

Task 1: Line fitting

For this task, please refer to *ransacLine.m*.

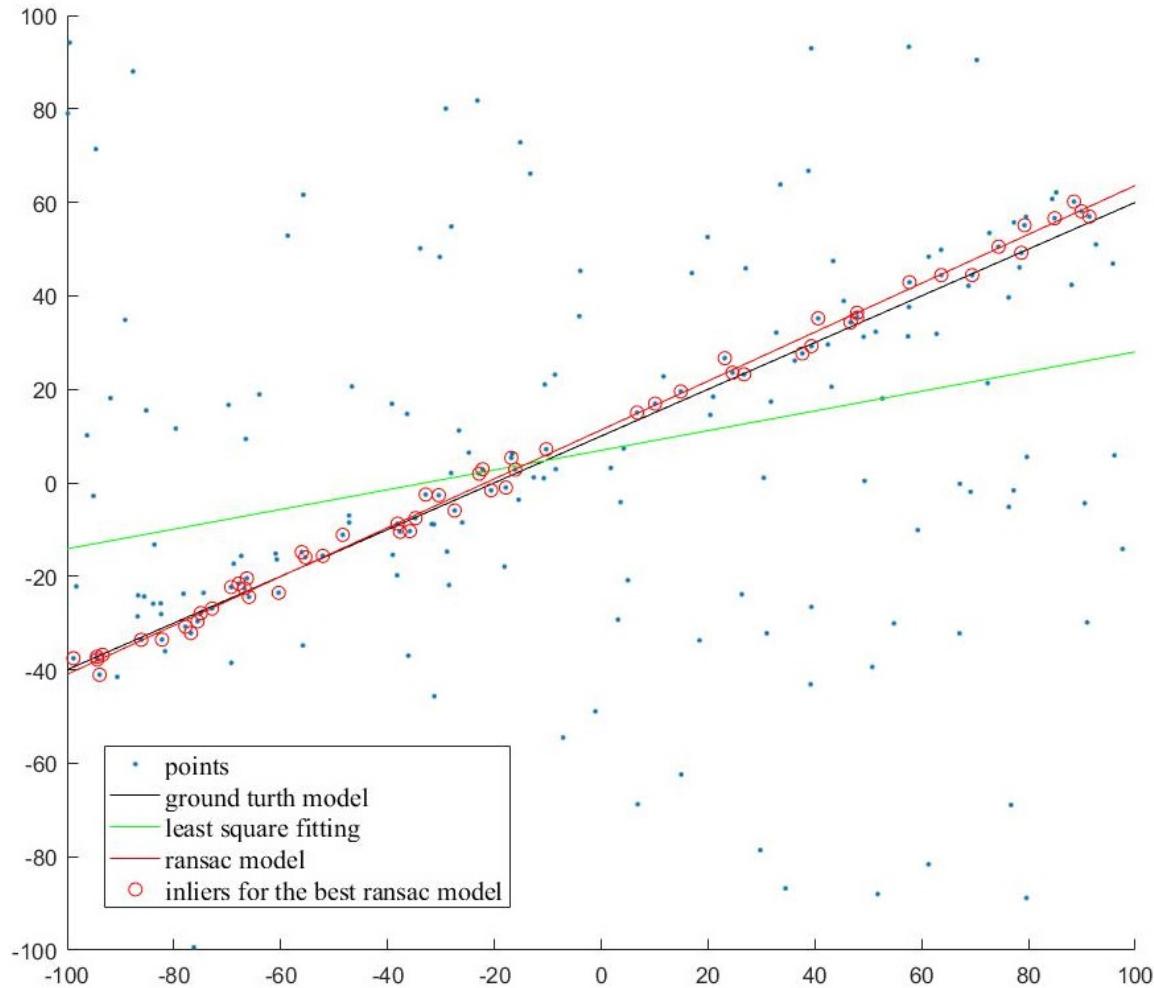


Figure 1: Least square and RANSAC line fitting result.

A line can be represented as $y = kx + d$. k and d can be determined from two sampled points on the line as Eq.1. The line can also be represented as Eq.2, from which we can calculate the distance from an arbitrary point p to the line l using Eq.3. Those points whose $d_{p,l} < \text{threshold}$ would be regarded as inliers. The sample resulting in the most inliers would be regarded as RANSAC's result while the corresponding k_l and d_l would be the fitted line's parameters. The final RANSAC result is shown in Fig.1.

$$k_l = \frac{y_2 - y_1}{x_2 - x_1}, \quad d_l = \frac{x_2 y_1 - x_1 y_2}{x_2 - x_1} \quad (1)$$

$$ax + by + c = kx - y + d = 0 \quad (2)$$

$$d_{p,l} = \frac{|a_l x_p + b_l y_p + c_l|}{\sqrt{a_l^2 + b_l^2}} = \frac{|k_l x_p - y_p + d_l|}{\sqrt{k_l^2 + 1}} \quad (3)$$

Another consideration is the number of RANSAC sampling iteration. Given the inlier ratio r and the sample number in each iteration N , we can get the relationship between the probability of at least one all-inliers sampling p and total iteration number M , as shown in Eq.4. In this case, $r = 0.5$ and $N = 2$. So we can get the iteration number for different p , as shown in Eq.5 and Eq.6.

The iteration number given by the testing programme is 300, which is way too larger than the necessary value. The sum of fitting error for the real model without noise (err_real), least square model for all the points (err_ls) and RANSAC model with different iteration numbers (err_ransac(M)) are reported in Table 1. For the consideration of generality, I conduct three sets of test and take the mean value. The results show us that the fitting error of RANSAC model is very close to the real model's and is far less than the fitting error of the least square model. Besides, the results also indicate that only 25 iterations are enough for RANSAC when the outlier ratio is 0.5.

$$p = 1 - (1 - r^N)^M \quad (4)$$

$$M(p > 0.99) \approx 16 \quad (5)$$

$$M(p > 0.999) \approx 25 \quad (6)$$

Table 1: Comparison of the line fitting error of different fitting methods

Test set \ fitting error	err_real	err_ls	err_ransac(300)	err_ransac(25)	err_ransac(16)
Set 1	39.094	174.927	38.623	40.521	56.8452
Set 2	40.658	158.288	44.141	43.277	45.075
Set 3	41.748	105.009	48.967	42.461	51.170
Mean	40.500	146.075	43.910	42.086	51.030

Task 2: Fundamental matrix estimation

For this task, please refer to *fundamentalMatrix.m* and *normalizePoints2d.m*.

Firstly, correspondence (≥ 8) are manually selected. Secondly, they are normalized using the same strategy using in CV Lab 1 and the normalization transformation T_1 and T_2 for both pixel sets are determined. Then,

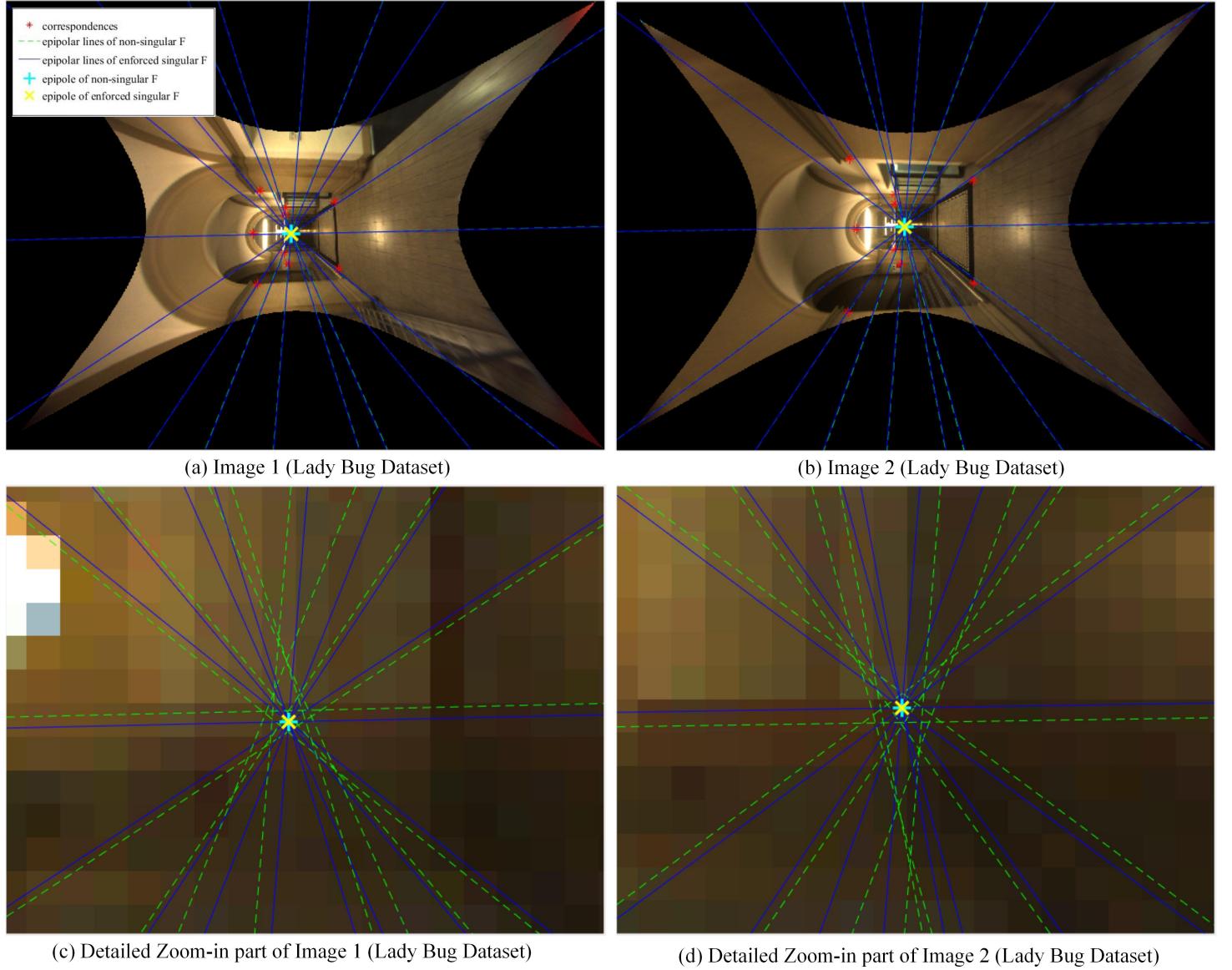


Figure 2: Non-singular and enforced-singular fundamental matrix estimation using 8-points method on Lady Bug Dataset

we can estimate the elements in the normalized fundamental matrix by applying the epipolar constraint as shown in Eq.7. The fundamental matrix is rescaled from the normalized one by applying Eq.8. Finally, I enforce the singularity constraint to F so that matrix \hat{F} 's singular value would be $(\sigma_1, \sigma_2, 1)$. This is done by applying **SVD** and forcing the third singular value to be zero.

$$x_2^T F x_1 = 0 \quad (7)$$

Assignment 4

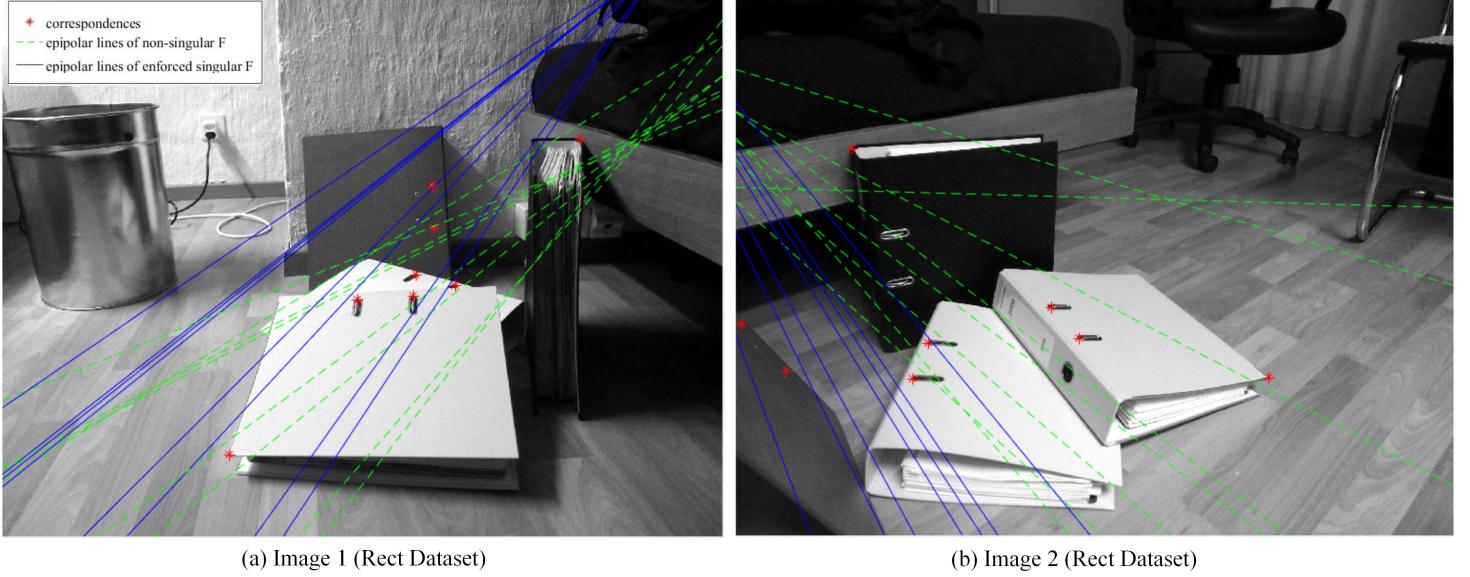


Figure 3: Non-singular and enforced-singular fundamental matrix estimation using 8-points method on Rect Dataset (degenerate case)

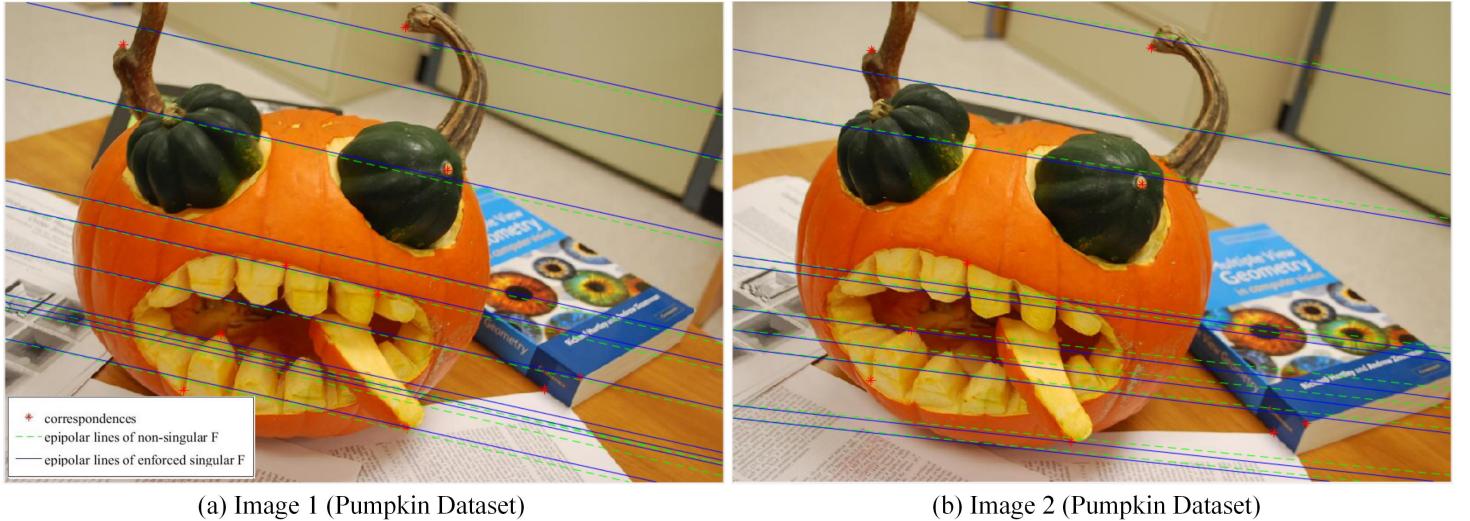


Figure 4: Non-singular and enforced-singular fundamental matrix estimation using 8-points method on Pumpkin Dataset (degenerate case)

$$F = T_2^T F_n T_1 \quad (8)$$

Given the non-singular fundamental matrix F and the enforced-singular fundamental matrix \hat{F} , epipolar lines on both the images can be calculated using Eq.9. Epipoles can also be determined as the left and

right null space of F or \hat{F} according to Eq.10.

$$l_2 = Fx_1, l_1 = F^T x_2 \quad (9)$$

$$Fe_1 = 0, e_2 F = 0 \quad (10)$$

The epipolar lines and the epipoles on both the images of the three datasets (Ladybug, Rect and Pumpkin) corresponding to the manually selected points and the fundamental matrix F or \hat{F} estimated by 8-points methods are shown respectively in Fig.2- Fig.4. According to Fig.2, it can be noticed that the epipolar lines and epipoles of F and \hat{F} are almost overlapped with each other. Selected points are approximately on their correspondences' epipolar lines. However, when zooming in the image, it is found that \hat{F} 's epipolar lines are almost intersected in the epipole while F 's epipolar lines are not intersected in one single point, which do not obey the epipolar geometry. So it's clear that the enforced-singularity fundamental matrix is the actual matrix wanted by us.

Unfortunately, for Rect and Pumpkin datasets, the manually chosen points may have a large amount of error. Besides, these points are very likely to lie on a common plane, so that the epipolar constraints would degenerate, which means only 8 correspondences (some of them are co-planar) is not enough to estimate the fundamental matrix. According to Fig.3 and Fig.4, selected points are not on their correspondences' epipolar lines. This problem would be solved in task 4 using dense feature matching and RANSAC algorithm. Please refer to Fig.7 and Fig.8 for epipolar lines and epipoles generated by correct fundamental matrix.

Task 3: Feature extraction and matching

For this task, the lib called **VLFeat** is downloaded.

To use it, a file called *startup.m* containing the script *run('VLFeatRootPath/toolbox/vl_setup')* is added to the working folder and launched. After that, the **SIFT** feature points can be extracted and the initial correspondences can be constructed.

The results are shown in Fig.6(a) - Fig.8(a), from which we can tell there are a lot of outliers within the candidate correspondences.

Task 4: Eight-point RANSAC

For this task, please refer to *ransac8pF.m*, *ransac8pF_adaptive_iter.m* and *distPointsLines.m*.

In this task, I keep randomly sampling 8 correspondences, from which the enforced-singularity fundamental matrix is estimated according to Task 2. Then the Sampson distance for each correspondence is calculated as the sum of the distance between the feature point and the epipolar line determined by fundamental matrix. The distance calculation is involved in *distPointsLines.m*. Those correspondences whose Sampson

Table 2: Inliers' number and mean Sampson distance of the inliers for RANSAC with different threshold distance

Threshold distance	#Inlier K	Inlier ratio	mean Sampson distance of inliers d_s	K/d_s
1	14	0.022	0.65	21.403
3	42	0.067	1.33	31.475
5	93	0.144	2.50	37.136
10	132	0.210	3.48	37.963
20	205	0.325	8.652	23.693

distance is less than RANSAC distance threshold would be regarded as inliers. Trial giving rise to largest number of inliers would be regarded as the best model so far.

For simple RANSAC, the iteration number is fixed as 1000. By varying the Sampson distance threshold, different groups of RANSAC consensus correspondences are determined, as shown in Fig.5 (only Pumpkin dataset is shown for saving the space) . Besides, the number of inlier correspondences K and mean Sampson distance of these inliers d_s are reported in Table 2. The result indicates that both the inlier number and mean Sampson distance would decrease as the threshold distance decreases and their ratio K/\bar{d}_s are very close for different threshold. In this case, since the iteration number is fixed, the found correspondences are not necessarily true, especially for larger threshold distance's cases. This phenomenon can also be noticed from Fig.5(b) and (c).

The iteration number should be determined adaptively to guarantee the presence of the optimal model (sampling) without being too time-consuming. In the case of 8-points method fundamental matrix estimation, for different inlier ratio of correspondences and different final probability of not missing the optimal model, the iteration number M is calculated according to Eq.4. The results are shown in Table 3. It is noticed that when the inlier ratio is small (for example, less than 0.1), RANSAC would take more than a billion iterations to gurantee the presence of the optimal sampling, which is still extremely time consuming. However, for a higher inlier ratio (for example, larger than 0.3), RANSAC would be efficient enough.

Next, we apply the adaptive RANSAC to all of the three datasets and count their total iteration numbers, which is reported in Table 4. In order not to have a too little inlier ratio which would lead to too many iterations, the threshold distance is set as 5 for all of the datasets. Ladybug dataset has the highest inlier ratio (≈ 0.33) among them, thus resulting in 19298 iterations, which take about 10 seconds. However, due to large rotation change of sight and similar feature patterns in the scenario, the inlier ratio for Rect dataset (≈ 0.15) ad Pumpkin dataset (≈ 0.22) are lower. So the iteration number for them is still very large, which may take several minutes and even hours to finish the RANSAC.

The optimal correspondences found by adaptive RANSAC are shown in Fig.6(b) - Fig.8(b). In Fig.6(c,d) - Fig.8(c,d), the epipolar lines and epipoles are demonstrated. It is noticed that almost all the inlier feature points are exactly on their corresponding epipolar lines.

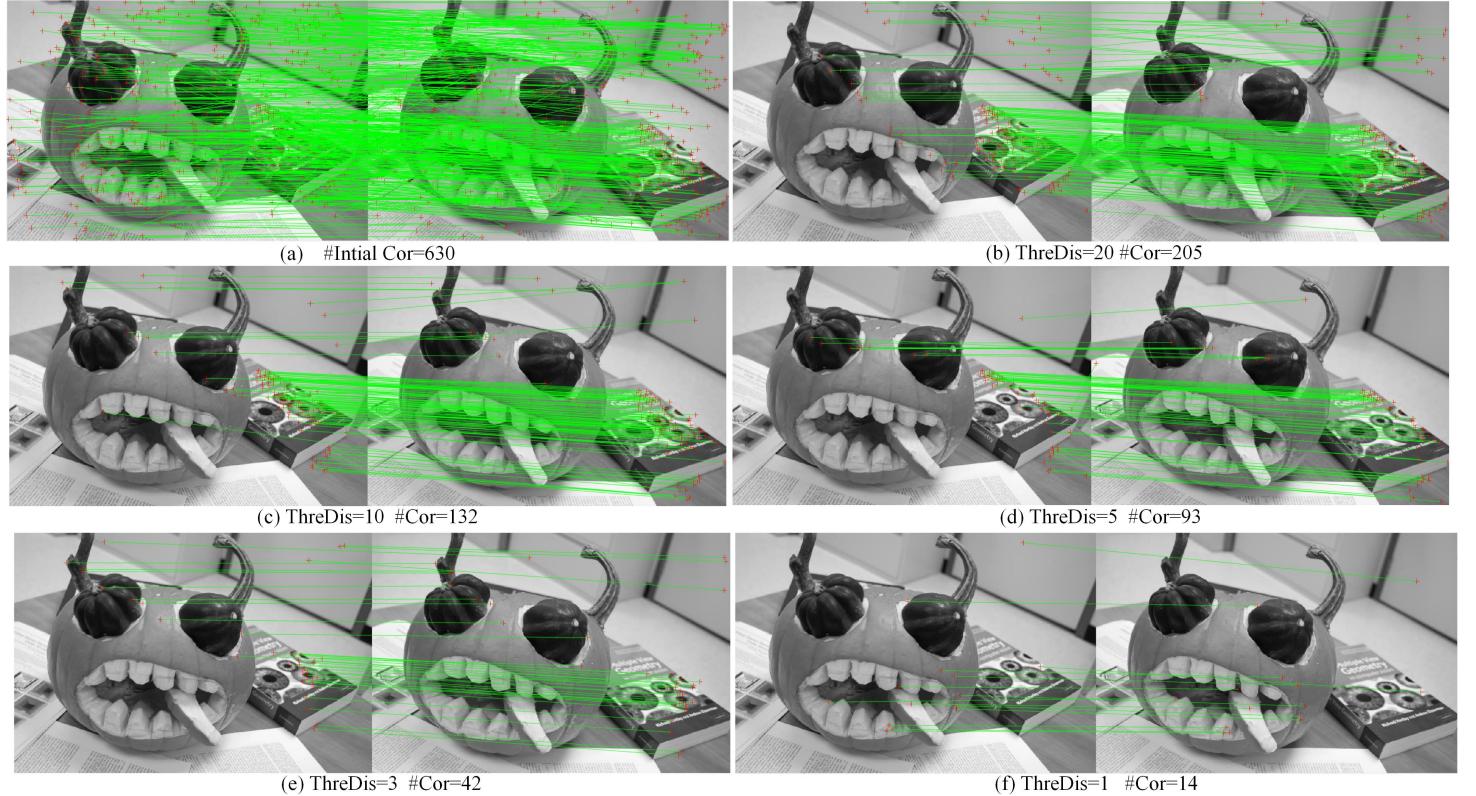


Figure 5: Correspondence determined by RANSAC for different Sampson distance threshold on Pumpkin Dataset (total iteration number M is fixed as 1000)

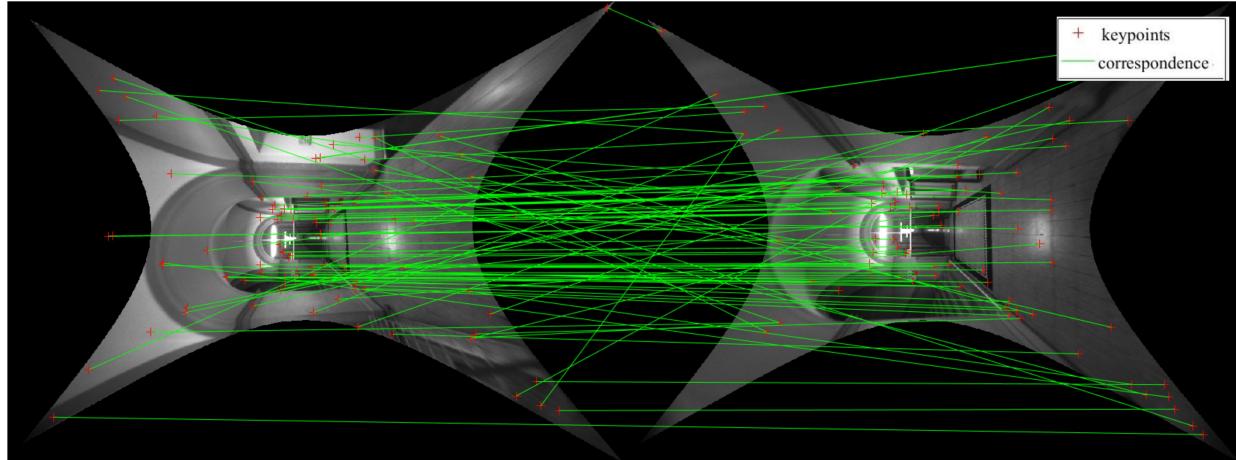
Table 3: Number of iterations for different p and r of 8-points RANSAC F matrix estimation

$p \setminus r$	0.05	0.1	0.2	0.3	0.4	0.5
0.9	5.89×10^{10}	2.30×10^8	8.99×10^5	3.51×10^4	3.51×10^3	588
0.95	7.67×10^{10}	3.00×10^8	1.17×10^6	4.57×10^4	4.57×10^3	765
0.99	1.18×10^{11}	4.61×10^8	1.80×10^6	7.02×10^4	7.02×10^3	1.18×10^3
0.999	1.77×10^{11}	6.91×10^8	2.70×10^6	1.05×10^5	1.05×10^4	1.76×10^3

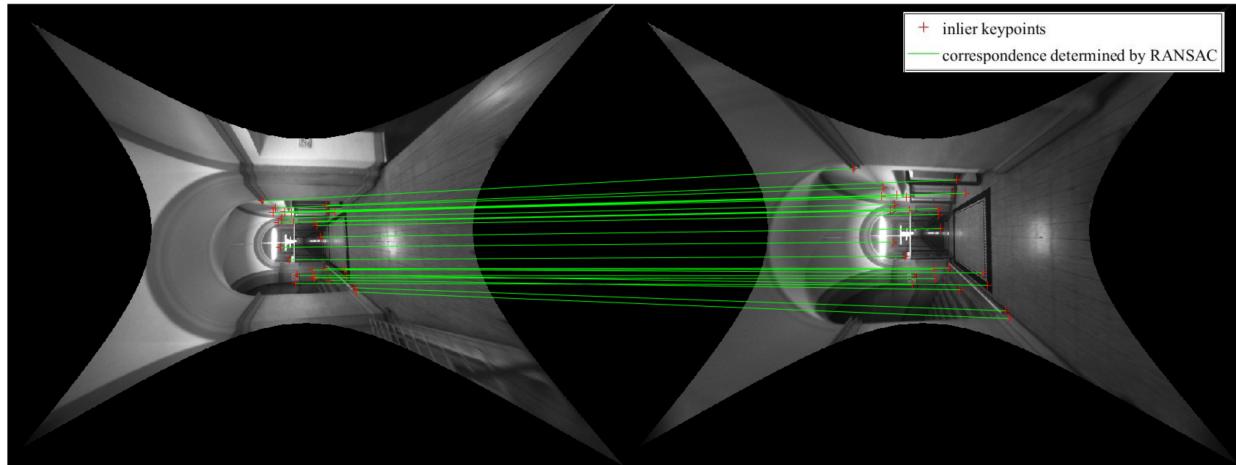
Table 4: Number of iterations for different dataset using adaptive RANSAC with threshold distance = 5

Dataset	Ladybug	Rect	Pumpkin
# total iteration M	19298	5531642	478238

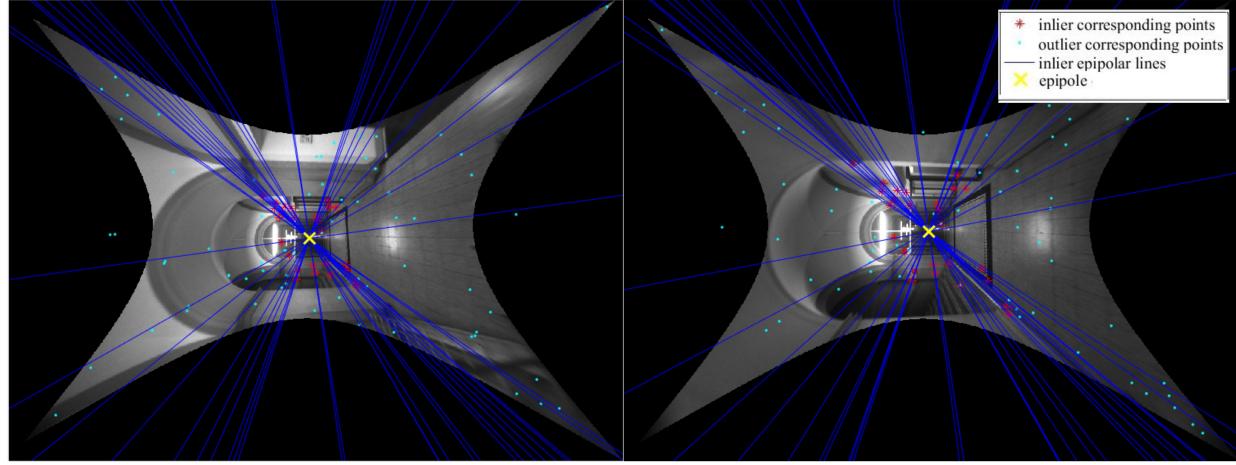
Assignment 4



(a) Initial correspondence between Image 1 and Image 2 (Ladybug Dataset)



(b) Correspondence determined by RANSAC between Image 1 and Image 2 (Ladybug Dataset)

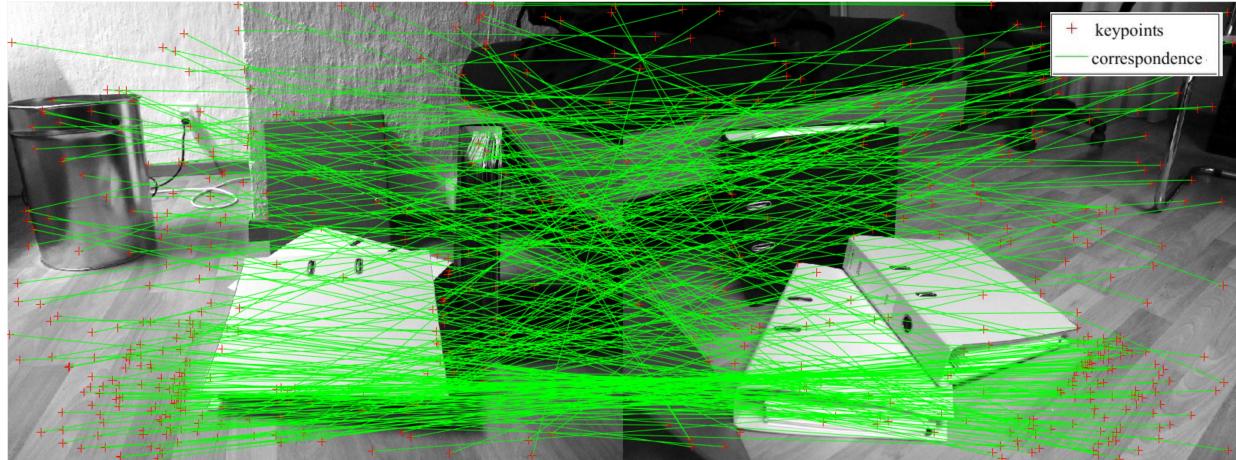


(c) Image 1 (Ladybug Dataset)

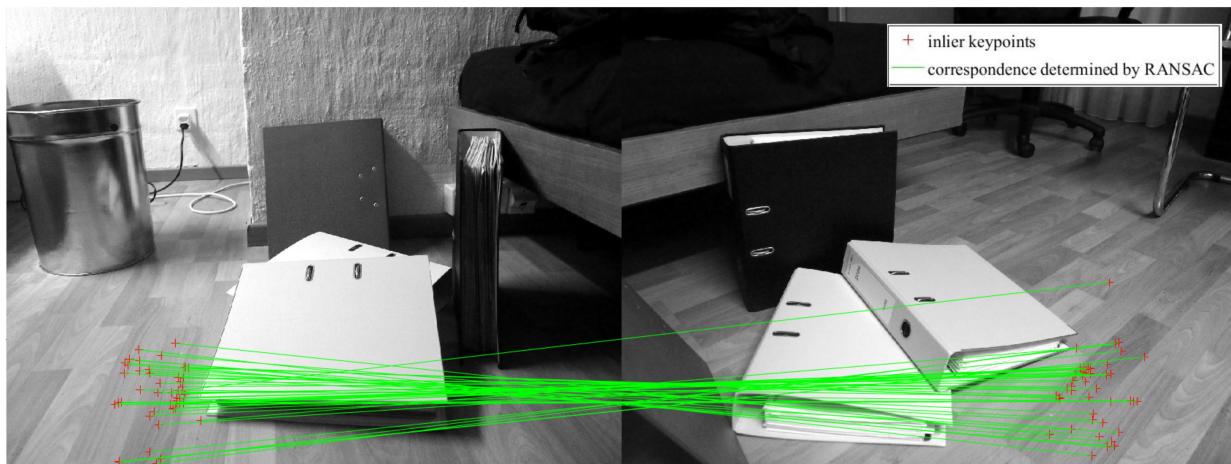
(d) Image 2 (Ladybug Dataset)

Figure 6: Correspondence and the fundamental matrix estimated from them determined by adaptive RANSAC on Ladybug Dataset

Assignment 4



(a) Initial correspondence between Image 1 and Image 2 (Rect Dataset)



(b) Correspondence determined by RANSAC between Image 1 and Image 2 (Rect Dataset)

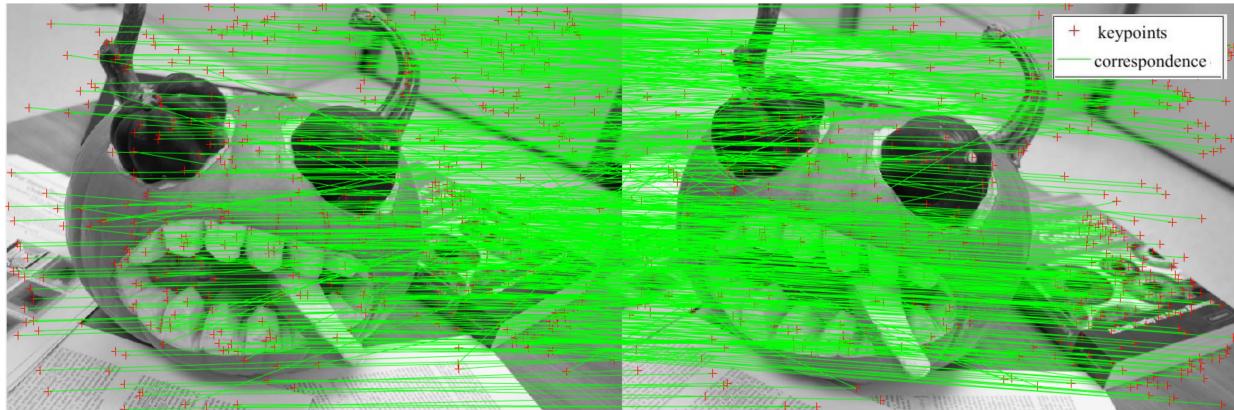


(c) Image 1 (Rect Dataset)

(d) Image 2 (Rect Dataset)

Figure 7: Correspondence and the fundamental matrix estimated from them determined by adaptive RANSAC on Rect Dataset

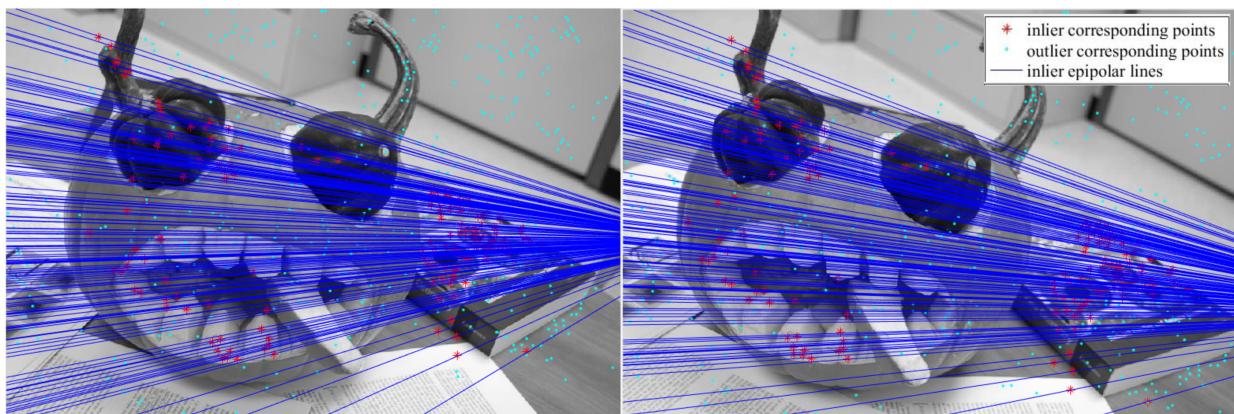
Assignment 4



(a) Initial correspondence between Image 1 and Image 2 (Pumpkin Dataset)



(b) Correspondence determined by RANSAC between Image 1 and Image 2 (Pumpkin Dataset)



(c) Image 1 (Pumpkin Dataset)

(d) Image 2 (Pumpkin Dataset)

Figure 8: Correspondence and the fundamental matrix estimated from them determined by adaptive RANSAC on Pumpkin Dataset