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Lecture 23: Hausdorff and Fréchet distance

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23.1 Introduction

Shape matching is an important area of research as it has applications to a number of problems, such as object recognition and analysis of protein structures. In this lecture, we discuss the Hausdorff and Fréchet distances.

Consider 2 point sets $P \subseteq \mathbb{R}^2$ and $Q \subseteq \mathbb{R}^2$, where the goal is to find the extent of similarity between P and Q. The first question that needs to be answered is: what do we mean by "similar" ? Mathematically, we want to find a mapping σ:$P \rightarrow Q$, that has one of the following properties:

- σ minimizes $\max_{p\in P} ||p - \sigma(p)||$ (minimizes maximum distance between mapped points) or,
- σ minimizes $\Sigma_{p\in P}||p - \sigma(p)||$ (minimizes sum of distances between mapped points) or,
- σ minimizes $\Sigma_{p\in P}||p - \sigma(p)||^2$ (minimizes sum of squared distances between mapped points)

The mapping σ does not have be one-to-one. The question is: how do we find σ ?

23.2 Hausdorff Distance

Let P and Q be two sets of points in $\mathbb{R}^d$.

The directed Hausdorff distance from P to Q, denoted by $h(P,Q)$, is $\max_{p\in P} \min_{q\in Q} ||p - q||$.

The Hausdorff distance between P and Q, denoted by $H(P,Q)$, is $\max\{h(P,Q), h(Q,P)\}$.

Intuitively, the function $h(P,Q)$ finds the point $p \in P$ that is farthest from any point in Q and measures the distance from p to its nearest neighbor in Q. Hausdorff distance is a measure of the mismatch between two point-sets. For $d = 2$, the Hausdorff distance can be computed in time $O(n \log n)$ (where n is the number of points), using a Voronoi diagram in $\mathbb{R}^2$. In $\mathbb{R}^3$ computing a Voronoi diagram could take quadratic time, so a different approach is needed to compute $H(P,Q)$ in subquadratic time.

Let $D(q,r)$ be the disk of radius r centered at point $q \in Q$. The decision problem for the Hausdorff distance could be written as:

Given $r \geq 0$, whether $h(P,Q) \leq r$? That is, $\forall p \in P$, $\exists q$ $||p - q|| \leq r$.

$$\Rightarrow \forall p \, \exists q \;\; p \in D(q,r) \tag{23.1}$$

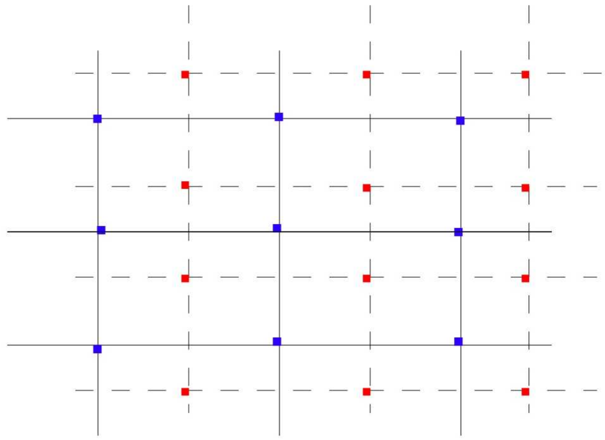

Figure 23.1: Translation: In the above figure, the points in blue represent one point-set, and the points in red represent the other. Clearly, the point-sets only differ in a translation factor.

$$\Rightarrow \forall p \ p \in \bigcup_{q \in Q} D(q, r) \tag{23.2}$$

$$\Rightarrow P \ \subseteq \bigcup_{q \in Q} D(q, r) \tag{23.3}$$

A point $p \in \mathbb{R}^d$ can be mapped to a point $Q(p) \in \mathbb{R}^{d+1}$ and a disk $D(q, r)$ can be mapped to a half-space h_q in $\mathbb{R}^{d+1}$ such that $p \in D(q, r)$ if and only if $Q(p) \notin h_q$. Hence, $p \in \bigcup_{q \in Q} D(q, r)$ iff $p \notin \bigcap_{q \in Q} h_q$, i.e.,

$$P \subseteq \bigcup_{q \in Q} D(q, r) \Leftrightarrow Q(P) \bigcap (\bigcap_{q \in Q} h_q) = \phi \tag{23.4}$$

A point-location data structure for convex polyhedra can be used to answer the decision query. When P and Q are sets of elements other than points (features, for example), a similar formulation is possible. A survey paper by Alt and Guibas describes geometric techniques to measure the similarity between discrete geometric shapes [1].

23.3 Hausdorff Distance under Translation

In some cases, the point-sets P and Q are very similar and a translation applied to one of the point sets would achieve the best matching. Figure 23.1 shows an example where a simple translation transforms one point-set to the other. So we permit translations. Let σ_t be the correspondence between $P + t$ and Q, where t represents the translation that is applied to P. The correspondence between the point-sets changes only at critical values of t. Let $\mu(P, Q)$ be the matching that minimizes the Hausdorff distance between $P + t$ and Q and $f(t)$ represent the Hausdorff distance for a given value of t.

Define $\mu(P, Q)$ as $\min_{t \in \mathbb{R}^2} H(P+t, Q)$. We also define $f(t)$ as $H(P+t, Q)$. Let π be a partition of $\mathbb{R}^2$ so that the map σ_t remains the same for all points in a face of π. Figure 23.2 shows an example of what π could look like. Within each face of π, the correspondence between $P+t$ and Q remains unchanged.

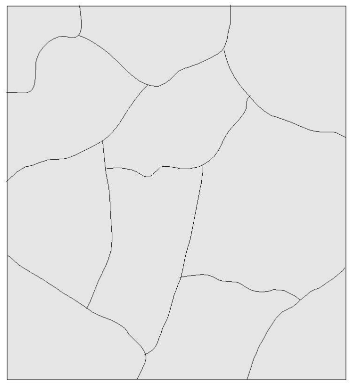

Figure 23.2: Partition π: Within each region of the partition, the correspondence remains unchanged.

Partition π has $O(n^3)$ faces and this bound is tight in the worst case. We can compute π in $O(n^3 \log n)$ time. In fact, it can be shown that $f(t)$ has $\Omega(n^3)$ local minima, but most of the minima are "shallow." There are efficient approximation algorithms for computing $\mu(P, Q)$. The notion of π and $f(.)$ can be introduced for other similarity functions as well. For example, let σ_t be the correspondence for the Euclidean minimum weight matching between $P+t$ and Q. We can again define the partition π. It is an open problem whether π has only polynomial number of faces in this case.

A problem with taking a '$\max$' is that outliers can have a significant effect, and hence, the Hausdorff distance is very sensitive to any outlier in P or Q.

23.4 Fréchet distance

The Fréchet distance is a measure that takes the continuity of shapes into account and, hence, is better suited than the Hausdorff distance for curve or surface matching. A popular illustration of the Fréchet distance is, as follows [2]: Suppose a man is walking a dog. Assume the man is walking on one curve and the dog on another curve. Both can adjust their speeds but are not allowed to move backwards. The Fréchet distance of the two curves is then the minimum length of leash necessary to connect the man and the dog.

The Fréchet distance between two curves is defined as follows:

$$Fr(P, Q) = \inf_{\alpha, \beta} \max_{t \in [0,1]} ||P(\alpha(t)) - Q(\beta(t))|| \tag{23.5}$$

where $P, Q : [0, 1] \to \mathbb{R}^2$ are parametrizations of the two curves and $\alpha, \beta : [0, 1] \to [0, 1]$ range over all

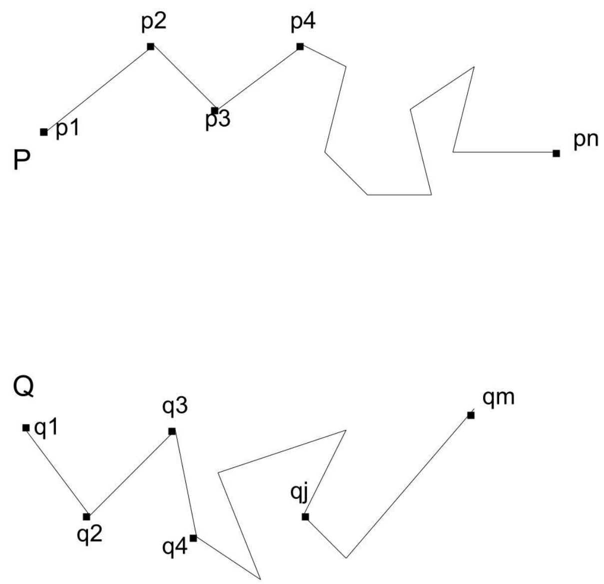

Figure 23.3: P and Q in the above figure could be the backbones of two protein structures. A matching between P and Q should be monotone for biological significance to be maintained here.

continuous and monotone increasing functions. If P and Q are polygonal chains with n and m line segments respectively, the decision problem for the Fréchet distance can be written as: whether $\phi(P, Q) \leq r$?

Before describing an algorithm for the Fréchet distance, consider a simpler problem. Let $P =< p_1, ..., p_n >$ and $Q =< q_1, ..., q_m >$ be two polygonal chains. Define a mapping σ from the vertices of P to those of Q such that:

1. if $q_{j_1} = \sigma(p_{i_1})$ and $q_{j_2} = \sigma(p_{i_2})$, and $i_1 < i_2$ then $j_1 \leq j_2$ (monotonicity)
2. $\max_i ||p_i - \sigma(p_i)||$ is minimum

Figure 23.3 shows an example where a matching between the backbones of two protein structures needs to be monotone for biological significance to be preserved. This problem can be solved in $O(mn)$ time using a dynamic programming approach. We extend this algorithm to Fréchet distance.

An $n \times m$-diagram, shown in 23.4, indicates by the areas enclosed by the blue curves for which points $p \in P$ and $q \in Q$, $||p - q|| \leq r$. The horizontal and vertical directions of the diagram correspond to the natural parametrizations of P and Q respectively. A square cell of the diagram corresponds to 2 edges (one from P and one from Q) and can be easily computed as it is the "intersection of the bounding square with an ellipse" [1]. Therefore, $\phi(P, Q) \leq r$ if there is a monotone increasing curve from the lower left to the upper right corner of the diagram (corresponding to a monotone mapping σ). Figure 23.5 shows an example of a monotonic path that defines a matching between point-sets P and Q. The decision problem mentioned just above can be answered in time $O(mn)$. The optimization problem can be solved in $O(mn \log{(mn)})$ time [3]. The Fréchet distance also suffers from outliers. Moreover, there is no good approximation algorithm known to calculate the Fréchet distance.

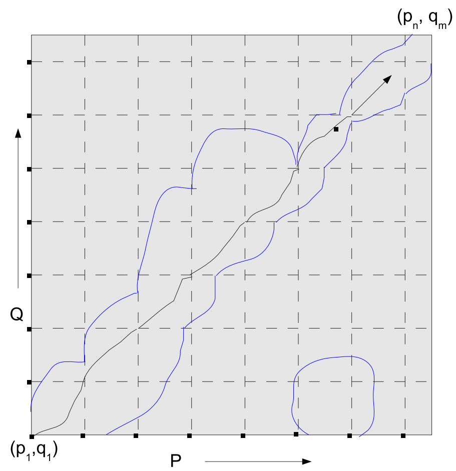

Figure 23.4: We place the points in P along the x-axis and the points in Q along the y-axis. The areas enclosed by the blue curves indicate for which points $p \in P$ and $q \in Q$, $||p - q|| \leq r$. A square cell of the diagram corresponds to 2 edges (one from P and one from Q) and can be easily computed as it is the intersection of the bounding square with an ellipse.

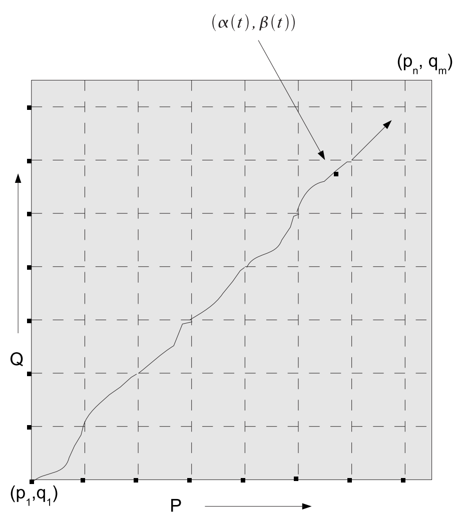

Figure 23.5: A monotonic path through this graph gives a matching between P and Q. Point $(\alpha(t), \beta(t))$ lies on this monotonic path.

References

[1] H. Alt, L.J. Guibas, *Handbook of Comput. Geom.*, pp. 121-153, 1999.
[2] H. Alt, M. Godau, *Int. J. Comput. Geom. and Appl.*, pp. 75-91, 1995.
[3] R. Cole, *J. ACM*, vol. 34, pp. 200-208, 1987.