

Comparison of Image Alignment Algorithms

Zhaowei Li and David R. Selviah

University College London

Abstract: This paper compares a new algorithm with two well-known algorithms for precise alignment of overlapping adjacent images. The new part of the algorithm is concerned with the selection of exactly matching pairs of feature points in the two images and its performance is compared with the performance of the Least Median of Square regression algorithm (LMedS), and the Random Sample Consensus (RANSAC) algorithm which are also compared against one another in a novel way. The RMS error of alignment achieved by the new algorithm is reduced by 39.58% and 24.07%, compared to LMedS and RANSAC respectively and moreover it is 95.25% and 97.35% faster, respectively.

1. Introduction

In recent years, the accuracy of aligning mosaic images to form a single panorama becomes more important as the resolution or number of pixels in each image increases. Image alignment algorithms find the correspondence relationship between the adjacent overlapping images and these are followed by image stitching algorithms which use the results of the alignment algorithm to seamlessly join the images [1]. The flow chart of the image alignment and stitching algorithm is shown in Figure 1.

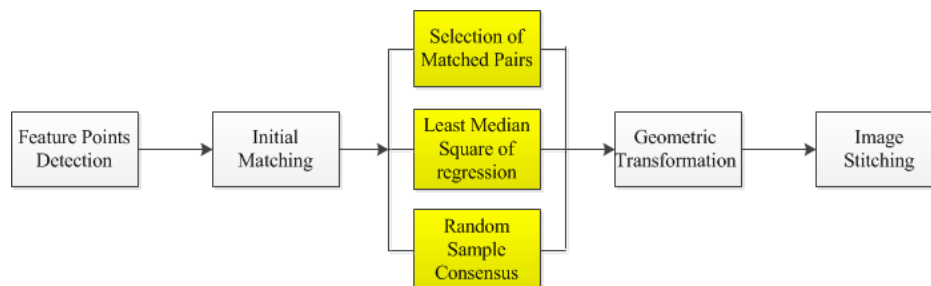


Figure 1: Flow chart of image alignment design procedure

The Scale Invariant Feature Transform (SIFT) [2], described in section 2, detects and extracts feature points in an image, and perform an initial matching process. The feature points are points which can easily be identified in the two images and it is necessary to find the feature points in one image which match those in the adjacent image and to reject points which do not match any in the other image. However, as many as 50% bad matches still remain in the initially matched points, so another method for further selection of well-matched points is necessary. Following the improved selection, a geometric transformation of one of the images is calculated so that the images can be superimposed on top of one another in good correspondence, which is then ready for the final image stitching step. In this paper we introduce our new method, in section 3, for selection of matching feature points to solve the image correspondence problem and compare against two well-known algorithms, Least Median Squares of Regression, LMedS and Random Sample Consensus, RANSAC.

2. SIFT Feature Detection and Initial Matching

The Scale Invariant Feature Transform (SIFT) [2] can detect and extract feature points which are invariant to changes in illumination, image noise, rotation, scaling, and small changes in viewpoint.

After features are extracted from images, the initial matching process can begin. Feature vectors from one image are compared to those from the other image in pairs. To give robustness, feature vectors from the other image which are within a certain similarity threshold are preserved. As a result, bad matches appear. In some cases one feature point in the first image may match two different feature points in the second image according to this method.

3. Refined Matching

Due to the problems with the SIFT initial matching algorithm, further selection is required. The existing methods for further selection of matched points are commonly known as Least Median of Square regression (LMedS) and Random Sample Consensus (RANSAC). Both methods are based on randomly selecting matched points and are both iterative methods. LMedS calculates the median of the square of the error and seeks to minimise this. Additionally, LMedS is robust as it can select feature point matches when the original sample has up to 50% of poorly matched points. However, the calculation speed is rather slow [3].

The RANSAC algorithm consists of two steps. First just enough feature point matching pairs are randomly chosen to compute model parameters. Next, this method checks the number of elements of the input feature point dataset which are consistent with the model just chosen. RANSAC repeats the two steps within a specified threshold until it finds the maximum number of elements within a model. It then selects this model and rejects mismatches. However, the calculation speed of this algorithm is also rather slow [4].

In conclusion, the two standard methods for selection of feature point matches between two adjacent overlapping images have both advantages and disadvantages. Therefore, a new algorithm [6, 7], Selection of Matched Pairs (SelMap) has been developed to perform the selection more accurately and faster and in this paper we compare its performance against that of the two standard algorithms in widespread use.

4. Experiment Method, Results and Discussion

In the experiment, two photographs were recorded through a microscope using a CCD camera, of an object consisting of printed paper which had been shaded using a graphite pencil. The object was moved sideways from one photograph to the other so that there was a 50% overlap between the photographs. When the SIFT algorithm was used on these two images a large number of feature points were identified and divided into matched pairs, however, plenty of the pairs were poorly matched. When the SelMap method was used, more accurate results than that achieved by SIFT are clearly seen as shown in Figure 2, which is displayed using a similar style as [3]. Figure 2 (a) and (b) show the two original images side by side. Figure 2 (c) shows blue lines constructed on the image joining pairs of matched feature points as determined by the SIFT algorithm. Figure 2 (d) shows the matched points selected by the SelMap algorithm from those chosen by the SIFT algorithm and Figure 2 (e) displays the remaining points chosen by the SIFT algorithm but rejected as poor matches by the SelMap algorithm. Finally Figure 2 (f) shows the joined images using the projective transformation.

Figure 3 compares the performance of the new algorithm against that of RANSAC and LMedS in terms of RMS error of Euclidian distance between matched pairs of points after the image transform and superposition of the images for all pairs of matched points selected by the algorithm and calculation time. In the ideal case, the distance should be zero, which means that the matched pairs of points are in exact correspondence.

In terms of RMS error, the SelMap method is clearly better than the two standard methods in terms of both error and time. The error is reduced by 39.58% and 24.07%, compared with LMedS and RANSAC respectively. The time is reduced by 95.25% compared to LMedS, and 97.35% compared to RANSAC.

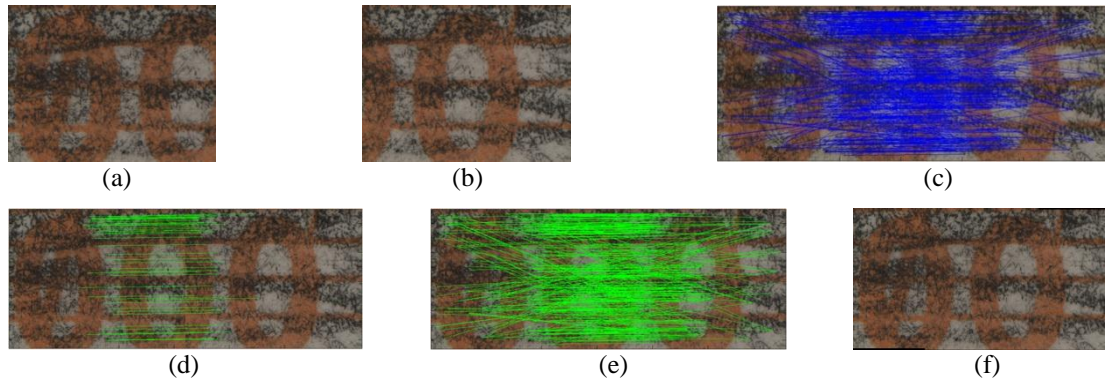


Figure 2 (a) and (b) are the two input images, (c) is the result of initial matching using SIFT, (d) is the result of the new matching selection method, (e) displays the pairs of matching points selected by SIFT but rejected by the SelMap method, (f) is the final aligned image using the new method

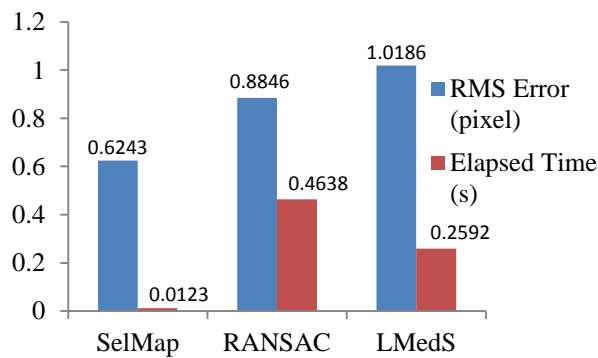


Figure 3 Algorithm Performance Comparison

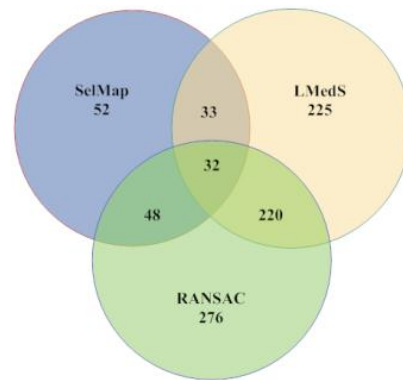


Figure 4 Number of similar and different selected pairs

Algorithms	SelMap vs. LMedS		SelMap vs. RANSAC		LMedS vs. RANSAC	
	SelMap	LMedS	SelMap	RANSAC	LMedS	RANSAC
RMS error of different points (pixels)	0.5444	1.0433	3.185×10^{-7}	0.8677	5.2329	1.2787
Number of different points	19	192	4	228	5	56
Number of same pairs	33		48		220	

Table 1 RMS error comparison of the three methods for selection of matched pairs of feature points

In a new analysis method, when comparing two methods for selecting matched pairs of feature vectors we find how many of the same pairs were identified by both of the methods and how many new pairs were identified by each of the methods compared to the other. The results are shown in Table 1 and figure 4 where the overlapping regions are the same pairs. After SIFT initial matching, there are 449 pairs of matched points selected. The SelMap chooses 52 pairs from these, while LMedS sorts out 225

matched pairs and RANSAC chooses 276 pairs. The new method finds 19 new pairs compared to LMedS and 4 new pairs compared to RANSAC. In order to investigate how good the new pairs found are we used only the new ones to calculate the RMS error and found that the error was much better for these new pairs being as low as about half a pixel compared to LMedS and almost perfect compared to RANSAC. From the table, the SelMap achieves 47.82% and 99.99% lower RMS error for the different pairs not selected by the LMedS and RANSAC algorithms, respectively.

5. Conclusion

The new SelMap method can achieve 39.58% and 24.07% lower RMS errors and 95.25% and 97.35% faster speeds than the established and widely used LMedS and RANSAC respectively. Furthermore, from Table 1, the RMS errors for the different new pairs of matched points selected by the SelMap are 47.82% and 99.99% lower than the two existing algorithms, thus this innovative method can pick out better corresponding feature points. The RMS for the new different matched points selected by the new method are 14.68% and 99.99% lower than the RMS error using all of the matched points selected by the new method. This shows that the new different matched pairs of feature points selected by the SelMap method are better than those which it has in common with the LMedS and RANSAC methods.

To sum up, the whole image alignment and stitching process can be successfully realized by several algorithms demonstrated above, and the final aligned image is observed to be of a good quality for all algorithms. However, the new Selection of Matched Pairs method can achieve better performance than the commonly used RANSAC and LMedS, with respect to alignment error, and calculation speed in the case of the two images and the projective transform used in this paper.

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