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AUTOMATIC THRESHOLDING FOR CORRESPONDENCE DETECTION

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We study the problem of thresholding the residual of template matching as a preprocess for selecting the correct matches between feature points in two images. In order to determine the threshold dynamically, we introduce a statistical model of the residual and compute an optimal threshold according to that model. The model parameters are estimated from the histogram of the residuals of candidate matches. Using real images, we show that our method can substantially upgrade the quality of the initial matches by simply adjusting the threshold.

Keywords: Template matching; image matching; feature point correspondence; correspondence detection; automatic thresholding.

1. Introduction

Establishing point correspondences over multiple images is the first step of many video processing applications. Two approaches exist for this purpose: tracking correspondences over successive frames, and direct matching between separate frames. This paper focuses on the latter.

The basic principle is local correlation measurement by template matching. Detecting feature points in the first and second images separately using a corner detector,[2,4,8,10,11] we measure the correlation between the neighborhoods of the two points for each candidate pair and match those that have a high correlation.

To do so, we need to set an appropriate threshold for distinguishing the correct matches from the incorrect ones. This problem has not been considered fully in the past, chiefly because template matching alone is insufficient for establishing point correspondences; an outlier removal technique based on voting, such as LMedS[9] and RANSAC,[3] needs to be applied thereafter. The thresholding task is usually passed on to the outlier removal stage.[1,12]

However, most outlier removal techniques do not work if the outlier ratio is as high as 50%. Hence, setting a good threshold at the template matching stage for removing incorrect matches is essential for the subsequent outlier removal procedure to be effective. If the threshold is too high, however, a lot of correct matches will be lost, which will reduce the number of final matches, making subsequent computations less reliable. Hence, we need a good balance between removing incorrect matches and retaining correct ones.

This paper presents an optimal thresholding method based on a statistical analysis. We introduce a parametric model of the template matching residual and compute an optimal threshold according to that model. The model parameters are estimated from the histogram of the residuals of the candidate matches. Since only the threshold is adjusted, our method should not be regarded as a stand-alone matching scheme. Rather, it is intended as a preprocess for subsequent outlier removal procedures. Using real images, we show that our method can substantially upgrade the quality of the initial matches by simply adjusting the threshold.

2. Template Matching

After feature points are detected from the two images using a corner detector, the similarity between point P in the first image and point Q in the second is measured by the following *residual* (*sum of squares*):

$$J(P,Q) = \sum_{(i,j)\in\mathcal{N}} |T_P(i,j) - T_Q(i,j)|^2 \,, \tag{1}$$

where $T_P(i,j)$ and $T_Q(i,j)$ are the intensity values of the templates obtained by cutting out an $n \times n$ pixel region $\mathcal{N}$ from around P and Q. If we normalize them to $\sum_{(i,j)\in\mathcal{N}} T_P(i,j)^2 = 1$ and $\sum_{(i,j)\in\mathcal{N}} T_Q(i,j)^2 = 1$, Eq. (1) is equivalent to the use of the *normalized correlation.*

Basically, each point P in the first image is matched to the point Q in the second for which $J(P,Q)$ is the smallest, but overlaps and conflicts must be resolved. So, we apply the following uniqueness enforcing procedure. We first choose the pair (P,Q) that has the smallest residual $J(P,Q)$. Then, we remove from among the candidate pairs those that involve P and Q. From the remaining pairs, we choose the pair (P',Q') that has the smallest residual $J(P',Q')$. We repeat this procedure until all pairs are exhausted.

3. Thresholding the Residual

If the above uniqueness enforcing procedure is applied to all the pairs, we may match those points for which no counterparts exist. So, we need to remove beforehand those pairs for which the residual is very large. For this, the threshold is usually set empirically.[1,12] For example, Zhang *et al.*[12] accepted those pairs for which the normalized correlation is larger than 0.8.

However, the threshold cannot be fixed, because the residual $J(P, Q)$ is determined not only by the image intensity fluctuations but also by the relative distortion of the two images. For example, if rotation and scale change exist between the two images, the residual $J(P, Q)$ is not zero even when no image noise exists. It follows that the threshold should depend on the magnitude of the rotation and scale change, which is unknown and different from image to image.

Our strategy is that we introduce a statistical model of the residual and compute an optimal threshold according to that model. The model parameters are estimated from the histogram of the residual. In the following, we assume that rotation and scale change may exist to a certain unknown degree between the two images but not to such an extent that local correlations between matching points are completely lost; in that case, template matching should not be used in the first place.

4. Statistical Model of the Residual

If the match (P, Q) is correct, the image intensity difference

$$\Delta T_{ij} = T_P(i,j) - T_Q(i,j) \tag{2}$$

in Eq. (1) is due to the relative distortion in the neighborhoods of P and Q, as well as small fluctuations of image intensity. We model such randomness by a Gaussian distribution of mean 0 and standard deviation σ_0. Then, J/σ_0^2 for a correct match should be subjected to a χ^2 distribution with n^2 degrees of freedom, provided that the intensity difference is independent of the pixel (n is the template size).

If the match (P, Q) is incorrect, the difference ΔT_{ij} is due to the inhomogeneity of the intensity within the image of that scene. We assume that ΔT_{ij} is subjected to a Gaussian distribution of mean 0 and standard deviation σ_1. Then, J/σ_1^2 for an incorrect match should be subjected to a χ^2 distribution with n^2 degrees of freedom, provided that the intensity difference is independent of the pixel.

Let $f_0(J)$ be the probability density of the residual J for correct matches, and $f_1(J)$ for incorrect ones. According to the above model, we have

$$f_0(J) = \frac{1}{\sigma_0^2}\,\phi_{n^2}\left(\frac{J}{\sigma_0^2}\right), \quad f_1(J) = \frac{1}{\sigma_1^2}\,\phi_{n^2}\left(\frac{J}{\sigma_1^2}\right), \tag{3}$$

where $\phi_d(x)$ denotes the probability density of the χ^2 distribution with d degrees of freedom. It has the form

$$\phi_d(x) = \frac{e^{-x/2}x^{d/2-1}}{2^{d/2}\Gamma(d/2)}, \tag{4}$$

where $\Gamma(x)$ is the Gamma function. This distribution has expectation d and variance $2d$.

5. Effective Template Size

The assumption that the image intensity difference is independent of the pixel is not realistic. However, exact modeling of this correlation is difficult, so we introduce the following approximation.

If there are N points in the first image and M points in the second, the number of correct matches is at most $\min(N, M)$, which is much smaller than the number NM of all possible pairs. Since most of the matches are incorrect, the probability density of the residual J for all the matches is approximately $f_1(J)$, which has an expectation of $n^2\sigma_1^2$ and a variance of $2n^2\sigma_1^4$. It follows that if we compute the mean μ_J and the variance σ_J^2 of J from the histogram of J, we should have

$$\mu_J \approx n^2\sigma_1^2\,, \quad \sigma_J^2 \approx 2n^2\sigma_1^4\,, \tag{5}$$

provided that each pixel value is independent. Eliminating σ_1 from these, we obtain $n^2 \approx 2\mu_J^2/\sigma_J^2$. However, n^2 should be much smaller than this due to correlations. So, we define the *effective template size* by

$$n = \frac{\sqrt{2}\mu_J}{\sigma_J}\,. \tag{6}$$

In other words, we regard each pixel value as if independent within the template of this size, which need not be an integer.

6. Model Parameter Estimation

Let p and $q\,(= 1 - p)$ be the fractions of the correct and incorrect matches, respectively. The probability density of the residual J for all the matches is

$$f(J) = pf_0(J) + qf_1(J) = \frac{J^{n^2/2-1}}{2^{n^2/2}\Gamma(n^2/2)}\left(\frac{pe^{-J/2\sigma_0^2}}{\sigma_0^{n^2}} + \frac{qe^{-J/2\sigma_1^2}}{\sigma_1^{n^2}}\right). \tag{7}$$

We determine the model parameters σ_0 and σ_1 by a maximum likelihood estimation. Let $J_1 \leq J_2 \leq \cdots \leq J_{NM}$ be all the NM residual values sorted in ascending order. From Eq. (7), their likelihood is

$$\prod_{i=1}^{NM} f(J_i) = \frac{\prod_{i=1}^{NM} J_i^{n^2/2-1}}{2^{n^2NM/2}\Gamma(n^2/2)^{NM}} \prod_{i=1}^{NM}\left(\frac{pe^{-J_i/2\sigma_0^2}}{\sigma_0^{n^2}} + \frac{qe^{-J_i/2\sigma_1^2}}{\sigma_1^{n^2}}\right). \tag{8}$$

Differentiating the logarithm of this with respect to σ_0^2 and σ_1^2 and letting the results be zero, we obtain

$$\sigma_0^2 = \frac{\sum_{i=1}^{NM} A_iJ_i}{n^2\sum_{i=1}^{NM} A_i}\,, \quad \sigma_1^2 = \frac{\sum_{i=1}^{NM} B_iJ_i}{n^2\sum_{i=1}^{NM} B_i}\,, \tag{9}$$

where we define

$$A_i = \frac{1}{1 + \frac{q}{p}(\frac{\sigma_0}{\sigma_1})^{n^2} e^{\frac{J_i}{2}(\frac{1}{\sigma_0^2} - \frac{1}{\sigma_1^2})}}\,, \quad B_i = \frac{1}{1 + \frac{p}{q}(\frac{\sigma_1}{\sigma_0})^{n^2} e^{\frac{J_i}{2}(\frac{1}{\sigma_1^2} - \frac{1}{\sigma_0^2})}}\,. \tag{10}$$

The values of σ_0 and σ_1 are obtained by iterations: guessing the initial values to be, for example,

$$\sigma_0 = \sqrt{\frac{\sum_{i=1}^{\lfloor pNM \rfloor} J_i}{n^2 \lfloor pNM \rfloor}}\,, \quad \sigma_1 = \frac{\sigma_J}{\sqrt{2\mu_J}}\,, \tag{11}$$

and substituting them into the right-hand sides of Eqs. (9), we obtain their updated values. This process is repeated until σ_0 and σ_1 converge. The first of Eqs. (11) is the value of σ_0 we would have if the $\lfloor pNM \rfloor$ matches with the smallest residuals were all correct. The second of Eqs. (11) is obtained by eliminating n^2 from Eqs. (5).

The fractions p and $q\,(= 1 - p)$ are set empirically. Since the number of correct matches between N points and M points is at most $\min(N, M)$, we let $p_{\max} = \min(N, M)/NM$ and set, for example, $p = 0.6p_{\max}$ if no knowledge is available about the correctness of the matches. The estimate of p need not be precise, as we will show later.

7. Detection Ratio Versus Inlier Ratio

Suppose we set a threshold J_c for the residual J and accept those matches with $J \leq J_c$ as correct. Let α be the ratio of the accepted correct matches among all the correct ones; we call it the *detection ratio.* A correct match with residual J is accepted with the probability

$$\alpha = P_0[J < J_c] = P_0\left[\frac{J}{\sigma_0^2} < \frac{J_c}{\sigma_0^2}\right], \tag{12}$$

where $P_0[\,\cdot\,]$ denotes the probability for correct matches. Let $\chi^2_{n^2}(\alpha)$ be the αth percentile of the χ^2 distribution with n^2 degrees of freedom. Since J/σ_0^2 for a correct match should be subjected to a χ^2 distribution with n^2 degrees of freedom, Eq. (12) implies that J_c/σ_0^2 equals $\chi^2_{n^2}(\alpha)$. Hence, the threshold J_c is given by

$$J_c = \sigma_0^2 \chi^2_{n^2}(\alpha)\,. \tag{13}$$

Some incorrect matches are necessarily accepted by this thresholding. An incorrect match with residual J is accepted with the probability

$$\gamma = P_1[J \leq J_c] = P_1\left[\frac{J}{\sigma_1^2} \leq \left(\frac{\sigma_0}{\sigma_1}\right)^2 \chi^2_{n^2}(\alpha)\right], \tag{14}$$

where $P_1[\,\cdot\,]$ denotes the probability for incorrect matches. Let $\Phi_{n^2}(X)\,(= \int_0^X \phi_{n^2}(x)dx)$ be the accumulated probability function of the χ^2 distribution with n^2 degrees of freedom. Since J/σ_1^2 for an incorrect match should be subjected to a χ^2 distribution with n^2 degrees of freedom, Eq. (14) implies

$$\gamma = \Phi_{n^2}\left(\left(\frac{\sigma_0}{\sigma_1}\right)^2 \chi^2_{n^2}(\alpha)\right). \tag{15}$$

Among the NM possible matches, the numbers of correct and incorrect matches are pNM and qNM, respectively. After the thresholding, we obtain αpNM correct

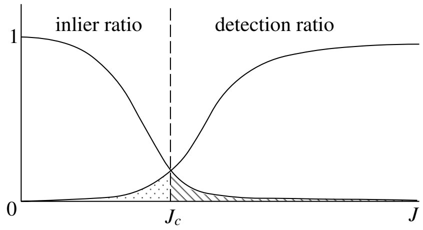


Fig. 1. Determining the threshold that balances the inlier ratio and the detection ratio.

matches and γqMN incorrect ones on average. Hence, the *inlier ratio*, i.e. the ratio of correct matches among the accepted matches, is approximately

$$\beta = \frac{\alpha pNM}{\alpha pNM + \gamma qMN} = \frac{\alpha p}{\alpha p + \gamma q}\,. \tag{16}$$

8. Threshold Selection

The threshold J_c is determined by the detection ratio α in the form of Eq. (13), but how should we set α? It should be large if we want to collect many correct matches, but the number of incorrect matches also increases, lowering the inlier ratio β as a result.

Here, we determine the threshold J_c so that the detection ratio α *equals* the inlier ratio β. This balances the probability $1-\alpha$ of rejecting correct matches and the probability $1-\beta$ of accepting incorrect ones (Fig. 1). Substituting Eq. (16) into Eq. (15) and letting $\beta = \alpha$, we obtain

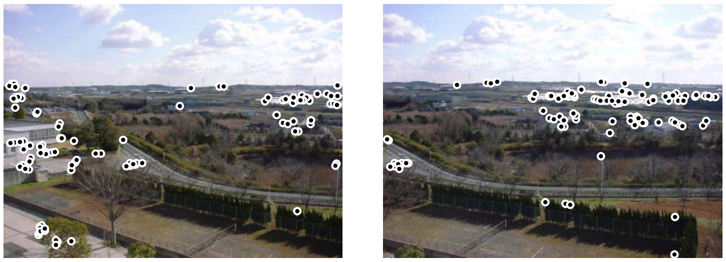
$$\alpha = 1 - \frac{q}{p}\,\Phi_{n^2}\left(\left(\frac{\sigma_0}{\sigma_1}\right)^2 \chi^2_{n^2}(\alpha)\right), \tag{17}$$

from which α is obtained by Newton iterations.

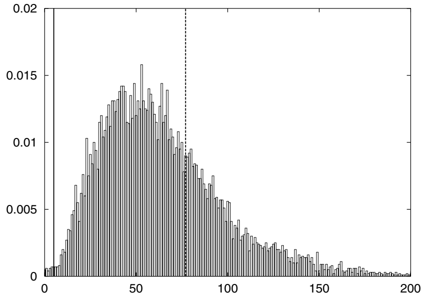
9. Real Image Examples

Figures 2(a) and (b) show two real images of a distant scene. We detected 100 feature points from each image using the Harris operator,[4] as marked there. Figure 2(c) is the histogram of the residuals of a 9×9 template for all candidate matches. Letting $p/p_{\max} = 0.6$, we estimated the effective template size n, the model parameters σ_0 and σ_1, and the optimal detection ratio α (= the inlier ratio β) as listed in Fig. 2(d). We see that n is much smaller than the actual size 9 due to correlations. The density $f(J)$ of the residual J estimated by Eq. (7) is superimposed onto the histogram in Fig. 2(c). The estimated density agrees with the histogram very well.

Figures 2(e) and (f) superimpose the densities $f_0(J)$ and $f_1(J)$ of correct and incorrect matches estimated by Eqs. (3) onto the histograms of correct and incorrect matches, separately. Here, we checked the correctness of the matches as follows.



(a) (b)



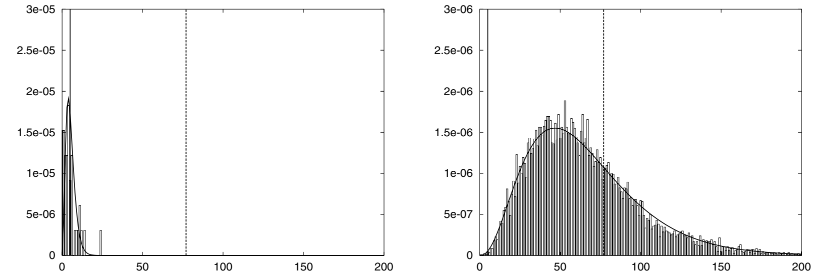
(c)

$n = 2.65$ (pixels)

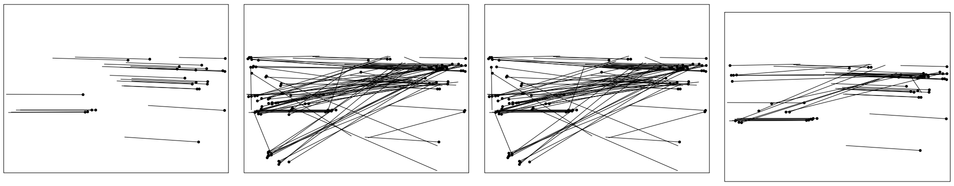
$\sigma_0 = 61.4$, $\sigma_1 = 280.1$, $\alpha = \beta = 87.8(\%)$

	Detection Ratio	Inlier Ratio
Proposed Thresholding	59.0	95.3
No Thresholding	87.2	34.0
Otsu Criterion	87.2	36.6
Zhang *et al.*	87.2	36.6

(d)



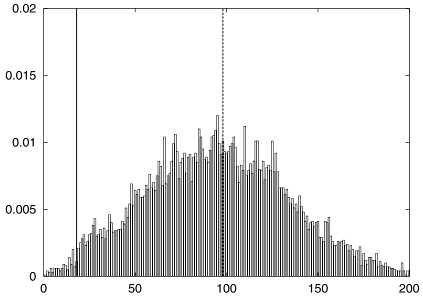
(e) (f)



(g) (h) (i) (j)

Fig. 2. (a), (b) Input images and detected feature points. (c) The residual histogram of all the matches. (d) The model parameters, the detection ratio (%), and the inlier ratio (%). (e) The residual histogram of correct matches and their estimated density. (f) The residual histogram of incorrect matches and their estimated density. (g) Matches resulting from the proposed thresholding. (h) Matches without thresholding. (i) Matches resulting from the Otsu thresholding. (j) Matches resulting from the method of Zhang *et al.* The vertical solid lines in (c), (e), and (f) indicate the threshold determined from the computed detection ratio α. The vertical dotted lines indicate thresholds obtained by the Otsu criterion.

(a) (b)



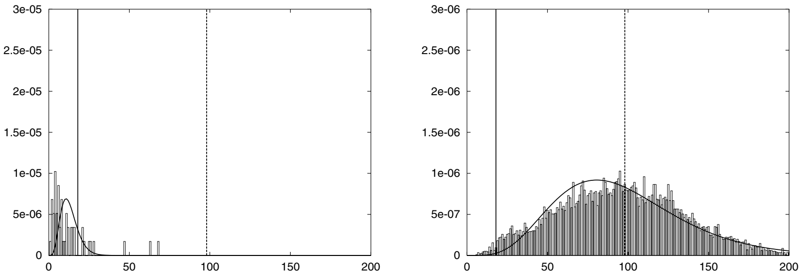
(c)

$n = 3.44$ (pixels)

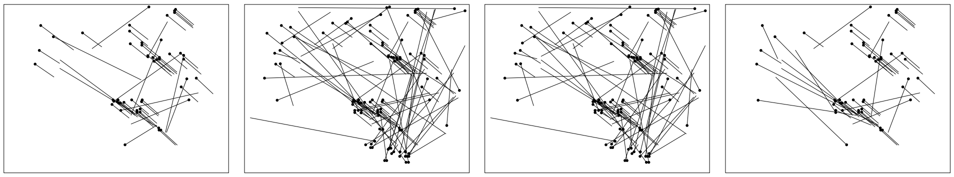
$\sigma_0 = 118.9$, $\sigma_1 = 311.6$, $\alpha = \beta = 79.1(\%)$

	Detection Ratio	Inlier Ratio
Proposed Thresholding	74.0	72.5
No Thresholding	86.0	43.0
Otsu Criterion	86.0	44.8
Zhang *et al.*	72.1	69.2

(d)

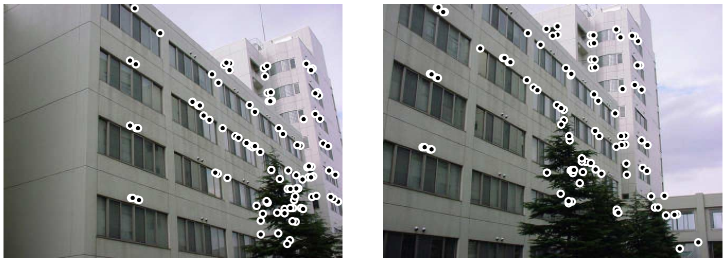


(e) (f)

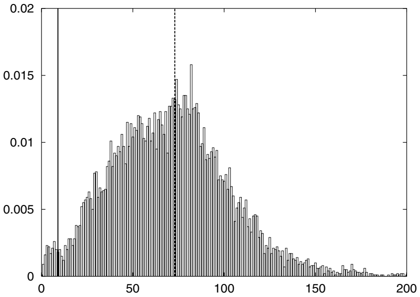


(g) (h) (i) (j)

Fig. 3. (a), (b) Input images and detected feature points. (c) The residual histogram of all the matches. (d) The model parameters, the detection ratio (%), and the inlier ratio (%). (e) The residual histogram of correct matches and their estimated density. (f) The residual histogram of incorrect matches and their estimated density. (g) Matches resulting from the proposed thresholding. (h) Matches without thresholding. (i) Matches resulting from the Otsu thresholding. (j) Matches resulting from the method of Zhang *et al.* The vertical solid lines in (c), (e), and (f) indicate the threshold determined from the computed detection ratio α. The vertical dotted lines indicate thresholds obtained by the Otsu criterion.



(a) (b)



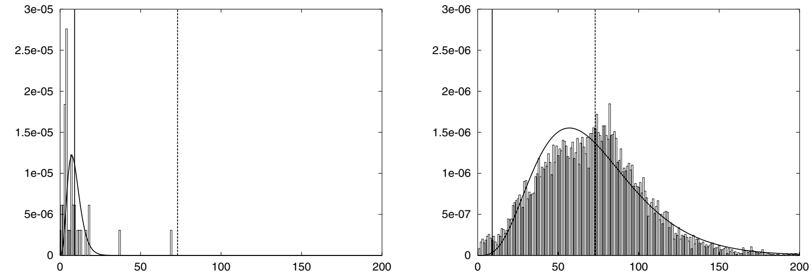
(c)

$n = 3.09$ (pixels)

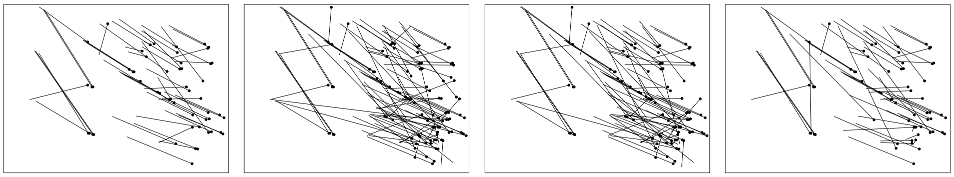
$\sigma_0 = 71.7$, $\sigma_1 = 255.6$, $\alpha = \beta = 89.5(\%)$

	Detection Ratio	Inlier Ratio
Proposed Thresholding	39.5	28.3
No Thresholding	39.5	15.0
Otsu Criterion	39.5	16.1
Zhang *et al.*	34.2	21.3

(d)



(e) (f)



(g) (h) (i) (j)

Fig. 4. (a), (b) Input images and detected feature points. (c) The residual histogram of all the matches. (d) The model parameters, the detection ratio (%), and the inlier ratio (%). (e) The residual histogram of correct matches and their estimated density. (f) The residual histogram of incorrect matches and their estimated density. (g) Matches resulting from the proposed thresholding. (h) Matches without thresholding. (i) Matches resulting from the Otsu thresholding. (j) Matches resulting from the method of Zhang *et al.* The vertical solid lines in (c), (e), and (f) indicate the threshold determined from the computed detection ratio α. The vertical dotted lines indicate thresholds obtained by the Otsu criterion.

Since two images of a distant scene are related by a *homography*, we optimally computed the homography $\mathcal{H}$ by *renormalization*[a] [5] from a large number of corresponding points selected by hand. For each candidate match (P, Q), we mapped the point P to the second image by the computed homography $\mathcal{H}$ and judged the match as correct if the point Q is within three pixels from its ideal position $\mathcal{H}P$. The result agrees very well with our prediction.

The vertical solid lines in Figs. 2(c), (e) and (f) indicate the computed threshold J_c. A well known scheme for automatic thresholding is the *Otsu discrimination criterion.*[7] The vertical dotted lines in Figs. 2(c), (e) and (f) indicate the corresponding threshold.

Figure 2(g) shows the final matches obtained by applying the computed threshold J_c followed by the uniqueness enforcing procedure; they are displayed as "optical flow" (line segments connecting the matching positions). For comparison, Fig. 2(h) shows the result without thresholding; Fig. 2(i) is the result using the Otsu criterion; Fig. 2(j) is the result thresholded by the normalized correlation 0.8 according to Zhang *et al.*[12] The actual detection ratio α and the inlier ratio β for these results are listed in Fig. 2(d).

We can see that without thresholding we can collect many correct matches but we also pick out many incorrect ones. As a result, the inlier ratio significantly drops. Our thresholding scheme balances the conflicting goals of collecting as many correct matches as possible and rejecting as many outliers as possible. The Otsu criterion shows little effect. The method of Zhang *et al.*[12] gives an intermediate result between the Otsu criterion and our method.

Figures 3 and 4 show other examples with corresponding results, and we can observe similar effects. From these, we can confirm that our method substantially upgrades the quality of the matches by simply adjusting the threshold.

10. Validation of Our Model

From the above experiments, we can see that the residual distribution of correct matches is included in the residual distribution of incorrect matches to a large extent with a long tail (Fig. 5). Therefore, if we want to pick out a large number of correct matches, we need a high threshold, which inevitably accepts many incorrect matches. Our analysis determines an optimal threshold by analyzing the distribution shapes. In this paper, we approximated the distributions by the χ^2 distribution density, adjusting the effective template size n and the parameters σ_0 and σ_1. As long as the approximation is good, the underlying statistical hypotheses (independent Gaussian distributions, etc.) are not so very essential.

Theoretically, the fraction p of correct matches could be estimated from the histogram, using the EM-algorithm, for example. Most often, however, we would end

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[a] The program is available from `http://www.ail.cs.gunma-u.ac.jp/Labo/programs-e.html`.

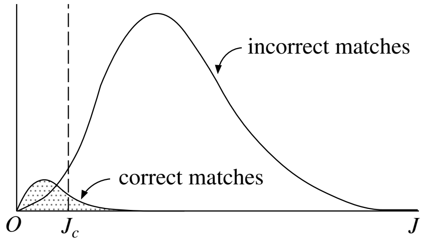

Fig. 5. The residual distribution of correct matches is included in the residual distribution of incorrect matches to a large extent.

up concluding that all matches are incorrect, because interpretation is statistically very likely. This is unavoidable unless we impose the constraint that a certain fraction of matches should be correct. This is the reason why we introduced the fraction p heuristically, rather than estimating it from the histogram.

We set the ratio $p/p_{\max}$ to 0.6, but this value need not be precise. Figure 6 shows the final results for $p/p_{\max} = 0.4, 0.6, 0.8, 1.0$ for the images in Figs. 2, 3 and 4, and the results are not so different, as we can see. Hence, we may safely set $p/p_{\max}$ to be around 0.6 if no prior information is given.

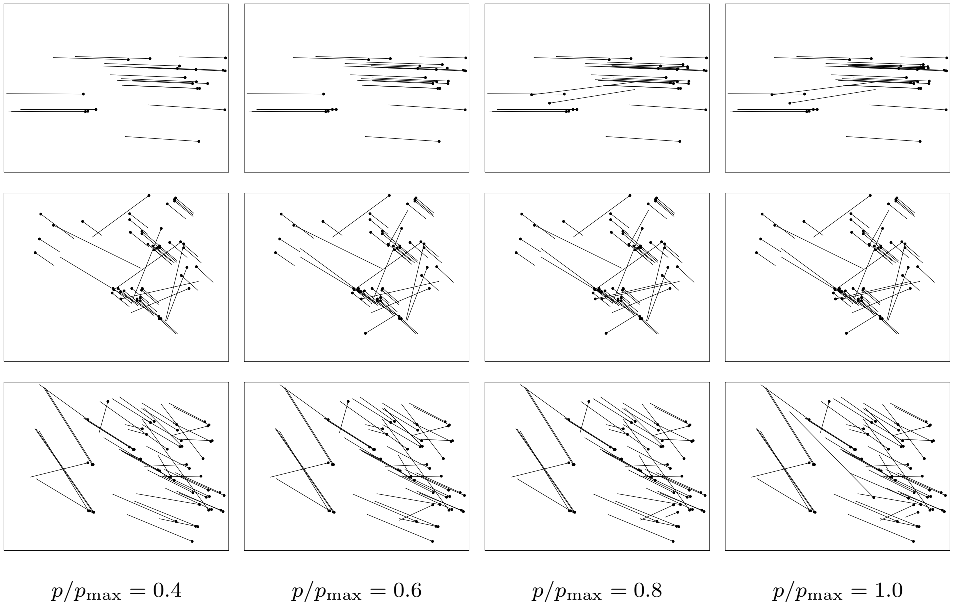

Fig. 6. Matches resulting from different estimates of the fraction p of correct matches for the images in Figs. 2, 3 and 4 (from above).

11. Conclusion

We have studied the problem of thresholding the residual of template matching for selecting correct matches between feature points detected in two separate images. We dynamically determined the threshold by introducing a statistical model of the residual and computed an optimal threshold according to that model. The model parameters were estimated from the histogram of the residual of candidate matches.

Since only the threshold is adjusted, our method alone cannot establish exact matches. Rather, it should be regarded as a preprocess for outlier removal based on voting. Using real images, we have shown that our method can substantially upgrade the quality of initial matches by simply adjusting the threshold. It has been confirmed that our method is very effective as a preprocess for automatic image mosaicing generation using LMedS[9] and RANSAC,[3] as demonstrated in Ref. 6.

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