A Novel Image Correlation Matching Approach

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Abstract—In this paper we present a novel approach which is combined local invariant feature descriptor named ARPIH (Angular Radial Partitioning Intensity Histogram) with histogram-based similar distance (HSD). The approach succeeds the ARPIH descriptor’s distinctive advantage and provides higher robustness in deformation image matching, such as rotation image, illumination changing image and perspective image, etc. Based on the MCD algorithm, we present the HSD algorithm. This algorithm transforms the image matching into the histogram matching by calculating the number of the similar points between template histogram and target histogram in order to decrease the calculation complicity and improve the matching efficiency. A large amount groups of images are used in testing the approach presented in this paper. The matching results presented here indicate that the presented algorithm is efficient to figure out both the geometric deformation image matching and the illumination changing image matching. Contrast with the traditional matching algorithm, the approach presented in this paper has the obvious advantage of high matching precision, robustness and performance efficiency.

Index Terms—image matching; local invariant feature; ARPIH; HSD

I. INTRODUCTION

Image matching defines the process of finding out the same or similar image modes from the target image according to the known image template [1]. With the development of technology, image matching technique is very important in many applications including modern spaceflight, military affairs, medicine and industry in latter-day information processing. Because of variant imaging conditions such as illumination, visual angle, rotation and sensors, more requirements of image matching are raised. It is the emphasis of research that how to find out a quick matching method with higher robustness for image deformations.

The recent researches indicate that the local information of image is enough to describe the image and can be used for image matching to avoid more errors in image segmentation [2]. Lowe [3] takes local DOG extremum as interest point and presents a particular local invariant descriptor- SIFT (scale invariant feature transform) descriptor through calculating local image grads histogram. The descriptor has the characters of image scaling, rotation and affine invariant which makes it figure out the deformations matching, such as local shelter, rotation and view point changing. It is proved to be distinctiveness and robustness. Reference [4] applies the SIFT descriptor to shaped fibers inspection, and built an automatic fiber recognition system. Schmid and Mohr [5] prove the local information is enough for image recognition. They take Harris corner as interest point and distill the rotation-invariant descriptor from its neighborhood area. This descriptor can ensure the correct matching of rotary image. Tuytelaars and Van Goal [6] construct a small affine invariant region at the corner and grayscale extremum. All the ways are common in searching for a specific structure of parallelogram, [3] and [5] are circumvolving and grayscale invariant, [6] is affine invariant. Lei Qin and Wen Gao [7] put forward a novel local invariant descriptor named angular radial partitioning intensity histogram (ARPIH), which describes images by a series of feature descriptors of grayscale and rotation-invariant. This method can solve the matching problems of geometric deformations and illumination changing, but it has some shortcomings of complex operation and long matching time. Xu Xiao-Ming and Yang Dan [8] presented a novel algorithm to design the descriptor of image feature points based on locality preserving projections (LPP). The proposed algorithm can preserve invariability on the geometric structure: the eigenvectors which are neighboring each other in the original space will maintain the same attribute in low-dimensional space; on the contrary, the dissimilar eigenvectors become apart farther each other. Therefore, the description generated by their algorithm can show the interrelationship between features and has strong robustness. But it has disadvantage of complexity in calculation.

Similarity measure which indicates using some measurement to confirm the similarity among the features to match normally takes use of some kind of cost functions or distance functions. The classical similarity measure includes correlation function and Minkowski Distance [9]. Recently people take Hausdorff Distance [10], mutual information [11] as matching measurement. Hausdorff Distance has the advantage of high sensitive to noise. And fractional Hausdorff Distance can process covered target and outliers, but it costs long time in computing. The mutual information-based method has been widely used in matching medical images because of its insensitive to illumination changing, but it also has the shortcoming of complex computation and the images must have wide overlap region. The performance of the traditional matching
methods which are based on adding the differences of the pixels' gray value will be degraded by the difference of the gray value and the distortion between the template image and the target image. Clark F. Olson [12] proposed the maximum-likelihood estimation which can be used for both edge template matching and gray-level image matching. The literature [13] puts up a novel correlation matching method based on the Maximum Close Distance (MCD). In order to decrease the influence to image from noise and local shelter, a novel distance measurement which replaces the correlative value with a robust statistics' value is proposed. It computes the number of the similar points rather than the distance of the gray level of the template and target images. Consequently, the matching stability is improved greatly with lower complex operation and shorter matching time compared with the traditional grayscale similar matching. But it is hardly to match geometric deformation images, such as rotational images, using this measurement.

Based on MCD we put forward a novel way of histogram-based similar distance (HSD) in this paper; what’s more, we combine the ARPIH and HSD skilfully. The strength histogram constructed by ARPIH is regarded as an image, and then the similar grade of two histograms is computed to figure out the deformation image matching, such as rotation image, illumination changing image, perspective image and local shelter image.

II. LOCAL INVARIENT DESCRIPTOR

A. Local invariant area

Image matching based on the local invariant information needs to a local invariant image region after the image is changed in gray scales or rotation. The algorithm by K. Mikolajczyk and C. Schmid [14] can describe this invariant region as \( (x, y, scale, alpha) \), among them, \((x, y)\) is one point in the region; \(scale\) stands for gray scale of the point, and \(alpha\) is the location of the point [3].

B. ARPIH descriptor

The structure of ARPIH descriptor is showed in Fig.1. The image region is fractionalized into 18 sub-regions according to the method shows in figure 1(a). The angle \( \theta \) is \( \pi/3, 2\pi/3, 4\pi/3, 5\pi/3, 2\pi \) and the ratio of radius \( r \) is \( 0.57 : 0.85 : 1 \) which is chosen by experience. Thus the number of pixels in every sub-region is more less the same.

In Fig.1 (a) the number in the sub-region is serial number of the sub-region, the Fig.1 (c) is the ARPIH descriptor.

ARPIH descriptor is a three-dimension histogram which incarnates the pixel grayscale distribution in the image region and the geometry relationship between the sub-regions. The \( x \) axis of histogram is the serial number of sub-region, and \( y \) axis is grayscale \( (0 \sim 255) \) which is evenly divided into 18 gray ranges. Then the pixels in every sub-region are distributed into every gray range by its own grayscale. For example, in ARPIH descriptor, the axis \( H(11, 9) \) shows the number of the pixels whose grayscale is between \((115,129)\) in the 11th sub-region. By ARPIH descriptor we can transform the matching between two image regions into the matching between two histograms in order to reduce the computing complexity and improve the performances of anti-deformation.

![Fractionalization of the sub-region.](image1a)
![Described image region.](image1b)
![ARPIH descriptor.](image1c)

Figure 1. Structure of ARPIH descriptor
III. HSD

A. MAD

When matching two images, the similar relation of the corresponding points is the main question to take into account. So the similarity measure only considers the distance of the corresponding points in the two images, that is to say, their similar relations, instead of calculating all the point’s distance from one aggregate to another one. First, we calculate the similarity of every pairs of corresponding points in the image region, and then accumulate the similarity according to the minimum absolute difference to get the distance of two images.

Define the template image as \( S(m,n) \), its size is \( M \times N \), the target image as \( I(u,v) \), its size is \( U \times V \). The position of template image in the target image is \( (i,j) \), supposes \( S'(m,n) = I(i + m, j + n) \), \( d(i,j) \) denotes the distance function between the same size image windows, \( (i^*, j^*) \) denotes the optimal matching position, \( P \) is the matching range, and \( P \) is defined as follows:

\[
P = \{ (i, j) \mid 0 \leq i \leq U - M, 0 \leq j \leq V - N \}
\]

The distance measurement function based on traditional mean absolute difference algorithm (MAD) is defined as follows:

\[
d(i,j) = \frac{1}{MN} \sum_{m=1}^{M} \sum_{n=1}^{N} R_{MAD}(S(m,n),S'(m,n))
\]  

(2)

Where

\[
R_{MAD}(S(m,n),S'(m,n)) = \| S(m,n) - S'(m,n) \|
\]

(3)

The optimal matching position is

\[
d(i^*,j^*) = \min \{d(i,j) \mid (i,j) \in P \}
\]

(4)

In this algorithm, every point has the same contribution to matching result, so its performance is easily degraded by noise of specific points and local shelter.

B. Hausdorff Distance[10]

Given two finite point sets \( A = \{a_1,a_2,a_3,\ldots,a_p\} \) and \( B = \{b_1,b_2,b_3,\ldots,b_q\} \), the Hausdorff distance is defined as

\[
H(A,B) = \max \{ h(A,B), h(B,A) \}
\]

(5)

Where

\[
h(A,B) = \max_{a \in A} \min_{b \in B} \| a - b \|
\]

(6)

\[
h(B,A) = \max_{b \in B} \min_{a \in A} \| b - a \|
\]

(7)

And \( \| \cdot \| \) is Euclidean norm on the points of \( A \) and \( B \). The function \( h(A,B) \) is called the directed Hausdorff distance from \( A \) to \( B \). It identifies the point \( a \in A \) that is farthest from any point of \( B \) and measures the distance from \( a \) to its nearest neighbor in \( B \) (using the given norm \( \| \cdot \| \)), that is, \( h(A,B) \) in effect ranks each point of \( A \) based on its distance to the nearest point of \( B \) and then uses the largest ranked such point as the distance (the most mismatched point of \( A \)). Intuitively, if \( h(A,B) = d \) then each point of \( A \) must be within distance \( d \) of some point of \( B \), and there also is some point of \( A \) that is exactly distance \( d \) from the nearest point of \( B \) (the most mismatched point).

The Hausdorff distance \( H(A,B) \) is the maximum of \( h(A,B) \) and \( h(B,A) \). Thus, it measures the degree of mismatch between two sets by measuring the distance of the point of \( A \) that is farthest from any point of \( B \) and vice versa. Intuitively, if the Hausdorff distance is \( d \), then every point of \( A \) must be within a distance \( d \) of some point of \( B \) and vice versa. Thus, the notion of resemblance encoded by this distance is that each member of \( A \) be near some member of \( B \) and vice versa.

Unlike most methods of comparing shapes, there is no explicit pairing of points of \( A \) with points of \( B \) (for example, many points of \( A \) may be close to the same point of \( B \) ). The Hausdorff distance measures the mismatch between two sets that are at fixed positions with respect to one another.

C. MCD

Combining with the advantages and characters of the two measurements above, MCD is defined as follows in the literature [12]:

\[
d(i,j) = \sum_{m=1}^{M} \sum_{n=1}^{N} R_{MCD}(S(m,n),S'(m,n))
\]

(8)

Where

\[
R_{MCD}(S(m,n),S'(m,n)) = \begin{cases} 1 & \| S(m,n) - S'(m,n) \| \leq T \, \text{else} \end{cases}
\]

(9)

Where \( d(i,j) \) means similarity, so the optimal matching position is

\[
d(i^*, j^*) = \max \{d(i,j) \mid (i,j) \in P \}
\]

(10)

The difference between the two algorithms is that the former computes the sum of the entire pixel’s grayscale absolute difference, while latter one only computes the number of the similar points, so that the stability of the matching algorithm enhanced greatly. What’s more, in the correlation plane, the MAD needs to get the valley value, but the MCD needs to get the peak value, that is to say, the position of the most similarity. Thus when computing we only consider the similar point number between the template image and target image to measure the similarity degree, and at the same time it discards
those points that have more differences with the template, the local massive noise points will not influence the matching result. In a word this algorithm has advantages of traditional similarity matching because it avoids the disadvantage of the broad non-protruding peaks by noise.

However, this method is obviously still related with the location of the pixels, so that it can not figure out the matching problems of geometric deformations, such as rotation and perspective.

D. HSD

Based on the idea of MCD, we bring forward the definition of HSD.

Suppose there are two histograms with the same size $M \times N$, they are $H(m,n)$ and $H'(m,n)$. We consider the two histograms are similar when they can satisfy the following conditions:

$$D_{HSD} \geq T_1$$

$$D_{HSD} = \sum_{m=1}^{M} \sum_{n=1}^{N} R_{HSD}(H(m,n),H'(m,n))$$

$$R_{HSD}(H(m,n),H'(m,n)) = \begin{cases} 1, & |H(m,n) - H'(m,n)| \leq T_2 \\ 0, & \text{else} \end{cases}$$

Where, $T_1$ and $T_2$ are the threshold values which are pre-established. The values of $T_1$ and $T_2$ are established according to the radial value $r$ of the ARPIH descriptor, essentially, according to the sub-region area of the ARPIH descriptor.

HSD has the ability of transforming the matching between two plane images to the matching between two histograms. It calculates the number of the similar points between template histogram and target histogram in order to decrease the calculation complicity and improve the matching robustness.

This method not only preserves the advantage of insensitive to the massive noise points, but also decreases the calculation complexity, and increases the performance efficiency in matching.

IV. IMAGE MATCHING BASED ON ARPIH AND HSD

Because of the ARPIH descriptor is in depended to the pixel points’ position to a certain extent, it has the capacity of making up the shortcoming of MCD in unable to figure out the matching problems of geometric deformations, such as rotation and perspective.

Meanwhile, the HSD algorithm has the advantage of high performance efficiency and insensitive to the massive noise points.

According to the advantage of the two formers, that is to say the presented algorithm can figure out the noise pollution images and geometric deformation images, such as rotation, perspective and illumination changing images, and perform efficiently.

V. MATCHING STEPS

This matching algorithm is executed according to the following steps:

Step 1: transform the square template image into circle template image. Based on the well-known Bresenham method [15] for the discretization of a circle, we get a circle region of the square template image. The center of the circle is exactly the center of the template image, and the diameter value $d$ of the circle is the side length of the square template image.

Step 2: Fractionize the circle region mentioned above into 18 sub-regions according to the method shows in figure 1(a).

Step 3: Calculate the ARPIH descriptor of the template image.

Step 4: Repeat Step1, select the sub-region from the top left corner of the target image in the same size with the template image.

Step 5: Repeat Step2 and Step3 to acquire the ARPIH descriptor of the sub-region mentioned in Step 4.

Step 6: Match the two histogram and compute $D_{HSD}$, then save it into arrays and record the relevant position.

Step 7: Glide the template image on the target one, and search the next sub-region with the same size as template image, then get its ARPIH.

Step 8: Repeat step 6 and step 7 until to finish a whole scan for target image, the matching position is the area which has the maximal $D_{HSD}$.

Fig.2 shows the matching flow of the matching algorithm.

VI. RESULT AND DISCUSSION

In order to validate the robustness, superiority and validity performance of the matching algorithm we presented when the target images are deformations such as rotation, perspective, and illumination changing, we make experiments on 45 groups of images by using the two algorithm, the algorithm proposed in this paper and the MCD, to make a contrast, and each group have four images, original image, rotate by 15 ° clockwise image, perspective image and illumination changing image are included.

All the experiments are operated on the windows XP professional operation system. The processor frequency of the computer is 2.4 GHz, and the EMS memory capacity is 1GB. The test software is compiled and executed under the Matlab 7.0 (Release 14) environment. Close all the other software when executing the test software.

An example result by using standard Lena image as the target image is shown in Fig. 3 and Fig. 4. Fig. 3 shows the matching result gotten by the presented algorithm in
this paper, and Fig. 4 shows the matching result gotten by the MCD algorithm.

Figure 2. Flow chart

The image (a) in Fig. 3 is the circle template image which radius is 53, and the image (a) in Fig. 4 is the square template image which size is 53 × 53. The image (b) in Fig. 3 shows the division mode of the template image for calculating its ARPIH. The image (b) in Fig. 3 is the ARPIH of the template image. The image (d) in Fig. 3 and image (b) in Fig. 4 are the original target images which size is 256 × 256. Image (e) in Fig. 3 and image (c) in Fig. 4 are gotten by rotating the original image by 15° clockwise. Image (f) in Fig. 3 and image (d) in Fig. 4 are the perspective images from the original image. Image (g) in Fig. 3 and image (e) in Fig. 4 are gotten by enhancing the brightness of the original image.
Figure 3. Matching result using the presented algorithm

Figure 4. Matching result using the MCD algorithm
In Fig. 3, the black circle in image (b), (c), (d) and (e) denote the matching areas gotten by the proposed algorithm in this paper. The pixel points that are on the intersection of the “×” in the matching areas are just the corresponding points of the maximal $D_{MCD}$, which are the best matching positions, and they are also the center of the matching circle areas.

Fig. 4 shows the results by the way of MCD in contrast with the former. The black squares in image (b), (c), (d) and (e) denote the matching areas. The pixel points that are on the center of the matching square areas are just the corresponding points of the maximal $R_{MCD}$, which are the best matching positions.

In addition, to further demonstrate that the presented algorithm in this paper compared with the traditional algorithm has the advantage of robustness, superiority and validity in image matching, we make the Table I which shows the statistical and analysis of the 45 groups of experiment results working by the presented algorithm and the MCD algorithm.

We can get the following conclusions according to the analysis items shown in Table 1:

First, for matching no-deformation images (the original image), the presented algorithm in this paper has no special advantage comparing with the traditional MCD algorithm.

Second, for matching geometric deformation images such as perspective image, rotation image and illumination changing images, the presented algorithm in this paper performs obviously more excellent than the MCD algorithm.

Third, compared with the presented algorithm in this paper and the traditional MCD algorithm, the former one obviously cost less executing time than the latter one, that is to say, the presented algorithm in this paper has the higher executing efficiency and cost less system resources than MCD algorithm.

In a word, all the test results prove that the presented algorithm in this paper has better performance of anti-deformation, stability and efficiency than the traditional algorithm.

VII. CONCLUSION

This paper presents a novel image correlation matching algorithm based on ARPIH descriptor and HSD algorithm. This correlation matching algorithm transforms the matching between two images into the matching between two special histograms which are structured by the ARPIH. The presented algorithm in this paper is proved to be efficient and effective to figure out the deformation image matching, such as the rotation image, perspective image and illumination changing image. The performance efficiency of the presented algorithm is also proved in the paper.

Above all, we can draw the conclusion that the presented algorithm in this paper is effective, feasible, robustness and efficient.

REFERENCES


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Baoming Shan was born in 1974 in Dongying, China. He received the B.S. degree and M.S. degrees from Qingdao University of Science & Technology in 1996 and 1999, respectively. His research interest covers digital image processing and computer vision, adaptive control, intelligent control of industrial process.