Rejecting Outliers Based on Correspondence Manifold

Finding reliable corresponding points between two images is a fundamental problem in computer vision. For given images, correspondence points are the projections of the same point in the scene. Many of the computer vision algorithms rely on the success of finding corresponding points between two images\cite{1-2}, for example, stereo vision, image registration, motion analysis, object recognition, etc. We focus on removing outliers from putative correspondences. Putative correspondences are usually established by matching the interest points with local information, for example, the intensity in a small region around the interest points or some kind of local descriptor\cite{3-4}. However, usually a large proportion of the putative correspondences are outliers because of the viewpoint change, occlusion, local ambiguousness, etc. And the outliers are usually enough to ruin the traditional estimation methods. Therefore, much of the endeavor in computer vision community is to overcome or alleviate this problem by rejecting the outliers directly before estimating, or by firstly resorting to some robust estimator tolerating the possible presence of outliers for a coarse estimation of the model parameters and then, identifying the outliers based on the coarse estimation. Recently, the researchers are paying more and more attention to outlier removing, especially with the development of $L_\infty$ vision framework\cite{5-6}.

This paper propose a novel scheme to reject outliers, which is independent of the model to be estimated and overcomes the following limitations of the available methods in published works:

1) Efficiency sharply goes down with the increase of outlier percentage;
2) Efficiency decreases dramatically with the increase of the number of estimated model parameters;
3) Outlier rejecting is coupled with model selection and model estimation.

The remainder of this paper is organized as follows. In the next section, the related work on outlier rejecting will be briefly reviewed and analyzed. Section 2 introduces correspondence manifold and its upward view. Section 3 presents our proposed scheme for outlier rejecting: firstly gives a learning method for correspondence view by a novel group diagnostic technique, and then, introduces an outlier rejecting method by statistical inference technique based on the estimated correspondence view. After discussing three issues on implementation in Sections 4 and 5, we demonstrate the performance of our proposed scheme and discuss its characteristics in Section 6. The work is concluded in Section 7.

1 Related work

We loosely classify the methods for identifying outliers into two types: case diagnostic procedures and resampling procedures. The remainder of this section will briefly review the two types of outlier rejecting methods and discuss their limitations.

1.1 Case diagnostic methods

Torr\cite{7} proposed an outlier removing method by extending Cook’s squared distance to orthogonal regression and studied its application in motion segmentation by estimating the fundamental matrix. For $L_\infty$ triangulation, Sim\cite{8} presented an outlier removing method by repeatedly estimating the model and throwing away the putative corresponding points with maximal residual. Li\cite{9} gave a novel algorithm for exactly removing up to $k$ putative correspondences as outliers by enumerating all local minima of the quasi-convex cost functions up to level $k$, where $k$ is the estimated upper bound of outlier number.

The case diagnostic methods are very successful when there is only a single outlier. When there are many outliers, this kind of methods usually suffer from the following two problems:

1) Masking effect\cite{10} and swamping effect\cite{11}. Masking effect means that some outliers are made invisible by the others, and swamping effect is meant that some inliers appear as outliers.

2) Computationally prohibitive\cite{9,12}. Because these kinds of methods are based on a greedy search scheme, it will be very expensive when there are many outliers.

Therefore, when there are many outliers, it is usually recommended to use the resampling methods\cite{13} or to pre-remove the most egregious mismatches by the resampling methods\cite{8-9} before using the case diagnostic method.

1.2 Resampling methods

The resampling procedures act by repeatedly generating hypotheses based on the estimation of a parametric model from a minimum number of randomly selected putative correspondences and evaluating them by some means, finally choosing the hypothesis with the highest score to identify outliers. Three of the most popular resampling methods are RANSAC (Random Sample consensus)\cite{7,13}, LMedS (Least median of squares)\cite{14-15}, and MLESAC\cite{16-17}. These methods try to obtain a minimum samples of outlier free putative correspondences to estimate a parametric model, and usually can tolerate a high percentage of outliers. Their
shortcoming is that the computational efficiency will decrease dramatically with the increase of the outlier percentage and the number of the model parameters to be estimated\cite{1}.

In conclusion, the available outlier-removing methods in published works suffer, directly or indirectly, from the problems of being model-dependent and sensitive to outlier percentage. In the next section, we propose a novel model-independent outlier-removing scheme to alleviate the above shortcomings based on correspondence manifold.

2 Correspondence manifold and correspondence view

In this work, we assume that the corresponding points lie on a consistent manifold, and outliers are rejected by checking their consistency with upward views of the manifold.

In correspondence problem, two of the commonly used constraints are\cite{1}:

1) Uniqueness constraint. Suppose there is an image pair $I$ and $I'$. The uniqueness constraint says that a point in image $I$ corresponds to only one point in image $I'$, and vice versa. In most cases, this is true. Hence, there are a couple of one-to-one mappings between image points by this constraint, one from $I$ to $I'$, the other from $I'$ to $I$. The mappings can be written as $f(u, v) = (g_1(u, v), g_2(u, v)) = (u', v')$ and $f'(u', v') = (g_1(u', v'), g_2(u', v')) = (u, v)$, where $(u, v) \in I$ and $(u', v') \in I'$.

2) Smoothness constraint. This constraint states that for two given correspondence pairs $p$ and $p'$, $q$ and $q'$, if $p$ is in the neighborhood of $q$, then, $p'$ and $q'$ should also be close to each other. Suppose $p$ and $p'$ are the images of the same scene point $Q$, and $P$ and $Q$ are two points on the same object, then, this constraint usually is true. Hence, we assume that $f(u, v)$ and $f'(u', v')$ are continuous.

Therefore, by the above two constraints, we can assume that there are two continuous mappings between image points. Furthermore, every pair of corresponding points $(u, v)$ and $(u', v')$ defines a point $(u, v, u', v')$ in the joint image space $R^3$\cite{10}. By the above constraints, the correspondences specify a continuous manifold $M_e$ in the joint image space, for example, if the camera performs perspective projection, then, the manifold is an algebraic variety\cite{1}, otherwise, if the camera is of the pinhole model with distortion or a more general model for fish-eye lenses, the manifold will become more complicated. For convenience, the manifold in this work is named correspondence manifold.

In fact, mapping $f(u, v)$ could be thought as the scenario that we stand on the coordinate plane $(u, v)$ to observe the correspondence manifold $M_e$, and $f'(u', v')$ is the upward view of $M_e$ when viewed on the coordinate plane $(u', v')$. Therefore, it is appropriate to call $f(u, v)$ and $f'(u', v')$ correspondence view.

Therefore, the correct matches should be consistent with the correspondence views and the correspondence manifold theoretically. And the putative corresponding points can be regarded as a sample set from the manifold, usually with some outliers. If we can learn the correspondence views from the putative corresponding points, then, the outliers can be removed by checking whether they are consistent with the correspondence views.

Due to the inherent ambiguity of the correspondence problem and the complexity and diversity of practical cases, there are unavoidably some exceptional examples to the above constraint assumptions.

1) Exception of the uniqueness constraint.

This exception arises when two or more scene points lie on a single ray from one camera but can be seen as separate points from the other camera, as illustrated in Figure 9.22 in [18]. Fortunately, at least one view $f(u, v)$ or $f'(u', v')$ can accommodate the special corresponding points of this kind.

2) Exception of the smoothness constraint.

This exception occurs when stereo depth changes sharply. Under this condition, the characteristics of correspondence views $f(u, v)$ and $f'(u', v')$ are illustrated in Fig. 1 with an example in 2-dimensional space that can be easily visualized. In Fig. 1 (a), the real function $G(U)$ is discontinuous; however, if we approximate it with a continuous $\hat{G}(U)$ as being illustrated in Fig. 1 (b), then, most of the points on $G(U)$ are still consistent with $\hat{G}(U)$. Similarly, when exceptions of this kind occur, we can approximate the $f(u, v)$ and $f'(u', v')$ with continuous $\hat{f}(u, v)$ and $\hat{f}'(u', v')$, respectively. And for notation convenience, we still refer to $f(u, v)$ and $f'(u', v')$ as $f(u, v)$ and $f'(u', v')$ when this exception occurs.

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{image1.png}
\caption{A sketch map (The characteristics of the correspondence views $f(u, v)$ and $f'(u', v')$ when the exception of smoothness constraint arises.)}
\end{figure}

In conclusion, we can assume that there are two continuous correspondence views $f(u, v)$ and $f'(u', v')$ between the locations of the corresponding pairs approximately. And if $f(u, v)$ and $f'(u', v')$ can be estimated, then, we can remove outliers by checking whether the putative corresponding points are consistent with correspondence views $f(u, v)$ and $f'(u', v')$.

3 Learn correspondence views and reject outliers

As was analyzed in Section 2, the correspondence manifold $M_e$ is the general trend of putative correspondences, and we can judge whether a putative corresponding pair follows the general trend $M_e$ by checking its consistency with views $f(u, v)$ and $f'(u', v')$. Therefore, we propose a novel scheme to reject outliers by the following two steps:

1) Learn the correspondence views from putative correspondences. Usually, a large percentage of putative correspondences are outliers, and many of them unduly influence the estimation of correspondence views. Here, we propose a group diagnostic technique to learn the correspondence views robustly.

2) Reject outliers. After learning correspondence views, we propose to reject outliers by checking consistency of the putative correspondences with the correspondence views based on statistical inference technique.

3.1 Learn correspondence view

The learning procedure of correspondence view, for example $f(u, v)$, can be divided into two function estimation problems: $g_1(u, v) = u'$ and $g_2(u, v) = v'$. However, because of the complexity and diversity of practical cases and
the exceptions presented in Section 2, it is a very demanding problem to estimate the correspondence view comparing with the usual function estimation problems:

1) The correspondence view is varying. Sometimes it is very steep (e.g. Fig. 1 (b)); if the function is more steep near point A, then, more of the corresponding points are consistent with it. Sometimes it is very flat, and usually these cases arise simultaneously and repeatedly. Therefore, the used estimation model should have a powerful ability to describe.

2) The data set are usually corrupted severely.

In correspondence problem, putative correspondences are usually corrupted with noise and a large proportion of outliers, sometimes more than 40% or 50% are outliers. Many of the putative pairs can unduly influence the estimation of correspondence views (called influentials in robust statistics[20]). Therefore, to learn the correspondence view correctly, the influentials should be detected at first.

Remark 1. Outliers and influentials are not equivalent: a distinct outlier is not deemed an influential, and an influential need not be an outlier[20]. Therefore, the outliers should be identified by checking whether they follow the general trend of putative correspondences, not by evaluating their influence[7].

In diagnostic statistics, the influentials are usually identified by a one-by-one greedy search scheme[7,10,20]. The methods of this kind usually work very well when there is a single influential or small numbers of them. The shortcomings of this kind of methods, however, are: 1) the efficiency will decrease dramatically with the increase of a number of the total samples or influentials; 2) it is much more difficult to diagnose influentials when there are multiple of them[7,10,12].

In this work, we propose a novel group diagnostic technique for identifying influentials and estimating correspondence view. Suppose $S$ is the set of putative correspondences and the size of $S$ is $n$. First, estimate the correspondence view from sample set $S$ and pick out a subset from $S$ as suspect influentials. Second, delete the suspect subset and reestimate the correspondence view with the remaining samples. And then, determine the influence of the suspect subset by comparing the above two estimations. If the influence is unduly large, then, the subset is regarded as influential set as a whole and repeat the above procedure, otherwise terminate the iteration process. The proposed scheme is presented as following.

Algorithm 1. A novel group diagnostic technique to identify influentials and estimate correspondence view $f(u,v)$. $f(u,v)$ can be estimated similarly.

Step 1. Estimate correspondence view $f(u,v)$ from $S$, and obtain $f(u,v)$.

Step 2. Choose a subset $S_i$ from $S$ as suspect influentials based on $f(u,v)$.

Step 3. Reestimate $f(u,v)$ with $S_i = S - S_i$, and get $f_i(u,v)$.

Step 4. Determine the influence of $S_i$ by comparing $f(u,v)$ and $f_i(u,v)$.

Step 5. If $S_i$ has unduly influence on $f(u,v)$, then reject $S_i$ as influential, and let $f(u,v) = f_i(u,v)$, $S = S - S_i$, and go to Step 2.

Step 6. If the influence of $S_i$ is appropriate, then, assume that there are no more influentials and terminate the procedure.

It can identify influentials efficiently. Usually more than 75% influentials could be identified within three iterations in our experiments, even if the percentage of the outliers is up to 55%. By the traditional diagnostic technique in the published works, however, only one sample is identified with $n + 1$ estimations, where $n$ is size of $S$. Therefore, the identifying procedure is sped up dramatically by the proposed scheme. Two questions immediately arise:

1) How to choose the suspect influential subset?

For a given estimation $f(u,v)$, we propose to select the suspect influentials by residual analysis

$$|e_i(p,p')| > \tau_n \sigma_i, \quad (p,p') \in S$$

where $\tau_n > 0$ is a given threshold, and $e_i(p,p')$ is the estimation error

$$e_i(p,p') = f_i(u,v) - g_i(u,v)$$

$${p = (u,v), \quad p' = (u',v')}, \quad i = 1,2$$

Suppose the estimation error $e_i$ follows Gaussian probability distribution with zero mean and standard deviation of $\sigma_i$. Then, for a given confidence level $0 < \alpha < 1$, we can choose the threshold in (1) by

$$P(|X| \leq \tau_n) = \alpha$$

where $X$ is a random variable following standard normal distribution $N(0,1)$. For example, if $\alpha = 0.9544$, then $\tau_n = 2$, and by (1), we can label the putative correspondences that have unduly influence on the estimation and simultaneously the non-influential corresponding points can be preserved with probability 0.9544.

In practice, the standard deviation $\sigma_i$ is unknown and its estimation

$$\hat{\sigma}_i = \sqrt{\frac{\sum_{(p,p') \in S} e_i^2(p,p')} {n}}$$

is used, where $\{e_i\}$ are defined in (2).

2) How to evaluate the influence of the suspect influential subset $S_i$?

Upon the assumption of the zero mean Gaussian distribution, if there are no influentials in $S$, then, the estimation of correspondence view should not be affected too much by deleting the suspect subset $S_i \subset S$, only if there is sufficient redundancy in $S$. Suppose $\hat{\sigma}_i^2$ and $\hat{\sigma}_\infty^2$ are, respectively, the estimations of $\sigma_i^2$ before and after the removal of suspect subset $S_i$. Because the zero mean Gaussian distribution is determined completely by its variance, we can evaluate the influence of $S_i$ by comparing $\hat{\sigma}_i^2$ and $\hat{\sigma}_\infty^2$. And to offset the disturbance of measurement units, we propose

$$\hat{\Delta}_i = \frac{(\hat{\sigma}_i^2 - \hat{\sigma}_\infty^2)}{\hat{\sigma}_\infty^2}$$

instead of $\hat{\sigma}_i^2 - \hat{\sigma}_\infty^2$ to be the evaluation criterion.

3.2 Reject outliers

In theory, the correspondences lie on at least one of the correspondence views. However, because of the coordinates of putative corresponding points are usually corrupted by noise, the corresponding points usually do not exactly satisfy the equation of correspondence view $f(u,v) = (u',v')$ or $f(u',v') = (u,v)$ in practice. Therefore, we need a measurement to reflect the consistency of a putative correspondence with the correspondence view.

Suppose $p = (u,v)$ and $p' = (u',v')$ are a pair of corresponding points, and let

$$e(p,p') = f(u,v) - (u',v') = (e_1,e_2)$$

$$\|p-p'\| = \sqrt{(u-u')^2 + (v-v')^2}$$
where $e_1$ and $e_2$ are defined in (2). Then, $c(p, p')$ scores the consistency of the putative pair $(p, p')$ with the correspondence view $f(u, v) = (u', v')$. However, it is a vector and not appropriate for identifying the outliers directly. Let

$$c(p, p') = e(p, p')D(f)^{-1} e^T(p, p')$$

(6)

where

$$D(f) = \begin{bmatrix} \sigma_1^2 & 0 \\ 0 & \sigma_2^2 \end{bmatrix}$$

and $\sigma_i^2$ is the variance of $e_i$, $i = 1, 2$. $c(p, p')$ is independent of the scale of $e_i$ and reflects the consistency of $(p, p')$ with the correspondence view $f(u, v)$. As a result, the outliers can be identified by $c(p, p') > \varepsilon$, where $\varepsilon > 0$ is a preset threshold.

A common problem is how to choose the threshold $\varepsilon$. Upon the assumption that $e_1$ and $e_2$ are independent random variables with Gaussian distributions $N(0, \sigma_1^2)$ and $N(0, \sigma_2^2)$, respectively, the measurement $c(p, p')$ will follow $\chi^2(2)$ distribution. And the threshold $\varepsilon$ can be chosen with the following condition:

$$P(Y < \varepsilon) = \alpha_c$$

(7)

where $Y$ is a random variable following $\chi^2(2)$ distribution, and $\alpha_c$ is a given confidence level. In the experiments of this work, $\alpha_c = 0.995$.

Similarly, a measurement $c'(p, p')$ can be defined to evaluate the consistency of putative pair $(p, p')$ with correspondence view $f'(u', v')$. And the final outlier-rejecting algorithm is presented as following.

Algorithm 2. Outliers rejection by checking the consistency of putative pairs with the estimated correspondences.

1. Assume $S$ is a set of putative correspondences
2. For every putative pair $(p, p') \in S$, compute the consistency $c(p, p')$ and $c'(p, p')$; if $c(p, p') > \varepsilon$ or $c'(p, p') > \varepsilon$ or $c(p, p')$ is independent of the scale of $e_i$ and reflects the consistency of $(p, p')$ with the correspondence view $f(u, v)$. As a result, the outliers can be identified by $c(p, p') > \varepsilon$, where $\varepsilon > 0$ is a preset threshold.

4 Some issues on implementation

4.1 Termination criterion

In Algorithm 1, the correspondence views are learned in an iterative paradigm. Some rule is needed to decide when to stop the iteration.

The influences of suspect influential subset in some experiments are presented in Fig. 2. Most of the influentials are usually identified at the first several iterations, including those observations with top undue influence on estimation. For example, in the experiment of Fig. 4, 424 influentials are detected in the first iteration, and approximately 97.13% of the influentials are identified in the first four iterations. Therefore, influence of the suspect subset is very high at the beginning. With more iterations, the influentials will become less and less, and the selected pairs are also usually the ones that have less influence on estimation than the ones selected in the first several iterations. Hence, the influence tends to vanish when the iterative number becomes large. In practice, we can use a threshold $\varepsilon_{INFL}$, and terminate the algorithm when $INFL \leq \varepsilon_{INFL}$.

After nearly all the influentials are identified, some of the vital observations, to correctly estimate the correspondence view, sometimes might be selected into the suspect subset; then, the influence $INFL$ might be less than zero, e.g., at the eighth iteration in the experiment A of Fig. 2. And in this case, the iterative procedure should be terminated.

4.2 Estimator

The learning procedure of correspondence view can be implemented by two regression problems (discussed in Section 3.1). However, because correspondence view is varying in practice, the regression model put in use should be able to approximate rich types of functions. In this work, we use the SVM regression method, which has been proved to be very effective on both theory and real application [21]. The implementation package used is LIBSVM [22] with radial basis kernel $e^{-\gamma(u-v)^2}$.

5 Size of suspect influential subset

The suspect influential subset is chosen by (1), and therefore, the parameter $\tau_{INFL}$ controls the size of the suspect influential subset. And further, $\tau_{INFL}$ influences the computational efficiency (see Fig. 3, Table 1) and capability (see Table 1) of our proposed scheme. For example, in the experiment of Fig. 3, when we preset $\tau_{INFL}$ with a smaller value 1.65, the influentials can be deleted dramatically in the first several iterations and the learning procedure can be finished within 10 iterations; however, when $\tau_{INFL}$ is preset with a larger value 2.24, only few of the influentials can be deleted at every iterations, and the learning of the correspondence view $f'(u', v')$ takes 36 iterations. Therefore, the smaller $\tau_{INFL}$ is, the more efficient the proposed scheme is.

![Fig. 2 Influence of suspect influential subset $S_c$](image)

![Fig. 3 Putative correspondence set is the one in experiment of Table 2 with inliers 16.13% (a) $\tau_{INFL} = 1.65$, the view is learned within 10 iterations; (b) $\tau_{INFL} = 1.96$, learning procedure is finished at the 15th iteration; (c) $\tau_{INFL} = 2.24$, learning procedure is finished at the 36th iteration)](image)
Table 1 Performance of our proposed scheme and parameter \( \tau_{\alpha} \) in diagnostic learning correspondence views (Putative correspondence set is the one in the experiments of Table 2 that has 16.13% inliers. Three \( \tau_{\alpha} \) thresholds 1.65, 1.96 and 2.24 are corresponding to confidence levels 0.9, 0.95 and 0.975, respectively.)

<table>
<thead>
<tr>
<th>( \tau_{\alpha} )</th>
<th>1.65</th>
<th>1.96</th>
<th>2.24</th>
</tr>
</thead>
<tbody>
<tr>
<td>Identified inliers (%)</td>
<td>96.74</td>
<td>98.14</td>
<td>99.07</td>
</tr>
<tr>
<td>Identified outliers (%)</td>
<td>98.21</td>
<td>98.63</td>
<td>97.76</td>
</tr>
<tr>
<td>Iterative times</td>
<td>[7, 10]</td>
<td>[14, 15]</td>
<td>[31, 36]</td>
</tr>
</tbody>
</table>

However, when a smaller value of \( \tau_{\alpha} \) is used, there will be more non-influentials selected into the suspect subset, which will result in a coarser estimation of correspondence view and less inliers being preserved (see Table 1). Therefore, a tradeoff should be made between computational efficiency and inliers preserving in practice.

6 Experiments and discussions

In this section, we test the performance of our proposed scheme and verify the validity of correspondence manifold on real image pairs. In all of the experiments, the putative correspondences are computed from the SIFT keypoints[4] by nearest neighbor method. The performance is assessed from the following aspects.

6.1 Identifying outliers

In Fig. 4 (a), an image pair of a lion is shown for establishing correspondence. All of the 2533 putative correspondences are presented in Fig. 4 (b), and approximately 44.14% are mismatches. By iteratively diagnosing the influencers, the two correspondence views \( f(u, v) \) and \( f'(u', v') \) are estimated with Algorithm 1. 99.82% of the outliers are correctly detected by checking their consistency with the estimated correspondence views. The percentage of outliers is dramatically reduced from 44.14% down to 0.15%. The identified inliers and the identified outliers are presented in Figs. 4 (c) and (d), respectively. More experimental results are presented in Fig. 5. And the experimental results in Fig. 5 show that the outlier detecting capability of our proposed scheme is not affected by the large view angle.

6.2 Robustness and efficiency

In this subsection, the robustness and efficiency of our proposed scheme are investigated on putative correspondences with different inlier percentage. The data set are generated by the following two means.

Denote \( P \) as the initial set of putative correspondences in the experiment of Fig. 4 (b), which consists of 1 415 inliers, and 1 118 outliers. The putative correspondences with different inlier percentages can be obtained by deleting some randomly chosen inliers from \( P \). For example, if we randomly choose 500 from \( P \) and delete them, the inlier percentage will be \( (1 415 - 500)/(2 533 - 500) \approx 45.01 \). The experimental results are presented in Table 2. It is shown that the results are satisfactory, wherein more than 98% of the outliers are detected correctly although the lowest inlier percentage is down to 16.13%. The experiments show that the capability of detecting outlier is very robust and the capability of recognizing correct matches is not weakened by the increase of the outlier percentage.

The putative correspondences with different inlier percentage can also be obtained by adding some randomly generated outliers into \( P \). And similar results are obtained.

Table 2 Robustness and efficiency of our proposed scheme

<table>
<thead>
<tr>
<th>Inliers number</th>
<th>1 415</th>
<th>515</th>
<th>315</th>
<th>215</th>
</tr>
</thead>
<tbody>
<tr>
<td>Original inlier ratio (%)</td>
<td>55.86</td>
<td>31.54</td>
<td>21.98</td>
<td>16.13</td>
</tr>
<tr>
<td>Identified outlier (%)</td>
<td>99.82</td>
<td>99.20</td>
<td>98.66</td>
<td>98.03</td>
</tr>
<tr>
<td>Identified inlier (%)</td>
<td>94.35</td>
<td>93.40</td>
<td>97.14</td>
<td>98.14</td>
</tr>
<tr>
<td>Iterative times</td>
<td>[6, 8]</td>
<td>[10, 10]</td>
<td>[11, 12]</td>
<td>[14, 15]</td>
</tr>
</tbody>
</table>

From the experimental results in Table 2, it is shown that although the required computational time will increase with the decrease in inlier percentage, the computational influence of the inlier percentage is not significant, in particular, comparing with the traditional resampling paradigms[1].

The above experimental results show that the proposed scheme can identify the inliers and outliers simultaneously with a high probability. That is to say, the correct matches are usually consistent with at least one of the upward view of the correspondence manifold, and mismatches are usually far away from both of the correspondence views. Therefore, the assumption of correspondence manifold is sound.

6.3 Necessity of utilizing both views

By the uniqueness and smoothness constraints, the matches should be consistent with correspondence views \( f(u, v) \) and \( f'(u', v') \) simultaneously in theory. Therefore, outliers can be removed by checking their consistency with correspondence view \( f(u, v) \) or \( f'(u', v') \). The experimental results in Table 3 show that more than 98% of the outliers are removed by any one of the two correspondence views.

Because of the complexity and diversity of practical cases, however, there are unavoidably exceptional examples to the uniqueness constraint and smoothness constraint. Therefore, some of the inliers are consistent with only one of the two correspondence views (as being shown by the experimental results in Table 4), hence, we should use the two views to preserve the inliers in practice.
7 Conclusions

In this work, we introduce correspondence manifold and correspondence view for outliers rejecting. The correspondence views are estimated by a novel group diagnostic technique. And the mismatches are removed by checking their consistency with correspondence views. The main advantages include that the identification procedure that is independent of camera model and the parameters to be estimated, and that the coupling between correspondence identification and model selection and estimation can be solved efficiently.

References

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