

Efficient Rotation Invariant Retrieval of Shapes with Applications in Medical Databases

Selina Chu, Shrikanth Narayanan, C.-C. Jay Kuo

Department of Computer Science
Department of Electrical Engineering
University of Southern California
Los Angeles, CA 90089

Email: selinach@sipi.usc.edu

Outline

- Shape recognition and representation
- Checking for rotation invariance of shapes
- Background
- Current method and problem
- Our framework
- Experimental setup and results
- Conclusion and future work

Shape Recognition

- Efficient content-based image retrieval
 - *Recognition of contours provide a mean to accelerate search*
- Direct comparison of images is intractable for large databases
 - *High dimensionality in raw data*
 - *Idiosyncrasies in details hinder the matching process*
- Conditions for effective shape matching
 - Similarity measure must be robust to various transformations and modest occlusions
 - Transformations, such as scaling and translation, can be dealt with by data representations or the similarity measure
 - Rotation invariance: More difficult compared with translation and scaling [22]

Representing Shapes

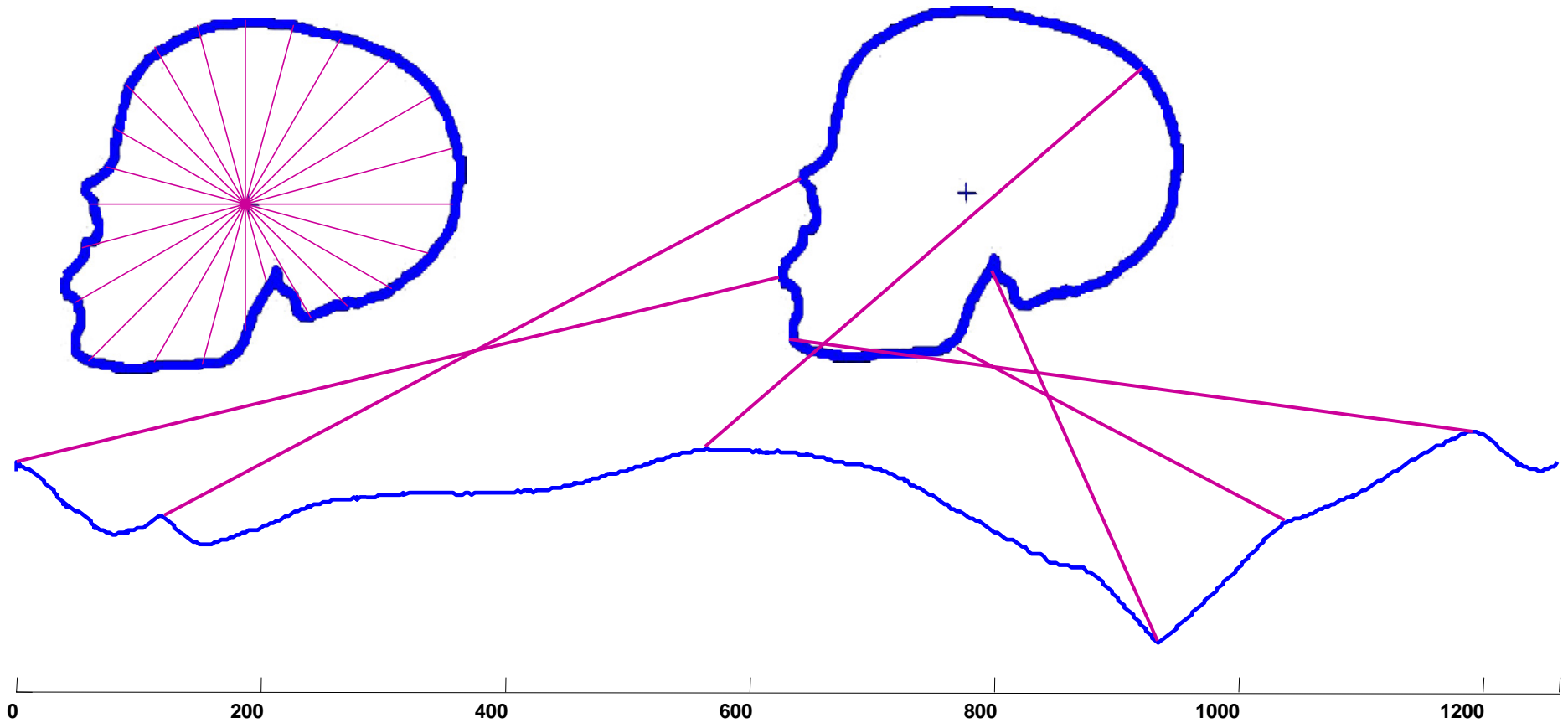


Represent shapes as one-dimensional data or time series:

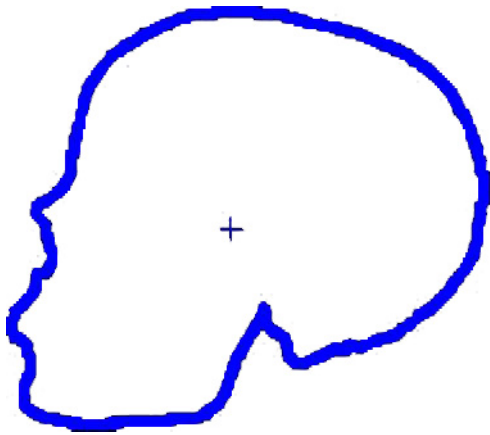
Numerous techniques for converting shapes to time series.

We'll see an example of a simple method...

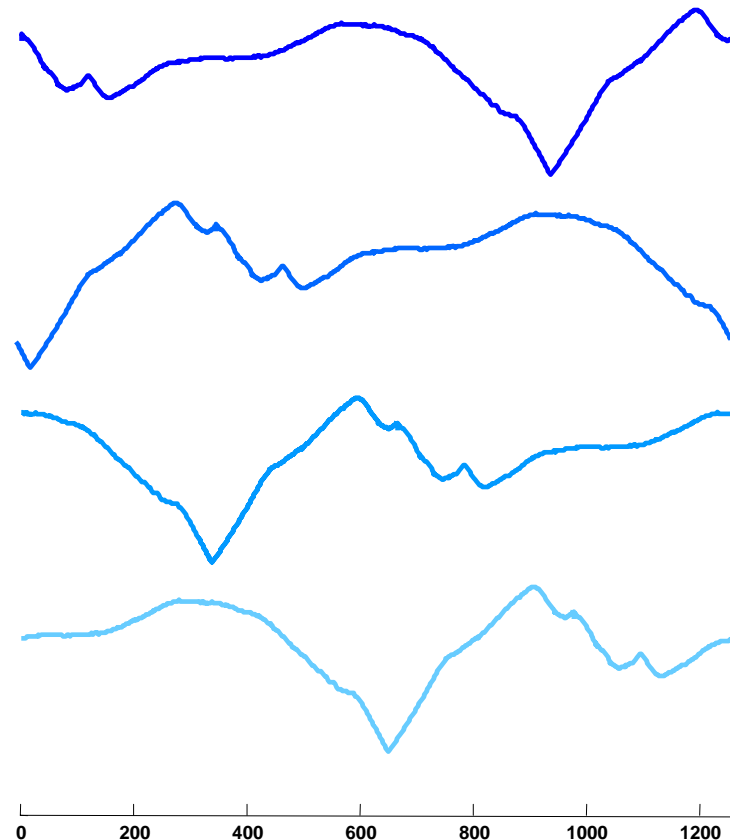
Representing Shapes as Time Series



Checking Rotation Invariance



Rotation invariance can be achieved by checking all possible circular shifts (for every sampled point)...



Dealing with Rotation Invariance

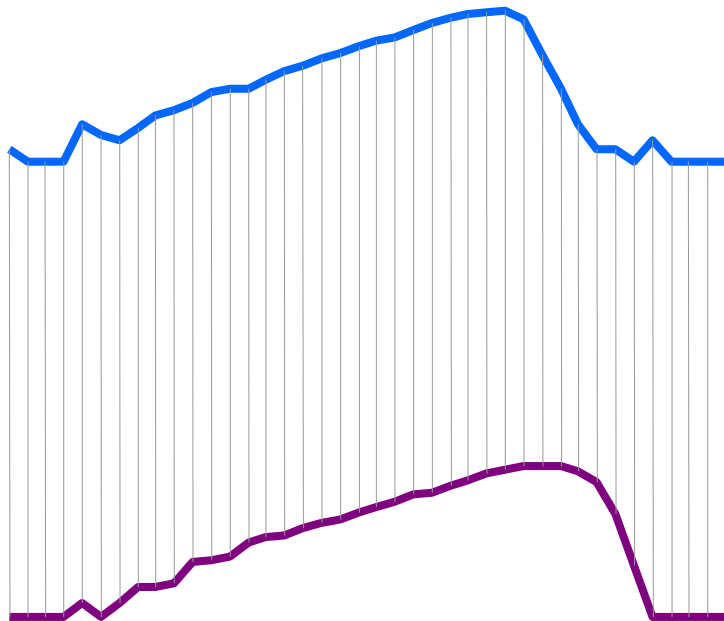
3 Major Techniques:

- Landmarking
 - To find the one “true” rotation and use that particular alignment as input into the distance measure
- Rotation Invariant Features
 - Extracting rotation invariant features, such as ratio of perimeter to area, fractal measure, elongatedness, curvature, entropy, perimeter of convex hull, etc.
- Brute force rotation alignment
 - Hold one shape fixed
 - While rotating the other shape (candidate object), find the similarity measure between the two, for all different rotations
 - Take minimum distance among all rotations
 - Repeat for every candidate in the database

Rotation Invariant Problem

- Was demonstrated that brute force rotation alignment produces the best precision/recall and accuracy [1]
- Powerful contour matching algorithms uses dynamic programming, i.e. dynamic time warping (DTW)
 - *Robust to occlusions*
 - *Many distance measures for shapes, DTW and LCS are used in majority of literatures*
- Comparison between two shapes alone is $O(n^3)$
- Complexity grows exponentially as we increase the size of database

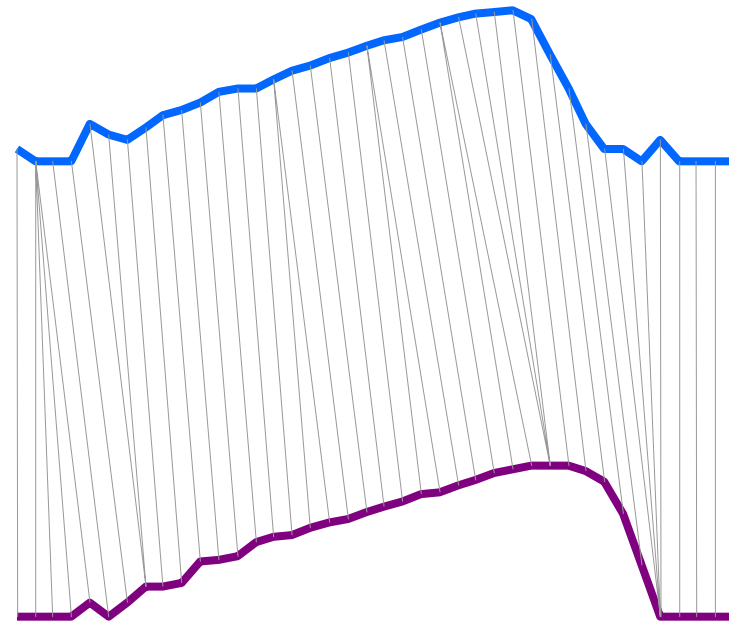
Fixed Time Measures



Fixed Time Axis
Sequences are aligned "one to one".

Euclidean Distance

Time Warped Measures



"Warped" Time Axis
Nonlinear alignments are possible.

Dynamic Time Warping

Computing the DTW distance

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

$$w_k = (i, j)_k$$

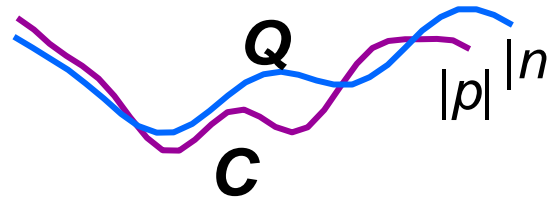
w_k is a matrix element that defines a mapping between Q and C.

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

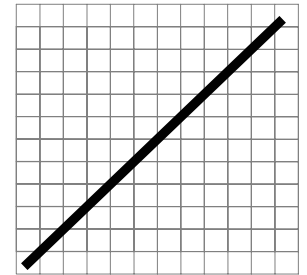
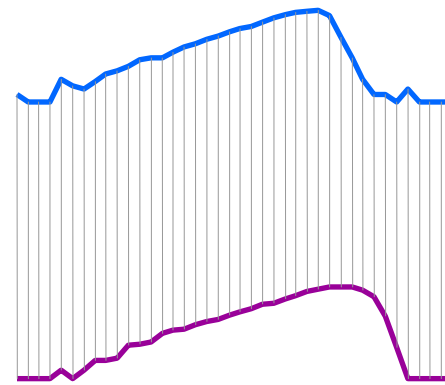
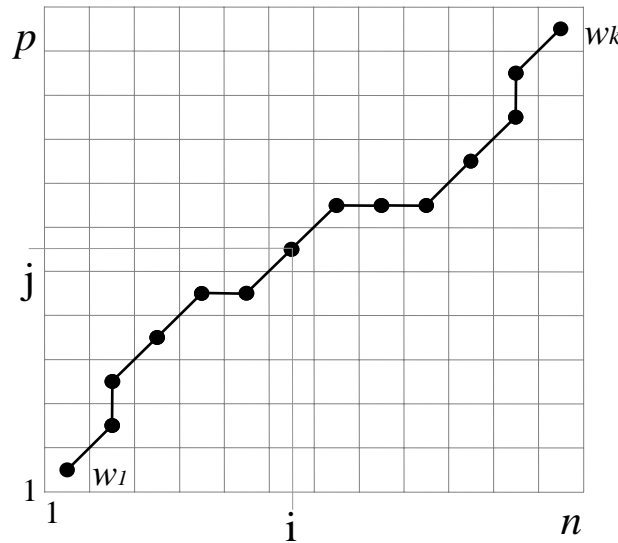
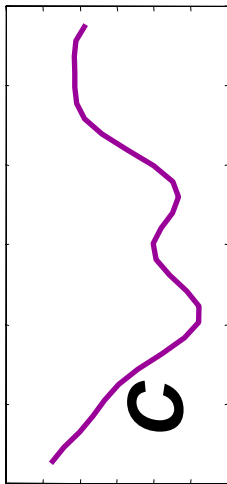
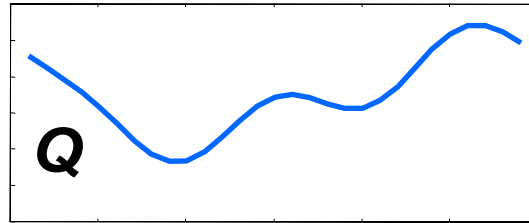
- $\gamma(i, j)$ is the cumulative distance of $d(i, j)$,
- $d(i, j)$ is the distance found in the current cell
- Find the minimum of the cumulative distances of the three adjacent elements

We'll see a visualization of that ...

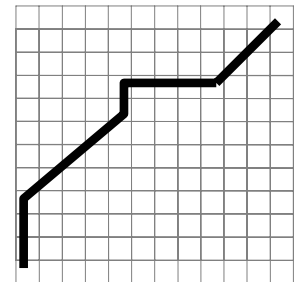
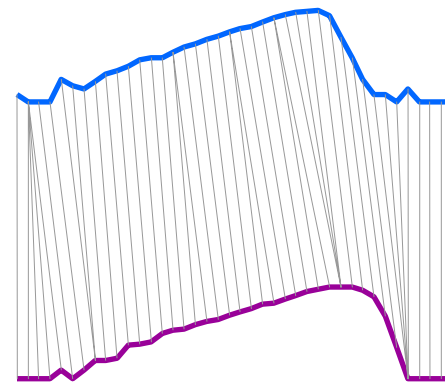
Computing the Dynamic Time Warp Distance



Note that the input sequences can be of different lengths

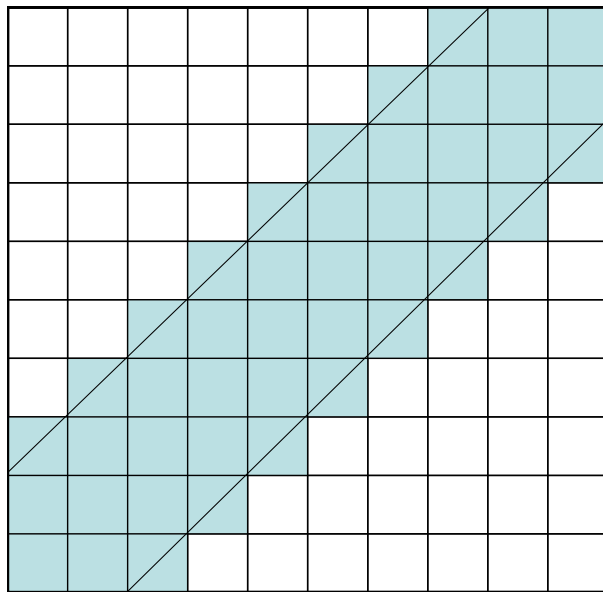


Euclidean distance is a special case of DTW

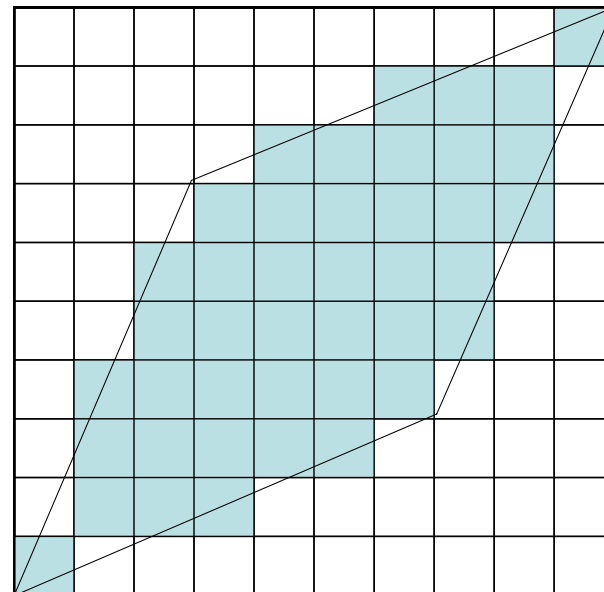


Global Constraints

Constraining the warping path:



Sakoe-Chiba Band

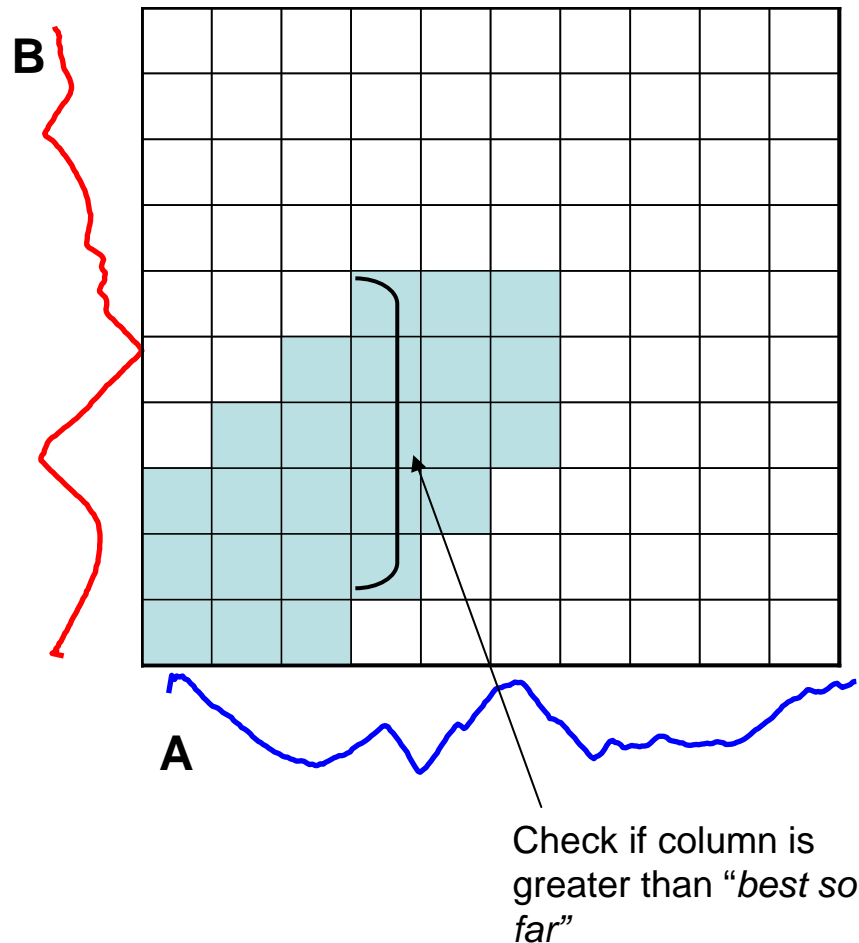


Itakura Parallelogram

More on speeding up DTW

Early abandonment...

Discard the candidate from further consideration when the minimum of a column in the distance matrix is greater than "*best so far*"



Optimizing search when using Euclidean Distance

- Trivially: Discard the candidate from further consideration as soon as the accumulated distance for that candidate exceeds the “*best so far*”

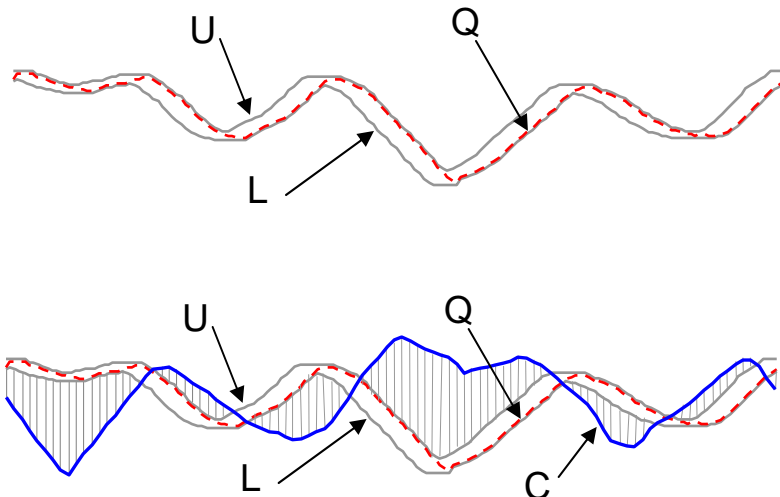
$$D(X, Y) = \sum_{i=1}^n (x_i - y_i)^2$$

Ignore the square root for
Euclidean distance

- Using `best_so_far` works as a lower bound for Euclidean distance because it obeys triangular inequality rule
- DTW: does not obey triangular inequality
- Lower bounding is not as trivial, but possible...

Lower Bounding for DTW

- Warping window with global constraints creates a bounding envelope around the time series, Q
- **Lower bound function:** squared sum of the distances of C that is outside of the envelope
- Obeys triangular inequality - to guarantee no false dismissals

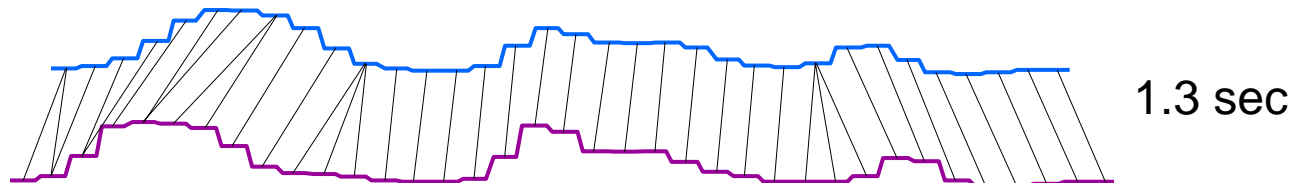
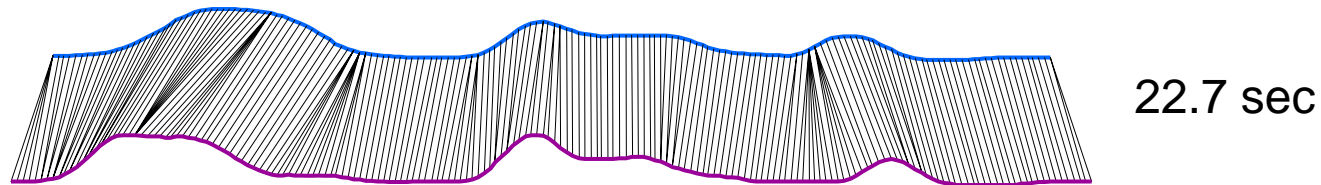


- r , the allowed range of warping
 - Sakoe Chiba: r is constant
 - Itakura: r is function of i
- U and L , upper and lower of envelope,
 - $U_i = \max(q_{i-r}, \dots, q_{i+r})$
 - $L_i = \min(q_{i-r}, \dots, q_{i+r})$ $\forall i \ U_i \geq q_i \geq L_i$

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

Representing the Data – Dimensionality Reduction

Piecewise Constant Approximation: approximates a time series by dividing into equal-length segments

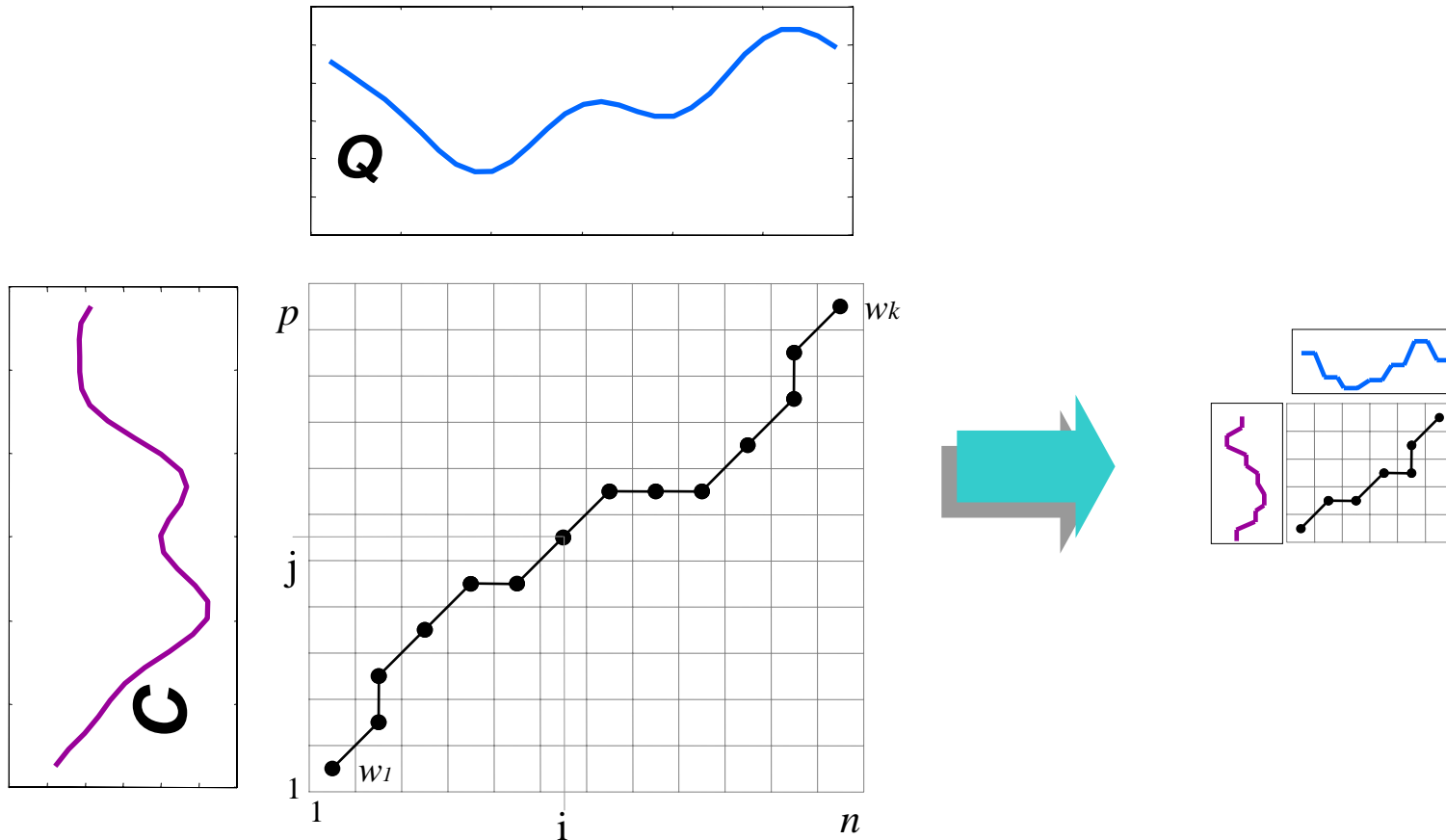


$$\bar{c}_i = \frac{N}{n} \sum_{j=\frac{n}{N}(i-1)+1}^{\frac{n}{N}i} c_j$$

C : time series
 n : original dimension
 N : reduced dimension

- Yi and Faloutsos, *Fast Time Sequence Indexing for Arbitrary L_p Norms*, VLDB 2000.
- Keogh et al. *Dimensionality Reduction for Fast Similarity Search in Large Time Series Databases*, Knowl. Inf. Syst. 2000.

An Approximation to Dynamic Time Warp Distance



Simple Idea: Approximate the time series with some compressed or downsampled representation and perform DTW on the new representation, resulting in a smaller distance matrix

Now What?

So how do we apply all these different techniques to the rotation invariance shape matching problem..

Lower bounding,
Dimensionality reduction,
And an iterative process

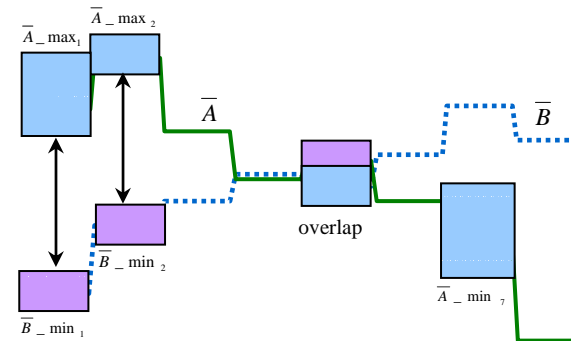
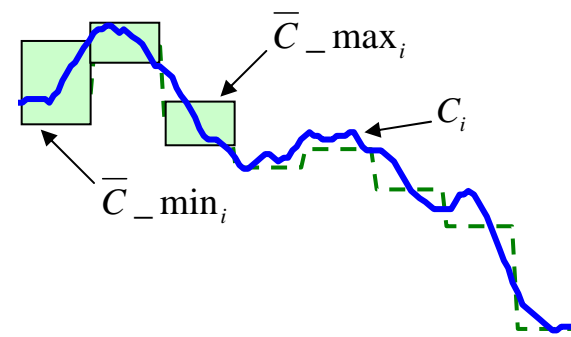
Lower Bounding for Rotation Invariant using Euclidean Distance

Similar to finding PAA using the mean; we can use the min and max instead:

$$\bar{C}_{\max_i} = \max\left(C_{\frac{n}{N}(i-1)+1}, \dots, C_{\frac{n}{N}(i)}\right) \quad \bar{C}_{\min_i} = \min\left(C_{\frac{n}{N}(i-1)+1}, \dots, C_{\frac{n}{N}(i)}\right)$$

Lower bound function: The length of the arrows, squared and summed, times the root of the compression ratio now lower bounds circular shifts of $D(A,B)$.

$$LB_{ED_rotation}(\bar{A}, \bar{B}) = \sqrt{\sum_{i=1}^n \frac{n}{N} \begin{cases} (\bar{A}_{\min_i} - \bar{B}_{\max_i})^2, & \text{if } \bar{A}_{\min_i} > \bar{B}_{\max_i} \\ (\bar{B}_{\min_i} - \bar{A}_{\max_i})^2, & \text{if } \bar{B}_{\min_i} > \bar{A}_{\max_i} \\ 0 & \text{otherwise (overlap)} \end{cases}}$$



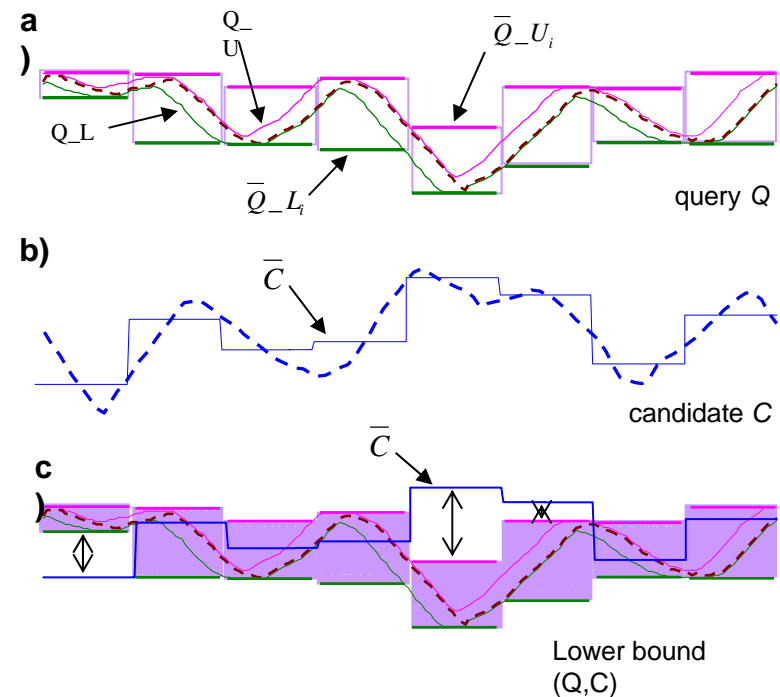
Lower Bounding for Rotation Invariant using DTW

Similarly, we can use the min and max instead on the bounding envelopes:

$$\bar{C}_{-U_i} = \max(\bar{C}_{i-r}, \dots, \bar{C}_{i+r}) \quad \bar{C}_{-L_i} = \min(\bar{C}_{i-r}, \dots, \bar{C}_{i+r})$$

Lower bound function: The length of the arrows, squared and summed, times the root of the compression ratio now lower bounds circular shifts of $D(A,B)$.

$$LB_DTW_rotation(\bar{Q}, \bar{C}) = \sqrt{\sum_{i=1}^N \frac{n}{N} \begin{cases} (\bar{C} - \bar{Q}_{-U_i})^2, & \text{if } \bar{C} > \bar{Q}_{-U_i} \\ (\bar{C} - \bar{Q}_{-L_i})^2, & \text{if } \bar{C} < \bar{Q}_{-L_i} \\ 0 & \text{otherwise (between_U_ \& _L)} \end{cases}}$$



Iterative Deepening Rotation Invariant Shape Matching

Best_so_far = inf;

Find approximations of the target shape using different compression ratio, from coarse to fine, until it's the true sequence

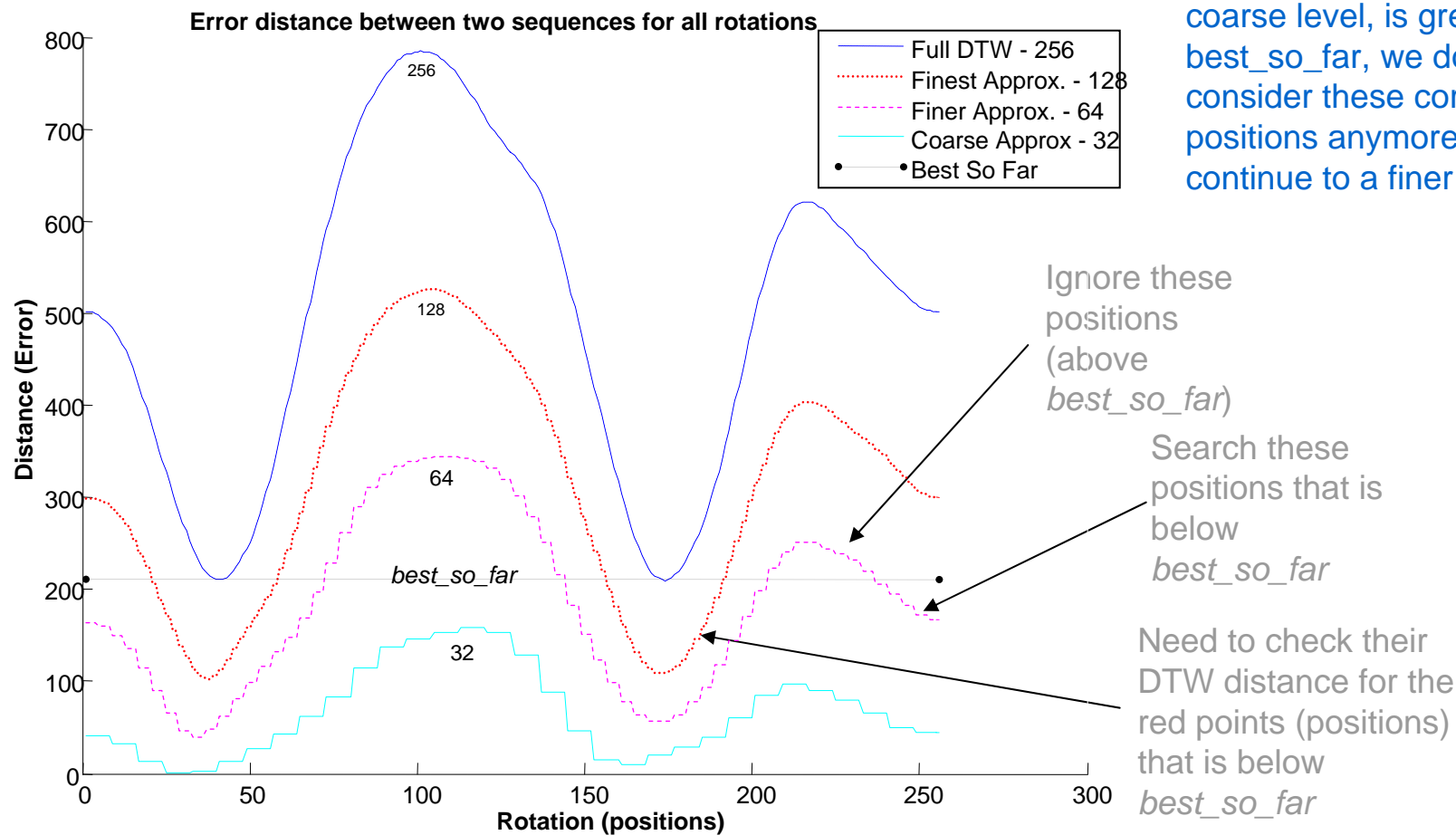
For every candidate in the database

1. Coarse approximation candidate shape
2. Find minimum lowerbounding distance between the approximated target and candidate, for all rotations
3. If result > best_so_far (result not promising)
 - prune the candidate from further consideration
4. Otherwise, we continue to a finer approximation of the data, go to step 2

End

Optimizing the Iterative Approach

Once we know that at a certain position, the lowerbound, at a coarse level, is greater than the *best_so_far*, we don't need to consider these corresponding positions anymore, as we continue to a finer level



Experimental Setup and Results

- Perform experiments on two publicly available datasets
 - 1024 samples per sequence
 - Leaves: 15 classes, 1125 instances
 - Chicken: 5 classes, 446 instances
- Levels of compression: 2^5 , 2^6 , ... , 2^{10}
- Leave-one-out cross validation, 1-nearest neighbor

Dataset	Size of database	Accuracy		Average time per query (minutes)			
		Accuracy: Euclidean Distance	Accuracy: DTW	Euclidean Distance (brute-force)	Iterative Deepening Euclidean Distance	DTW (brute-force)	Iterative Deepening DTW
15-class	1125	86.7%	89.2%	0.329 (20s)	0.068 (4s)	192.18*	0.293 (18s)
5-class	446	80.0%	80.0%	0.092 (6s)	0.031 (2s)	72.78	0.267 (16s)

*Randomly sampled targets for retrieval due to time constraints (40%)

Observations

- 70% of the computational time (for iterative approach) is spent on the initial minimum distance calculation
 - Once we have a best_so_far value, it acts as a catalyze for quickly pruning out other irrelevant choices
- The lowerbound for filtering out poor matches becomes even tighter as more sequences are observed.
- As the size of the database increases, our iterative method will achieve a greater speedup

Conclusion

- Introduce novel framework for speeding up rotation invariant shape matching
- Took the slow but accurate approach and speeded up by 3-4 orders of magnitude, depending on the size of database
- And it guarantee no false dismissals
- Future works include a more detailed analysis this work, with datasets, and extending to other similarity search problems

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Thank you

selinach@sipi.usc.edu

<http://sipi.usc.edu/~selinach>



Questions?