FTW: Fast Similarity Search under the Time Warping Distance

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Motivation

- Time-series data
 - many applications
 - computational biology, astrophysics, geology, meteorology, multimedia, economics
- Similarity search
 - Euclidean distance
 - DTW (Dynamic Time Warping)
 - Useful for different sequence lengths
 - Different sampling rates
 - scaling along the time axis

- DTW allows sequences to be stretched along the time axis
 - Minimize the distance of sequences
 - Insert 'stutters' into a sequence
 - □ THEN compute the (Euclidean) distance



- DTW is computed by dynamic programming
 - Warping path: set of grid cells in the time warping matrix



DTW is computed by dynamic programming

$$p_{1}, p_{2}, ..., p_{i,j} \qquad q_{1}, q_{2}, ..., q_{j}$$

$$D_{dtw}(P,Q) = f(N,M)$$

$$f(i,j) = \left\| p_{i} - q_{j} \right\| + \min \begin{cases} f(i,j-1) & p\text{-stutter} \\ f(i-1,j) & q\text{-stutter} \\ f(i-1,j-1) & \text{no stutter} \end{cases}$$

- Global constraints limit the warping scope
 - Warping scope: area that the warping path is allowed to visit



• Width of the warping scope *W* is user-defined



Motivation

- Similarity search for time-series data
 DTW (Dynamic Time Warping)
 - scaling along the time axis
 - But...
 - High search cost *O(NM)*
 - prohibitive for long sequences

Our Solution, FTW

- Requirements:
 - 1. Fast
 - 2. No false dismissals
 - 3. No restriction on the sequence length
 - It should handle data sequences of different lengths
 - 4. Support for any, as well as for no restriction on "warping scope"

Problem Definition

Given

• S time-series data sequences of unequal lengths $\{P_1, P_2, ..., P_S\},\$

- \Box a query sequence Q,
- an integer k,

• (optionally) a warping scope W,

Find the k-nearest neighbors of Q from the data sequence set by using DTW with W

Overview

- Introduction
- Related work
- Main ideas
- Experimental results
- Conclusions

Related Work

- Sequence indexing
 - □ Agrawal et al. (FODO 1998)
 - □ Keogh et al. (SIGMOD 2001)

• ...

- Subsequence matching
 - □ Faloutsos et al. (SIGMOD 1994)
 - Moon et al. (SIGMOD 2002)
 - ••••

Related Work

Fast sequence matching for DTW

- Yi et al. (ICDE 1998)
- □ Kim et al. (ICDE 2001)
- Chu et al. (SDM 2002)
- Keogh (VLDB 2002)
- □ Zhu et al. (SIGMOD 2003)

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None of the existing methods for DTW fulfills all the requirements

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 LBS (Lower Bounding distance measure with Segmentation)

P⁴: Approximate sequences

$$p_i^R$$
: segment range
 p_i^U : upper value
 p_i^L : lower value
 $p_i^R = (p_i^L : p_i^U)$

□ *t*: length of time intervals*



Compute lower bounding distance
 Distance of the two ranges p_i^R and q_j^R: distance of their two closest points





Compute lower bounding distance
 Distance of the two ranges p_i^R and q_j^R: distance of their two closest points

$$D_{seg}(p_{i}^{R}, q_{j}^{R}) = \begin{cases} \left\| p_{i}^{L} - q_{j}^{U} \right\| & (p_{i}^{L} > q_{j}^{U}) \\ \left\| q_{j}^{L} - p_{i}^{U} \right\| & (q_{j}^{L} > p_{i}^{U}) \\ 0 & (otherwise) \end{cases}$$

Exact DTW distance



• Compute lower bounding distance from P^4 and Q^4

Use a dynamic programming approach

$D_{lbs}(P^A, Q^A) \leq D_{dtw}(P, Q)$



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Use a dynamic programming approach

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Main Idea (2) – EarlyStopping

- Exploit the fact that we have found k-near neighbors at distance d_{cb}
 - *d_{cb}*: k-nearest neighbor distance (the Current Best)
 the exact distance of the best k candidates so far

Main Idea (2) – EarlyStopping

Exclude useless warping paths by using d_{cb}
 Omit g(1,3) if g(1,2) > d_{cb}
 Omit g(4,1) if g(3,1) > d_{cb}



• Q: How to choose *t* (length of time intervals)?



- Q: How to choose *t* (length of intervals)?
- A: Use multiple granularities, as follows:



- Compute the lower bounding distance from the coarsest sequences as the first refinement step
- Ignore P if $D_{lbs}(P^A, Q^A) > d_{cb}$, otherwise:



- ... compute the distance from more accurate sequences as the second refinement step
- ... repeat



- until the finest granularity
- Update the list of k-nearest neighbors if $D_{dtw}(P,Q) \le d_{cb}$



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Experimental results

Setup

□ Intel Xeon 2.8GHz, 1GB memory, Linux

Datasets:

Temperature, Fintime, RandomWalk

□ Four different time intervals (for *n*=2048)

 $t_1=2, t_2=8, t_3=32, t_4=128$

Evaluation

- Compared FTW with LB_PAA (the best so far)
- Mainly computation time

Outline of experiments

- Speed vs db size
- Speed vs warping scope W
- Effect of filtering
- Effect of varying-length data sequences

Itakura Parallelogram



Wall clock time as a function of data set size



Wall clock time as a function of data set size



Wall clock time as a function of data set size



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Sakoe-Chiba Band



Wall clock time as a function of warping scope



Wall clock time as a function of warping scope



Wall clock time as a function of warping scope



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Effect of filtering

- Most of data sequences are excluded by coarser approximations (t_4 =128 and t_3 =32)
 - Using multiple granularities has significant advantages



Frequency of approximation use

Outline of experiments

- Speed vs db size
- Speed vs warping scope W
- Effect of filtering
- Effect of varying-length sequences

Difference in Sequence Lengths

5 sequence data sets

Random(2048,0): length 2048 +/- 0

Random(2048,32): length 2048 +/- 16

Random(2048,64), Random(2048,128), Random(2048,256)



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Conclusions

- Design goals:
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Conclusions

Design goals:
✓. Fast (up to 220 times faster)
✓. No false dismissals
✓. No restriction on the sequence length
✓. Support for any, as well as for no restriction on "warping scope"





 Sequential scan of feature data should boost performance (speed-up factors SF=5, SF=10)

$$PA_{SF} = \frac{PA_{fd}}{SF} + PA_d$$

 PA_{ds} : page accesses for data sequences PA_{fd} : page accesses for feature data

