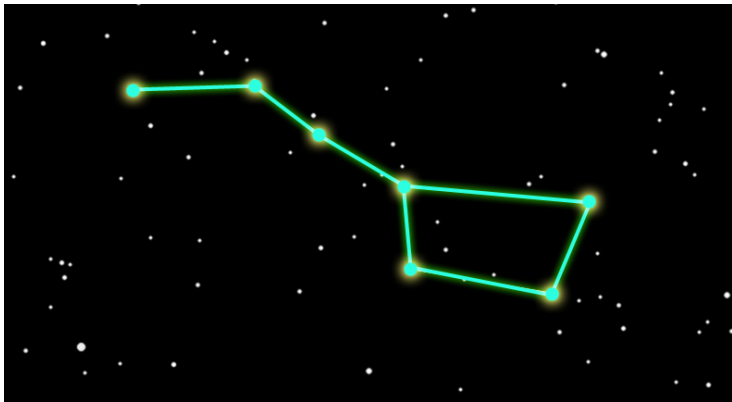


# Computational Geometry

## Point Pattern Matching

Kevin Böckler



# Topics

- 1 Introduction
- 2 Matching of Point Patterns
- 3 Matching of Curves & Areas
- 4 Shape Interpolation

## 1 Introduction

- Motivation
- Hausdorff-Distance

## 2 Matching of Point Patterns

- Exact Matching
- Approximated Matching
- Pattern recognition

## 3 Matching of Curves & Areas

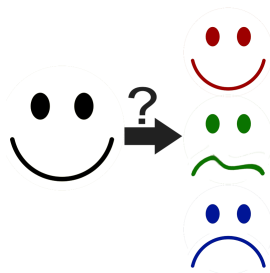
- Approximated Matching
- Better distance for shapes

## 4 Shape Interpolation

- Polygonal chain matching
- Difficulties

# Applications

- Distance of two shapes  
or: How similar is one shape compared to another?
- Applications:
  - Computer vision/computations
  - Molecular biology
  - Sign recognition
  - Morphing



# The Problem

Input:

- two shapes (set of points),  $P, Q \subset \mathbb{R}^2$
- allowed transformations  $T$  of  $P, Q$

Output:

$f \in T$ , which solves one of the following problems:

- Exact matching
- Approximated matching
- Optimal matching

# Transformations

We define a transformation as follows:

## Transformation

A transformation  $f$  is a function which maps one shape to another:

Let  $A$  be a shape, e.g. a set of points:

$$A = \{a \in \mathbb{R}^2 \mid a \in A\}$$

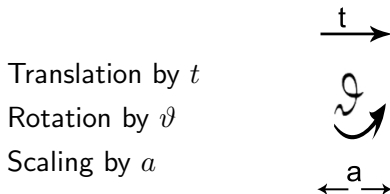
$$f : \mathbb{R}^2 \rightarrow \mathbb{R}^2$$

Applying  $f$  on a shape means transforming of each element by  $f$ :

$$f(A) = \{f(a) \mid a \in A\}$$

# Transformations

We look at the following transformations:



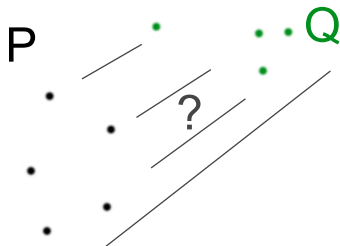
## Combinations

**Rigid Motion** means translation and rotation

**Similarity** means translation, rotation and scaling

Rigid Motions are interesting!

# Hausdorff-Distance



What is the distance between two shapes?

How similar are two shapes?

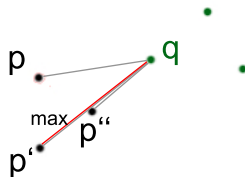
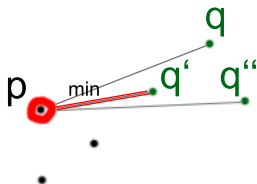


# Hausdorff-Distance

## Definition

The Hausdorff-Distance is the maximum of the minimal distances:

$$\delta_H(P, Q) = \max_{p \in P} \min_{q \in Q} \|p - q\|_2$$



# Overview of the problems

Input:  $P, Q \subset \mathbb{R}^2$  and  $T$  of  $P, Q$

Output:  $f \in T$  with property of matching:

Exact matching

$$\delta_H(f(P), Q) = 0$$

Approximated matching

with  $\varepsilon$  as allowed error tolerance

$$\delta_H(f(P), Q) \leq \varepsilon$$

Optimal matching

$$\delta_H(f(P), Q) = \min_{f' \in T} \delta_H(f'(P), Q)$$

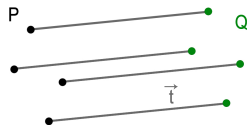
- 1 Introduction
  - Motivation
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- 2 Matching of Point Patterns
  - Exact Matching
  - Approximated Matching
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  - Polygonal chain matching
  - Difficulties

# Exact matching

## Definition

An exact matching of two sets  $P, Q$  is a valid function which transforms each point  $p \in P$  to a point  $q \in Q$ .

or:  $\delta_H(f(P), Q) = 0$



Given: sets  $P, Q$  and  $T = T_{\text{translations}}$

Output:  $f(x) \in T_{\text{translations}}$

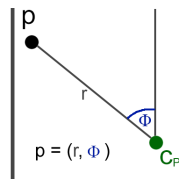
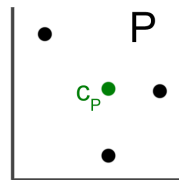
Exact matching means a translated point is equal to a point of  $q$ :

$$\forall p \in P : p' = f(p) = q, q \in Q$$

# A simple algorithm for rigid motions

- 1 Compute the centroids  $c_P, c_Q$
- 2 Sort all points of  $P, Q$  as pairs of  $(\Phi_i, r_i)$  and put them into a sequence
- 3 A matching is found, if the sorted sequence of  $P$  is a cyclic shift of the sequence of  $Q$
- 4 If there is a matching, just compute the transformation by looking at the first pair of each  $P, Q$

Runtime:  $O(n \log(n))$



# Extend with Scaling

Considering Scaling is simple:

- Start the algorithm by finding a scaling factor
  - ① Compute the diameters of  $P, Q$
  - ② The scaling factor  $a$  is  $\frac{d_P}{d_Q}$
- Computing scaling needs additional linear time

# Exact matching does not work!

- Exact matching  $\neq$  Reality
- Approximation is more effective

## Problem: Approximated Matching

Approximated matching means matching all points  $p \in P$  to the  $\varepsilon$ -neighborhood of a point  $q \in Q$ .

- one-to-one matching
- many-to-one matching

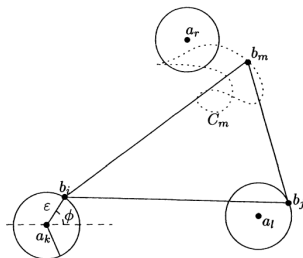
**For a given  $P, Q, T, \varepsilon$ : is there a matching?**

For a given  $P, Q, T$ : find the smallest  $\varepsilon$

# One-to-one Matching: Approaching under rigid motions

Given: sets  $A, B$  and  $T = T_{\text{rigid motions}}$

Output: Is there a matching  $f \in T$  so, that  $B$  is matched to  $A$  within  $\varepsilon$ ?



- For each pair  $(b_i, b_j)$  find an interval of degree  $\Phi$
- All relationships are edges in a bipartite graph
- A matching does exist, if there is a perfect matching in this graph



# One-to-one Matching: Approaching under rigid motions

Runtime of this approach:

- 1 Procedure has to be done  $n^4$  times for all 4-tuples
- 2 For each procedure look at all 2-tuples' curves and calculate intervals  
 $\Rightarrow$  Analysis showed runtime:  $O(n^8)$

Other approaches:

- Translation only in  $O(n^{1.5} \log(n))$
- Disjoint  $\varepsilon$ -neighborhoods lead to  $O(n^4 \log(n))$
- + Assuming,  $\varepsilon$  is not too close at optimal  $\varepsilon_{\min}$ :  $O(n^2 \log(n))$

# Many-to-One Matching: Hausdorff-Distance

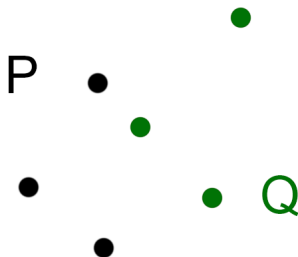
Matching by minimizing the Hausdorff-Distance

Input: Sets  $P, Q$  with  $m = |P|, n = |Q|$

- Many-to-One Matching
- Hausdorff-Distance computation in
  - $O(mn)$  by computing straight forward
  - $O(m + n \log(m + n))$  by using Voronoi-Diagrams
- General idea:
  - 1 Take a transformation
  - 2 Compute the new Hausdorff-Distance
  - 3 Compare the result and repeat until a good transformation has been found

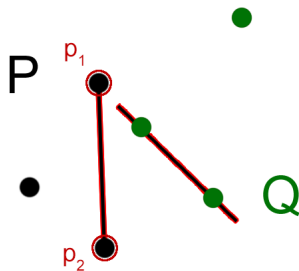
# Many-to-One Matching: Goodrich approximation

- 1 For one diametrically opposing pair of points  $p_1, p_2 \in P$ :
- 2 Do a best match to each pair of points  $q_1, q_2 \in Q$
- 3 Take the matching with the best resulting Hausdorff-distance  
$$T_{\min} = \min_T \delta_h(T(P), Q)$$



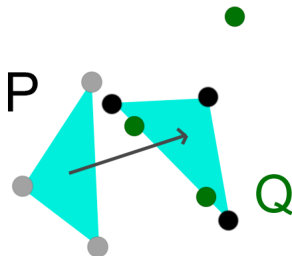
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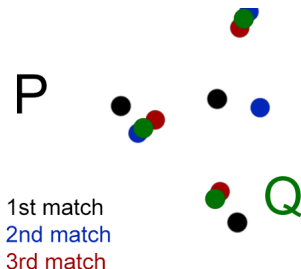
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# Many-to-One Matching: Goodrich approximation

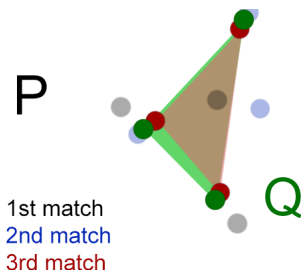
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# Many-to-One Matching: Goodrich approximation

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- 3 Take the matching with the best resulting Hausdorff-distance

Runtime of the Goodrich approximation:

$$m = |P|, n = |Q|$$

- 1  $O(m)$
- 2  $O(n^2)$
- 3  $O(n^2 m \log(n))$

Runtime is  $O(n^2 m \log(n))$



# Alignment Method

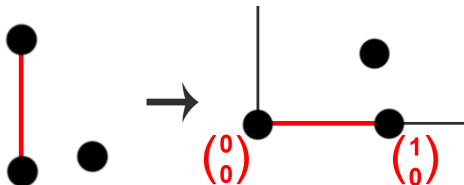


Given a model  $M$  and a scene  $S$ :  
Does  $S$  contain  $M$ ?

## Reference Frame

A reference frame of a set  $M$  in dependency of two offset points  $a, b \in M$  represents a new coordinate system with properties:

- $a$  is assigned as the origin  $(0, 0)$
- $b$  is assigned as an alignment vector  $(1, 0)$
- all other points relate to these two points



# Alignment Method



Given a model  $M$  and a scene  $S$ :  
Does  $S$  contain  $M$ ?

The Algorithm:

- 1 Create reference frames for each pair  $a, b \in M$
- 2 Create reference frames for each pair  $p, q \in S$
- 3 Find one reference frame of  $M$ , whose points lie all in a  $\varepsilon$ -neighborhood of a reference frame of  $S$

# Alignment Method

- Provides Similarity-Transformation
- Exhaustive method
- Worst-case runtime is  $O(|M|^3|S|^2 \log(|S|))$

Question: Given multiple scenes  $S_i$ , does one of them contain  $M$ ?  
or: Given multiple models  $M_i$ , does  $S$  contain a model  $M_i$ ?

- Solution: Hashing of models and scenes
- Voting in hashtables

# Short Summary: Matching of Point Patterns

## Algorithms:

- Exact matching: Sorting and searching for vectors
- Approx matching: Theoretical argumentation
- With respect to the Hausdorff-distance: Goodrich Approximation
- Pattern recognition: Alignment Method

## Outlook:

- 3D with projections
- Randomization? - Not yet

## 1 Introduction

- Motivation
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## 2 Matching of Point Patterns

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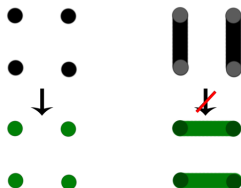
## 3 Matching of Curves & Areas

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- Difficulties

# The difference of line segments and point sets



## New Problem

Given two sets of line segments  $A, B$  with cardinalities  $n = |A|, m = |B|$ .

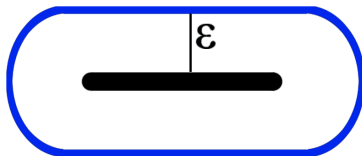
- infinite points
- Hausdorff-Distance:
  - harder to compute
  - with voronoi diagram intersections:  $O(n \log(n))$

# Translations for approximated matching

## Definition

A **racetrack**  $A_\varepsilon$  is a disk of radius  $\varepsilon$  around a given line segment  
 $A_\varepsilon = A \oplus C_\varepsilon$ , where  $C_\varepsilon$  is a circle with radius  $\frac{\varepsilon}{2}$

Example: set  $A$ , consisting of a single line segment



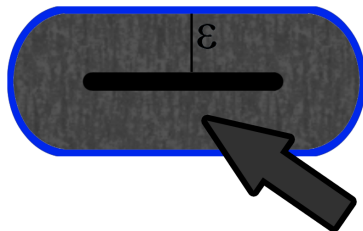
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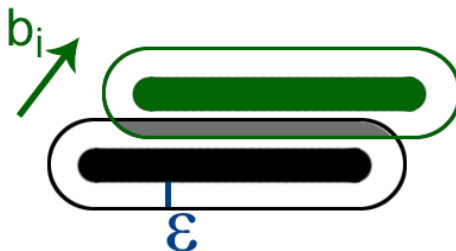


# Translations for approximated matching

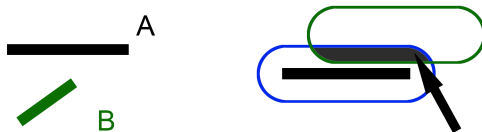
## A translated racetrack

Let  $A_i^\varepsilon$  be the intersection of  $A_\varepsilon$  and the translated racetrack  $A_\varepsilon$  by a vector  $b_i$

$$A_i^\varepsilon = A_\varepsilon \cap (A_\varepsilon \oplus b_i)$$



# Translations for approximated matching



## Theorem

*There is a matching exactly if  $S = \bigcap_{i=1}^m A_i^\varepsilon \neq \emptyset$ .*

*This is equivalent to the existence of a cell with depth  $m$*

- Depth determination with line sweep algorithm
- Complexity:  $mn$  arcs and lines,  $(mn)^2$  intersections points

$\Rightarrow$  Translations are performed in  $O((mn)^2 \log(mn))$

# Extend with Rotations

Procedure:

- 1 Rotate arrangement around the origin by  $\theta \in (0, 2\pi)$
- 2 Translate as before

Difficulty: Arrangement changes with rotation

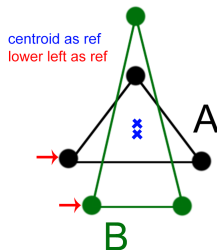
- Looking at events, when the arrangement changes
- Rigid motions are performed in  $O(m^3 n^3 \log(mn))$

# Idea of reference points

## Definition

A reference point  $r_A$  is a representative point of a shape  $A$  so that a perfect matching of  $A$  to  $B$  bounds the distance of  $T(r_A)$  to  $r_B$  by a constant factor  $\alpha$ , which is called the *quality of the reference point*

$$\alpha \delta(T_{\text{perfect}}(A), B) = \delta(T_{\text{perfect}}(r_A), r_B)$$



Which reference point has the higher local quality?

# Reference point for translation

## Theorem

*Translating  $A$  to  $B$  by matching  $r_A$  to  $r_B$  is at most  $a + 1$  times worse than the optimal matching*

- Finding a reference point as above needs linear time
- Translating  $r_A$  to  $r_B$  needs constant time

The translation algorithm has a runtime of  $O(n)$

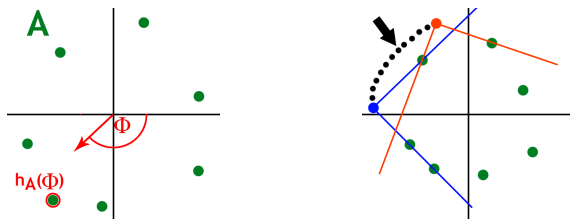
# Steiner point for rigid motions

What about rigid motions?

- Center of the boundary of the convex hull:  $a = 4\pi + 4 \approx 16.6$
- Steiner point:
  - Input has to be a convex body
  - Works for similarities
  - $a = \frac{4}{\pi} \approx 1.27$  (2D)
  - $a \approx 1.5$  (3D)

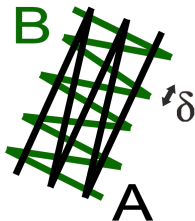
# Steiner point for rigid motions

- 1 Rotate lower-left Reference Point around A
- 2 Keep orthogonal tangents to A
- 3 Take the average over all those rotated points



- Support function  $h_A(\Phi)$  is largest extent in direction of  $\Phi$
- The desired point is  $h_A(\Phi) \begin{pmatrix} \cos \Phi \\ \sin \Phi \end{pmatrix}$
- Average is found by  $\frac{1}{\pi} \int_0^{2\pi} h_A(\Phi) \begin{pmatrix} \cos \Phi \\ \sin \Phi \end{pmatrix} d\Phi$

# Distance for line segments



Problem:

Two sets  $A, B$  with quite small Hausdorff-distance  $\delta_H$  but high disparity

## Better description of distance

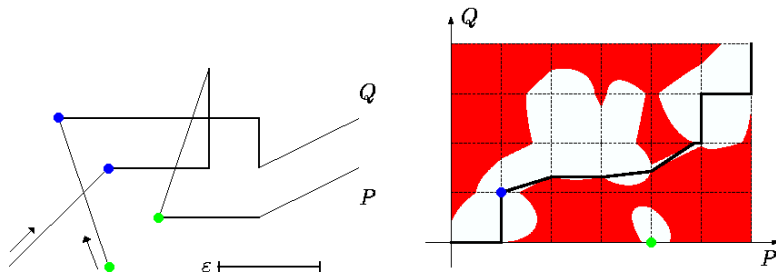
The Fréchet Distance is the greatest distance which can appear when walking along two monoton paths through both given shapes



# Fréchet Distance

Parametrization with a P/Q - diagram

- Input: Polygonal chains of line segments  $P, Q$  and distance  $\varepsilon$
- Output: *True*, if  $\delta_F(P, Q) \leq \varepsilon$



- P/Q - diagram needs runtime  $O(mn)$  with  $m = |P|, n = |Q|$

# Short Summary : Matching of curves & areas

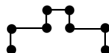
- Shapes are more complex than sets of points
- Distances of curves are different from point patterns

## Methods:

- Racetrack intersections
- Reference Point approximation
- Fréchet Distance

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# Introduction

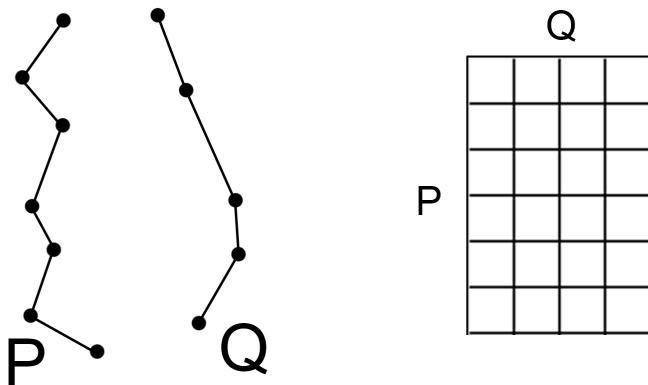


## Definition

Let  $P$  and  $Q$  be two shapes of size  $m = |P|, n = |S|$ . Morphing describes the mapping of  $P$  to  $Q$ .

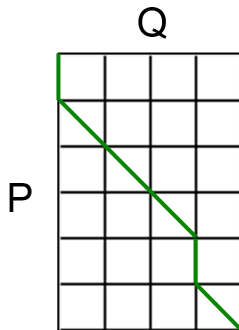
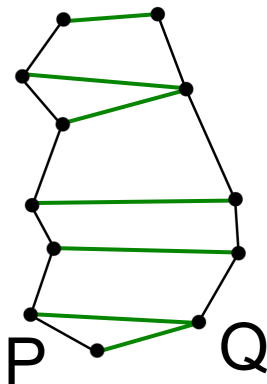
- The general process of morphing:
  - ① Find features and match them
  - ② Motions for each feature pair
  - ③ Transformation = combining motions + constraints
- For simplicity we will look on polygonal chains

# Linear chain matching



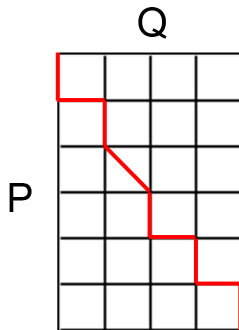
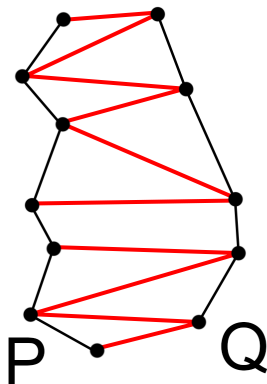
- 1 Construct a grid of  $P \times Q$
- 2 Monotone walkthrough the grid represents matching

# Linear chain matching



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# Linear chain matching



- 1 Construct a grid of  $P \times Q$
- 2 Monotone walkthrough the grid represents matching

# Linear chain matching

Optimal path in  $O(nm)$  with dynamic programming

What are suitable matching constraints?

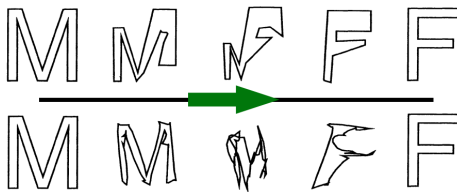
- Shortest distance
- parallel matching line segments

Last step:

- For each matching  $(p, q) \in P \times Q$  do a linear mapping



# Difficulties with chain matching



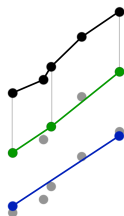
- Goal: minimize intersections
- Reason: Choosing the wrong origin from the shape
- Solution: Select constraints
  - e.g. keep parallel sides while morphing
  - runtime:  $O(n \log(n))$

# Lessons learned

- Definition, features and similarities of shapes
  - elements of a shape
  - distance
  - transformations
- Approximative approaches matching two sets of points
  - Goodrich approximation
- Finding a shape in another one
  - Alignment method
- Areas are point sets with infinite elements
  - Complex shapes
  - Reference Points

## Outlook:

- Three dimensions
- Shape simplification
  - Redundancy
  - Complexity



# Sources

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