



Approximate input sensitive algorithms for point pattern matching[☆]

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ABSTRACT

We study input sensitive algorithms for point pattern matching under various transformations and the Hausdorff metric as a distance function. Given point sets P and Q in the plane, the problem of point pattern matching is to determine whether P is similar to some portion of Q , where P may undergo transformations from a group G of allowed transformations. All algorithms are based on methods for extracting small subsets from Q that can be matched to a small subset of P . The runtime is proportional to the number k of these subsets. Let d be the number of points in P that are needed to define a transformation in G . The key observation is that for some set $B \subset P$ of cardinality larger than d , the number of subsets of Q of this cardinality that match B , is practically small, as the problem becomes more constrained. We present methods to extract efficiently all these subsets in Q . We provide algorithms for homothetic, rigid and similarity transformations in the plane and give a general method that works for any dimension and for any group of transformations. The runtime of our algorithms depends roughly linearly on the number of subsets k , in addition to an $n \log n$ factor. Thus our approximate matching algorithms run roughly in time $O(n \log n + km \log n)$, where m and n are the number of points in P and Q , respectively. The constants hidden in the big O vary depending on the group of transformations G .

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1. Introduction

A central problem in pattern recognition, computer vision, and robotics, is the question of whether two point sets P and Q resemble each other. One approach to this problem, first used by Huttenlocher and Kedem [17] and further developed by Huttenlocher et al. [18], is based on the minimum Hausdorff distance between point sets in the plane. The Hausdorff distance between two point sets P and Q is defined as

$$H(P, Q) = \max(h(P, Q), h(Q, P))$$

where the directional distance from P to Q is

$$h(P, Q) = \max_{p \in P} \min_{q \in Q} d(p, q)$$

Here, $d(\cdot, \cdot)$ represents a more familiar metric on points; for instance, the standard Euclidean metric (the L_2 metric) or the L_1 or L_∞ metrics.

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The *minimum Hausdorff distance* problem is to find

$$D(P, Q, G) = \min_{T \in G} h(T(P), Q)$$

where G is the group of allowed transformations. The *pattern matching* problem is, given a parameter $\delta > 0$, to find a transformation $T \in G$ such that $h(T(P), Q) \leq \delta$.

Algorithms for solving the minimum Hausdorff distance exactly for transformations other than translation have high computation time even for rigid transformations. The best known algorithm for rigid transformations was given by Chew et al. [10], and requires $O(m^3 n^2 \log^2 mn)$ time, where $|P|=m$ and $|Q|=n$. To overcome the high complexity of exact algorithms, approximation and randomization were considered by several authors for both the minimum Hausdorff distance and the pattern matching problems [3,8,9,14–16,20–22]. Let δ^* be the minimum directional Hausdorff distance between P and Q . The approximate algorithm finds a transformation that maps P within distance $(1 + \varepsilon)\delta^*$ from Q for some $\varepsilon > 0$.

The *alignment scheme* [19,15,14] is a common heuristic for geometric matching that works as follows: pick a small subset B of P , called a *base*. For every subset of Q of size $|B|$ compute the transformation T that maps B to the respective subset of Q , and verify the quality of each transformation T by computing $h(T(P), Q)$, or by counting the number of points, p_i in P , such that $h(T(p_i), Q) \leq \delta$. Based on this scheme, Goodrich et al. [14] considered the

approximation of the minimum Hausdorff distance under rigid motion. They showed that there is a discrete rigid transformation which approximates the minimum Hausdorff distance to a distance within factor 4, and that it can be computed in time $O(mn^2 \log n)$. Cho and Mount improved this approximation in [8]. Gavrilov et al. [15] presented an approximation algorithm based on the approximation definition of Heffernan and Schirra [16] and the alignment scheme. The running time of their algorithm is $O(mn^{4/3} \Delta^{1/3} \log n)$ for rigid motion, where Δ is the bound on the diameter of the point sets. In the same paper they presented a reduction from geometric pattern matching to string matching obtaining a running time of $O(n(n + \Delta) \text{polylog}(n))$ for rigid motion. Cardoze and Schulman [9] presented a randomized algorithm based on a reduction to a dense problem and using FFT. The time complexity of their algorithm is $O(n^2 \log n + \log^{O(1)} \Delta)$ for rigid motion. In [3], we gave a randomized algorithm for a different kind of approximation under *similarity* transformations (translation, rotation and scale). The running time of that algorithm was $O(n^2 \text{polylog}(n))$ but it is of less interest from the practical point of view. There is a fairly large number of works that explore the transformation space in a branch and bound fashion in order to find a good transformation [20–22]. Although these algorithms cannot guarantee a good upper bound on the runtime, they can be fast in practice.

We extend the methods in [14,15] and give an asymptotically faster algorithm under rigid transformations, and provide new algorithms for homothetic (translation and scale), and similarity transformations. We call a subset B of P , δ -equivalent to a subset C of Q , with respect to G , if there is a transformation T in G such that $h(T(B), C) \leq \delta$. Our goal is to find all k subsets $C_i \subseteq Q$, with their respective transformations $T_i \in G$, such that $h(T_i(B), C_i) \leq \delta$ for $i = 1, \dots, k$. We call the set B a *base*. A base, \mathcal{B} , is a *minimal base* if $|\mathcal{B}| = d$ is the smallest number of pairs $(p_i, q_j) \in P \times Q$ that are required to uniquely determine a transformation in G . As will be seen below, this minimum number depends on the number of parameters in a transformation in G , but is not necessarily equal to it.

We focus on *input sensitive* algorithms rather than on the worst case complexity. By input sensitive we mean that we take into account the number k of subsets $C_i \subseteq Q$ that are δ -equivalent to B . We present methods for extracting efficiently all subsets in Q that are δ -equivalent to a pre-chosen base B . We provide algorithms for G being *rigid*, *homothetic*, or *similarity* transformation in the plane. The runtime of these algorithms depends linearly on k , in addition to an $n \log n$ factor. Thus our alignment algorithms run roughly in time $O(n \log n + km \log n)$, where m and n are the number of points in P and Q , respectively.

Let d be the size of the minimal base. The key observation is that for a base B of size larger than d , and even as small as $d + 1$, the number of subsets of Q that are δ -equivalent to B , is very small in practice. The reason for this is that the larger the size of the base is, the problem becomes more constrained, thus it is expected that a smaller number of subsets of Q are δ -equivalent to B .

We call the problem of finding the subsets for rigid, homothetic, and similarity transformation in the plane the *specific dimension cases*. We show that the same idea works also for the *general case* for any family G of transformations and for points in any dimension. For this general case, we do not present theoretical results, but observe good performance in practice. We make use of branch and bound algorithms [20–22] in a novel way, where we first find all subsets in Q that are δ -equivalent to B and then all other points in P are verified in the same way as in the alignment scheme. Next we check the dependence of the runtime on the cardinality of B , where B is of a fixed size. Our experiments show that the time performance of the general case is commonly better for a larger (but fixed) size of B .

Our contributions in this paper are summarized below:

- Presenting a general input sensitive scheme that uses bases that are *not* minimal within the alignment framework to greatly reduce the runtime of matching algorithms. We compare our runtime with that of Mount et al. [20].
- Developing efficient algorithms to extract subsets in Q that are δ -equivalent to a given base for rigid, homothetic and similarity transformations in the plane, in time roughly $O(n \log n + k)$, where n is the number of points in Q , and k is the number of the subsets in Q .
- Combining branch and bound algorithms with our scheme to obtain input sensitive, fast in practice, algorithms for any transformation, and for point sets in any dimension.
- Showing empirically that there is an optimal size of the base that gives the best runtime, depending on the configuration of the sets.

2. Pattern matching and the alignment scheme

The study of combinatorial distance bounds was initiated by Paul Erdős [11] when he posed the question: “Given a set of n points in the plane, how many pairs of points can be a unit distance apart?” Erdős showed an upper bound of $O(n^{3/2})$. Szemerédi and Trotter [23] reduced the upper bound to $O(n^{4/3})$. Akutsu et al. [4], and Boxer [5], made the key observation that these bounds could be used to improve the analysis of exact point set matching algorithms. Consider the following naive algorithm to determine whether a point set P of size m , is contained in point set Q of size n in the plane ($m \leq n$) for rigid transformations. Fix a pair of points $p_1 \neq p_2 \in P$. Then, for each pair of points, $q_1 \neq q_2 \in Q$, determine (uniquely up to reflection) the rigid transformation, T , mapping $p_1 \mapsto q_1$, $p_2 \mapsto q_2$, if one exists. For each T , check if every point in $T(P)$ coincides with a point in Q , and if so, return T . We refer to this algorithm as *naive alignment*. This algorithm has running time $O(mn^2 \log n)$, where a factor of $m \log n$ comes from the cost of transforming P and determining the nearest neighbor in Q for each point in $T(P)$. However, given a pair (p_1, p_2) , we need only to consider all k pairs (q_1, q_2) such that $|p_1 - p_2| = |q_1 - q_2|$. By the combinatorial distance bounds, we know that there are $O(n^{4/3})$ such pairs in Q , and Agarwal et al. [1] have given an effective way of extracting these distances in time $O(n^{4/3} \log n)$. This immediately improves the running time of the naive algorithm to $O(kn^{4/3} \log n)$.

The question is whether the above method can be extended to deal with the directional Hausdorff distance as a measure, and for other types of transformations (i.e., homothetic and similarity). Here we would like the points of P to be δ -equivalent to points in Q . Namely, for example, for rigid transformations, instead of equal distance between pairs of points, the distance relation will be $|p_1 - p_2| - \delta \leq |q_1 - q_2| \leq |p_1 - p_2| + \delta$. There are no combinatorial bounds for the δ -equivalent case but Gavrilov et al. in [15] showed that if the points in Q are separated (i.e., that the distance between each pair of points in Q is greater than some given minimum distance) then there are analogue bounds to those of [23] on the number of pairs of points in Q of “almost” unit distance.

In this paper we take a different approach. In practical cases of point set matching it is often observed that the number of pairs of a given distance in Q (for the rigid problem, e.g.), even in the approximate case, is much smaller than its upper bounds. Given this observation, it is natural to look for algorithms that are *input sensitive* in the sense that their runtime depends on the actual number of such pairs. In the next section we show how to find these k pairs in Q for rigid transformations, and the respective δ -equivalent subsets of Q for other transformations.

Let G be a group of transformations and let u be the number of parameters in a transformation in G . We have $u = 3$ for homothetic and rigid transformations, $u = 4$ for similarity transformation, in the

plane. A transformation $T \in G$ is uniquely determined (or overdetermined) in the plane by $d = \lceil u/2 \rceil$ pairs of corresponding points (one point in P and one in Q). If u is even, T is uniquely determined by d pairs. If u is odd, the parameters of T are overdetermined by d pairs.

The key idea is thus to use this algorithm:

1. pick a base B of d' points from P , where $d' \geq d + 1$ if u is even, and $d' \geq d$ if u is odd,
2. extract all subsets $C_i \subseteq Q$ that are δ -equivalent to B , and
3. for each transformation T_i such that $h(T_i(B), C_i) \leq \delta$ verify whether $h(T_i(P), Q) \leq \delta$.

The challenging part is to develop efficient and fast algorithms for determining all the subsets C_i . We describe our algorithms for finding these sets for each of the specific dimension cases.

We start by defining our approximation as in [15,16].

Definition 2.1 (Heffernan and Schirra [16]). (δ, β) -approximate pattern matching algorithm returns, for given $\delta, \beta > 0$, point sets P and Q and a group of transformations, G :

- If $D(P, Q, G) \leq \delta$, then return a transformation $T \in G$ such that $h(T(P), Q) \leq (1 + \beta)\delta$.
- If $D(P, Q, G) > (1 + \beta)\delta$, then return None.
- Otherwise, when $D(P, Q, G) \in (\delta, (1 + \beta)\delta)$, return “do not know”.

Definition 2.2. The δ -neighborhood of a point p in the plane is the set $\{x \in R^2 \mid d(p, x) \leq \delta\}$, where $d(\cdot, \cdot)$ is some metric in R^2 (e.g., L_1, L_2, L_∞).

Definition 2.3. The δ -neighborhood of a point set Q in the plane is the union of the δ -neighborhoods of all points in Q .

3. Specific dimension cases

3.1. Rigid motion

Given two point sets P and Q in the plane, and given $\delta, \beta > 0$, we find a pair of points (p_1, p_2) that determine the diameter of P , then we find all pairs of points $C_i = (q'_i, q''_i)$ in Q that are δ -equivalent to (p_1, p_2) , map P to Q using the transformation, T_i , determined by each C_i and verify whether $h(T_i(P), Q) \leq \delta$.

Gavrilov et al. [15] show that if all k pairs in Q that are δ -equivalent to (p_1, p_2) are known, a (δ, β) -approximation (Definition 2.1) can be computed in time

$$O\left(m \frac{k}{\beta^3} \min\left(\left(\frac{\delta}{\beta}\right)^2, \log n\right)\right)$$

Definition 3.1. Given a grid of cell-size ε , a set C of circles of a fixed radius r , each centered at the center of some grid cell, and given a set U of grid cells, the set of all pairs (u, c) , $u \in U, c \in C$ such that c intersects u is called the incidence set of U and C .

To find all incidences we develop the discretized tool below. We will later apply this tool to determine the subsets C_i of Q . Let $r = |p_1 - p_2|$ and let $\varepsilon = c\delta$ for some $c > 1$. For each point $q \in Q$ we create a circle of radius r centered at the center of the cell containing q . We create a list of points for each grid cell, corresponding to all points of Q that fall inside each cell. We then set U to be the set of all non empty grid cells (the cells containing points of Q). We compute all incidences using the tool and then, since an error bounded by $\sqrt{2}\varepsilon$ might have occurred, we have to examine all the points in the incident cells, and their neighbors in the grid, to extract all exact δ -equivalent points in Q . Note that we might have to test also pairs in

Q that are not in the required range. This depends on the grid we choose, so we can trade off between the runtime of the extraction algorithm and the additional spurious pairs it reports by choosing the constant c . The algorithms of [15] gives runtime of $O(n\sqrt{\Delta/\varepsilon} + k)$ under this slightly different setup, for the tool we need, where Δ is the side-length of the bounding square of U and k is the number of incidences. As seen in the next lemma, we do better when n is large.

Lemma 3.2. Let $\varepsilon > 0$ be a constant and let G_ε be a grid with cell-size ε . Let C be a set of distinct circles of radius r , the center of each coincides with the center of a grid cell, and let U be a set of distinct grid cells, bounded by a square of side-length Δ . Then, all incidences (u, c) , $u \in U, c \in C$ can be computed in time $O((\Delta/\varepsilon)^2 \log \Delta/\varepsilon)$.

Proof. We use a similar method as used by Fonseca for the half-box quadtree in [13]. Let B be the bounding square of U . We divide B into four identical boxes. Recursively we compute the incidences for each subdivision with the subset of C that intersects it, using the cell-size ε as the minimum box size. For each box of this size we report all circles that intersect this box. Since the number of circles that intersect a box of size A is $O((A/\varepsilon)^2)$, the runtime $T(A)$ for a box of diameter A satisfies, for $A = \varepsilon$, $T(\varepsilon) = O(1)$. The recursion for $T(A)$ is $T(A) = O((A/\varepsilon)^2) + 4T(A/2) = O((A/\varepsilon)^2 \log \Delta/\varepsilon)$, which proves the lemma when $A = \Delta$. \square

Combining Lemma 3.2 with [15] we have:

Lemma 3.3. Let G_ε be a grid with cell-size ε , C a set of n distinct circles of a fixed radius r , and centered in n grid cells. Let U be a set of any n grid cells. Then, all incidences (u, c) for $u \in U, c \in C$ can be computed in time $O(\min(n\sqrt{\Delta/\varepsilon} + k, (\Delta/\varepsilon)^2 \log \Delta/\varepsilon))$.

Proof. For $n \leq (\Delta/\varepsilon)^{3/2}$ we use the method from [15] getting time $O(n\sqrt{\Delta/\varepsilon} + k)$. For $n > (\Delta/\varepsilon)^{3/2}$ we use the method from Lemma 3.2 getting time $O((\Delta/\varepsilon)^2 \log \Delta/\varepsilon)$. \square

For an arbitrary set of points and circles, which is the case for our point matching problem, we create the grid G_ε in a bounding square of the set Q ; we round all points in Q to their nearest center of cell in G_ε , we compute U , the set of (up to n) grid cells that contain points of Q , and set r to be $|p_1 - p_2|$. This gets us to the conditions of Lemma 3.2, adding a term of $O(n)$ to the runtime. Using the lemma above we extract all the pairs (q'_i, q''_i) from Q that are δ -equivalent to (p_1, p_2) .

The next theorem thus follows:

Theorem 3.4. Let G_ε be a grid with cell-size ε , C a set of n distinct circles of a fixed radius r , and let Q be a set of n points. Let C' be the set of circles obtained from C by rounding the center of each circle to the center of the nearest cell in the grid, and let U be the set of non empty grid cells obtained from Q by inserting each point to the cell it belongs. Then, all incidences (u, c) for $u \in U, c \in C'$ can be computed in time $O(\min(n\sqrt{\Delta/\varepsilon} + k, n + (\Delta/\varepsilon)^2 \log \Delta/\varepsilon))$.

By applying the (δ, ε) -approximation method of [15] the point matching problem is then solved.

3.2. Homothetic transformations

Homothetic transformations consist of scale and translation only and $d = 2$ pairs of points (one from P and one from Q) overdetermine a transformation. Let p_1, p_2 be two fixed points in P . We wish to find the set of all k pairs q'_i, q''_i , $i = 1, \dots, k$, from Q , that are δ -equivalent to p_1, p_2 with respect to homothetic transformation. Here we use L_2 as the underlying metric for the Hausdorff distance.

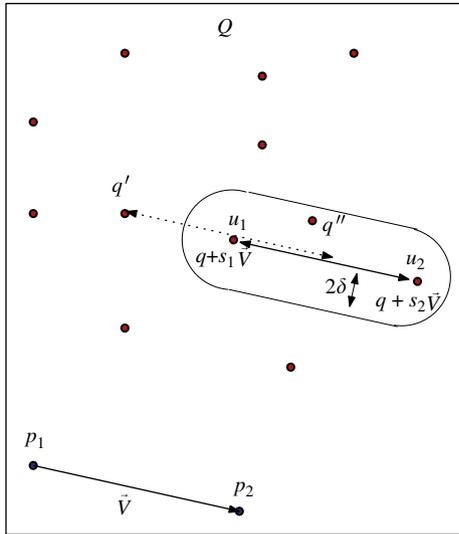


Fig. 1. δ -equivalent pairs under homothetic transformation.

Lemma 3.5. Given a point set Q in the plane, two arbitrary points p_1, p_2 , and scale restrictions $s_1 < s_2$, we can find all pairs q', q'' that are δ -equivalent to $p_1, p_2 \in P$, under homothetic transformation with scale s , $s_1 \leq s \leq s_2$, in $O(n \log n + k)$ time, where k is the number of these pairs.

Proof. We impose the constraints s_1 and s_2 as they exist in any practical application. Clearly, if there is no restriction on the scale axis then the algorithm is easily transformed into a 1D intersection problem. Consider Fig. 1. We have a point set Q , and two points p_1 and p_2 that form a vector \vec{V} . If we transform p_1 to coincide with some $q' \in Q$, then under homothetic transformation with scale s between s_1 and s_2 , the homothetic transformation of p_2 is free to move on the line segment between u_1 and u_2 .

In order for (p_1, p_2) to be δ -equivalent to (q', q'') , $T(p_1)$ can be in the δ -neighborhood of q , and $T(p_2)$ can be in the racetrack which is the Minkowski sum of segment (u_1, u_2) with a disc of radius δ . We look for q'' whose δ -neighborhood intersects the racetrack. This is equivalent to finding q'' inside the racetrack which is the Minkowski sum of the segment (u_1, u_2) with a disc of radius 2δ .

For given pair, p_1, p_2 , all these racetracks are parallel to each other thus we can use range searching for querying all points of Q inside these racetracks. Each racetrack is the union of a rectangle and two discs. We thus query all points inside every rectangle by orthogonal range searching and query all points in the discs using halfspace range searching in 3D after a standard lifting [7,2] (in practice we can use simpler approximate halfspace range searching [13]). Every pair of a racetrack and a point, corresponds to a pair in Q that is δ -equivalent to p_1, p_2 . Building the range tree (after transforming the coordinate system so that the rectangles are axis aligned) takes $O(n \log n)$ time and query the points in the n rectangles takes $O(n \log n + k)$ time where k is the number of reported points. Building the halfspace range searching data structure takes time $O(n \log n)$ and query all n discs takes $O(n \log n + k)$ time [2] and the lemma follows. For a given racetrack, all points in the overlap region between the rectangle and the discs are reported twice. \square

Note that for homothetic transformation we do not require p_1 and p_2 to be the diameter points.

3.3. Similarity transformations

Similarity transformations have four parameters—translation, rotation and scale. We parameterize the transformation so that it is

linear (see [3]). According to the key idea, given a base B of three fixed points p_1, p_2 and p_3 in P , we want to find all subsets of three points in Q that are δ -equivalent to B under similarity transformation. The set of all transformations that map p_1 to some point q in Q is a 2-flat in transformation space, i.e., the intersection of two hyperplanes in R^4 [3]. If we use L_∞ as the underlying metric, the set of all transformations that map p_1 to the δ -neighborhood q is the Minkowski sum of this 2-flat with a planar square of side-length 2δ . Let us call the Minkowski sum of a 2-flat with the square a stick in 4D. Mapping each of p_1, p_2 and p_3 to the neighborhoods of all points of Q , respectively, we get three sets, A, B and C , each consisting of a set of parallel sticks in 4D [3]. Our problem is thus reduced to find all the regions where three sticks, one from each set, intersect.

Finding such intersections in R^4 is not efficient enough, thus we discretize the rotation axis in R^4 , and use the homothetic method as a subroutine for each cell in the rotation axis as follows. We discretize the rotation axis into $O(1/\epsilon)$ slices, where ϵ is the maximum rotation that moves every point in P by less than distance $\delta/2$. We then solve the matching problem for each one of the rotations using the 3D homothetic algorithm above. We thus have an algorithm which runs in $O((1/\epsilon)n \log n + k)$ time for extracting all pairs q', q'' of points in Q , such that there is some homothetic transformation T_i as (approximately) required. q', q'' are the set of all pairs in Q that are approximately δ -equivalent to p_1 and p_2 under similarity transformations. The amount of approximation is determined by ϵ .

4. The general quadtree method

The scheme for the general cases is as follows: let P, Q be point sets in R^D of m and n points, respectively, and let d be the dimension of the transformation space G . Let B be a base of l points in P , where l is greater than the number of pairs of points required to uniquely determine a transformation in G . We are given some $\epsilon > 0$ that determines the accuracy of our approximation in R^D . We set another parameter ϵ' in transformation space such that for any two transformations T_1, T_2 , and every $p \in P$, $|T_1 - T_2|_\infty < \epsilon' \Rightarrow |T_1(p) - T_2(p)| \leq \epsilon$ (here we interpret T_1 and T_2 as points in R^d). As before, let $B \subset P$ be a base of cardinality l . An object in transformation space corresponds to the set of transformations that map a point p in B to the δ -neighborhood of a point $q \in Q$. Since we map l points of P to all points of Q , we get sets A_1, \dots, A_l in transformation space. The objects in each A_i , are, as before, all parallel, each A_i is the set of objects corresponding to the transformation that maps one point $p \in B$ to all points of Q .

We now have to find all intersections of l objects from l different sets. This is done by applying a branch and bound method recursively in the following manner. We divide the transformation space into a d -dimensional quadtree and recurse to smaller boxes only if needed. To determine if a box has to be recursed, we check whether it is intersected by at least l objects from l different sets. To simplify the computation this is done by switching back to the spatial space (R^D). For a given quad tree box W in R^d and each point $p \in B$ we construct the polytope into which p is mapped by the transformations in W , and check, whether there are points of Q in the polytope. In order to simplify the computation even more we bound the polytope by axis parallel bounding box (to allow orthogonal range search, see below). A point $q \in Q$ in this bounding box corresponds to an object in transformation space that has a potential intersection with the explored box W .

Checking if this bounding box is empty of points in Q can be done in polylogarithmic time if we build an orthogonal range search structure in $O(n \log^{d-1} n)$ time and space. We stop the recursion when the size of the cell is smaller than ϵ' and report all cells that are intersected by l objects. These objects correspond to l pairs $p \in P$,

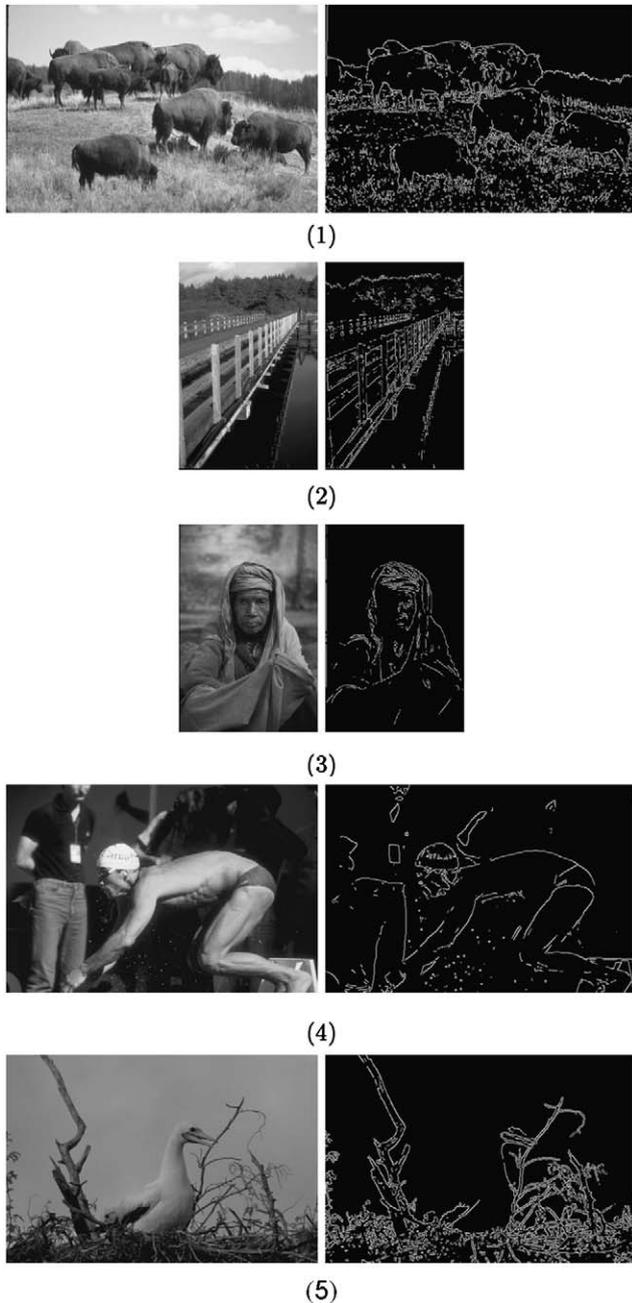


Fig. 2. Real data—images and their edge map that was taken as point sets.

$q \in Q$, such that q_1, \dots, q_l is approximately δ -equivalent to p_1, \dots, p_l . The amount of approximation is determined by ε .

The general case is similar to several other works that use *branch and bound* methods [20–22]. The important difference is that they work directly on the two sets P, Q , and we find a small number of sets in Q that are δ -equivalent to a base of fixed small number of points.

The method described in this section is the method we implemented. In the next section we present the results of our experiments.

5. Experimental results

We implemented and tested our algorithms on Pentium 4, 3 GHz with 1 GB RAM memory. Our experimental results contain a number of tests. We found that the general algorithm described in Section 4 is very fast in practice and since it allows to take a base of arbitrary

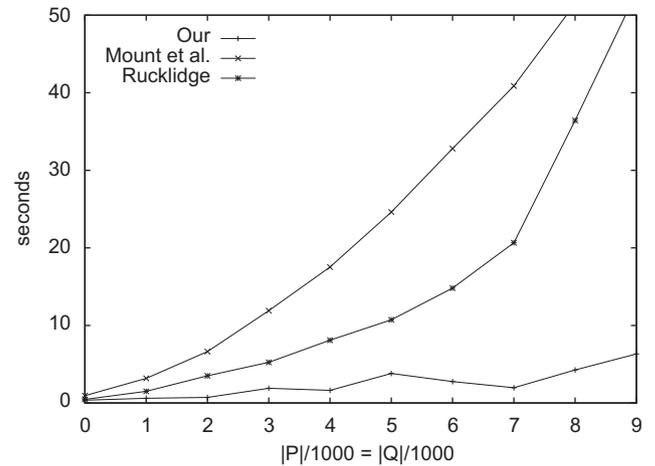


Fig. 3. Similarity transformations in the plane—random data set. The results of the algorithm of Mount et al. [20], the algorithm of Rucklidge [22] and our algorithm from Section 4 with a base of 16 points are shown.

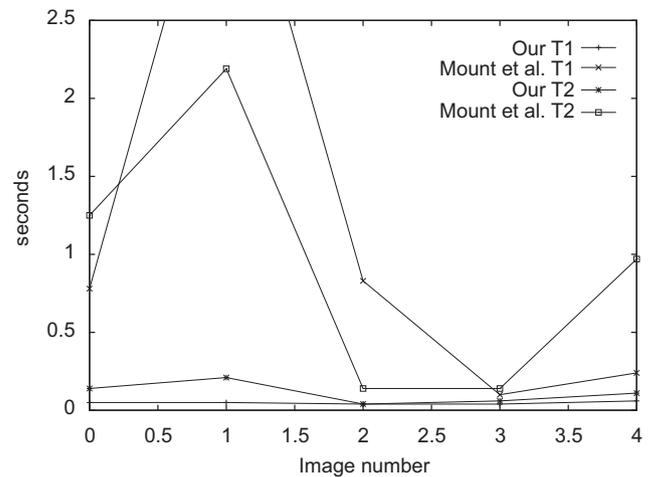


Fig. 4. Similarity transformation in the plane—real world data. Results of running the algorithm of Mount et al. and our algorithm from Section 4 with a base of 16 points are shown for two transformations, T_1 and T_2 (see the text).

fixed size, in most of the cases (for large enough data sets) it outperforms the algorithms in Section 3, (although the algorithms from Section 3 have better worst case upper bounds with respect to the number of candidates being found). We thus compare our algorithm for similarity transformation (from Section 4) in the plane with the implementation of Mount et al. [20] and the algorithm of Rucklidge [22]. We note that the algorithm of Gavrilov et al. [15] is only suitable for *rigid* transformation, thus it cannot be used for comparison under similarity transformations.

Two settings were considered, random input where the sets P and Q were taken randomly inside a bounding box, and real world inputs taken to be edge points extracted from images (e.g., for a registration problem). The images we considered are shown in Fig. 2. On the left are the gray level images, and on the right their corresponding edge maps computed using *Canny's* edge detector [6]. The point sets were taken to be points in these edge maps sampled by factor of 2. It should be noted that the algorithm of Mount et al. supports three different approaches, a pure branch and bound, branch and bound with partial pinning and branch and bound with full pinning. The latter was shown to be the faster so we used this version. In addition, their algorithm supports outliers (they use quantile Hausdorff

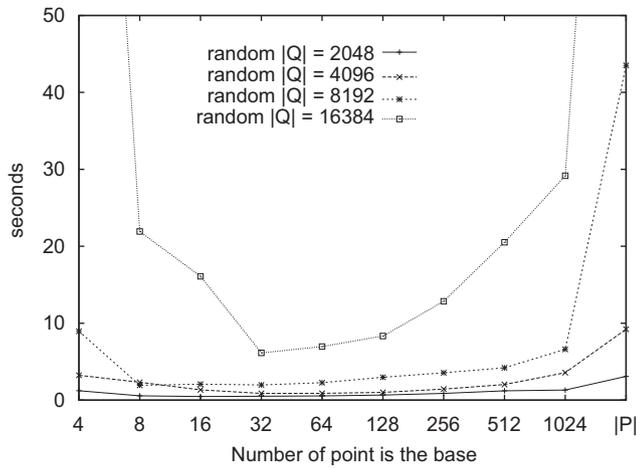


Fig. 5. The runtime of our algorithm from Section 4 with respect to the size of the base–similarity transformations in the plane for random data.

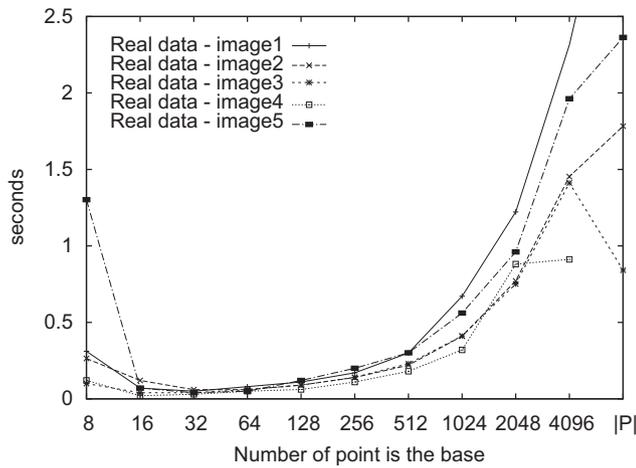


Fig. 6. The runtime with respect to the size of the base–similarity transformations in the plane for real data (image1).

distance). For the comparison to be fair, we set the tunable parameter to quantile = 1.0, so it is completely comparable to the setting of our algorithm.

In the first test (random data, Fig. 3), we set $P = T(Q)$, where T is composed of rotation of 45° , $scale = 0.5$, and $translation = (100, 100)$. We added random noise to P uniformly sampled from $[-\delta, \delta]$. We compare our results to the results of two other algorithms, Mount et al. [20] and the algorithm of Rucklidge [22]. The algorithm of Rucklidge is essentially identical to our branch and bound algorithm without the input sensitive part. Thus it is used demonstrate how the input sensitive part affects the results. We then let the algorithms find the transformation and measured the runtimes. The point sets were randomly selected from the world in resolution $[-2048, 2048] \times [-2048, 2048]$. We set $\delta = 1.0$ for all tests. For the algorithms of Mount et al. [20], there are many other parameters that we set according to the recommendations in their paper and according to the tests in their package. In the second test, we set $P = T_i(Q)$, $i = 1, 2$, where T_1 is composed of rotation of 45° , $scale = 0.5$, and $translation = (100, 100)$ and T_2 is composed of rotation of 60° , $scale = 0.3$, and $translation = (100, 100)$. We compare our algorithm to the algorithm of Mount et al. for all the images of real data under these transformations (Fig. 4).

Let d be the number of pairs of points that are required to define a transformation in a group G of transformations. It is natural to ask whether picking a base of size larger than $d + 1$ but fixed, can result in a better runtime. It appears empirically that this is indeed the case. It appears that there is some optimum (depending on the configuration of P and Q) that gives the best runtime. Our experiments show that the gap between the optimal number of points in the base and $d + 1$ is significant. Although we do not currently know how to analytically predict the optimal number of points in advance, the existence of this optimum is reasonable, since it is a trade off between the computation time in the extraction of equivalent sets, and the verification step that depends on this number of sets. Large base decreases the number of equivalent sets while increasing the extraction process. Small base, decreases the extraction time while the expected equivalent sets is higher. We tested what is the optimal number of base points for both random and real inputs. We plot the runtime with respect to the number of points in the base for varied size of random inputs and from all real data sets extracted from the images. These results can be viewed in Figs. 5 and 6. Our tests show that a fixed number around 16 works very well in all cases. It was

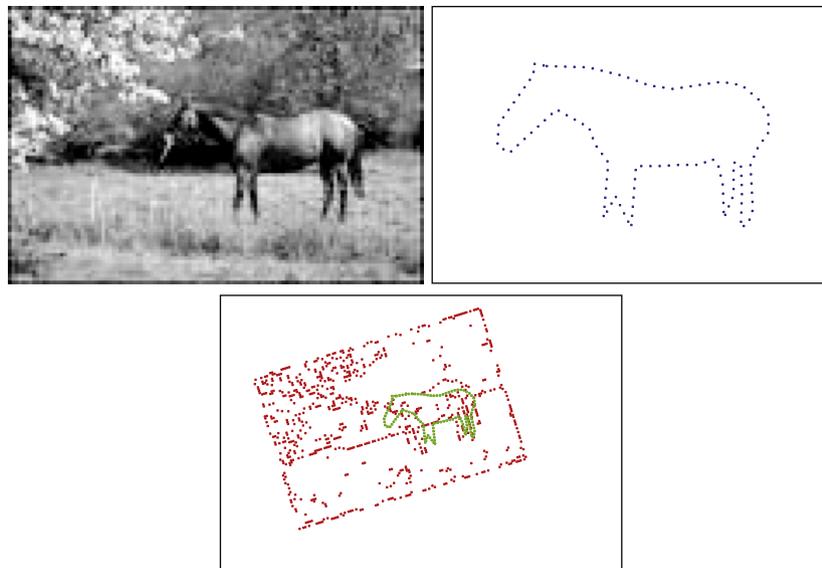


Fig. 7. Finding a model in image: an input image is on top left. On top right, a model of a horse. The extracted point set (by Canny's edge detection) scaled, rotated and translated and the transformed model in green is on the bottom. The computation time using our method from Section 4 with eight base points is 360 ms. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

also shown that we achieve an impressive speed up relative to the case of taking all the points as done in [20–22].

In the last test, we show that our algorithm also works (though somewhat limited) in cases where not all the points of P can be matched to points in Q . In principle, a standard randomization can be used to repeat the basic algorithm in Section 4 as many times as needed, given an estimation on the fraction of points of P that can be matched. However, as the number of points in the base is getting higher, the number of times is getting higher exponentially, thus it is not efficient for large bases. In the test in Fig. 7, we used a base of size 8. Here we extract points (by Canny's edge detection) from an input image, transformed them and let the algorithm find a synthetic model (composed as a pointset) inside the (transformed) image. The results are in Fig. 7.

6. Conclusions

We presented a set of input sensitive algorithms for point pattern matching that are very fast in most practical cases. All algorithms are based on a simple alignment scheme and their speed comes from fast methods to extract all subsets from Q that are δ -equivalent to a given set from P . The runtime is proportional to the number of these subsets. We showed experimental results for similarity transformations that give evidence of the speed of these algorithms. We also asked whether better runtime can be achieved for base of arbitrary fixed size and showed empirically that there is a significant optimum.

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