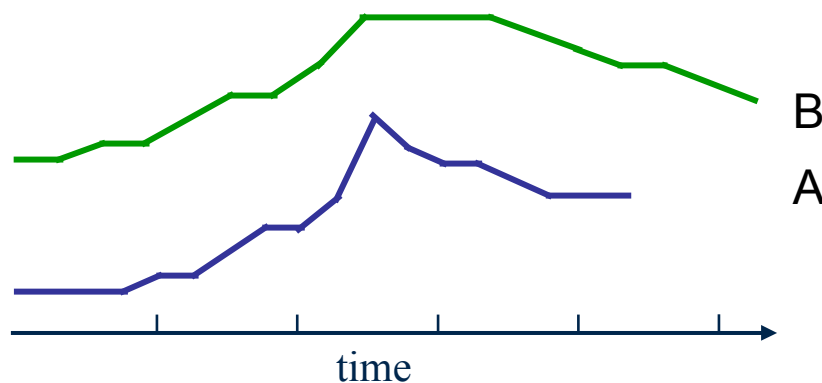


Sequence Matching
using
Dynamic Time Warping

Issues with Sequence Matching

- Sequential data from natural process may vary not only in magnitude but also in the time-evolution of the process
- Two realizations of the same process may differ in the temporal length
 - Speech recognition, Action recognition, Gene expression etc.,



$$D(A, B) = ?$$

Sequences of Same Length

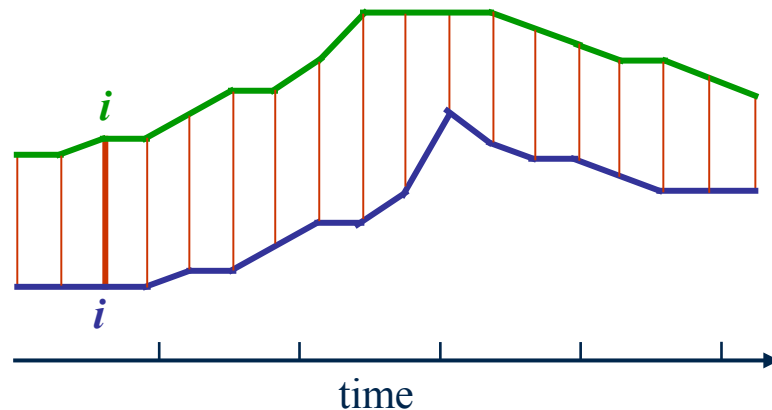
- If the sequences A and B are of same length

$$A = (\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_N)$$

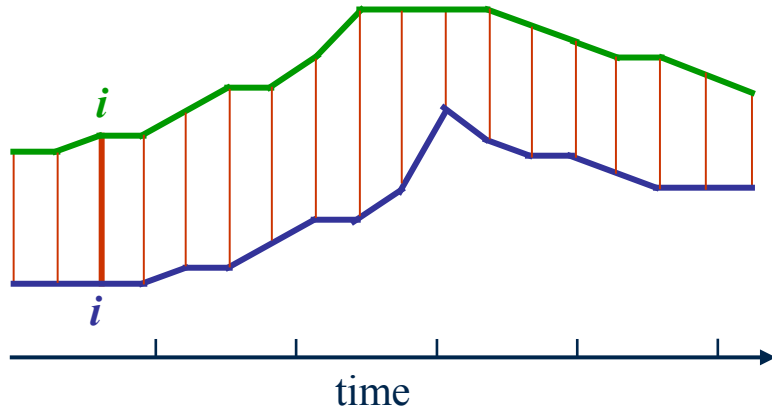
$$B = (\mathbf{y}_1, \mathbf{y}_2, \dots, \mathbf{y}_N)$$

$$D = \frac{1}{N} \sum_{n=1}^N \|\mathbf{x}_n - \mathbf{y}_n\|_2$$

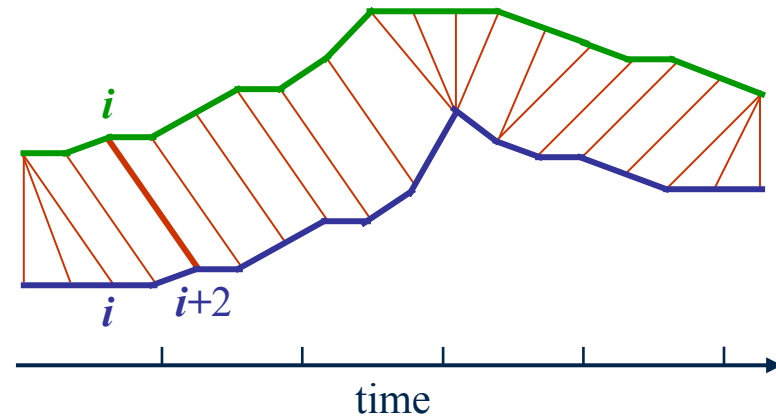
- It cannot be used for misaligned sequences



Motivation for DTW



Distance between corresponding points produce a poor similarity measure



- A nonlinear (elastic) alignment produces a more intuitive similarity measure
- Allows similar shapes to match even if they are out of phase in time

Varying Length Sequences

$$A = (\mathbf{x}_1, \mathbf{x}_2, \dots, \dots \mathbf{x}_M)$$

$$B = (\mathbf{y}_1, \mathbf{y}_2, \dots, \mathbf{y}_N)$$

- Find the best alignment path
 $(p_1, q_1), (p_2, q_2) \dots (p_k, q_k)$

Boundary conditions:

$$(p_1, q_1) = (1, 1)$$

$$(p_k, q_k) = (M, N)$$

- Distance between the sequences is given by

$$D(A, B) = \frac{1}{K} \sum_{i=1}^K \|\mathbf{x}_{p_i} - \mathbf{y}_{q_i}\|_2$$

Varying Length Sequences

$$A = (\mathbf{x}_1, \mathbf{x}_2, \dots, \dots \mathbf{x}_M)$$

$$B = (\mathbf{y}_1, \mathbf{y}_2, \dots, \mathbf{y}_N)$$

- Find the best alignment path
 $(p_1, q_1), (p_2, q_2) \dots (p_k, q_k)$

Boundary conditions:

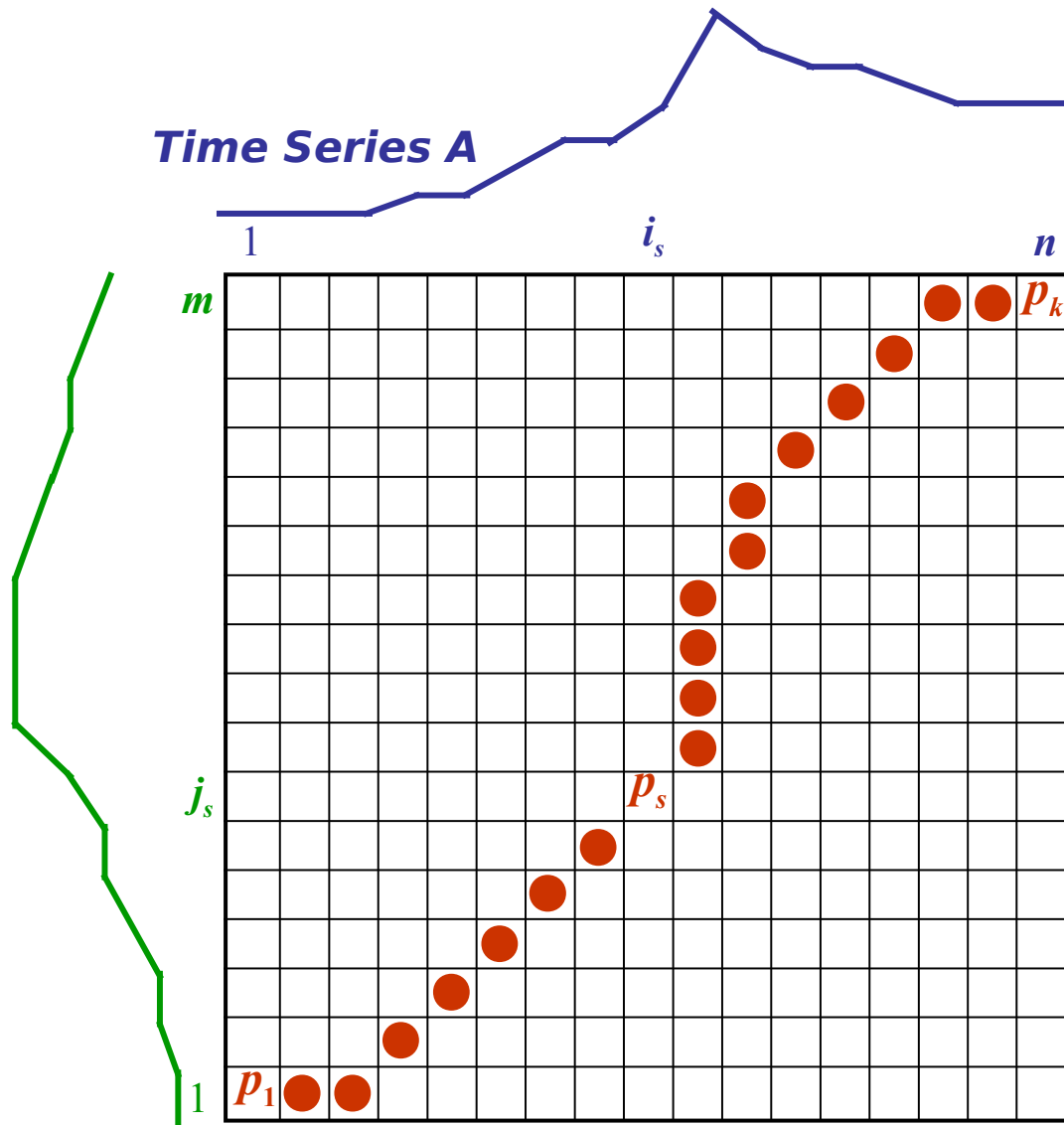
$$(p_1, q_1) = (1, 1)$$

$$(p_k, q_k) = (M, N)$$

- Distance between the sequences is given by

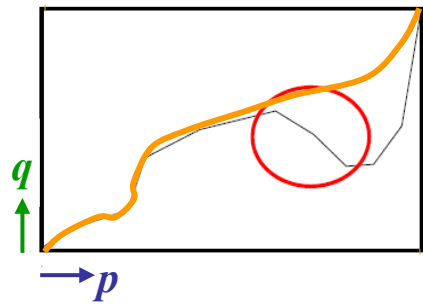
$$D(A, B) = \frac{1}{K} \sum_{i=1}^K \|\mathbf{x}_{p_i} - \mathbf{y}_{q_i}\|_2$$

Warping Path from Distance Matrix



Constraints on the Warping Path

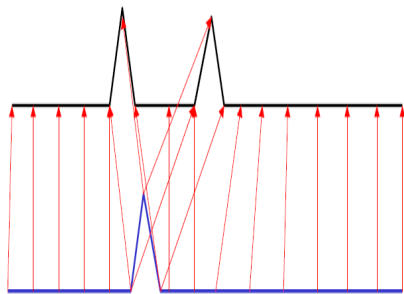
Monotonicity: The alignment path should not go back in “time” index.



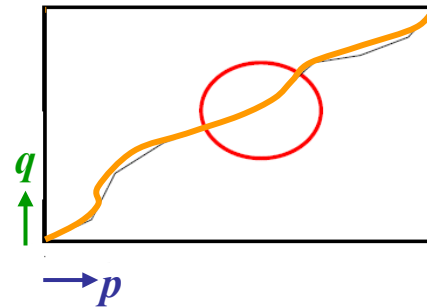
$$p_{k-1} \leq p_k$$

$$q_{k-1} \leq q_k$$

Guarantees that features are not repeated in the alignment.



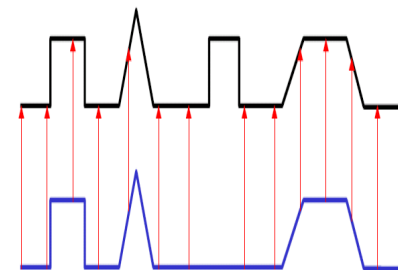
Continuity: The alignment path should not jump in “time” index.



$$p_k - p_{k-1} \leq 1$$

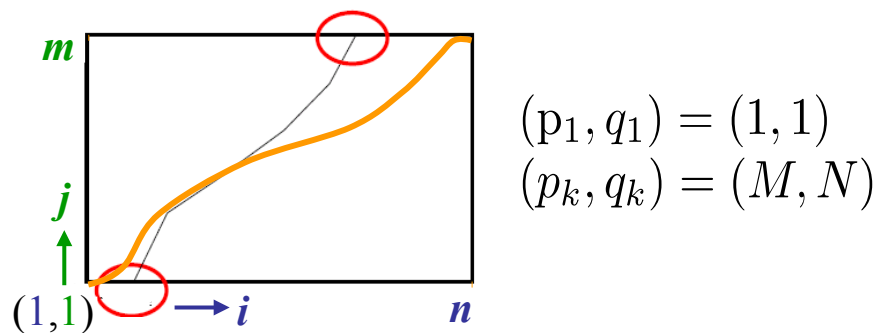
$$q_k - q_{k-1} \leq 1$$

Guarantees that the alignment does not omit important features.

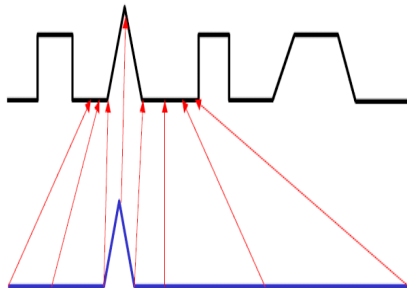


Constraints on the Warping Path

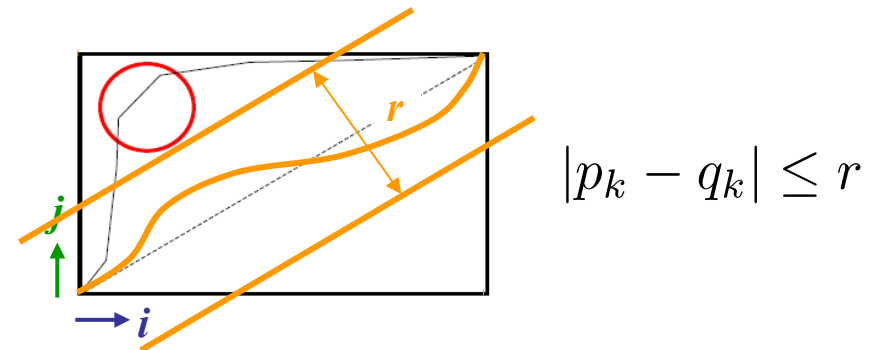
Boundary Conditions: The alignment path starts at the bottom left and ends at the top right.



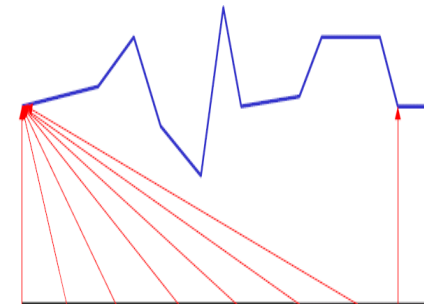
Guarantees that the alignment does not consider partially one of the sequences.



Warping Window: A good alignment path is unlikely to wander too far from the diagonal.



Ensures that the alignment does not try to skip different features and gets stuck at similar features.



DTW Algorithm

- Compute distance matrix D ($M \times N$)
- Augment D with an initial row and column
- Compute accumulated distance matrix A :
 - Initialize $A(0,0) = D(0,0)$
 - For $i=1$ to M and $J=1:N$
 - $A(i,j) = D(i,j) + \min(A(i-1,J), A(i-1,j-1), A(i,j-1))$
 - $P(i,j) = \operatorname{argmin} (A(i-1,J), A(i-1,j-1), A(i,j-1))$
- Backtracking: Start from $P(M,N)$ and backtrack.

Distance Matrix Computation

4	0	9	9	16	4	4	1
4	0	9	9	16	4	4	1
5	1	16	4	25	9	1	0
1	9	0	36	1	1	25	16
6	4	25	1	36	16	0	1
1	9	0	36	1	4	25	16
2	4	1	25	4	0	16	9
3	1	4	16	9	1	9	4
B							
A	4	1	7	0	2	6	5

7	Inf	0 28 (0,4)	9 37 (0,6)	9 40 (2,6)	16 47 (2,6)	4 21 (4,6)	4 14 (5,6)	1 8 (6,6)
6	inf	0 28 (0,4)	9 37 (0,5)	9 31 (2,5)	16 38 (2,5)	4 17 (4,5)	4 10 (5,5)	1 7 (5,5)
5	inf	1 28 (0,4)	16 34 (1,4)	4 22 (1,4)	25 29 (3,4)	9 13 (3,4)	1 6 (4,4)	0 6 (5,5)
4	inf	9 27 (0,3)	0 18 (0,3)	36 39 (2,3)	1 4 (2,3)	1 5 (3,4)	25 30 (4,4)	16 42 (5,3)
3	inf	4 18 (0,2)	25 27 (1,2)	1 3 (1,2)	36 39 (2,3)	16 42 (3,2)	0 26 (4,2)	1 27 (5,3)
2	inf	9 14 (0,1)	0 2 (1,1)	36 38 (1,1)	1 26 (3,1)	1 26 (3,1)	25 50 (4,1)	16 57 (5,1)
1	inf	4 5 (0,0)	1 2 (0,0)	25 27 (1,1)	4 25 (2,0)	0 25 (3,1)	16 41 (4,1)	9 49 (5,0)
0	inf	1 1 (-1,1)	4 5 (0,0)	16 21 (1,0)	9 30 (2,0)	1 31 (3,0)	9 40 (4,0)	4 44 (5,0)
-1	0	inf	inf	inf	inf	inf	inf	inf
	-1	0	1	2	3	4	5	6

Global vs Local Optima

Similarity/Distance Matrix

4	0	1	9	16	4	4	1
4	0	1	9	16	4	4	1
5	1	4	4	25	9	1	0
1	9	4	36	1	1	25	16
6	4	9	1	36	16	0	1
1	9	4	36	1	1	25	16
7	9	16	0	49	25	1	4
3	1	0	16	9	1	9	4
B							
A	4	3	7	0	2	6	5

Subsequence Matching

