

Robust Clustering of Multi-Structure Data with Enhanced Sampling

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Abstract - This paper deals with the improvement of clustering results by enhancing performance of sampling. The proposed clustering framework is established on a J-linkage framework [4] with guided sampling technique for multi-structures [7]. We tested the proposed method on publicly available dataset, verifying the validness of the proposed method.

Keywords - clustering, guided sampling, multiple structure estimation

1. Introduction

This paper describes robust clustering of data from multiple geometric structures where each structure is represented by a parametric model. The parametric models include geometric structures such as line, circle, homography or fundamental matrix. The clustering can be done by associating data with underlying models, and grouping the data according to models which data belong to. Hence, finding underlying models is a key for clustering, and it is the model fitting problem that deals with fitting models to data. Given multiple structure data, the model fitting is not trivial because a structure needs to be estimated from data that contain outliers. There are two types of outliers: a gross outlier and a pseudo outlier. The gross outlier is an erroneous data instance that does not belong to any genuine structures. The pseudo outlier of a structure indicates an inlier data instance of other valid structures. Hence, data clustering can be viewed as classification of given N structure data into N cluster inliers and gross outliers.

The most dominant approach for the model fitting is 'hypothesize-and-verify' scheme that adopts RANSAC [1] to cope with outliers. This scheme generates a set of model candidates, called *hypotheses*, from random subsets of the data and associates hypotheses with data, evaluating the hypotheses by a quality criterion. There are several approaches according to how to associate hypotheses with data. One prevailing scheme is a greedy approach for the association. A common method is a sequential fitting-and-removing procedure that runs RANSAC sequentially [2][3]. Each iteration of the procedure selects a hypothesis that maximizes a quality measure, often the number of inliers. Then, the inliers of the hypothesis are removed from the data, going to the next iteration. This sequential RANSAC, however, can be easily inaccurate as

fitting error in current iteration is amplified in subsequent iterations. Another greedy method [4] adopts agglomerative clustering, overcoming the drawback of sequential RANSAC. Although the greedy methods are simple to implement and relatively fast, it is generally sub-optimal, not guaranteeing global optimality of the solution. To handle the optimization issue, recent works have formulated the model fitting as global optimization problem [5][6].

Many previous works have improved the performance of model fitting, focusing on a way of data-hypotheses association, i.e., from greedy one to global optimization. Here, instead of focusing on data-hypotheses association, we have tried to improve model fitting performance by enhancing the quality of generated hypotheses. Instead of random hypothesis generation that most of previous works have adopted, we generate enhanced hypotheses on a guided sampling scheme.

2. Clustering with Enhanced Sampling

2.1 J-linkage as a Clustering Framework

We adopt J-linkage [4] as a clustering method, as it has shown excellent performance in many literatures. The J-linkage mainly consists of two steps: first step is to build preference sets of the input data, and second step is clustering by agglomerative clustering technique.

2.2 Enhancing Sampling on J-linkage Framework

In order to improve clustering results, instead of random sampling, we adopt multi-structure sampling method [7], called Multi-GS. Figure 1 shows the proposed clustering framework that combines J-linkage with the Multi-GS.

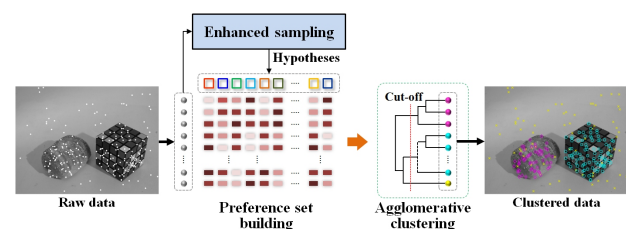


Fig. 1. The proposed clustering framework with enhanced sampling

3. Experimental Results

3.1 Experimental Setup

To verify the proposed method, we tested it on the AdelaideRMF dataset [8]. This dataset offers a set of image pairs for fundamental matrix estimation, including data of keypoint correspondences with their SIFT matching scores and the ground truth structure labels of the data. We used the following parameters for the experiments:

- The number of trials for each image set: 200
- The number of hypotheses for each trial: 200
- Cut-off distance for agglomerative clustering: 0.8

3.2 Discussion

Table 1 summarizes the clustering results of the proposed method, compared to the previous random method. Figure 2 shows the clustering results overlaid with input images, compared to the ground truth. The results show the proposed method outperformed the previous random method.

4. Conclusion

In this paper, we have improved clustering results on J-linkage framework [4] by enhancing sampling. Future work includes the improvement of the clustering framework to cope with the problems of J-linkage.

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Table 1 Pair-counting precision, recall, and F-measure on AdelaideRMF dataset. Upper value in each cell indicates a mean, and a value in () is a standard deviation.

Image set	Method	P	R	F
breadcube	Random	0.983 (0.045)	0.623 (0.147)	0.753 (0.112)
	Proposed	0.972 (0.033)	0.853 (0.170)	0.900 (0.110)
dinobooks	Random	0.710 (0.088)	0.506 (0.129)	0.581 (0.100)
	Proposed	0.707 (0.060)	0.807 (0.111)	0.750 (0.068)
breadcartoy-chips	Random	0.879 (0.124)	0.302 (0.102)	0.438 (0.119)
	Proposed	0.874 (0.109)	0.715 (0.168)	0.776 (0.134)

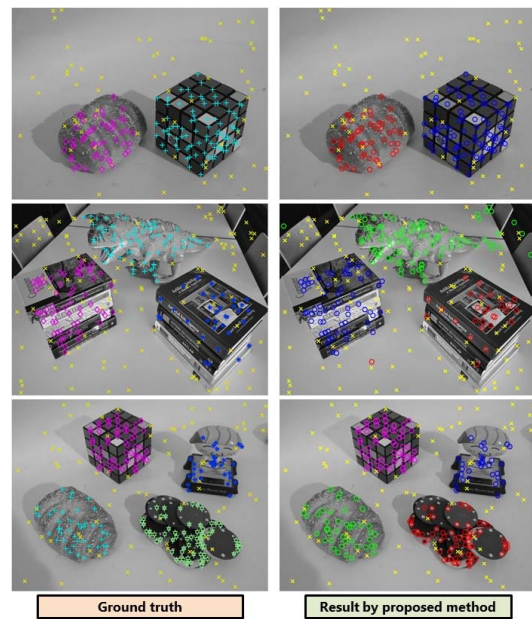


Fig. 2. Clustering result by proposed method (From top to bottom: breadcube, dinobooks, breadcartoy-chips). Each marker indicates each cluster.