A Fast Hausdorff Matching Algorithm between Infrared and Optical Image using PBIL Strategies

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Abstract—Aiming at the problem of low precision of traditional gray correlation matching and bad real-time feature of partial Hausdorff distance matching, a new image matching algorithm between Infrared and Optical Image based on Hausdorff distance and Population-based Increased Learning algorithm (PBIL) strategies is presented. Results of experiment show this algorithm is fast and has high accuracy in matching, and the convergence is very stable.

Keywords- Hausdorff distance; Infrared image; image matching; PBIL

I. INTRODUCTION

Multisensor image matching has become more and more important in target recognition systems. The existing methods use Optical image as a template and use Optical image or SAR image as real-time image. But, Optical imaging device and SAR device can not work all-weather, and infrared imaging equipment has many advantages, such as all-day working, good covert large detection range, powerful recognizing camouflage ability, large penetration range. Then it is a good method that using Optical image as a template and infrared image as real-time image. Because of the difference between Optical image and infrared image, it is difficult to get good matching performance using correlation-based technique in engineering application, which restricts application of this method.

Image edge is a basic feature, reflecting stable structure of images. Thus the edge can be used as feature for infrared and Optical image matching. The Hausdorff distance is a metric between point sets, can measure the similarity of two point sets. The Hausdorff distance is not based on finding corresponding mode and image points. Thus, it is more tolerant of perturbations in the location of points because it measures proximity rather than exact superposition. It has proven to be effective in object tracking and object recognition, when the image have noise or object partial shade\textsuperscript{[1-6]}.

However, the classified Hausdorff distance is extremely sensitive to outliers and sensitive to degradation such as noise and occlusions, and it is time-consuming because it considers every possible position within the test image. It is difficult to use in engineering application. So it is important to improve robustness of the classical Hausdorff distance and take effective searching strategy. In this paper, we propose a modified Hausdorff matching algorithm using PBIL strategy. Population-based Increased Learning algorithm\textsuperscript{[7]} integrate genetic search strategy based function optimization with competitive learning strategy, regard evolution as a learning process, revise the produce probability according to knowledge come from competitive learning, then produce the offspring according to the probability. The PBIL algorithm has strong robustness and Parallel searching ability, so it can achieve rapid convergence rate and satisfied result, which has applied to practical problems\textsuperscript{[8,11-13]}. Results of experiment show this approach is fast in computing, and has high accuracy in matching, and the convergence is very stable.

II. MODIFIED HAUSDORFF DISTANCE

A. Classical Hausdorff distance

The Hausdorff distance also is called max-min distance. The computation of the Hausdorff distance is a technique to measure the degree of similarity among different objects. Given sets \( A = \{a_1, a_2, \cdots, a_n\} \), \( B = \{b_1, b_2, \cdots, b_n\} \) the Hausdorff distance \( H(A,B) \) between A and B is defined as\textsuperscript{[4]}:

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

\[
h(A, B) = \max \{\min_{a \in A} d(a, b)\}
\]

\[
h(B, A) = \max \{\min_{b \in B} d(b, a)\}
\]

Where \( h(A,B), h(B,A) \) is called the directed Hausdorff distance from A to B or B to A and \( d(\cdot, \cdot) \) is a distance norm of A and B. We use the Euclidean distance. The distance is defined as:

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

The traditional Hausdorff distance calculating is easily, however, it would typically occur in the presence of occlusions, noise and image distortions. Huttenlocher proposed partial Hausdorff distance\textsuperscript{[9]}, Dubuisson and Jain...
proposed mean value Hausdorff distance\textsuperscript{[1]}. These modifications overcome the traditional shortcomings of Hausdorff distance, however, there are many different disadvantages in modified methods which affect the practical application\textsuperscript{[2]}. It may be fall into False match, once the image have pseudo edge or strong noise.

\section*{B. Modified Hausdorff distance}

The mean value can improve the efficiency of estimation, and it adapts to a Gaussian noise case. The partial operation can improve the robustness of estimation when the object is occluded or the images have pseudo edge. So we propose a new modified Hausdorff distance which combine partial Hausdorff distance and mean Hausdorff distance.

The new Hausdorff distance is defined as follows:

\[
    h(I, M) = \frac{1}{H} \sum_{i=1}^{N} \rho(d_B(a))
\]

Where \( H \) is number of edge pixels, \( H = \text{round}(f \times N), f \in [0, 1] \), and \( N \) is number of edge pixels of the test image. The cost \( \rho \) is a Symmetric convex function, has the only minimum at zero. \( \rho \) can be defined as:

\[
    \rho(x) = \begin{cases} 
    0 & |x| \leq \tau \\
    \tau & |x| > \tau 
    \end{cases}
\]

where \( \tau \) is a threshold to eliminate outliers, so the outliers which yield large errors are discarded.

The new Hausdorff distance, which can reduce the sensitivity to noise and occlusion, make the matching more robust than the classical three Hausdorff distance.

\section*{III. PBIL Algorithm}

PBIL is a probability learning algorithm based on evolutionary strategy which takes evolution as a learning process. The population of solutions is produced according to the probability matrix which is initialized as equal for all gene positions. Under the direction of the evaluation and analysis to solutions, learning probability is updated and the optimal one is copied to next generation.

A simple and universal procedure of the PBIL algorithm is given as follows:

- Initialize probability vector;
- While (Not termination condition)
  - Produce the population of solutions according to probability vector;
  - Evaluate the population;
  - Acquire knowledge from best individual of the population;
  - Update the probability vector according to the knowledge;
- Output the solution;

\section*{IV. Matching Algorithm}

We develop an algorithm based on new modified Hausdorff distance and PBIL. Canny edge detector is the optimal edge detection algorithm, so we adopt Canny edge detector as the edge detector.

The traditional Full Search algorithm compute similarity at every position in the search area. Since there is only one optimal matching position, so most of the matching is computed at the Non-optimal position. The data and time required in the matching is large enough to real-time matching application. So we improve the efficiency by modified PBIL algorithm, which avoid full searching, and accelerate the matching speed.

The encoding length of problem is assigned as \( n \), \( s \) is the \( i \) position of the encoding, also named gene bit. Each gene bit position may be 0 or 1. So the problem can be defined as:

\[
    \min f(s)
\]

We define \( p \) as learning probability: \( p_i (1 \leq i \leq n) \) denotes the probability of the gene position chooses the 1.

The reference image is Optical image, and the real-time image is infrared. Template is chosen form the real-time image. We encode the position \((i, j)\) to be matched with two 16 bit binary string. We connect the two genes, then the individual solution’s length is 32 bit. The objective function is above modified Hausdorff distance. The Solution is the optimal matching position. The algorithm is described as follows:

\textbf{Step1:} Initialize probability \( p: p_i = 0.5 \; ; \; i=1,2,…32; \)

\textbf{Step2:} Produce initial solution population with the Pop\_size according to probability \( p \), the initial solution population should exit throughout the whole image.

\textbf{Step3:} Evaluate each solution and obtain the optimal one

\[
    B = [b_1, b_2, \ldots, b_{32}]
\]

\textbf{Step4:} Update the probability based on the best individual,

\[
    p_i = p_i + (b_i - p_i) \times \epsilon \; ; \; i=1,2,…32; \; \epsilon \; \text{is the revising probability coefficient called evolution operator}
\]

\textbf{Step5:} Produce solution population with the Pop\_size-1, and the optimal one is copied to next generation.

\textbf{Step6:} Search the 3×3 field around the optimal one with Greedy algorithm.

\textbf{Step7:} Output the optimal solution if termination criterion is met then stops; otherwise jump to step 3

The algorithm adopts Elite Strategies at step 5, copy the optimal population to next generation, which avoid destroying the optimal population. The algorithm adopt Greedy algorithm to search the 3×3 field around the optimal population at step 6, which can find better population. The two strategies not only enlarge the search field, but also insure the global convergence.
V. EXPERIMENTAL ANALYSIS

We chose a 734 × 473 Optical image as base image, and chose a 68 × 56 template from the infrared image of the same scene. Figure 1 is base image. Figure 2 is the template. Figure 3 is the matching result. Algorithm is implemented on a standard PC (2.0 G Pentium IV) using a MATLAB implementation of the algorithm.

Results of different parameters are compared, and The proposed algorithm is also compared with the traditional FS algorithm.

A. Parameter Setting

The algorithm is affected by population size, revising probability coefficient $\varepsilon$. So we make parameter setting test to get proper parameters.

The algorithm is evaluated by accuracy frequency. We test the algorithm 50 times using different population size and revising probability coefficient $\varepsilon$. First, the population size is test by set revising probability coefficient $\varepsilon$ to 0.02, termination iteration number is set to 100. Then we get the optimal revising probability coefficient according to above identified population size. Figure 4 shows the performance of the different population size. Figure 5 shows the performance of different revising probability coefficient. The experimental results show that algorithm is not sensitive to population size (over 50), but larger population will increase the computing time. The probability coefficient has greater impact on performance, for this problem, the better probability coefficient is 0.05.

B. Termination criterion and convergence

Information entropy, termination probability and the largest number of iteration are applied here as termination criterion. Entropy is used to reflect the consistence of system information. At the end of the evolution it should be 0 or close to 0 at least. The formula is as follows:

$$S_{\text{entropy}} = - \sum_{i=1}^{n} \sum_{j=1}^{m} P_{ij} \ln P_{ij} \quad (9)$$

Termination probability means that all the gene position values are bigger than a positive number close to 1. The two termination criterions can reflect the convergence of the algorithm to control iteration number and computing time.

We test algorithm using above termination probability and the largest number of iteration separately. The population size is 50 and probability coefficient is 0.02, and entropy is set 0.001, termination probability is 0.99, number of largest iteration is 100. Table 1 shows the computing time at every termination criterion. We record the average objective function values of 50 population every iteration according to above parameters, Figure 6 shows the
evolutionary trend. We can see that the proposed algorithm has rapid Evolutionary rate and better Convergence performance.

Tab 1 performance of different termination criterion

<table>
<thead>
<tr>
<th>Termination criterion</th>
<th>Average time (s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Iteration number (100)</td>
<td>0.91</td>
</tr>
<tr>
<td>Termination probability (0.99)</td>
<td>1.24</td>
</tr>
<tr>
<td>Entropy (0.001)</td>
<td>1.86</td>
</tr>
</tbody>
</table>

C. Compared with FS

We also compared our algorithm with traditional full searching algorithm. In the experiment, the population size is 50, probability coefficient is 0.02, and number of largest iteration is 80. Table 2 shows the result. We can see that PBIL algorithm get the similar accuracy as FS algorithm, but the time cost is just 1/20 of FS.

Fig.6 Evolutionary trend

Tab 2 Compared PBIL with FS

<table>
<thead>
<tr>
<th>Algorithm</th>
<th>FS</th>
<th>PBIL</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of test</td>
<td>50</td>
<td>50</td>
</tr>
<tr>
<td>$t_{max}$/s</td>
<td>16.321</td>
<td>0.811</td>
</tr>
<tr>
<td>$t_{min}$/s</td>
<td>15.963</td>
<td>0.731</td>
</tr>
<tr>
<td>$t_{av}$/s</td>
<td>16.126</td>
<td>0.765</td>
</tr>
<tr>
<td>accuracy</td>
<td>49</td>
<td>48</td>
</tr>
<tr>
<td>accuracy/%</td>
<td>98</td>
<td>96</td>
</tr>
</tbody>
</table>

The experimental results show that, the proposed algorithm give Good solution of the image matching problem. The algorithm can get the optimal result quickly at the appropriate parameters.

VI. CONCLUSION

In this paper, we have proposed an infrared and Optical image matching algorithm using Hausdorff distance and Population-based Increased Learning algorithm. Results of experiment show this algorithm is fast and has high accuracy in matching, and the convergence is very stable. We also compared our algorithm with traditional full searching algorithm. The experimental results show our algorithm has good performance at speed and accuracy. So it is important to combine Hausdorff distance with PBIL algorithm for image matching.

VII. REFERENCES