

Lab Assignment - Model Fitting

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1 Line fitting

From both the figure 1 and table 1, we can see that the fitting result using RANSAC is much closer to the true model, compared with that using least squares fitting.

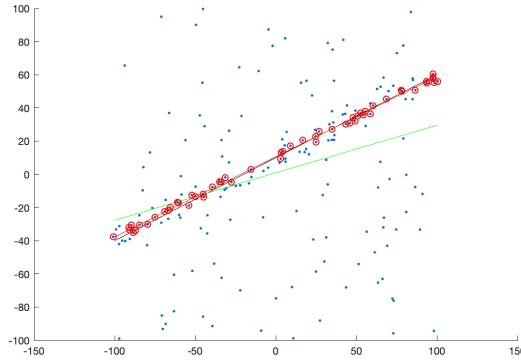


Figure 1: Fitting result of real model(black line), RANSAC(red line), least squares(green line), blue dots are data points, red circles are inliers using RANSAC

Method	real	RANSAC	least-squares
Error	37.8871	38.9741	156.0087

Table 1: error of different methods

2 Fundamental matrix estimation

We compute fundamental matrix with and without singularity constraint, the result F and \hat{F} are similar.

1. Ladybug

$$F \approx \hat{F} = \begin{bmatrix} 0.0000 & 0.0001 & -0.0598 \\ -0.0001 & -0.0000 & 0.0705 \\ 0.0490 & -0.0616 & 1.1702 \end{bmatrix}$$

2. Rect

$$F \approx \hat{F} = \begin{bmatrix} -0.0000 & 0.0000 & 0.0001 \\ 0.0000 & 0.0000 & -0.0005 \\ 0.0000 & -0.0034 & -0.0228 \end{bmatrix}$$

3. Pumpkin

$$F \approx \hat{F} = \begin{bmatrix} 0.0000 & -0.0000 & -0.0011 \\ 0.0000 & -0.0000 & 0.0041 \\ 0.0006 & -0.0038 & 0.0702 \end{bmatrix}$$

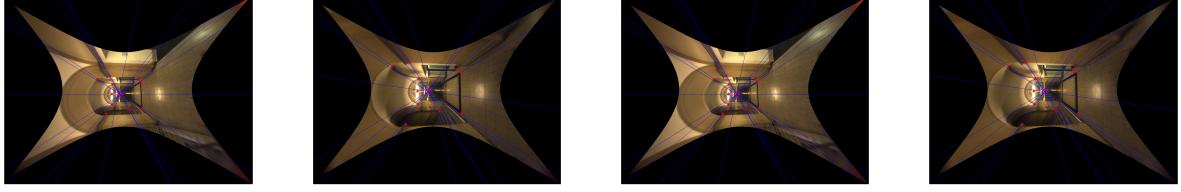


Figure 2: (a) ladybug1 F (b) ladybug2 F (c) ladybug1 \hat{F} (d) ladybug2 \hat{F}

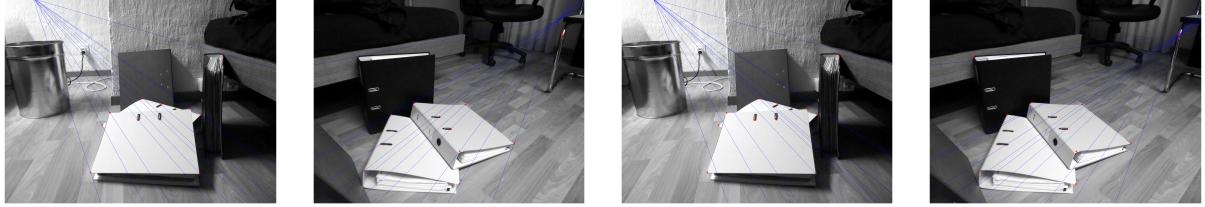


Figure 3: (a) rect1 F (b) rect2 F (c) rect1 \hat{F} (d) rect2 \hat{F}



Figure 4: (a) pumpkin1 F (b) pumpkin2 F (c) pumpkin1 \hat{F} (d) pumpkin2 \hat{F}

By comparing the first two columns and last two columns in figure 2,3,4, we can find that although F and \hat{F} numerically look similar, \hat{F} generally perform better than F from the quality result. This can be easily seen from the figure 3, where the red circle representing the epipole in (b) is far from the intersection of blue epipolar lines, while the circle in (d) almost sits at the intersection.

3 Feature extraction and matching

We display the feature extraction and matching result using VLFeat in figure 5. All three results have many mismatches.

4 Eight-point RANSAC

4.1 Simple RANSAC

Comparing figure 6 and figure 5, we see that simple RANSAC, i.e., incorporate the eight-point algorithm inside a RANSAC loop and keep the termination criterion fixed at 1000 trials, help to reduce mismatches. From the table 2, we also find that the smaller the error threshold we set, the less points are counted as inliers, the smaller the error of inliers is.

4.2 Adaptive RANSAC

We set threshold=5, probability=0.99, and compute the number of trials for each image pairs. The result are shown in figure 7.

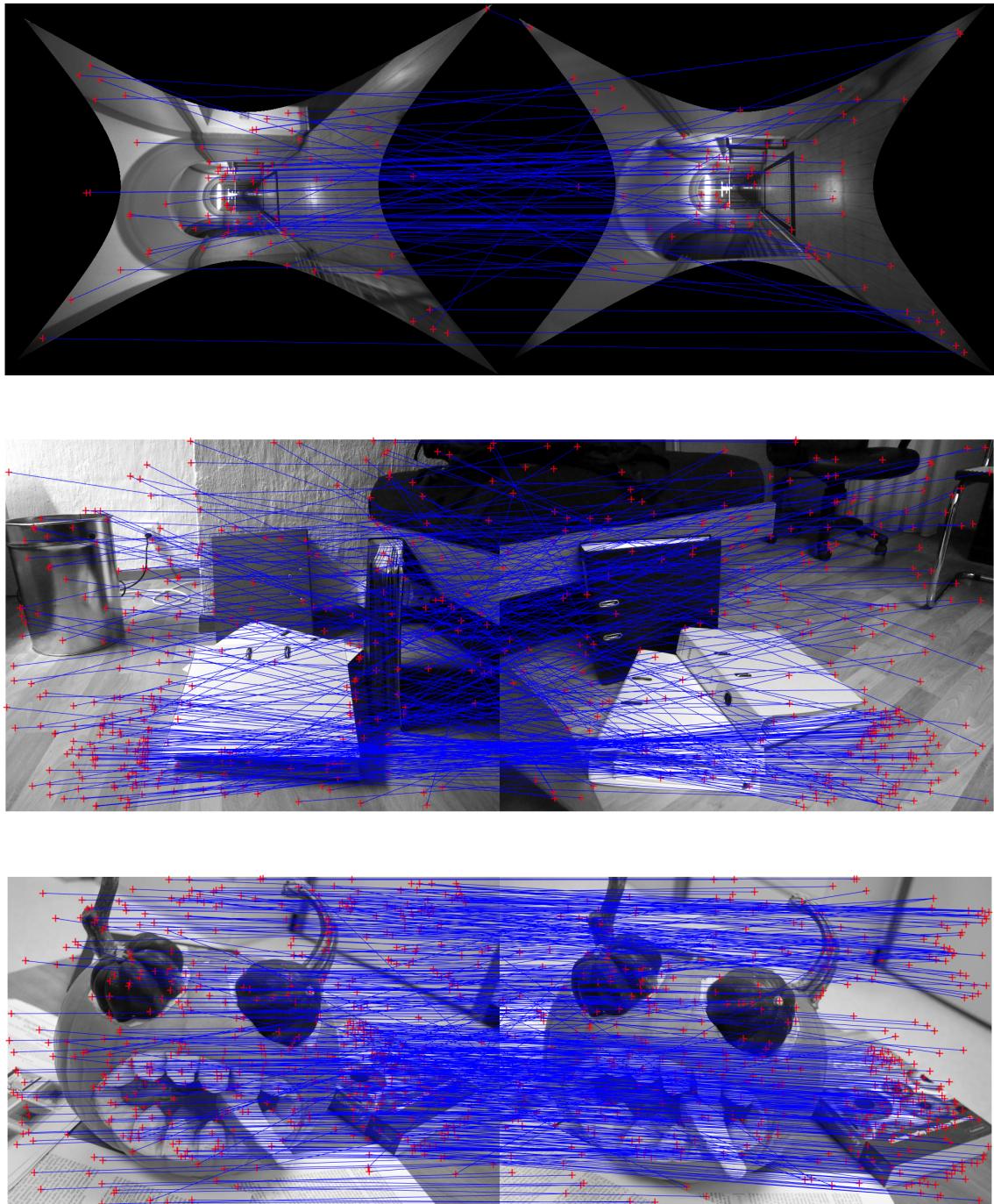


Figure 5: Matching result using VLFeat (a) ladybug (b) rect (c) pumpkin

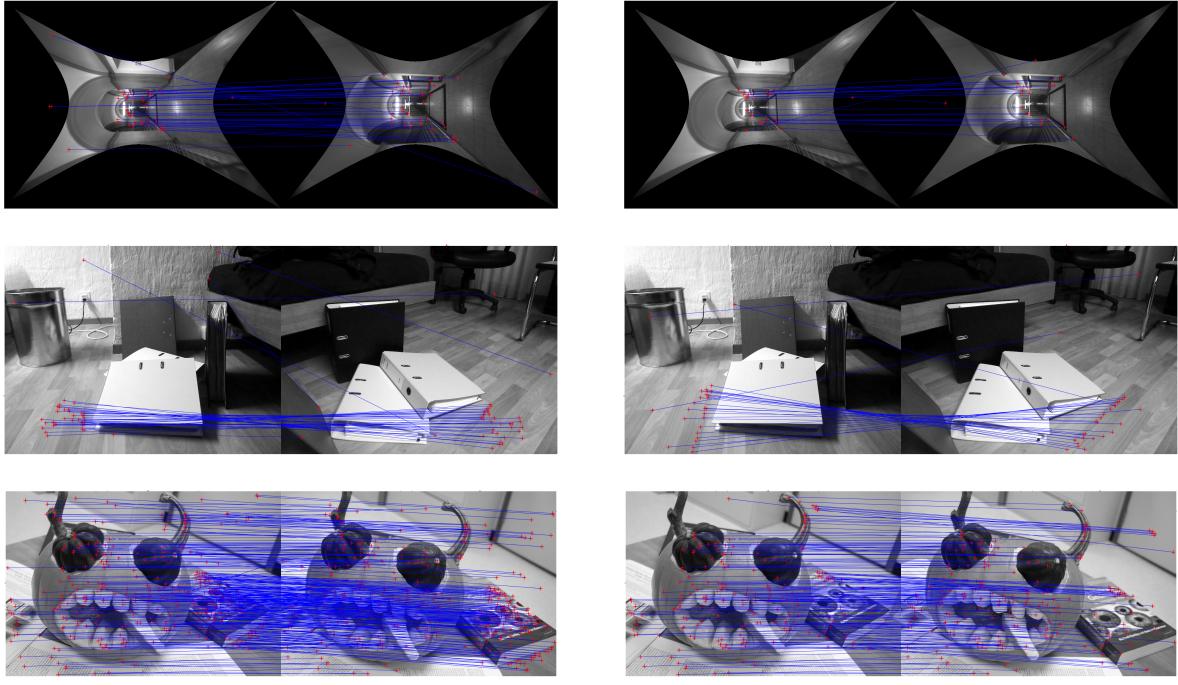


Figure 6: left: threshold=5, right: threshold=2

Data	ladybug		rect		pumpkin	
error threshold	5	2	5	2	5	2
total inlier counts	50	27	43	27	414	220
best inlier ratio	0.50	0.27	0.13	0.08	0.66	0.35
mean error of inliers	1.75	0.98	2.34	0.69	1.75	0.93

Table 2: total inlier counts / best inlier ratio / mean error of inliers with different error threshold using simple RANSAC

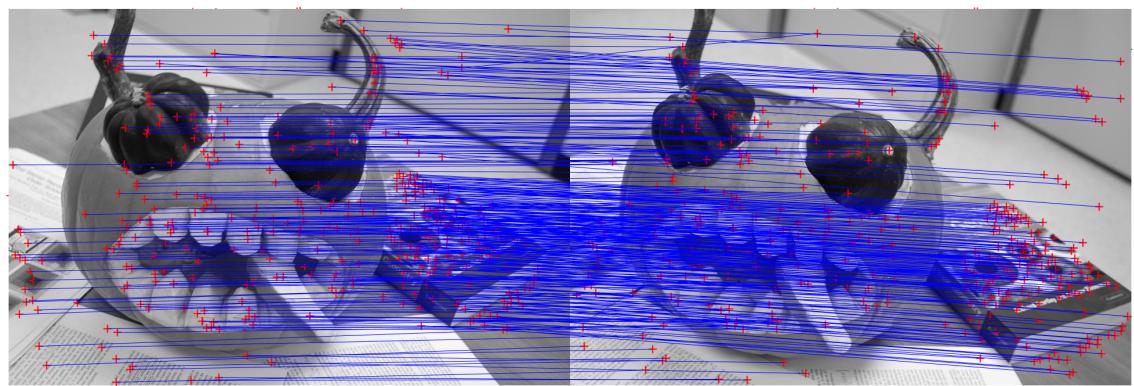
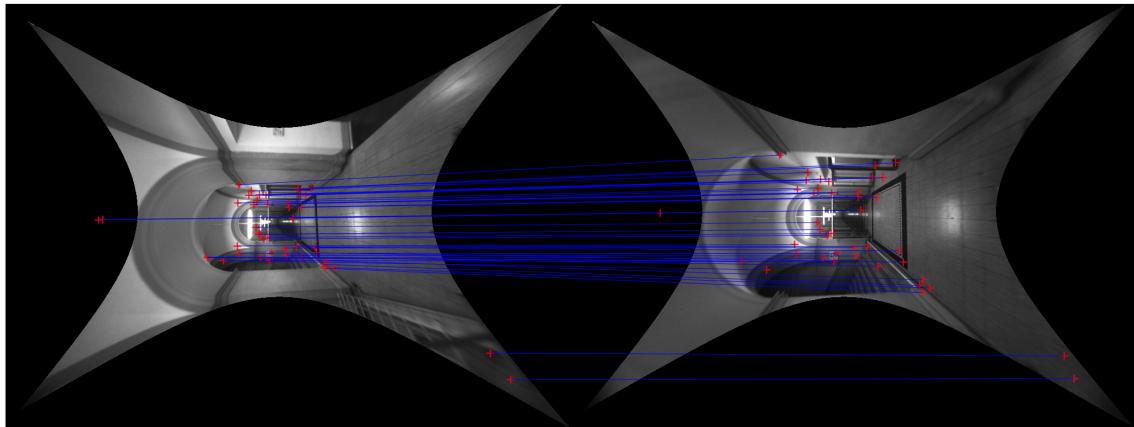


Figure 7: (a) ladybug: $M=51$ (b) rect: $M=415$ (c) pumpkin: $M=185819$