Lecture

Information Retrieval for Music and Motion
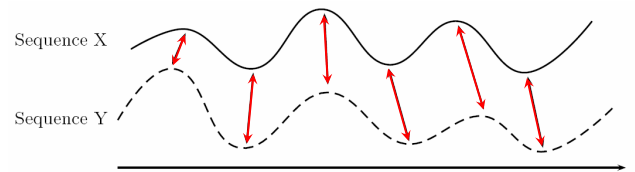
Meinard Müller

Summer Term 2008

Dynamic Time Warping

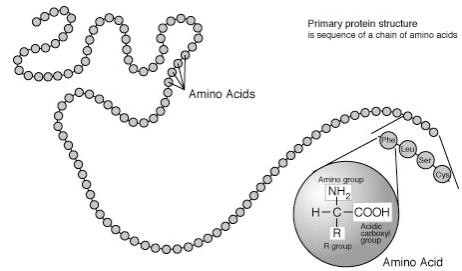UNIVERSITÄT DES SAARLANDES

M²CI CLUSTER OF EXCELLENCE

mpii max planck institut informatik

Alignment

Sequence X

Sequence Y

2

Alignment

DNA = Sequence of Nucleotids

3

Alignment

Primary protein structure is sequence of a chain of amino acids

Amino Acids

Amino group
NH_2
$H-C-COOH$
R
R group

Acidic carboxyl group

Amino Acid

Protein = Sequence of Amino Acids
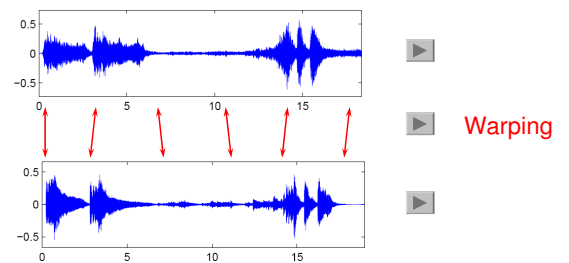
4

Alignment
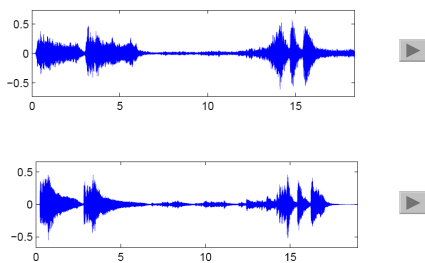
Music = Sequence of Audio Samples
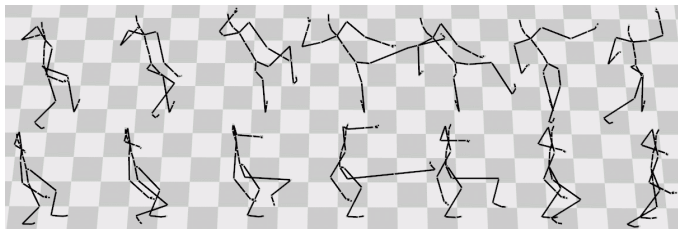
5

Alignment
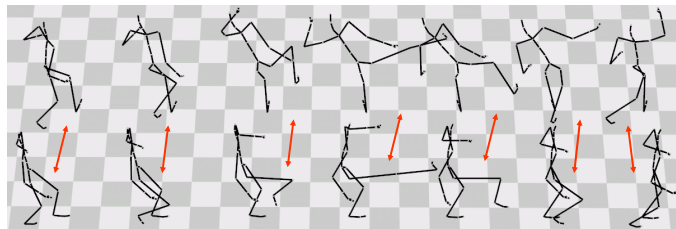

Warping

Music = Sequence of Audio Samples
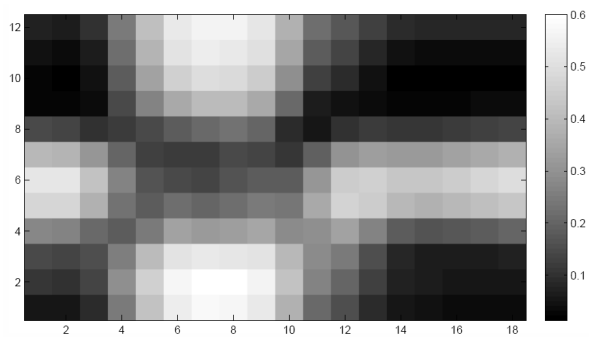
6

Alignment

Motion = Sequence of Poses

Alignment

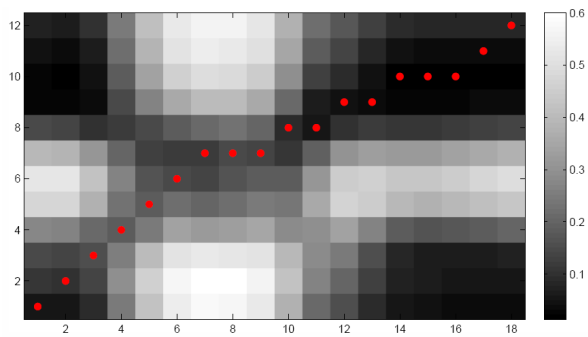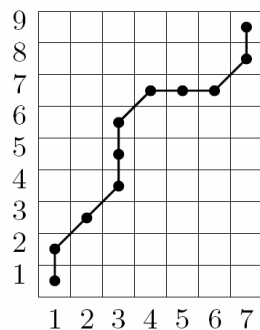Motion = Sequence of Poses

Cost Matrix
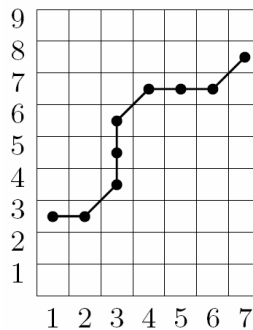
Cost Matrix

Cost-minimizing warping path
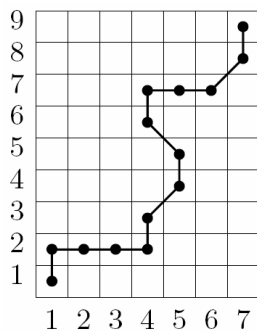
Warping Path
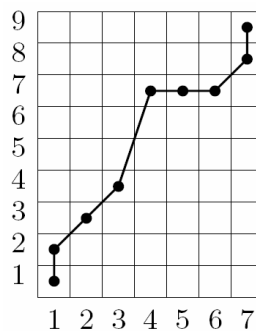
Warping Path

Violation of
Boundary Condition

Warping Path
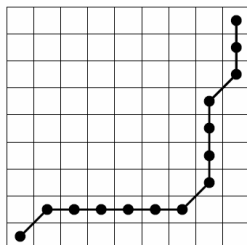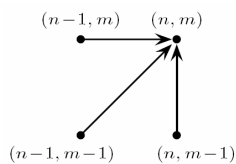

Violation of
Monotonicity Condition
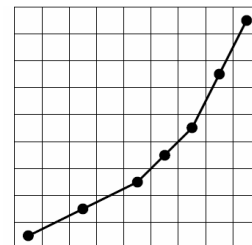
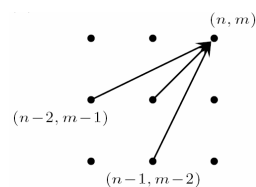## Warping Path

Violation of
Step Size Condition
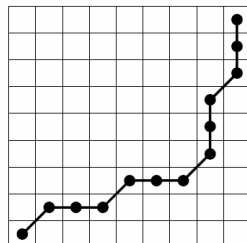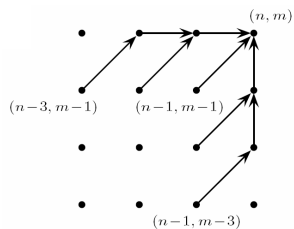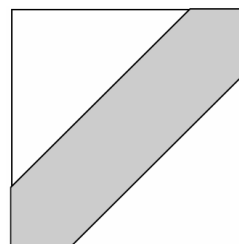
Variation of Step Size Condition

$(n-1, m)$ (n, m)

$(n-1, m-1)$ $(n, m-1)$

Variation of Step Size Condition

(n, m)

$(n-2, m-1)$

$(n-1, m-2)$

Variation of Step Size Condition

(n, m)
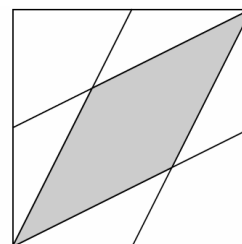
$(n-3, m-1)$ $(n-1, m-1)$

$(n-1, m-3)$

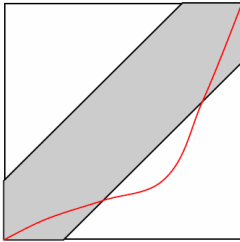## Strategy: Global Constraints
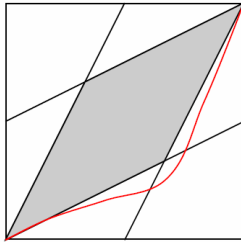
Sakoe-Chiba band   Itakura parallelogram

Strategy: Global Constraints
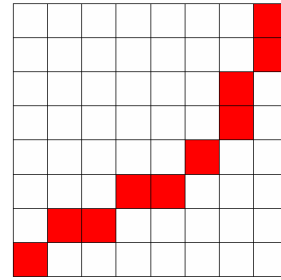
Sakoe-Chiba band   Itakura parallelogram

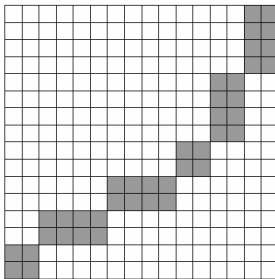

Problem: Optimal warping path not in constraint region

Strategy: Multiscale Approach
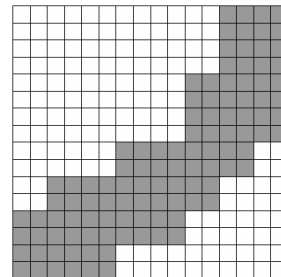

Compute optimal warping path on coarse level

Strategy: Multiscale Approach

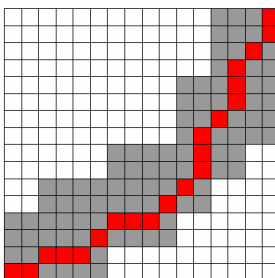Project on fine level

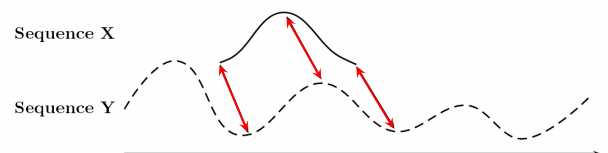## Strategy: Multiscale Approach

Specify constraint region

Strategy: Multiscale Approach

Compute *constrained* optimal warping path

Subsequence DTW

Sequence X

Sequence Y