A Method of Using Genetic Algorithm in Image Stitching

Lingfeng Zhao, Yujie Huang,Minge Jing, Xiaoyang Zeng, Yibo Fan

State Key Laboratory of ASIC & System, Fudan University, Shanghai, China

Abstract—Image stitching is an important part of computer vision, and how to do it more efficiently with high quality is a heated topic. In this paper, the authors propose a new method called TMGA for image stitching to get an improved performance in calculating Transform Matrix by using Genetic Algorithm. The proposed TMGA not only counts the number of interior points, but also takes standard error and degree of dispersion into consideration compared the traditional methods. The results demonstrate that the proposed algorithm can gain a high-quality transform matrix and improves the result of the stitching.

Keywords—Image Stitching, Transform Matrix, Genetic Algorithm

I. INTRODUCTION

Image stitching is a popular topic in computer vision [1], as it is the basis of many other works like object recognition. So how to improve the quality of stitching is very important.

Generally, there are four basic steps of image stitching: keypoint detection [2, 3], keypoint matching [4], calibration [5] and blending. There are some issues in the existing algorithms for image calibration. Theoretically, it merely needs four paired keypoints to get a perspective transform matrix. Whereas, it takes a lot of risk without regarding to the other matching keypoints since there exists some mismatches and it is difficult to discard them thoroughly. Another drawback of utilizing only four pairs is that it will lead to a local matching while a "ragged" occurs in the other area, especially for the images with some degree parallax. Therefore, it is generally accepted to use more keypoints pairs to generate a more accurate and global transform matrix. Now, the question is how to choose some of pairs of keypoints obtained in the previous step to gain a more proper transform matrix.

In this work, we present a method called TMGA which uses genetic algorithm in image calibration to improve the quality of the stitched picture by providing a more appropriate transform matrix. Compared with traditional method, TMGA improves the efficiency of iterations, as there exists an inheritable relationship between iterations. Besides, a specific fitness function is designed to make the matrix covers more points, to minimize deviation and to get a dispersive distribution of points.

II. RELATED WORK

Given the paired keypoints, one common way to get the transform matrix is using a random sample consensus method called RANSAC [5]. The brief idea of it is to randomly choose some matched keypoints and calculate their transform matrix. Then, repeat this process until a particular condition is met and finally select the best matrix. To judge the transform matrix, a single criterion which compares the number of interior points is utilized. The more interior points, the better transform matrix.

RANSAC is a so popular calibration algorithm as many progressive image stitching methods such as APAP [6], ANAP [7], SEAGULL[1] and other works [8] adopt it as a basic step.

To get better results, they require paired keypoints with more accuracy and dispersion. However, pure RANSAC cannot provide high quality results because of the following three reasons. Firstly, in RANSAC, the error of distance between transformed points and the original ones is the only standard of interior points. This may result in preference in selecting points and cannot get a global optimal result. Fig. 1 shows this issue where the part of tree is perfectly aligned while the part of step and well lid is distorted extremely.



Fig. 1. Local optimal align result

Furthermore, the randomness in RANSAC keeps it from some mismatched points to an extent. However, absolute randomness also makes its convergence inefficient because there is no inheritance relationship between iterations. Fig. 2 shows the randomness between iterations. It is argued that that the randomness makes it gain a transform matrix but the efficiency is too slow.

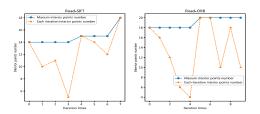


Fig. 2. RANSAC interior points number during iteration

Besides, RANSAC calculates transform matrix based on four selected paired points, which makes the matrix strictly fit to these four points [5]. Nevertheless, it is generally accepted that more than four keypoints is rather proper to gain an optimal transform matrix by using the least squares method described in [6].

III. GENETIC ALGORITHM IN IMAGE STITCHING

To use GA in image stitching, we define our optimization problem as the calculation of a transform matrix which can fit more interior points. After several experiments, we propose an algorithm of using GA in calibration.

Firstly, we take the transform matrix as the individual in GA, and its genes are elements of the matrix. The aim is to get an individual to fit more interior points.

Secondly, we randomly choose groups of paired points (each group contains more than four pairs of keypoints), and then calculate transform matrix for each group using least squares method.

Thirdly, we apply normal GA process, including selecting, making crossover and mutating, to each individual in every iteration. After some generations, the best one is chosen as the final solution. As mentioned before, it is not enough to only take the count on interior points into consideration in the fitness function because it is hard to make a choice when the numbers of interior points of two individuals are the same which is a common situation since the number of interiors is an integer. Therefore, the other two criteria are added: standard error and dispersion degree of interior points. As the name suggested, standard error of interior points means standard deviation of distance between interior points and the corresponding transformed points. So when the numbers of interior points are the same, those matrixes with smaller error are better candidates. Degree of dispersion measures how those keypoints disperse, and the farther the distances between the keypoints are, the more global optimal the matrix is.

To weigh these three criteria, the latter two are normalized. Standard error is easy to be normalized by dividing the number of interior points. And for degree of dispersion, first we calculate centroid of interior points, then we sum the distance between any two interior points to the centroid. The result will be a huge number, so we divide it by the sum of all keypoints to the centroid and use a hyperbolic tangent (tanh) to normalize it. Let \mathbb{N} be the number of interior points, D is the standard error of interior points, \mathbb{E} is the degree of dispersion divided by total distance. A fitness function which considers three elements above is obtained as Eq.2:

V=N-D/N+tanh(E/N) (1)

IV. EXPERIMENT RESULT

Here we choose 8 pairs of images [9] to compare the difference of RANSAC and TMGA based on the matching keypoints of two well-known algorithms-ORB [3] and SIFT [5]. That is to say, we compare four different methods: ORB with TMGA, ORB with RANSAC, SIFT with TMGA and SIFT with RANSAC. Due to space constraints, we only pick one images to visually explain clearly the differences between TMGA and RANSAC as shown in Fig.3.



Fig.3. Road with ORB. Left is RANSAC, right is TMGA method

In what follows, we present some data comparisons on these two methods in Fig.4 and Fig.5. They include the comparison on the number of interior points, degree of dispersion. As we expected, almost all of the results show that the proposed TMGA gets enhanced results. Take the comparison in the number of interior shown in Fig.4 as an example, there is only one exception in 16 examples while ten convincing cases manifest the benefit of TMGA over RANSAC. The similar conclusion can be drawn in the degree of dispersion as shown in Fig.5.

Through Fig.4 and Fig.5, it can be concluded that TMGA method covers more interior points in most circumstances. Besides, it gains more degree of dispersion. It is worth mentioning that TMGA costs almost the same time as RANSAC, and get better performance.

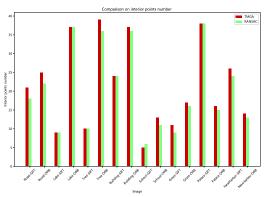


Fig. 4. Comparison on interior point number

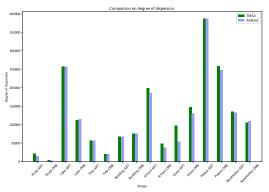


Fig. 5. Comparison on degree of dispersion

V. CONCLUSIONS

In this paper, a method of using genetic algorithm in calibration is proposed and it improves the performance of image stitching compared with the widely used RANSAC. The main contribution of this paper is using genetic algorithm and a specially designed fitness function to improve the quality of transform matrix in image stitching with small parallax. It can be further improved by change some parameters in evolving process, like mutations rate and population. And of course, by propagating more generations, it can get a better result.

REFERENCES

- Kaimo Lin, Nianjuan Jiang, Loong-Fah Cheong, "SEAGULL: Seam-Guided Local Alignmentfor Parallax-Tolerant Image Stitching", European Conference on Computer Vision, 2016.
- [2] DAVID G. LOWE, "Distinctive Image Features from Scale-Invariant Keypoints", International Journal of Computer Vision, P91–110, 2004.
- [3] Rublee, Ethan, Vincent Rabaud, Kurt Konolige, and Gary Bradski. "ORB: An efficient alternative to SIFT or SURF." In Computer Vision (ICCV), 2011 IEEE international conference on, pp. 2564-2571. IEEE, 2011.
- [4] Marius Muja and David G. Lowe: "Fast Matching of Binary Features". Conference on Computer and Robot Vision (CRV) 2012.
- [5] https://people.cs.umass.edu/~elm/Teaching/ppt/370/370_10_RANSAC.p ptx.pdf
- [6] Zaragoza, Julio, et al. "As-projective-as-possible image stitching with moving DLT." Proceedings of the IEEE conference on computer vision and pattern recognition. 2013.
- [7] Lin, Chung-Ching, et al. "Adaptive as-natural-as-possible image stitching." Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition. 2015.
- [8] Dongming, Cheng, and Pang Yu. "Research on sift image recognition algorithm combined with RANSAC." International Journal of Advanced Research in Computer Science 9, no. 1 (2018): 1-3.
- [9] http://sme.fudan.edu.cn/faculty/personweb/jinminge/orginalimages/Building-left.JPG