Matching Surfaces with Characteristic Points

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Abstract

We study approximation algorithms for a matching problem that is motivated by medical applications. Given a small set of points $P \subset \mathbb{R}^3$ and a surface S, the optimal matching of P with S is represented by a rigid transformation which maps P as 'close as possible' to S. Previous solutions either require polynomial runtime of high degree [2] or they make use of heuristic techniques which could be trapped in some local minimum. We propose a modification of the problem setting by introducing subsets of characteristic points $P_c \subseteq P$ and $S_c \subseteq S$, and assuming that points from P_c must be matched with points from S_c. We will show that especially in the case $|P_c| \geq 2$ this restriction results in new fast and reliable algorithms for the matching problem.

1 Introduction

Today an increasing number of surgeries is supported by medical navigation systems. The basic task of such a system is to transform real world data (positions in the operating field) into a 3-dimensional model (CT or MR) and to display the transformed position in the model. Real world data are gaged by optical, electromagnetic or mechanical tracking systems. A common technique for computing the transformation is based on markers which are fixed on bones. The markers have to be fixed already during the model acquisition. Their positions in the model are computed using appropriate image processing methods. Later, at the beginning of the surgery, at least three markers must be gaged with the tracking system. Since the total number of markers is small, one could compute the correct matching transformation even by brute force techniques. A more advanced approach making use of geometric hashing techniques is presented in [3].

There is strong need to develop algorithmic methods for computing a transformation without using markers. The main reason for that is an anatomical one: in many cases (e.g. spinal surgery) it would be very hard or even impossible to fix markers before the surgery. One solution is to gage a few points on the surface of a bone and to compute the corresponding points in the model. This point registration is a hard algorithmic problem, which cannot be solved by the following standard approaches:

1) The gaged points could be anywhere on the model surface and hence, a combinatorial search does not work.

2) The number of gaged points is too small to apply surface reconstruction and surface matching algorithms.

Moreover, the registration is part of the surgery and thus real time algorithms are required. In contrast to that, it is possible to spend more time for preprocessing the model. Here, we try to retrieve some ideas of the landmark approach to that new setting. The role of markers could be played by so-called characteristic points. Such points can be determined by the surgeon, based only on their anatomic properties, e.g., the root of the nose or of the thorn of a vertebra. If a set of characteristic points is known in the model and the surgeon can track at least three of them, the old landmark registration algorithms can be applied. Our main goal is to solve the registration problem if only two characteristic points can be tracked. To compute the transformation in that case, one must track some more (non-characteristic) points on the surface.

In this paper we present our approach for solving this problem and sketch some first results. In the next section we introduce some notations and give a formal definition of the problem. In section 3 we present the basic algorithm and show how to use this method for the approximation of the optimal matching.

2 Problem description

We consider two point sets P and S in $\mathbb{R}^3$. Usually we assume that S is the (infinite) set of points on a triangulated surface. The corresponding triangulation will be denoted by $\mathcal{S}$. However, this assumption is not crucial. If S is a finite, dense sample of points on a surface, the algorithms presented in the next sections, can be applied with small changes.

Our main goal is to register P into a model S. The quality of the registration will be evaluated by the *directed Hausdorff distance*. The distance between a point a and a compact point set B in d-dimensional space $\mathbb{R}^d$ is defined as

$$\mathrm{dist}(a, B) = \min_{b \in B} ||a - b||$$

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where $||\cdot||$ is the Euclidean norm in $\mathbb{R}^d$. For two compact sets A, B in the one-sided Hausdorff distance from A to B is defined as

$$\overrightarrow{H}(A,B) = \max_{a\in A} \operatorname{dist}(a,B) = \max_{a\in A}\min_{b\in B} ||a-b||.$$

The size of a problem instance (P, S) depends on two parameters: k, the number of points in P, and n, the number of triangles in $\mathcal{S}$. We remark that in our applications $k << n$ can be assumed. Moreover, we assume that two subsets of characteristic points $S_c \subseteq S$ and $P_c \subseteq P$ are given. In order to prepare a precise analysis of our algorithms we introduce additional parameters $k_c = |P_c|$ and $n_c = |S_c|$. Both parameters should be seen as some reasonable constants. The special role of characteristic points is expressed by the additional requirement, that each $p \in P_c$ must be mapped onto (or close to) a characteristic point $q \in S_c$.

To proceed to algorithmic solutions we have to classify several types of matchings.

Definition 1 *Given two parameters $\mu, \eta \geq 0$ a rigid transformation $t : \mathbb{R}^3 \to \mathbb{R}^3$ is called (μ, η)-matching if the following two conditions hold:*

1. $\mu(t) := \overrightarrow{H}(t(P \setminus P_c), S) \leq \mu$, *and*
2. $\eta(t) := \overrightarrow{H}(t(P_c), S_c) \leq \eta$.

If ϵ is an upper bound for $\mu(t)$ and $\eta(t)$ we denote t as an *ϵ-matching*. In line with the notations above, we have $\epsilon(t) = \max(\mu(t), \eta(t))$. The minimal $\epsilon(t)$ is denoted by ϵ_{opt}, and a corresponding matching is an *optimal matching*. For a given $\lambda > 1$, a matching t is a *λ-approximate matching*, if $\epsilon(t) \leq \lambda\epsilon_{opt}$.

Furthermore, we introduce the notion of *semioptimal matchings*. To this end we fix a set $\overline{S} = \{\bar{s}_1, \bar{s}_2, \ldots, \bar{s}_{k_c}\}$ of predefined matching positions for the characteristic points $P_c = \{p_1, p_2, \ldots, p_{k_c}\}$. Now we restrict our attention to matchings t with $t(p_i) = \bar{s}_i$ for $i = 1, \ldots, k_c$. Let us denote this set of matchings by $\mathcal{M}_{\overline{S}}$. We assume that P_c and $\overline{S}$ are congruent, because otherwise $\mathcal{M}_{\overline{S}} = \emptyset$.

A matching $t \in \mathcal{M}_{\overline{S}}$ is a $(\mu(t), \eta_0)$-matching, where $\eta_0 = \overrightarrow{H}(\overline{S}, S_c)$ is a common value for all matchings in $\mathcal{M}_{\overline{S}}$. A matching $t \in \mathcal{M}_{\overline{S}}$ is called *semioptimal matching* (with respect to $\overline{S}$) if $\mu(t)$ is minimal.

A trivial case with $|\mathcal{M}_{\overline{S}}| \leq 6$ occurs, if P_c contains three or more non-collinear points. If additionally the side lengths of the triangle spanned by the three points are pairwise different, there is only one matching in $\mathcal{M}_{\overline{S}}$. Thus, we will focus our attention to matchings with two characteristic points. In a first step we design an algorithm to compute semioptimal matchings for a given set $\overline{S}$. Then, based on the semioptimal solution, we show how to compute a λ-approximate matching for any $\lambda > 1$.

3 The 2 point case

3.1 Semioptimal matching

Now, let us assume that the matching positions $\overline{s_1}, \overline{s_2}$ for the two characteristic points p_1, p_2 are already given (see figure 1). First, we present an algorithm which reports (for any μ) all transformations t with the given matching positions for p_1 and p_2 and with $\mu(t) \leq \mu$.

Basic Algorithm (outline)

1. Fix a rigid transformation $t_0 : \mathbb{R}^3 \to \mathbb{R}^3$ such that $t_0(p_1) = \overline{s_1}$, $t_0(p_2) = \overline{s_2}$. For all $p_i \in P \backslash \{p_1, p_2\}$ let $C_i = C(p_i)$ be the circle with the following properties (see figure 1):

   i) the center of C_i is on the line defined by p_1 and p_2,

   ii) C_i is lying in a hyperplane perpendicular to $\overline{p_1, p_2}$, and

   iii) p_i is on C_i.

2. Consider the transformed circle $t_0(C_i)$ and let the point $p'_i(\alpha)$ rotate along this circle starting from $t_0(p_i)$, i.e., $p'_i(0) = t_0(p_i)$. Compute sets of intervals $I_i = \{\alpha \mid \ dist(p'_i(\alpha), S) \leq \mu\}$, for $i = 3, \ldots, k$.

3. Compute $I = \cap_{i=3}^{k} I_i$. For each $\alpha \in I$, $r_\alpha(s, s') \circ t_0$ is a rigid transformation mapping P onto S, where $r_\alpha(s, s')$ is the rotation around axis $\overline{s, s'}$ with angle α.

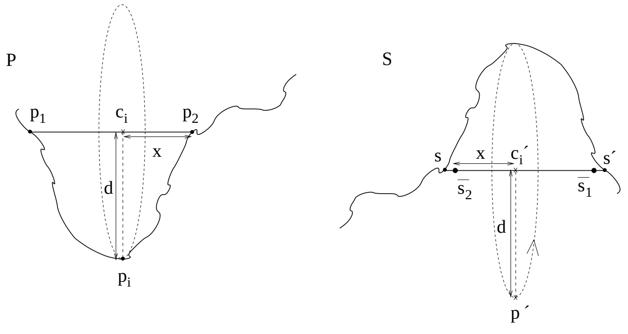

Figure 1: Corresponding points and the rotation of the point p'_i

A straightforward analysis shows that the algorithm runs in $O(kn \log n)$ time.
We remark that this time bound can be improved by a refined analysis under some assumption about the surface representation. The main idea is a subdivision of the bounding box of the surface S into $\sqrt{n} \times \sqrt{n} \times \sqrt{n}$ subboxes. The assumptions on the surface representation imply that each subbox intersects only a constant number of surface triangles. Since each cycle

intersects at most $O(\sqrt{n})$ subboxes, one can compute an interval set I_i considering only $O(\sqrt{n})$ triangles (if μ is not larger than the minimal subbox side length). We will leave the details of this analysis to a full paper.

The algorithm above can be used as a decision algorithm answering the question whether for a given μ there is some matching t with $t(p_1) = s, t(p_2) = s'$ and $\mu(t) \leq \mu$ for all other points of P. Thus, using binary search one can approximate a semioptimal matching. However, it is also possible to compute the precise value μ of a semioptimal matching by the following modification of the basic algorithm. Instead of computing the interval sets $I_i = \{\alpha \mid \operatorname{dist}(p'_i(\alpha), S) \leq \mu\}$ we compute the functions $f_i(\alpha) := \operatorname{dist}(p'_i(\alpha), S)$. This function is the lower envelope of the distance functions of a rotating point to the surface triangles. Thus, the description complexity of f_i is $O(n \log n)$, see [5]. Then, instead of computing $I = \cap_{i=3}^{k} I_i$, we compute the upper envelope f of all functions f_i. The minimum of f is the μ-value of a semioptimal matching.

3.2 The approximation problem

There are two groups of standard approaches to this Problem. The first group consists of simulated annealing [6] and ICP variants [1], [4]. These methods have proved to be useful in many practical situations, but, they have the disadvantage that they could be trapped in a local minimum, and thus it is hard to prove something about the approximation ratio. The second group consists of discretization patterns, inducing the repeated computation of the semioptimal solution for a dense discrete set of transformations. We will exploit this approach to compute a λ-approximation of the optimal matching, where $\lambda > 1$ is an arbitrary constant.

A common key problem of many approximation problems focusses on the fact the the value of an optimal solution is unknown. Here we are able to derive upper and lower bounds for ϵ_{opt} from the results of some semioptimal matchings. Since each pair (s, s') of characteristic points on S could constitute the approximated destination of (p_1, p_2) we apply this procedure for each such pair. More precisely, we compute the semioptimal matching $t_{s,s'}$ mapping (p_1, p_2) onto the point pair $(\overline{s_1}, \overline{s_2})$, where $(\overline{s_1}, \overline{s_2})$ forms the same line and has the same center as (s, s'), but $||\overline{s_1} - \overline{s_2}|| = ||p_1 - p_2||$. We denote the best value obtained in this way by $\delta = \min_{s,s' \in S_c}\{\epsilon(t_{s,s'})\}$.

Furthermore, we introduce the radius r_P and the relative radius R_P of the point set P with respect to the center of the characteristic points as follows:

$$r_P = \max_{p \in P} ||\frac{p_1 + p_2}{2} - p||, \quad R_P = \frac{r_P}{\frac{||p_1 - p_2||}{2}} = \frac{2\, r_P}{||p_1 - p_2||}.$$

Proposition 1 $\delta \geq \epsilon_{opt} \geq \frac{\delta}{R_P + 2}$.

Given an approximation factor $\lambda > 1$ we try to improve the best value δ obtained so far by small changes of the predefined matching positions $\overline{s_1}, \overline{s_2}$. The bounds above can be used to design a grid based set of pertubed matching positions which is dense enough to include a λ-approximation of an optimal matching.

Let us set two grids around points s and s' in the following manner. First, a 2-dimensional squared grid, centered at the point s', normal to segment (s, s'), with size $2\sqrt{3}\delta$ and with size of the subsquares $\frac{(\lambda-1)\delta}{8(R_P+1)R_P}$. Second, a 3 dimensional grid centered at the point s, parallel to the 2-dimensional grid, with size 2δ and size of subcubes $\frac{\sqrt{3}(\lambda-1)\delta}{6(R_P+1)}$. Using these grids for fixing a dense set of matching positions $(\overline{s_1}, \overline{s_2})$, at least one of the semioptimal matchings $t_{\overline{s_1},\overline{s_2}}$ is a λ-approximation of the optimal matching.

The number of the grid combinations, defining possible matching positions $(\overline{s_1}, \overline{s_2})$, is $(\frac{16\sqrt{3}R_P(R_P+1)}{\lambda-1} + 1)^2 (\frac{\sqrt{3}(R_P+1)}{\lambda-1} + 1)^3$. This implies the following estimation of the total run time:

Lemma 2 *The run time complexity of the λ-approximation presented above is* $O(n_c^2\, k\, n \log n\, \frac{R_P^5}{(\lambda-1)^5})$.

We remark that the factor n in this formula can be improved in the same way as discussed in the analysis of the semioptimal matching. Moreover, in the applications the ratio R_P can be regarded as a small constant.

References

[1] P. J. Besl and N. D. McKay. A method for registration of 3-d shapes. *IEEE Trans. on Pattern Recognition and Machine Intelligence*, 14(2):239–256, February 1992.

[2] M. Hagedoorn. Pattern matching using similarity measures. *PhD thesis, Utrecht University*, 2000.

[3] F. Hoffmann, K. Kriegel, S. Schönherr, and C. Wenk. A simple and robust algorithm for landmark registration in computer assisted neurosurgery. *Technical report B 99-21, Freie Universität Berlin*, 1999.

[4] S. Rusinkiewicz and M. Levoy. Efficient variants of the icp algorithm. In *Third International Conference on 3D Digital Imaging and Modeling*, pages 145–152, 2001.

[5] M. Sharir and P. Agarwal. Davenport-Schinzel sequences and their geometric applications. *Cambridge University Press*, 1995.

[6] P. J. M. van Laarhoven and E. H. L. Aarts. Simulated Annealing: Theory and Applications. *D.Reidel Publishing Company, Kluwer*, 1987.