Efficiently comparing face images using a modified Hausdorff distance

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Abstract: Comparing face images using the Hausdorff distance is one of the face matching and fast screening techniques. As a fast screening technique, the computational efficiency is a key issue. An efficient method for Hausdorff distance-based face matching and fast screening is proposed. The method utilises dominant points, instead of edge maps, as features for measuring similarity. A new formulation of Hausdorff distance is designed for significance-based dominant point matching. The experiments demonstrate that the proposed approach significantly improves the computational speed and storage economy. It provides a very efficient way to use the Hausdorff distance measure for face matching and fast screening.

1 Introduction

Computerised human face recognition has been an active research area in recent years. It has many practical applications, such as bank card identification, 'mug shot' searching, access control, security monitoring and surveillance systems. Face recognition is used to identify one or more persons from still images or a video image sequence of a scene by comparing input images with faces stored in a database. In a face identification system, face features are extracted/coded offline from the original images and stored in the face feature database. In the identification stage, the same features are extracted from the input face, and the features of the input image are compared with the features of each model image in the database. In most systems, searching is the most computationally expensive operation due to the large number of images available in the database. Efficient search algorithms and fast screening algorithms are prerequisites of identification systems.

Takács [1] proposed a face matching and fast screening approach for large face databases. The similarity measure is conducted using a modified Hausdorff distance on edge maps of face images. 92% accuracy was achieved in his identification experiment. He argued that the process of face recognition might start at a much earlier stage and edge images could be used for fast screening of faces without the involvement of high-level cognitive functions.

As a fast screening technique, the computational efficiency is an important issue. This study extends the work of [1] and proposes an efficient method for Hausdorff distance-based face matching and fast screening using dominant points. It significantly reduces the computational time and the storage requirement. Experimental results demonstrate that the proposed approach is 28 times faster

than that of the method in [1] with a cost of 1.74% accuracy degradation. Furthermore, the storage space is reduced to 18.5% of that of the existing method.

2 Dominant point detection

Edges are the most fundamental features of objects in the 3-D world. The edges in an image reflect large local intensity changes that are caused by the geometrical structure of the object, the characteristics of the surface reflectance of the object and the viewing direction. Edge detection is an important technique in computer vision and pattern recognition systems since the edges usually correspond to some important properties of the objects, such as object shape and boundary.

Edge extraction has been studied most extensively, and many reliable algorithms have been proposed and implemented. A few examples from a large collection of algorithms that have been presented to the computer vision community are given in [2–6]. The continuing development of edge detectors is producing increasingly complex edge detection algorithms. However, the 'increased sophistication is not producing a commensurate improvement in performance' [7]. Heath *et al.* [8, 9] investigated the performance of different edge detectors. They compared the edge detectors based on experimental psychology and statistics, in which humans rated the outputs of low-level vision algorithms. One of their clear results was that 'no one single edge detector was best overall; for any given image it is difficult to predict which edge detector will be best' [9].

The proposed face matching method using dominant points as features does not rely on any specific edge detector. It is a general method where any edge detector can be used. In this study, an edge detector based on the algorithm of Nevatia and Babu [6] is used, followed by a thinning process to generate one-pixel-wide edge curves.

The dynamic two-strip algorithm (Dyn2S) [10] is utilised to detect dominant points, the points with high curvatures, on the facial edge curves. The Dyn2S algorithm is briefly summarised here to provide the necessary background to this paper. The algorithm is based on a feature point approach to segment a curve. A strip is fitted to the left and right of each point on the curve, and the points inside each strip are approximated as a straight line. The

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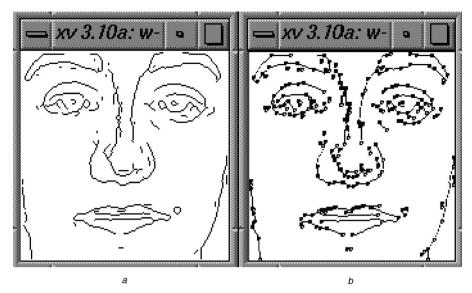


Fig. 1

a Illustration of a face edge map

b Dominant points superimposed on the edge map

orientation and width of the strip are adjusted automatically. Longer and narrower strips are favoured. In addition, the curvature and a measure of merit of each point can be calculated. The elongatedness of a strip is defined as the ratio of its length and width. The merit of a point can be computed as $E^{left} \cdot S \cdot E^{right}$, where $S = |180^{\circ} - \theta|$ is the acuteness of the angle θ between the two strips, and E^{left} and E^{right} are the elongatedness of the left and right strips. Minimum and maximum strip widths are chosen. An initial strip of minimal width extends from a point P on the curve to encompass as many points as possible to one side. Its width is then incrementally increased and its orientation is adjusted to include as many points as possible until the maximum strip width is reached. The elongatedness measure for each strip is recorded. The same procedure is applied to the other side of P. The left and right strips with the highest elongatedness measures are retained. A subset of significant points is chosen using local maxima. They are selected in a three-step procedure. First, points with a small merit compared to their neighbours are eliminated. Secondly, a number of points are reinstated to avoid over-elimination. They are chosen from any points that are not covered by one of the strips selected in the first step. Finally, points that align approximately on a straight line are deleted except for the two endpoints on the curve. The remaining points are the feature points extracted. The merit in this algorithm provides an objective evaluation of the prominent strength of each point and will be used as a significance measure of the dominant point in the proposed modified Hausdorff distance measure. The results of applying these processes to human faces are illustrated in Fig. 1.

3 Modified Hausdorff distance

The Hausdorff distance is a shape comparison metric based on binary images. It is a distance defined between two point sets. Unlike most shape comparison methods that build a point-to-point correspondence between a model and a test image, Hausdorff distance can be calculated without explicit point correspondence. Huttenlocher *et al.* [11] argued that the Hausdorff distance for binary image matching is more tolerant to perturbations in the locations of points than binary correlation techniques, since it measures proximity

rather than exact superposition. Here, we modify the Hausdorff distance measure and apply it to dominant point matching.

Given two finite point sets $M = \{m_1, m_2, \dots, m_p\}$ (representing a model in the database) and $T = \{t_1, t_2, \dots, t_q\}$ (representing a test image), the Hausdorff distance is defined as

$$H(M,T) = \max(h(M,T), h(T,M)) \tag{1}$$

where

$$h(M,T) = \max_{m_i \in M} \min_{t_j \in T} ||m_i - t_j||$$
 (2)

and $||m_i - t_j||$ is the Euclidean norm of the points m_i and t_j . The function h(M, T) is called the directed Hausdorff distance from M to T. It identifies the point $m_i \in M$ that is the farthest from any point of T and measures the distance from m_i to its nearest neighbour in T. The Hausdorff distance H(M, T) is the maximum of h(M, T) and h(T, M). Thus, it measures the degree of mismatch between two sets by measuring the distance of the point of M that is farthest from any point of T, and $vice\ versa$.

Dubuisson and Jain [12] investigated 24 forms of different Hausdorff distance measures and indicated that a modified Hausdorff distance (MHD) measure has the best performance. The directed MHD is defined as

$$h(M,T) = \frac{1}{P} \sum_{m_i \in M} \min_{t_j \in T} ||m_i - t_j||$$
 (3)

where P is the number of points in M. The definition of the undirected MHD is the same as (1). The Hausdorff distance defined as (1) and (2) is very sensitive to outlier points. A few outlier points, even only a single one, can perturb the distance greatly, though the two objects might be very similar. The MHD can alleviate the sensitivity of the Hausdorff distance, which uses (1), to outlier points. The partial Hausdorff distance (PHD) was suggested by Huttenlocher $et\ al.\ [11]$ and other researchers [13-16]. The PHD takes the kth smallest nearest neighbour distance as the objective function to deal with occluded objects and arbitrary outliers. It is robust in the sense used in robust statistics [17], though the comparative study of [12] reported that the MHD performed better than the PHD in

their experiments. A comparison experiment on face images is conducted and reported in Section 4.

In this paper, MHD is modified and employed to match dominant points rather than binary pixels. Dominant point representation demands much less storage requirement and thus is more computationally efficient than binary image matching. A new modified Hausdorff distance (M²HD) is proposed by introducing the merit value of each dominant point into the computation of the Hausdorff distance. The directed M²HD is defined as

$$h_{M^2HD}(M,T) = \frac{1}{\sum_{m_i \in M} W_{m_i t_j}} \sum_{m_i \in M} W_{m_i t_j} \cdot \min_{t_j \in T} \|m_i - t_j\|$$
(4)

where $W_{m_it_j}=1/2(W_{m_i}+W_{t_j})$ is the average merit of dominant points m_i and t_j . In this study, W_{m_i} and W_{t_j} are merits provided by the Dyn2S algorithm previously mentioned. Other dominant point detection algorithms, which provide merits or significances of points, can also be used. Every $\min_{t_j \in T} \|m_i - t_j\|$ (i.e. the distance of a matched pair) is weighted by the average merit of m_i and t_j because its contribution to $h_{M^2HD}(M,T)$ is assumed to be proportional to the significances of the two dominant points. $h_{M^2HD}(M,T)$ identifies its nearest neighbour point in T and attaches a merit-based weight to the distance from m_i to the identified point. The undirected M^2HD is rewritten as follows:

$$H_{M^2HD}(M,T) = \max(h_{M^2HD}(M,T), h_{M^2HD}(T,M))$$
 (5)

4 Experimental results

A face database [18] of 30 persons with two frontal and two profile views per person, from the University of Bern, was used to test the capability of the proposed M²HD approach. Each image has a size of 512×342 pixels with 256 grey levels and variations of the head position, size and contrast. The lighting conditions during image acquisition were carefully controlled. One profile image and one frontal face image of each person were used as models, while the other pair was used as input in the frontal and the profile face matching experiments, respectively. Though there are 60 pairs of models and inputs, one can have 120 matching tests if the roles of model and input are interchanged. Sample sets of the frontal and the profile faces are shown in Figs. 2 and 3.

In order to remove the influences of hair, neck and other foreign objects, such as shirt collars, the face matching process should be restricted to the personal identity area containing only the eyebrows, eyes, nose, mouth and chin. For this purpose, the automatic profile location algorithm [19] was employed to detect the nose tip and chin points. The distance between these two points was used as a reference to normalise the image size, align the face position and crop the facial area. For the frontal faces, the eye locations are detected for normalisation, alignment and cropping.

The identification accuracy using the existing MHD method and the proposed M2HD method are given in Table 1. Their storage sizes are summarised in Table 2. By using dominant points, the MHD recognition accuracy (top one identification) decreased to 93.34% due to the use of less feature points and dominant point extraction errors. The proposed M²HD dominant point matching improved the performance by integrating the significance of each dominant point, which correctly identified 94.17% (top one identification) of the test faces from the University of Bern face database [18]. This rate only dropped 1.74% from the 95.84% of the MHD method on edge maps. However, its average storage space dropped significantly by 81.5%. The computational complexities of MHD and M²HD are both of the order of O(PQ) for point sets of size P and Q. In other words, the computational time of the M²HD on dominant points is only 3.4% (= $(18.5\%)^2$) of that of MHD on edge maps. Note that this improvement in running time is achieved due to the smaller set of dominant points used by M²HD than the edge pixels used by MHD. These results show that compared to the MHD method on edge maps, the M²HD method on dominant points only required 3.4% of the computational time and 18.5% of the storage space. The cost to the above benefits was a mere 1.74% decrease in accuracy. In this study, all edge maps of faces were generated using a fixed threshold that gave similar amount of edges as in [1]. Figures 2 and 3 provide some examples of the edge maps and dominant points obtained in our experiments. The experimental results (Tables 1 and 2) show that a much smaller subset (270 dominant points) of edge pixels (1451 pixels) can be used to represent the face edge map and to achieve similar recognition accuracy. No matter what threshold is used in the edge detection to generate the edge maps, the dominant points are always a much smaller subset of its edge map. The MHD and the M²HD can be efficiently computed by preprocessing the

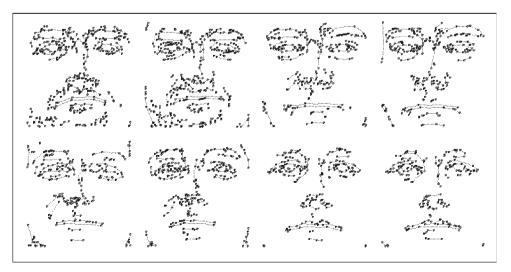


Fig. 2 Sample pairs of face edge maps with detected dominant points



Fig. 3 Sample pairs of profile edge maps with detected dominant points

Table 1: Accuracy* (%) comparison of the MHD and the M²HD on face database [18]

	MHD on EM	M ² HD on DP	Decrease (%)	MHD on DP
Accuracy	95.84	94.17	1.74	93.34

^{*}Top one identification

EM: edge map; DP: dominant point

Table 2: Comparison of average storage space (number of points) on face database [18]

	Edge map (MHD)	Dominant point (M ² HD)	Dominant points Edge map (%)	Decrease (%)
Frontal view	1451	270	18.6	81.4
Profile view	423	78	18.4	81.6
Average	_	_	18.5	81.5

point sets in time $O(P\log P)$ and $O(Q\log Q)$ into a data structure requiring O(P) and O(Q) space (e.g. a Voronoi diagram in the plane), and then running queries in time $O(\log P)$ and $O(\log Q)$ per query. (See [20–22] for technical details.) Thus, the desired measures can be computed in time $O((P+Q)\log(max(P,Q)))$.

The face database from Purdue University [23] was used for the fast screening comparison. For details on the collection of the database, readers can refer to [24]. 224 images of 112 subjects were tested. The 112 images of 112 people taken in the first session were used as models, while the other 112 images taken after two weeks were used as test images. Note that this is a single model test.

The experimental results are summarised in Fig. 4 in terms of top N screening/identification. In the top one identification, the correct match is only counted when the best matched face from models is the identical face (i.e. the

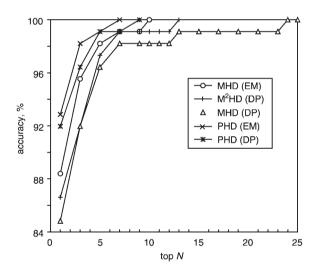


Fig. 4 Experimental results of fast screening on face database [23]

EM: edge map; DP: dominant point

face image from the same person) of the input. In the top Nscreening, the correct match is counted when the identical face of the input is among the best N matched faces from models. It was found that the accuracy of the proposed M²HD matching on dominant points was slightly lower than that of the MHD matching on edge maps (see Fig. 4). The M²HD on dominant points correctly identified all the test images using top 13 screening (i.e. screening the best 13/112 = 11.6% matches), while the MHD on edge maps correctly identified them using top ten screening (i.e. screening the best 8.9% matches). The screening result of the M²HD on dominant points, which could be used as candidates of another fine-tuning matching process, increased by 2.7%. However, the computational time and the storage space of the M²HD on dominant points were reduced to 3.7% (= $(19.3\%)^2$) and 19.3% of those of the MHD on edge maps, respectively (see Table 3). The MHD

Table 3: Comparison of average storage space (# of points) on face database [23]

	Edge map (MHD)	Dominant point (M ² HD)	Dominant points Edge map (%)	Decrease (%)
Storage space	1401	271	19.3	80.7

matching applied to dominant points was also tested and plotted in Fig. 4 as a comparison reference. By using dominant points, the MHD performed worse than the MHD on edge maps. Note that top 24 screening (i.e. screening the best 21.4% matches) is required by the MHD matching on dominant points to achieve 100% accuracy. This is believed to be due to the significant reduction in feature points and/or dominant point extraction errors. There are many other dominant point or interest point detection algorithms; a more robust method could alleviate this problem. The proposed M²HD dominant point matching improved the performance by incorporating the significance of each dominant point.

This study extends the work of [1] to provide an efficient way for Hausdorff distance-based face matching and fast screening using dominant points. Takács [1] used the MHD that demonstrated the best performance among 24 forms of different Hausdorff distances in [12]. However, the PHD [11] is robust to outliers and partial occlusions which seems to be in contrast to the comparative results of [12]. Here, a comparative experiment of the PHD on face images is conducted, as suggested by an anonymous reviewer. Figure 4 also shows the screening/identification results of the PHD using median nearest neighbour (NN) distance on edge maps and dominant points, respectively. It is found that the PHD with median NN distance outperformed the MHD, which is opposed to the result in [12].

Conclusions

Current face identification approaches require computer systems to search through a large quantity of face feature sets in the database and pick the ones that best match the features of an unknown input face. Comparing face images using the Hausdorff distance is one of the face matching and fast screening techniques. As a fast screening technique, the computational efficiency is a critical issue.

In this paper, an efficient method for Hausdorff distancebased face matching and fast screening has been proposed. The method utilises dominant points instead of edge maps as features for similarity measurement. A new formulation of Hausdorff distance is designed for merit-based dominant point matching. The identification and screening experiments demonstrated that compared to the existing MHD approach on edge maps, the proposed M²HD dominant points matching approach only required 3.4% of the computational time and 18.5% of the storage space. The cost of the above benefits was a mere 1.74% decrease in accuracy. These results indicate that the M²HD face matching method significantly improves the computational

speed and storage economy. It provides a very efficient way for Hausdorff distance-based face matching and fast screening. However, it is found that the PHD, using median nearest neighbour distance, performed better than the MHD in our experiments. Nevertheless, considering storage and running time, the efficiency improvements by using dominant points to replace edge maps are valid for the PHD as well. The proposed dominant point face matching method breaks down only when the dominant points cannot be detected or if they are detected in error. Though one of the face databases used in this research is a large publicly available database, it would be interesting to see, as part of future research, how the proposed method performs when the database becomes larger.

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