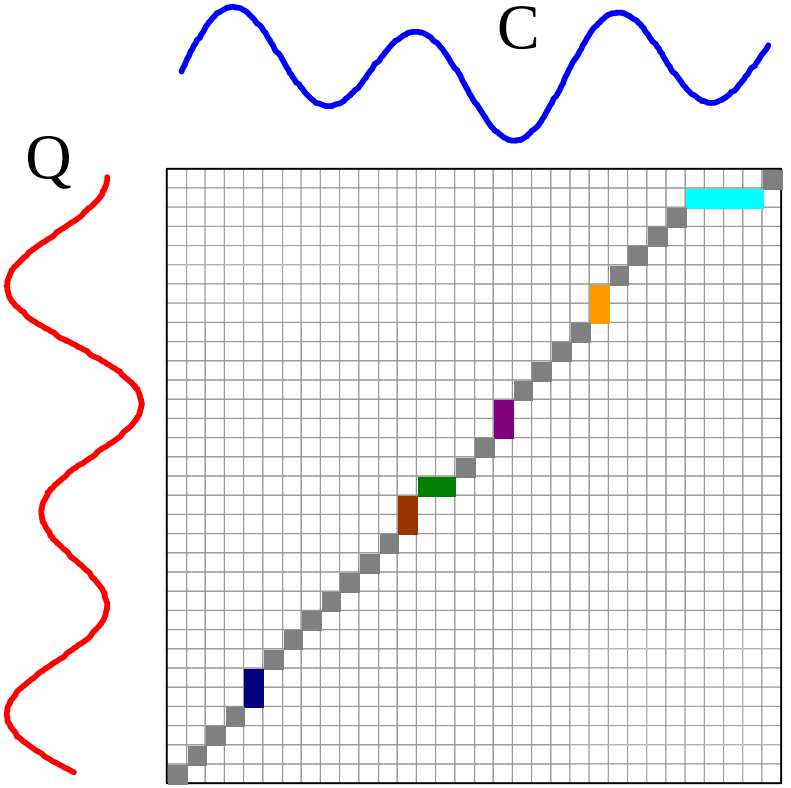
How is DTW Calculated?

$$DTW(Q,C) = \min\left\{ \sqrt{\sum_{k=1}^{K} w_k} \Big/ K \right.$$

$$\gamma(i,j) = d(q_i,c_j) + \min\{ \gamma(i\text{-}1,j\text{-}1) , \gamma(i\text{-}1,j) , \gamma(i,j\text{-}1) \}$$





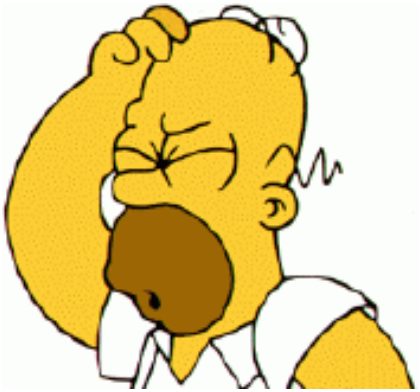


Warping path *w*

DTW is much better than Euclidean distance for classification, clustering, query by content etc.

But is it not true that "*dynamic time warping cannot be speeded up by indexing* *", and is $O(n^2)$?

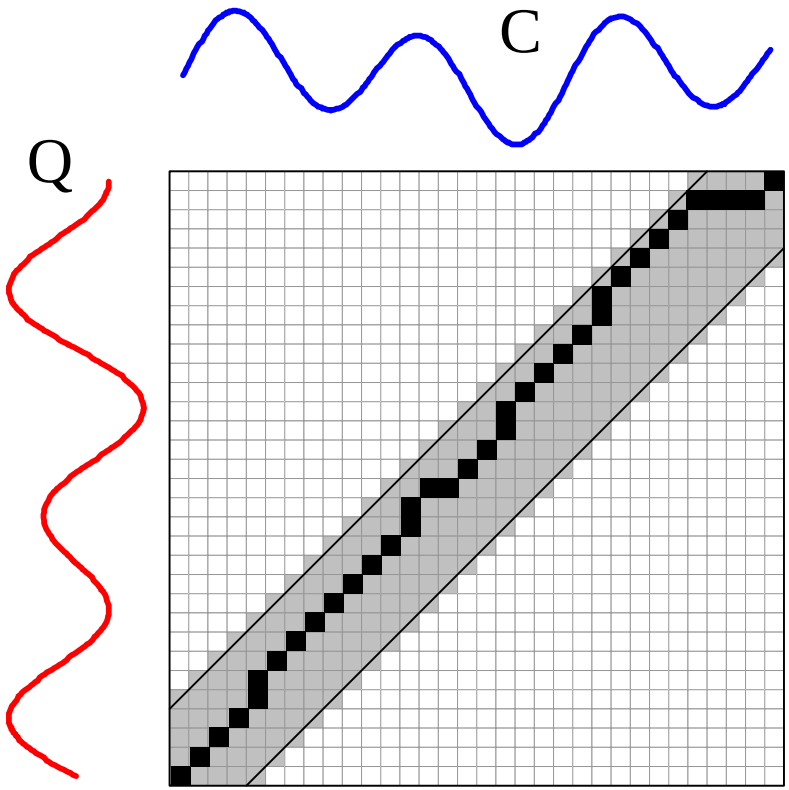
Dooh



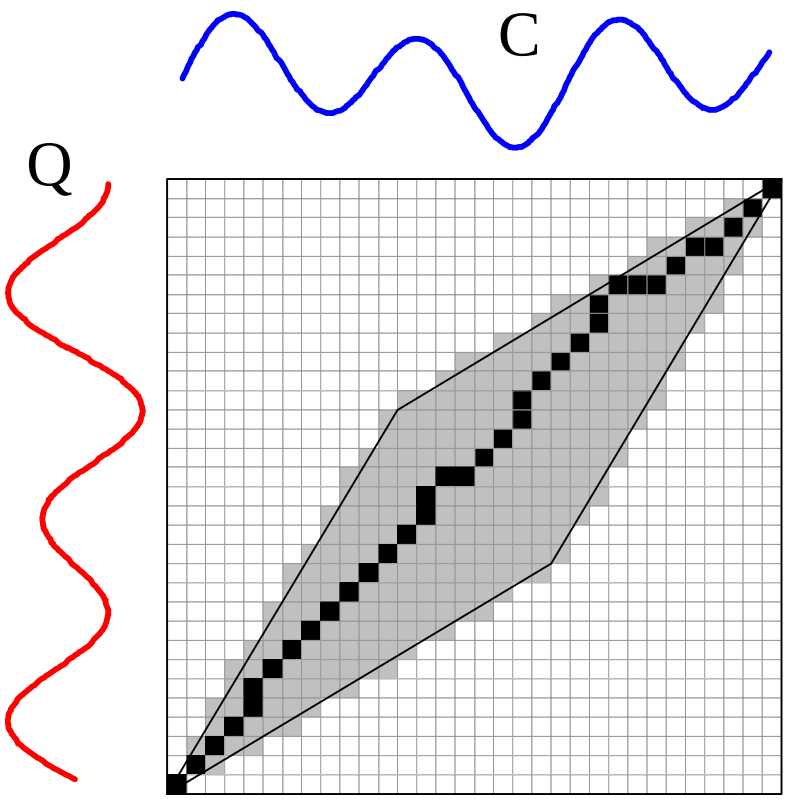
* Agrawal, R., Lin, K. I., Sawhney, H. S., & Shim, K. (1995). Fast similarity search in the presence of noise, scaling, and translation in times-series databases. VLDB pp. 490-501.

Global Constraints

- Slightly speed up the calculations
- Prevent pathological warpings



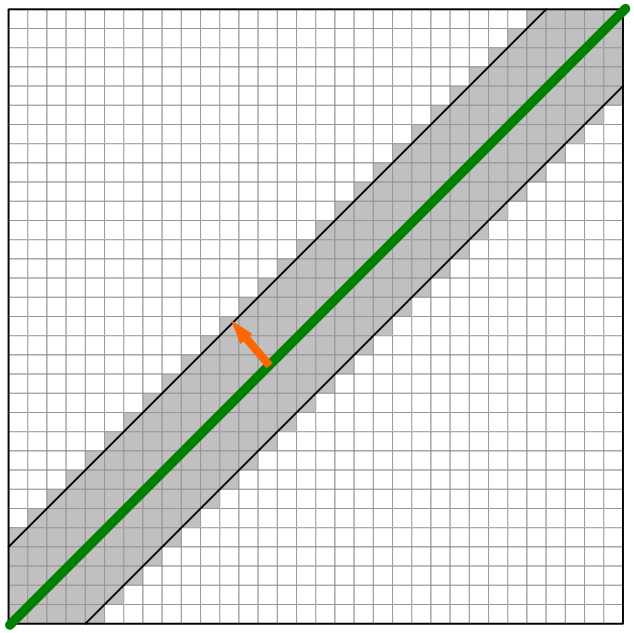
Sakoe-Chiba Band



Itakura Parallelogram

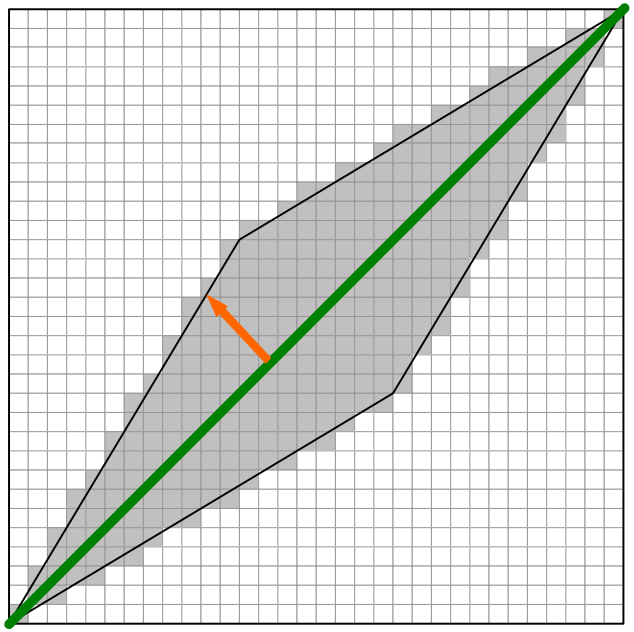
A global constraint constrains the indices of the warping path $w_k = (i,j)_k$ such that $j-r \leq i \leq j+r$

Where r is a term defining allowed range of warping for a given point in a sequence.



Sakoe-Chiba Band

$r =$



Itakura Parallelogram

Lower Bounding

We can speed up similarity search under DTW by using a lower bounding function.

Intuition

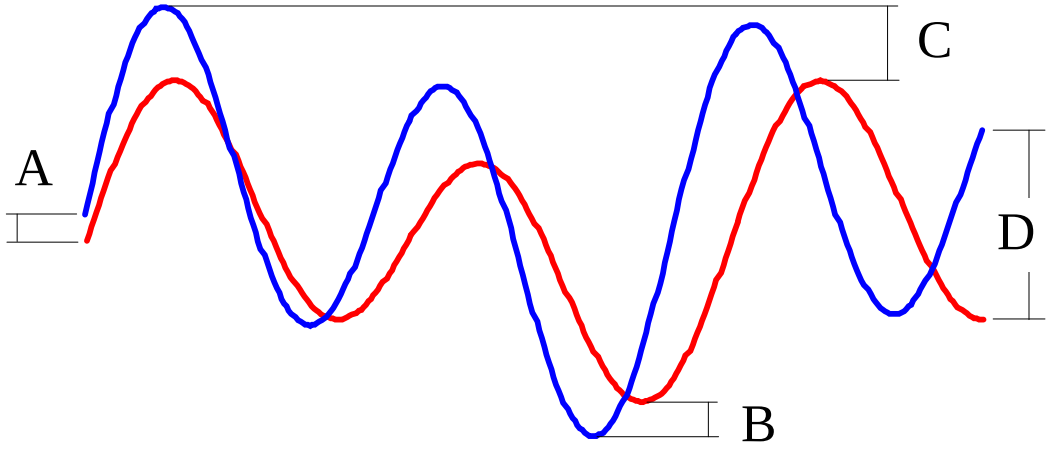
Try to use a cheap lower bounding calculation as often as possible.

Only do the expensive, full calculations when it is absolutely necessary.

Algorithm Lower_Bounding_Sequential_Scan(Q)

```
1.  best_so_far = infinity;
2.  for all sequences in database
3.    LB_dist = lower_bound_distance( C_i, Q);
4.    if LB_dist < best_so_far
5.      true_dist = DTW(C_i, Q);
6.      if true_dist < best_so_far
7.        best_so_far = true_dist;
8.        index_of_best_match = i;
9.      endif
10.   endif
11. endfor
```

Lower Bound of Kim et. al.

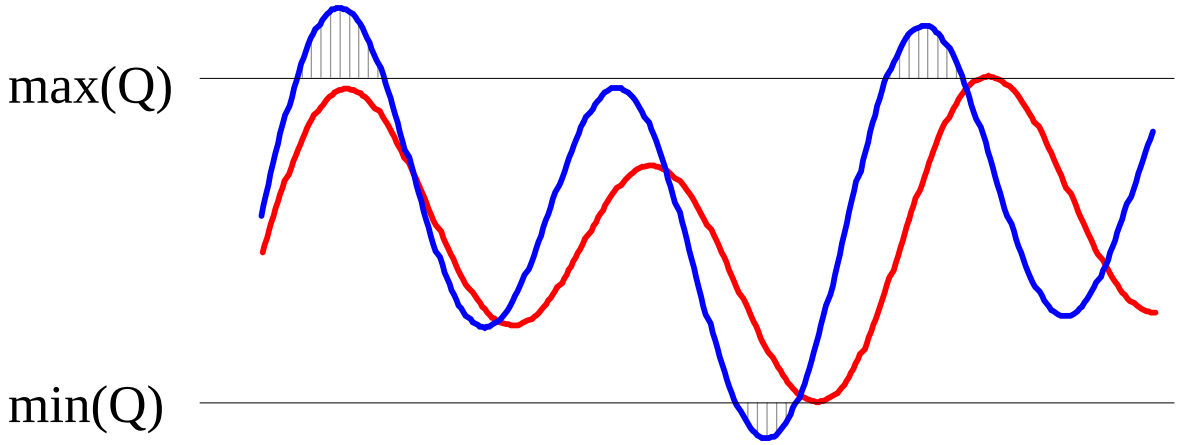


LB_Kim

Kim, S, Park, S, & Chu, W. *An index-based approach for similarity search supporting time warping in large sequence databases*. ICDE 01, pp 607-614

The squared difference between the two sequence's first (A), last (D), minimum (B) and maximum points (C) is returned as the lower bound

Lower Bound of Yi et. al.



LB_Yi

Yi, B, Jagadish, H & Faloutsos, C. *Efficient retrieval of similar time sequences under time warping*. ICDE 98, pp 23-27.

The sum of the squared length of gray lines represent the minimum the corresponding points contribution to the overall DTW distance, and thus can be returned as the lower bounding measure

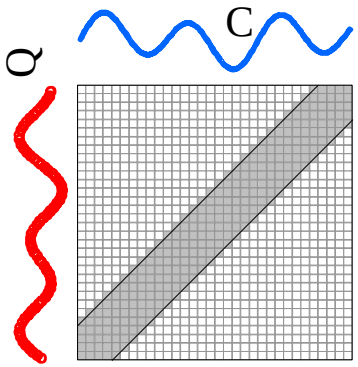
What we have seen so far…

• Dynamic Time Warping (DTW) is a very robust technique for measuring time series similarity.

• DTW is widely used in diverse fields.

• Since DTW is expensive to calculate, techniques to speed up similarity search have been introduced, including global constraints and two different lower bounding techniques.

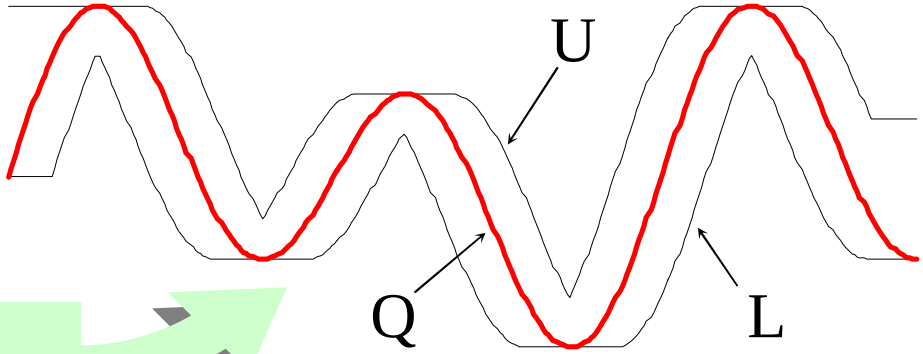
A Novel Lower Bounding Technique I

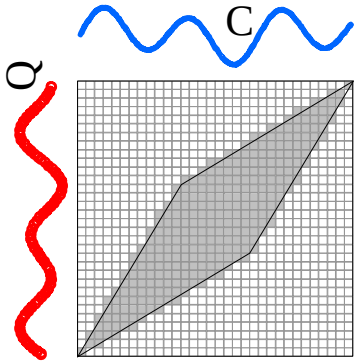


Sakoe-Chiba Band

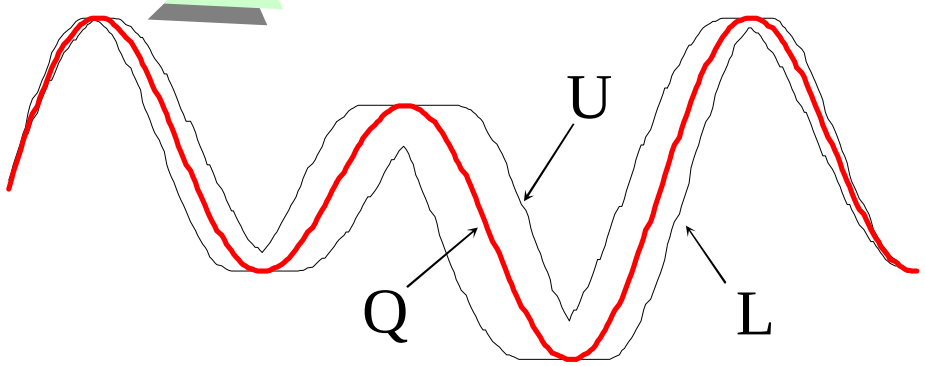
$U_i = \max(q_{i-r} : q_{i+r})$

$L_i = \min(q_{i-r} : q_{i+r})$

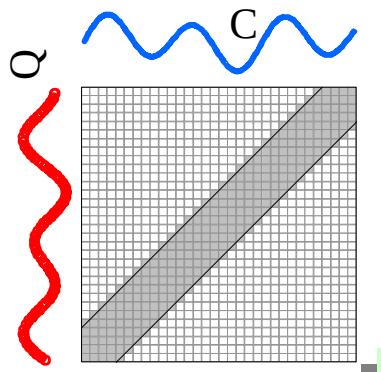




Itakura Parallelogram

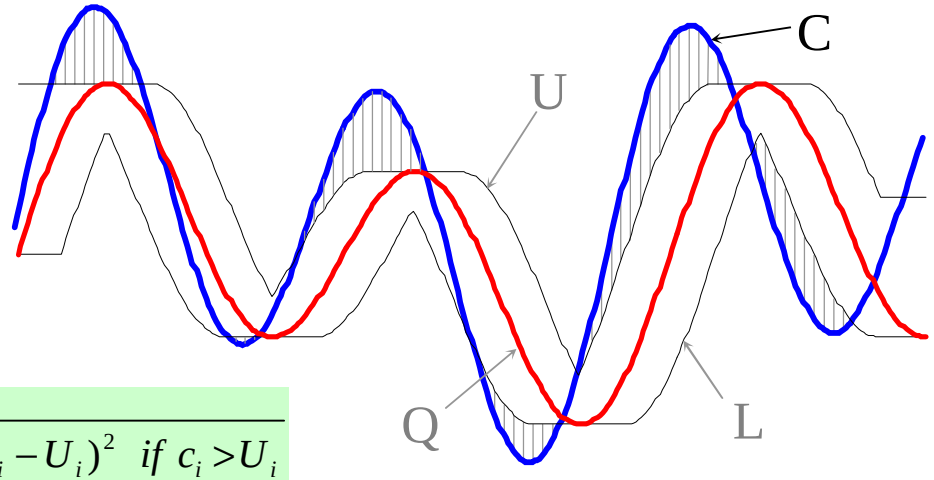


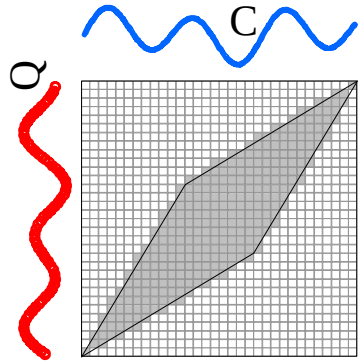
A Novel Lower Bounding Technique II



Sakoe-Chiba Band

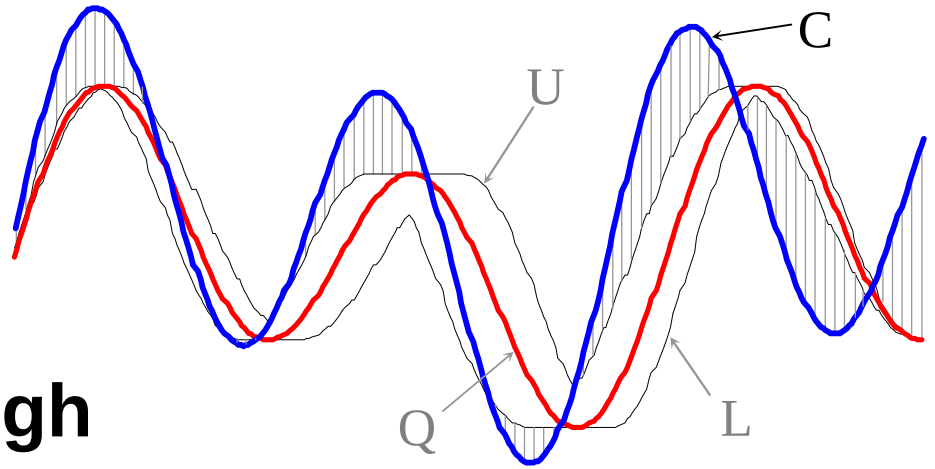
$$LB_Keogh(Q,C) = \sqrt{\sum_{i=1}^{n} \begin{cases} (c_i - U_i)^2 & if\ c_i > U_i \\ (c_i - L_i)^2 & if\ c_i < L_i \\ 0 & otherwise \end{cases}}$$



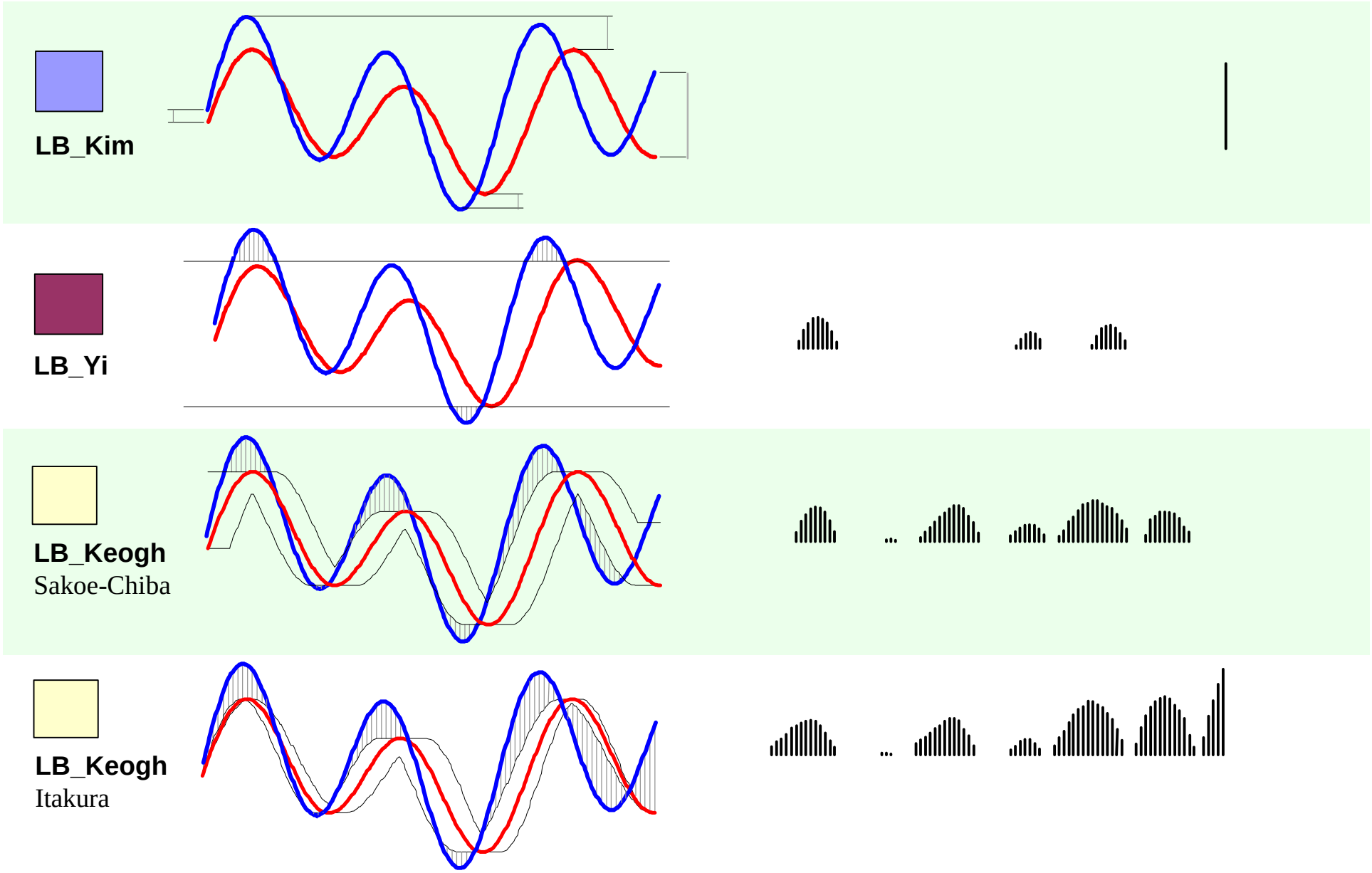


Itakura Parallelogram

LB_Keogh



The tightness of the lower bound for each technique is proportional to the length of gray lines used in the illustrations



Before we consider the problem of indexing, let us empirically evaluate the quality of the proposed lowering bounding technique.

This is a good idea, since it is an *implementation free* measure of quality.

First we must discuss our experimental philosophy…

Experimental Philosophy

• We tested on **32** datasets from such diverse fields as finance, medicine, biometrics, chemistry, astronomy, robotics, networking and industry. The datasets cover the complete spectrum of stationary/ non-stationary, noisy/ smooth, cyclical/ non-cyclical, symmetric/ asymmetric etc

• Our experiments are completely reproducible. We saved every random number, every setting and all data.

• To ensure true randomness, we use random numbers created by a quantum mechanical process.

• We test with the **Sakoe-Chiba Band**, which is the worst case for us (the **Itakura Parallelogram** would give us much better results).

Tightness of Lower Bound Experiment

• We measured T

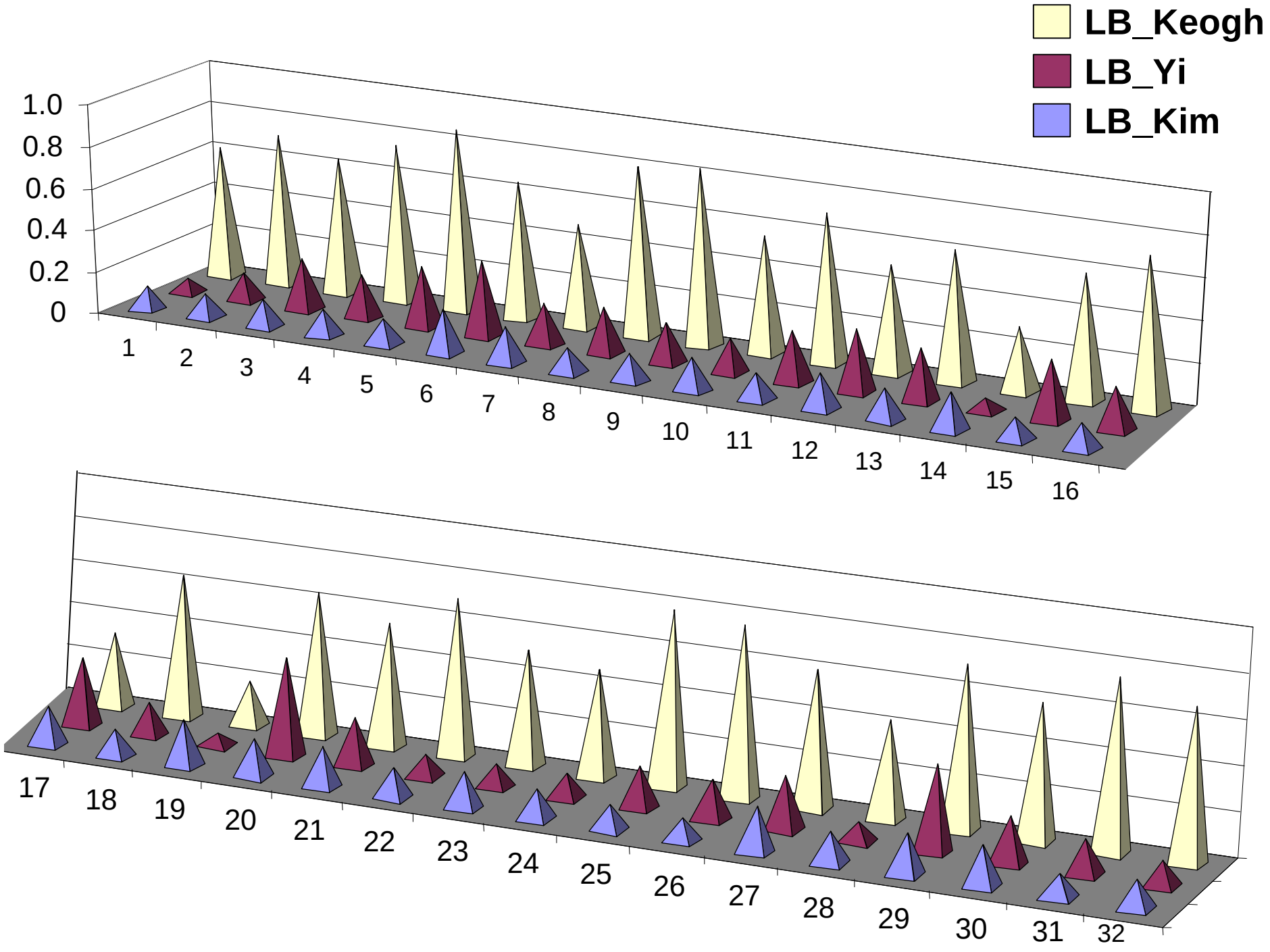
$$T = \frac{Lower\ Bound\ Estimate\ of\ Dynamic\ Time\ Warp\ Distance}{True\ Dynamic\ Time\ Warp\ Distance}$$

• For each dataset, we randomly extracted 50 sequences of length **256**. We compared each sequence to the 49 others.

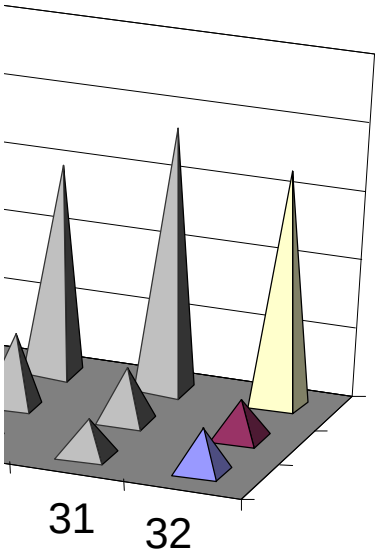
$0 \leq T \leq 1$
The larger the better

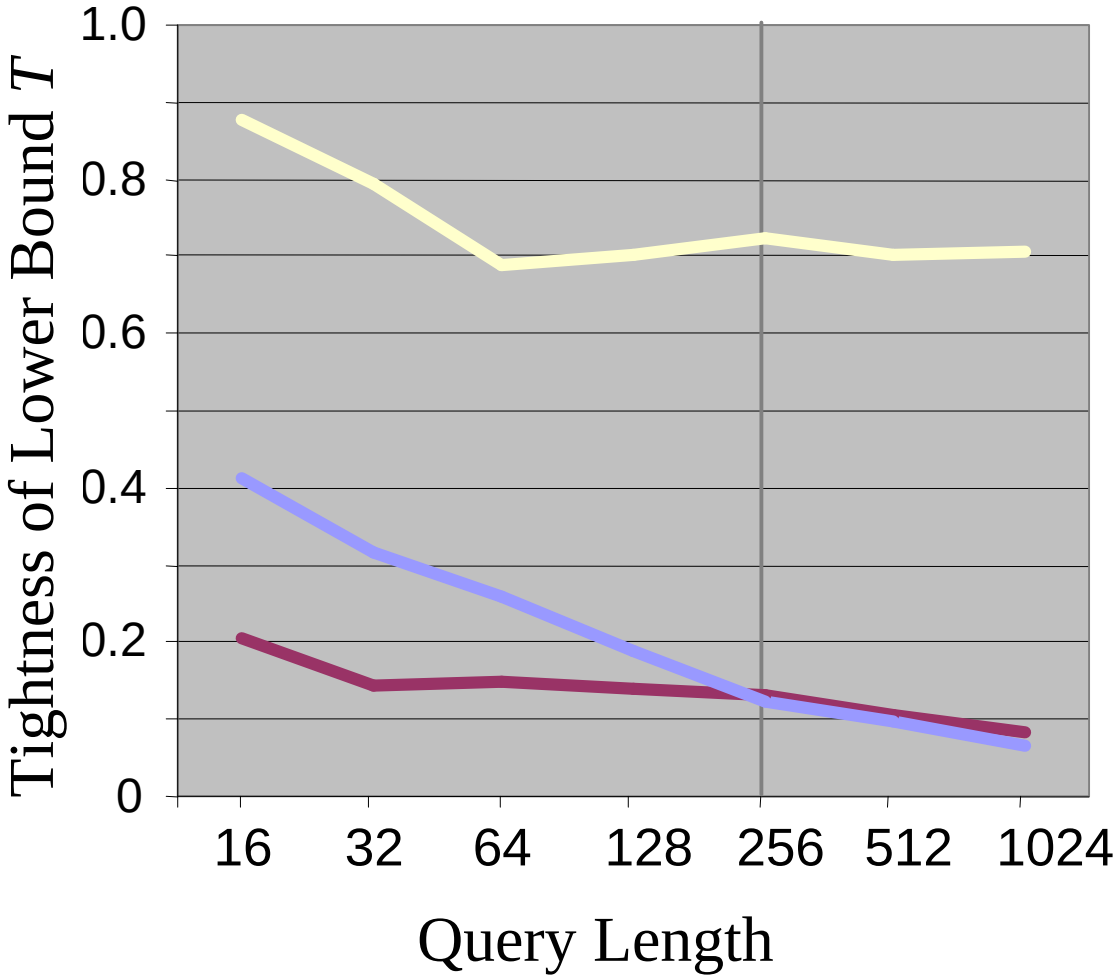
• For each dataset we report T as average ratio from the 1,225 (50*49/2) comparisons made.

Query length of 256 is about the mean in the literature.


LB_Keogh
LB_Yi
LB_Kim
1.0
0.8
0.6
0.4
0.2
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32

Effect of Query Length on Tightness of Lower Bounds





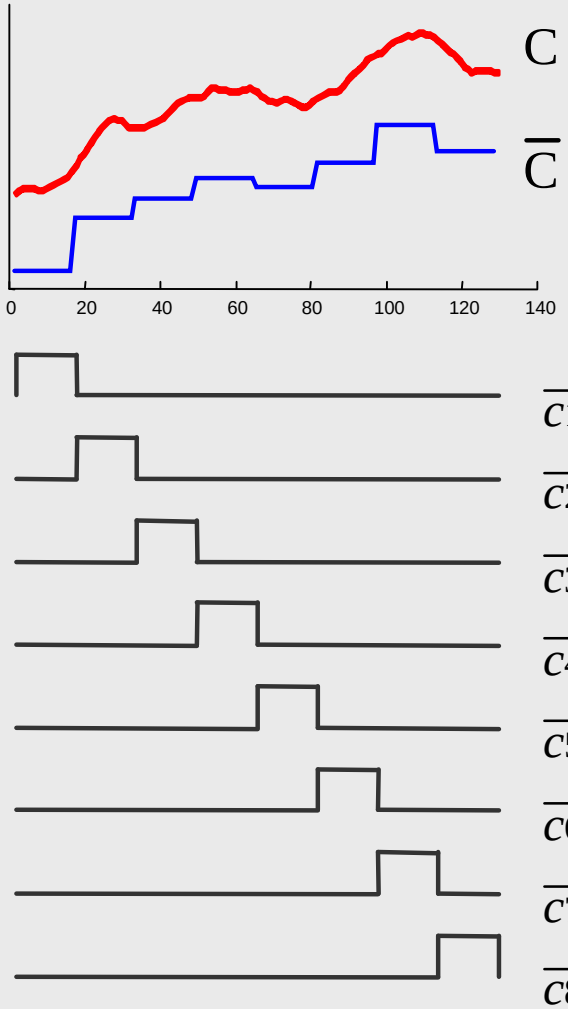
These experiments suggest we can use the new lower bounding technique to speed up sequential search. That's super!

Excellent!
But what we really need is a technique to index the time series

A Dimensionality Reduction Technique

Piecewise Aggregate Approximation (PAA)

$$\overline{C}_i = \frac{N}{n} \sum_{j=\frac{n}{N}(i-1)+1}^{\frac{n}{N}i} c_j$$



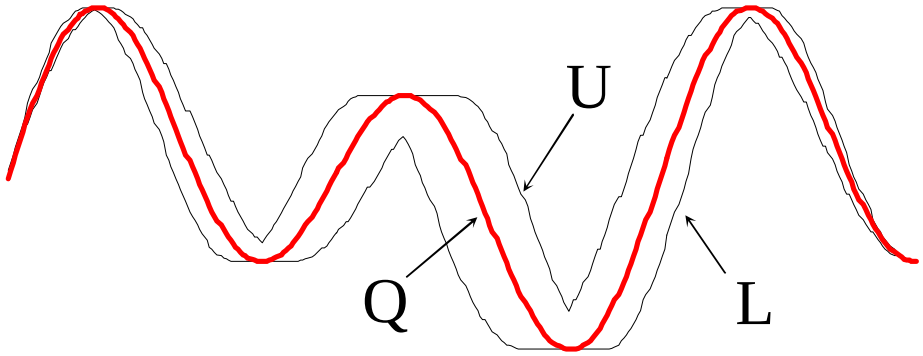
Advantages of PAA (for Euclidean Indexing)

- Extremely fast to calculate
- As efficient as other approaches such as wavelets and Fourier transform (empirically)
- Support queries of arbitrary lengths on the same index
- Supports weighted Euclidean distance
- Simple! Intuitive!

Keogh, E,. Chakrabarti, K,. Pazzani, M. & Mehrotra, S. (2000). *Dimensionality reduction for fast similarity search in large time series databases.* KAIS. pp 263-286.

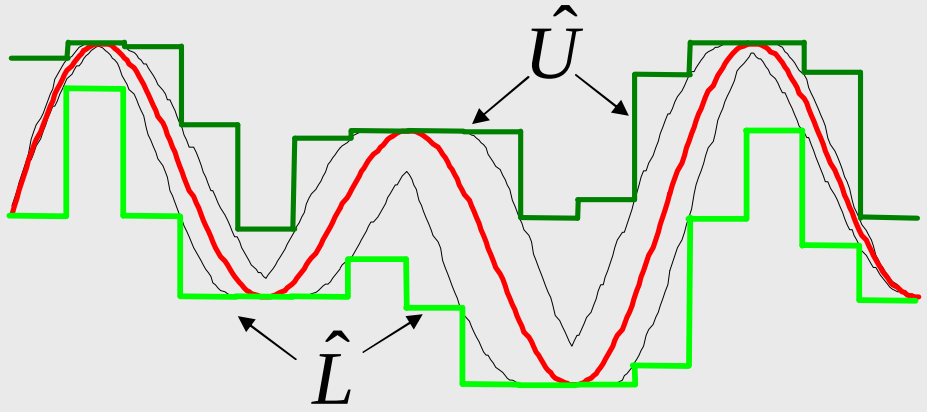
Yi, B, K., & Faloutsos, C.(2000). *Fast time sequence indexing for arbitrary Lp norms.* VLDB. pp 385-394.

We create special PAA of U and L, which we will denote $\hat{U}$ and $\hat{L}$.



$$\hat{U}_i = \max\left(U_{\frac{n}{N}(i-1)+1}, \ldots, U_{\frac{n}{N}(i)}\right)$$

$$\hat{L}_i = \min\left(L_{\frac{n}{N}(i-1)+1}, \ldots, L_{\frac{n}{N}(i)}\right)$$

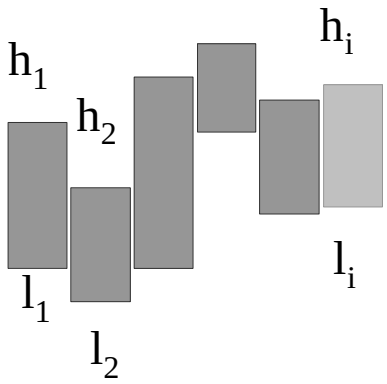


Our index structure contains a leaf node **U**. Let R = (L, H) be the MBR associated with **U**

MBR R = (L,H)

L = $\{l_1, l_2, \ldots, l_N\}$

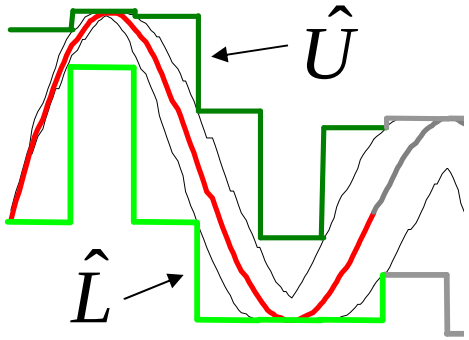
H = $\{h_1, h_2, \ldots, h_N\}$



We have seen how to define $\hat{U}$ and $\hat{L}$

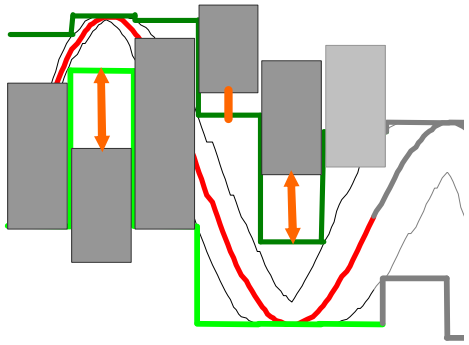
$$\hat{U}_i = \max\left(U_{\frac{n}{N}(i-1)+1}, \ldots, U_{\frac{n}{N}(i)}\right)$$

$$\hat{L}_i = \min\left(L_{\frac{n}{N}(i-1)+1}, \ldots, L_{\frac{n}{N}(i)}\right)$$



We can now define the MINDIST function, which returns the distance between a query Q and a MBR R

$$MINDIST(Q,R) = \sqrt{\sum_{i=1}^{N} \frac{n}{N} \begin{cases} (l_i - \hat{U}_i)^2 & \text{if } l_i > \hat{U}_i \\ (h_i - \hat{L}_i)^2 & \text{if } h_i < \hat{L}_i \\ 0 & \text{otherwise} \end{cases}}$$



MINDIST(Q,R)

Having defined the **MINDIST** function we can use (slightly modified) classic K-Nearest Neighbor and Range Queries

Algorithm RangeSearch(Q, ε, T)

```
1. if T is a non-leaf node
2. for each child U of T
3.     if MINDIST(Q,R)≤ ε   RangeSearch(Q, ε, U);
                            // R is MBR of U
4.     else                 // T is a leaf node

5.     for each PAA point C in T
6.     if LB_PAA(Q,)≤ ε
7.         Retrieve full sequence C from database;
8.     if DTW(Q,C) ≤ e  Add C to result;
```

Seidl, T. & Kriegel, H. (1998). Optimal multi-step k-nearest neighbor search. *SIGMOD*. pp 154-165.

Algorithm KNNSearch(Q,K)

```
Variable queue: MinPriorityQueue;
Variable list: temp;

1.  queue.push(root_node_of_index, 0);
2.  while not queue.IsEmpty() do
3.    top = queue.Top();
4.    for each time series C in temp
          such that DTW(Q,C) ≤ top.dist
5.    Remove C from temp;
6.    Add C to result;
7.    if |result| = K return result ;
8.  queue.Pop();
9.   if top is an PAA point C
10.  Retrieve full sequence C from database;
11.   temp.insert(C, DTW(Q,C));
12. else if top is a leaf node
13.  for each data item C in top
14.    queue.push(C, LB_PAA(Q,));
15. else                  // top is a non-leaf node
16.  for each child node U in top
17.    queue.push(U, MINDIST(Q,R)) // R is
                          MBR associated with U.
```

Pruning Power Experiment

• We measured P

$$P = \frac{Number\ of\ objects\ that\ do\ not\ require\ full\ DTW}{Number\ of\ objects\ in\ database}$$

• We randomly extract 50 sequences of length **256**. For each of the 50 sequences we separate out the sequence from the other 49 sequences, then find the nearest match to our withheld sequence among the remaining 49 sequences using the sequential scan

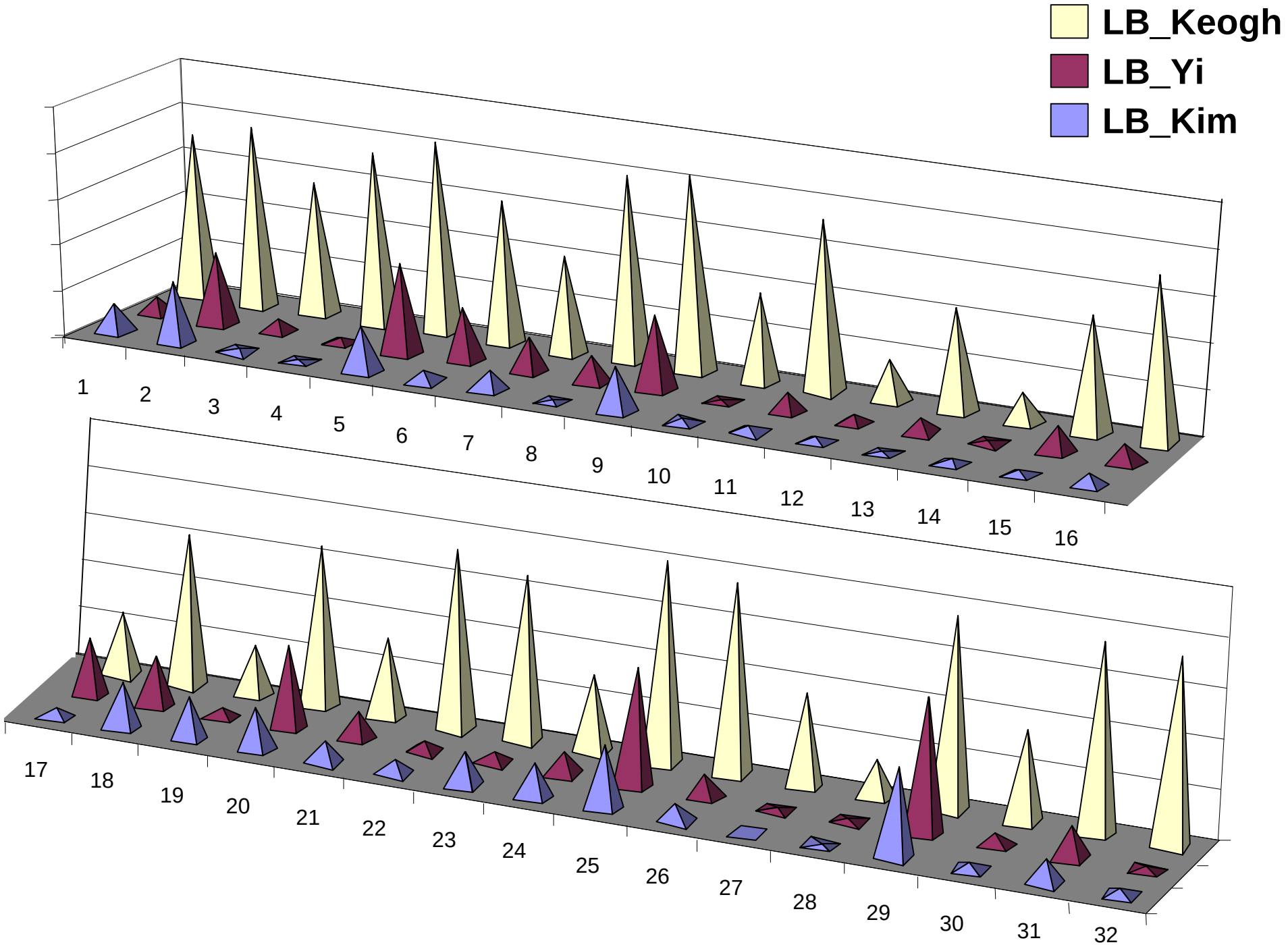
$0 \leq P \leq 1$

The larger the better

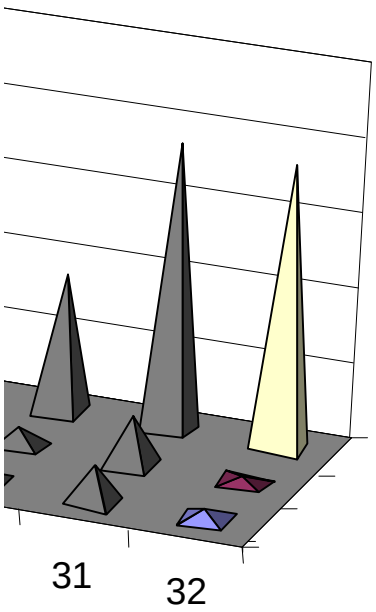
• We measure the number of times we can use the fast lower bounding functions to prune away the quadratic-time computation of the full DTW algorithm.

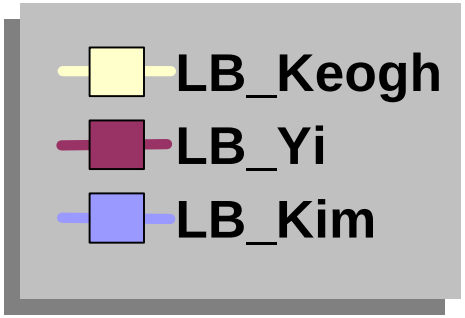
Query length of 256 is about the mean in the literature.

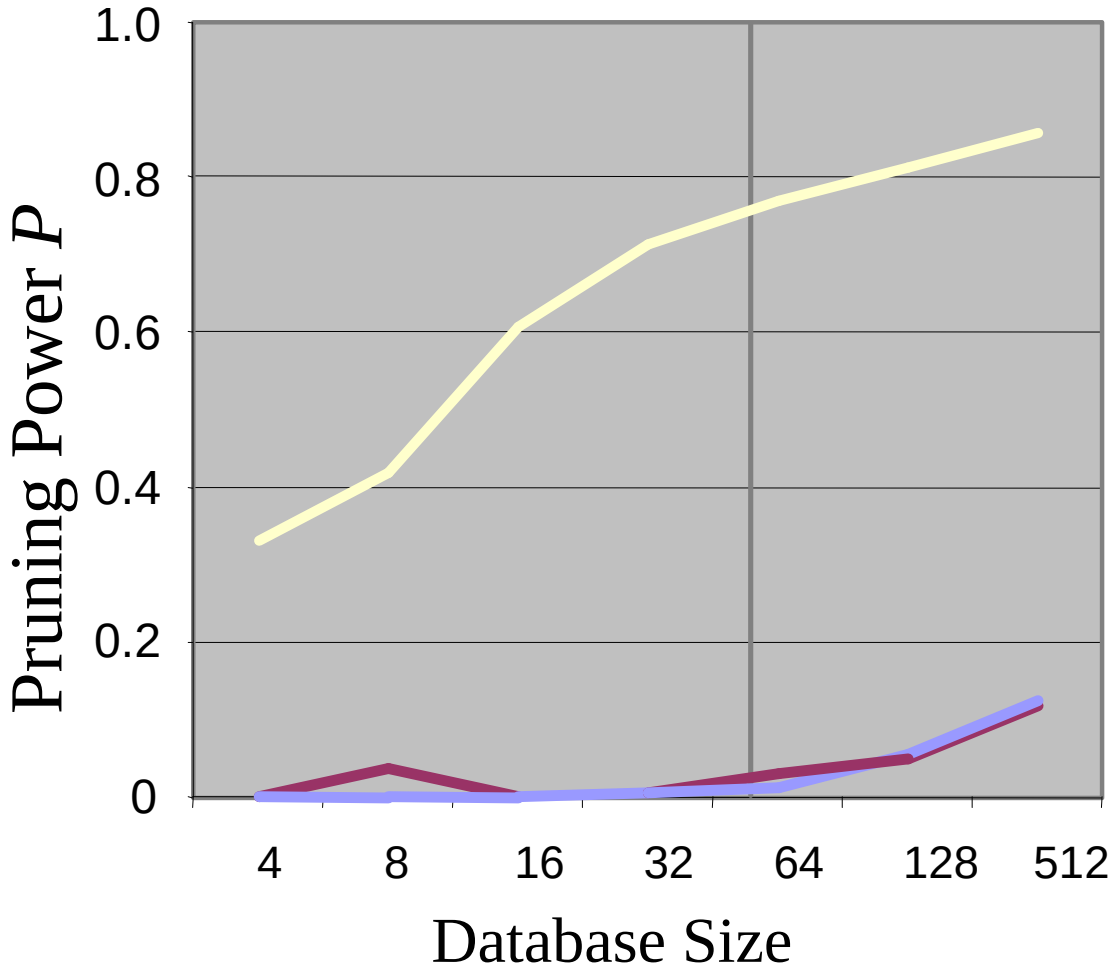
• For fairness we visit the 49 sequences in the same order for each approach.


LB_Keogh
LB_Yi
LB_Kim
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32

Effect of Database Size on Pruning Power







Experiment on Implemented System

System: AMD Athlon 1.4 GHZ processor, with 512 MB of physical memory and 57.2 GB of secondary storage. The index used was the R-Tree

Algorithms: We compare the proposed technique to linear scan. LB_Yi does not have an index method and LB_Kim never beats linear scan

Metric

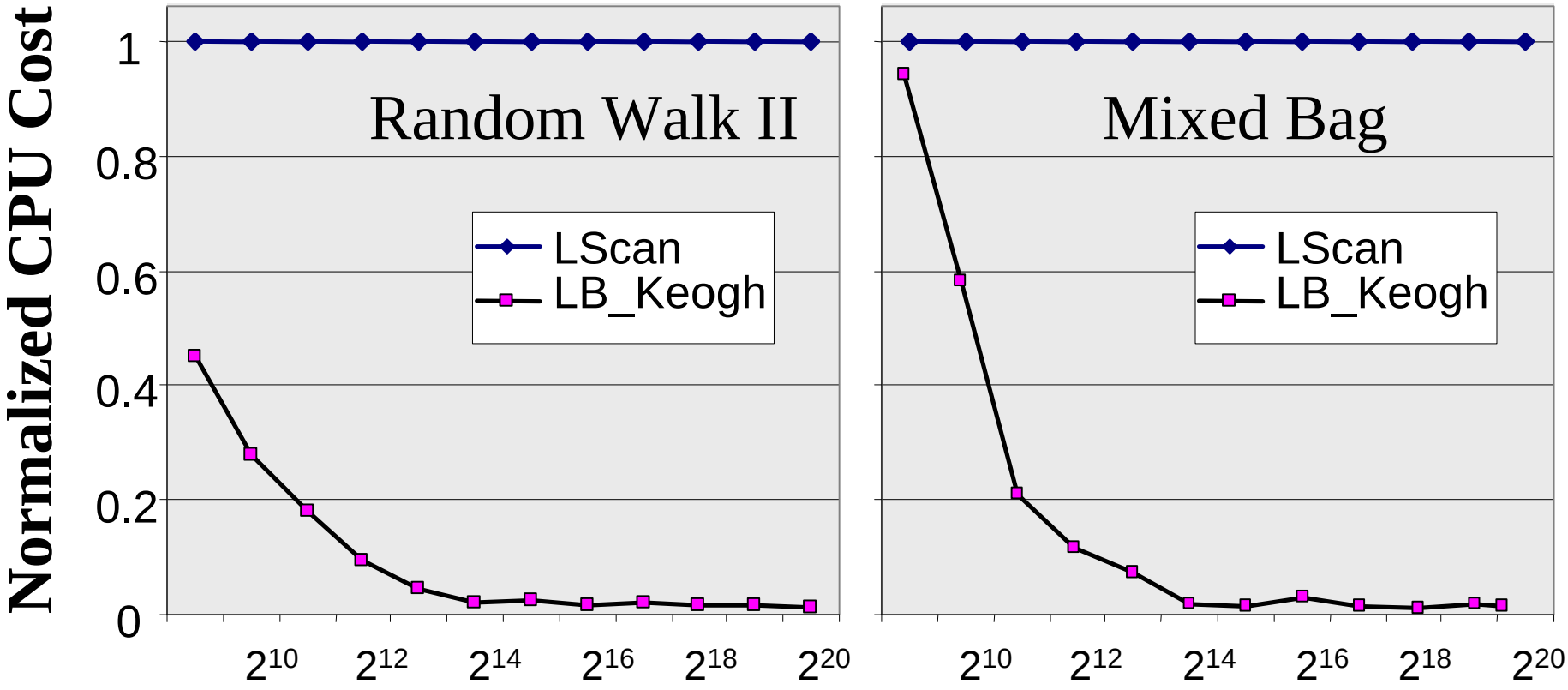
Definition: *The Normalized CPU cost*: The ratio of average CPU time to execute a query using the index to the average CPU time required to perform a linear (sequential) scan. The normalized cost of linear scan is 1.0

Datasets

- **Mixed Bag**: All 32 datasets pooled together. 763,270 items

- **Random Walk**: The most common test dataset in the literature. 1,048,576 items

Implemented System Experiment

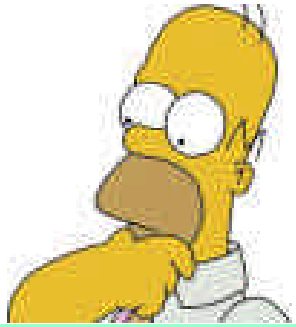


Note that the X-axis is logarithmic

Conclusions

- We have shown that DTW is better distance measure than Euclidean distance.
- We have introduced a new lower bounding technique for DTW.
- We have shown how to index the new lower bounding technique.
- We demonstrated the utility of our approach with a comprehensive empirical evaluation.

Questions?



Thanks to Kaushik Chakrabarti, Dennis DeCoste, Sharad Mehrotra, Michalis Vlachos and the VLDB reviewers for their useful comments.

Datasets and code used in this paper can be found at..

www.cs.ucr.edu/~eamonn/TSDMA/index.html