PUTATIVE MATCH ANALYSIS A Repeatable Alternative to RANSAC for Matching of Aerial Images

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Abstract: One disadvantage with RANSAC is that it is based on randomness and will therefore often yield a different set of inliers in each run, especially if the dataset contains a large number of outliers. A repeatable algorithm for finding both matches and the homography is proposed that will yield the same set of matches every time and is therefore a useful tool when trying to evaluate other algorithms involved and their parameters.

1 INTRODUCTION

In the process of finding corresponding points in two or more images it necessary to determine which points are true matches, so called inliers, and which points are not matching, so called outliers. RANSAC (Fishler and Bolles, 1981) is one of the far most used algorithms for this purpose and many variants have been proposed in literature (Chum et al., 2003; Chum et al., 2004; Chum and Matas, 2005. Chum and Matas, 2008; Michaelsen et al., 2006. Sattler et al., 2009). The main disadvantage with RANSAC is that it is not repeatable (Zuliani, 2009) since it is based on random sampling, as the name itself suggests: RANdom SAmple Consensus. Hence it is difficult using RANSAC while trying to run tests of other algorithms involved and changing their parameters, as the set of inliers may vary in each run.

We propose a repeatable algorithm that is not based on randomness, which will find the same inliers and thus the same homography (Vincent and Laganiere, 2001) every time the same set of matches is given to the algorithm. As it performs an analysis based on the putative matches, we have chosen to call it *Putative Match Analysis* or PUMA for short.

2 PUTATIVE MATCH ANALYSIS

The first step of PUMA is to construct what we have chosen to call a Relative Polar Matrix (RPM). The

matrix is constructed in the following way as shown in figure 1.



Figure 1: The RPM is constructed by taking the matches in the two images (a) and translating all matches one at a time so that one point coincide (b). A pair of vectors are constructed from that point to each pair of inliers. When a true match is used as base it will yield vectors with close to equal relative length and angle for true matches but not for false ones. A false match (c) on the other hand will yield varying cosines and lengths.

The two matched images (a) are translated so that one matching pair coincide, one at a time and each of these comparisons are shown in the four images to the right (b, c). First of all the green match is translated so the points overlap and the relative length of the vector from this point to a matching pair as well as the cosine of the angle between these are computed for all putative matches. The relative length of these vectors v_1 and v_2 is:

$$r = \frac{\min(\|v_1\|, \|v_2\|)}{\max(\|v_1\|, \|v_2\|)}$$
(1)

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Hence both the cosine of the angle: ρ between vectors and relative length: r will always be in the interval [-1..1] and [0..1] respectively. The first column of the matrix will contain the results for this first match and each row contains the pairs of (r, ρ) to each pair of matches. Those that are true inliers (the yellow and blue), will yield similar values of (r, ρ) even if the images have different rotation and scale. However, the false matches will yield pairs of (r, ρ) that have different values. Similarly when a false match coincide (c), all putative matches will yield quite different values of (r, ρ) . This procedure is repeated for each match, hence the second column will contain the pairs relative to this match and so on.

The first example of using this algorithm is shown in figure 2 where one of the images is rotated and scaled down just to show that the technique works well for both cases.



Figure 2: Matching of two aerial images where one of them is rotated and scaled. The method proposed finds the outlier in red even for this extreme situation.

In figure 3 the RPM matrix is visualized showing one matrix for ρ , to the right and one for r, to the left.



Figure 3: The RPM matrix is visualized showing one symmetric matrix for r, to the left and one for ρ in the middle. In this case there is just one outlier giving a clear trace in the matrices.

Each one of them are symmetric so all the information could be packed into one matrix as the

diagonal contains no information as the points cannot be compared to themselves. In this example there is one outlier that gives a clear trace in the matrix as its value differs from the others that are similar.

The second step of PUMA can be performed in several ways using the clustering technique of your choice. Each column in the RPM matrix contains a cluster that can be visualized using (r, ρ) as coordinates. Figure 4 upper left shows all points in the RPM plotted in the same plot and obviously it is hard to say what cluster we are looking for.



Figure 4: The upper left: all points in the RPM. Upper right: one set of the RPM is used in the plot and clearly it contains an outlier as it is quite scattered. Bottom left: a set containing an inliers is used and the outlier (red) is seen far from the cluster center (violet). Bottom right: the outlier has been removed and the whole RPMS is plotted and the cluster contains only putative inliers.

In the upper right the set that corresponds to the outlier is plotted. As expected the points are more scattered. In the bottom left one set is plotted and the outlier, depicted in red, is clearly seen far from the centre, depicted in violet. In the bottom row right the whole RPM is plotted after removing the outlier so that it now contains putative inliers. Still there are a couple of points lying a bit off centre that can be dealt with by choosing a smaller threshold for the clustering.

Clustering can be done in many ways (Jain and Dubes) and k-means clustering (MacQueen, 1967) is one popular clustering algorithm. Nevertheless, the problem here is a bit different as there is one cluster set for each row (or column as the RPM is

symmetric after removing any doubles) and the columns are also related to each other. PUMA was developed to work for aerial images, which will form one cluster that we search for. The clustering approach used here is very simple and starts by computing the average μ_i for each row *i* of (r, ρ) , thus giving a "centre" that is a bit perturbed by the outliers. Then the distance between each point on the row (r_i, ρ_i) and μ_i is stored in a matrix, which we have chosen to call the *Relative Distance Matrix* (*RDM*). In each iteration the set with an outlier furthest away from the average centre is located and that outlier is therefore removed and the RDM is updated accordingly.

In figure 4 bottom left is in fact the set having the largest distance shown. The outlier is easily found by locating the column with the largest value. In this case it is column 65 that has its largest value in row 9, indicating that it is the set with number 65 (column and row) that must be deleted as it gave the largest distance for set number 9. So even if it is set number 65 that is shown in the upper right in the picture, it is actually set number 9 in the lower right that helps us finding the most extreme outlier.

3 RESULTS

Two areal images, shown in figure 5, with different orientation were used and in order to produce more false matches the Harris operator (Harris and Stephens 1988) was used instead of the more accurate SIFT (Lowe, 2004). In this case the there were about 84.4% of false matches.



Figure 5: Putative matches produced using the Harris detector, with about 84.4% false matches.

In figure 6 is shown the whole set of clusters plotted in the top left and the set corresponding to the most extreme outlier in the top right where the cluster is obviously scattered. In the bottom left there is the set with the largest distance between the centre and a point, ie. an outlier and will be removed later in the algorithm. In the bottom right is the result after removing all outliers down to a certain threshold.



Figure 6: The upper left: all points in the RPM. Upper right: one outliers set of the RPM, which clearly contains an outlier as it is quite scattered. Bottom left: a set containing another outlier (red) and the cluster centre (violet) has the maximum distance. Bottom right: all the outliers have been removed and the whole RPM is plotted and the cluster contains only putative inliers.

The cluster is found in the upper right corner, which corresponds to a little scaling and a small rotation, about 18 degrees. The result contains all 34 columns regarded as inliers by the algorithm.



Figure 7: The result after executing the PUMA algorithm. Out of 218 putative matches 34 were chosen as inliers.

Figure 7 shows the result of PUMA yielding 34 inliers out of 218 putative matches. It should be noted that the basic implementation of RANSAC did not come to a correct consensus due to the high amount of outliers, however by forcing RANSAC to

continue it found all inliers after an average of about 32000 iterations.

Figure 8 shows both the RPM and the RDM for the whole set as well as for the case when 5 outliers are remaining. Clearly it is hard to see which rows and columns to remove in the upper row, while it becomes more and more clear as the outliers are removed.



Figure 8: The RPM matrix is visualized showing one symmetric matrix for ρ , to the left and one for r in the middle. And the RDM to the right. In the upper row is the whole set and in the lower row (scaled to be larger) is the set with five remaining outliers that gives a clear trace in the matrices.

The homography can be computed using this set of inliers and the set of inliers can easily be pruned using ordinary RANSAC by setting a desired threshold. As all matches are regarded as inliers RANSAC will now without problem find all inliers within that specific threshold.

4 CONCLUSIONS

The PUtative Match Analysis (PUMA) is a repeatable, brute force algorithm that can be used whenever it is necessary to test other parameters in an application and when it is crucial that the set of inliers are always the same for the same set of data. Hence, it can be used as a robust tool for testing and development of computer vision applications with small non affine distortions as in the aerial images used as examples. Due to its high computational cost it will be outperformed by RANSAC in most situations, but when there are many outliers, PUMA can be a good choice for a reasonable number of matches as it has proven to find the inliers even for a rather high amount of noise in the set.

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