

1 RANSAC

1.1 Fitting a Line

1. Two points to fit a line as $y = mx + b$
2. The probability of picking a sample set with no outliers is $(1 - r)^s = 0.9^2 = 0.81$
The probability of picking a sample set with one or more outliers is $1 - (1 - r)^s = 0.19$
3. The probability of picking only sample sets with outliers is $(1 - (1 - r)^s)^N = 0.19^N$
The probability of picking any set with inliers is $1 - (1 - (1 - r)^s)^N = 1 - 0.19^N$
To let $1 - 0.19^N > 0.95$, we need $N \geq 2$
Therefore, 2 trials.

1.2 Fitting Transformations

1. Four degrees of freedom due to four entries of the 2X2 matrix. One sample can provide two equations thus two samples (regarding x_i, y_i as one sample) are required to find M.
2. Ideally, $[y_{i1}, y_{i2}]^T = M[x_{i1}, x_{i2}]^T$.
Therefore, $A = [\dots, [x_{i1}, x_{i2}, 0, 0], [0, 0, x_{i1}, x_{i2}], \dots]$, $b = [\dots, y_{i1}, y_{i2}, \dots]^T$
3. Reference: The page 42 of lecture8.pdf. Regarding the problem of $\arg \min_v \|Av - b\|^2$, I set up two equations per point as Prof. Liu did.

However, in `numpy.linalg.lstsq`, the function supports Y to be 2-dimensional, so when I actually implement this part, I follow the instruction of the API of `numpy.linalg.lstsq` function.

To solve $X_{stack} @ W = Y$, I denote $X_{stack} = [X, 1]$, where X is a $N \times 2$ matrix and 1 is an all-one vector of size $N \times 1$.

Then I got

$$W = [[2.04098127, -3.0696843], [-1.01644528, 0.94335775], [-1.87154926, -3.05145812]]$$

Therefore

$$S = [[2.04098127, -1.01644528], [-3.0696843, 0.94335775]]$$

$$t = [-1.87154926, -3.05145812]^T$$

4. In the following figure, I plot X, Y, \hat{Y} with different colors. As we can see, Y and \hat{Y} align with each other very well.

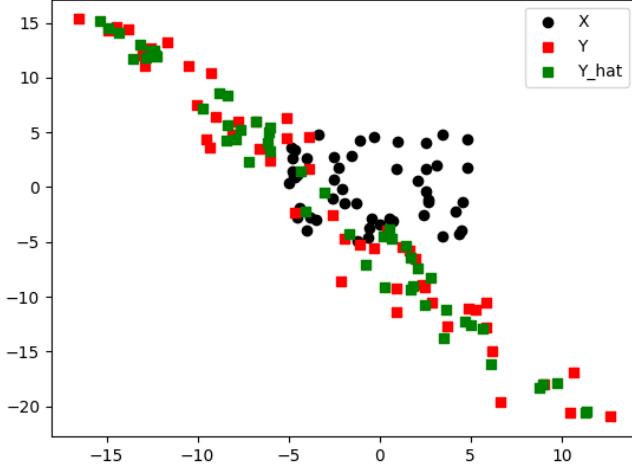


Figure 1: X , Y , \hat{Y} in one figure

5. The fitting result is good!

First, with S , I transform data X , which is clustered as a square, into a line that is paralleled with data Y . Second, with t , I align the line with data Y , getting the result \hat{Y} , shown as green square scatters in the Figure 1.

6. I report matrix H of each case as below:

```
[[[-5.84619486e-01 -9.38188546e-04 7.85709946e-02]
 [-1.48861804e-03 -3.619334740e-01 4.27826653e-01]
 [-2.62615122e-05 -2.09196954e-05 -5.81387269e-01]]
 [[ 3.68911272e-01 8.92258783e-04 -3.93043451e-01]
 [ 2.75059839e-05 5.96028476e-01 -2.41643577e-02]
 [ 2.17658979e-07 1.34347784e-05 5.94639553e-01]]
 [[-2.53193239e-01 -3.99057890e-03 5.69038181e-01]
 [-5.45228988e-03 -2.52238879e-01 6.2801972e-01]
 [-1.21872179e-04 -1.08513265e-04 -3.91808736e-01]]
 [[ 4.29709571e-12 5.77350269e-01 -3.07598061e-10]
 [ 5.77350269e-01 1.15147653e-12 -9.97508158e-11]
 [ 5.31784754e-14 2.87491195e-14 5.77350269e-01]]
 [[-7.91063985e-03 2.28491079e-13 6.01208628e-01]
 [-5.35800683e-14 -7.91063985e-03 7.38974625e-01]
 [ 2.89392053e-15 -1.06881468e-15 7.91063985e-03]]
 [[ 1.38048111e-01 2.19005570e-01 -6.17163607e-01]
 [ 2.20297434e-01 1.36451811e-01 -6.05518007e-01]
 [ 7.60197607e-05 4.81267787e-05 3.43927668e-01]]
 [[ 1.34941272e-01 7.96016480e-03 -1.11241055e-02]
 [-1.37954817e-02 1.513780758e-01 9.63220032e-01]
 [-5.34941898e-03 -1.11646326e-05 1.75235524e-01]]
 [[-1.44485744e-01 8.35368093e-03 -7.39389853e-01]
 [ 8.19996491e-03 -1.69535496e-01 -6.11590373e-01]
 [ 7.82502801e-05 -1.85804532e-05 -1.71768495e-01]]]
```

Figure 2: H of 8 cases

7. I display the figure of each case as below:

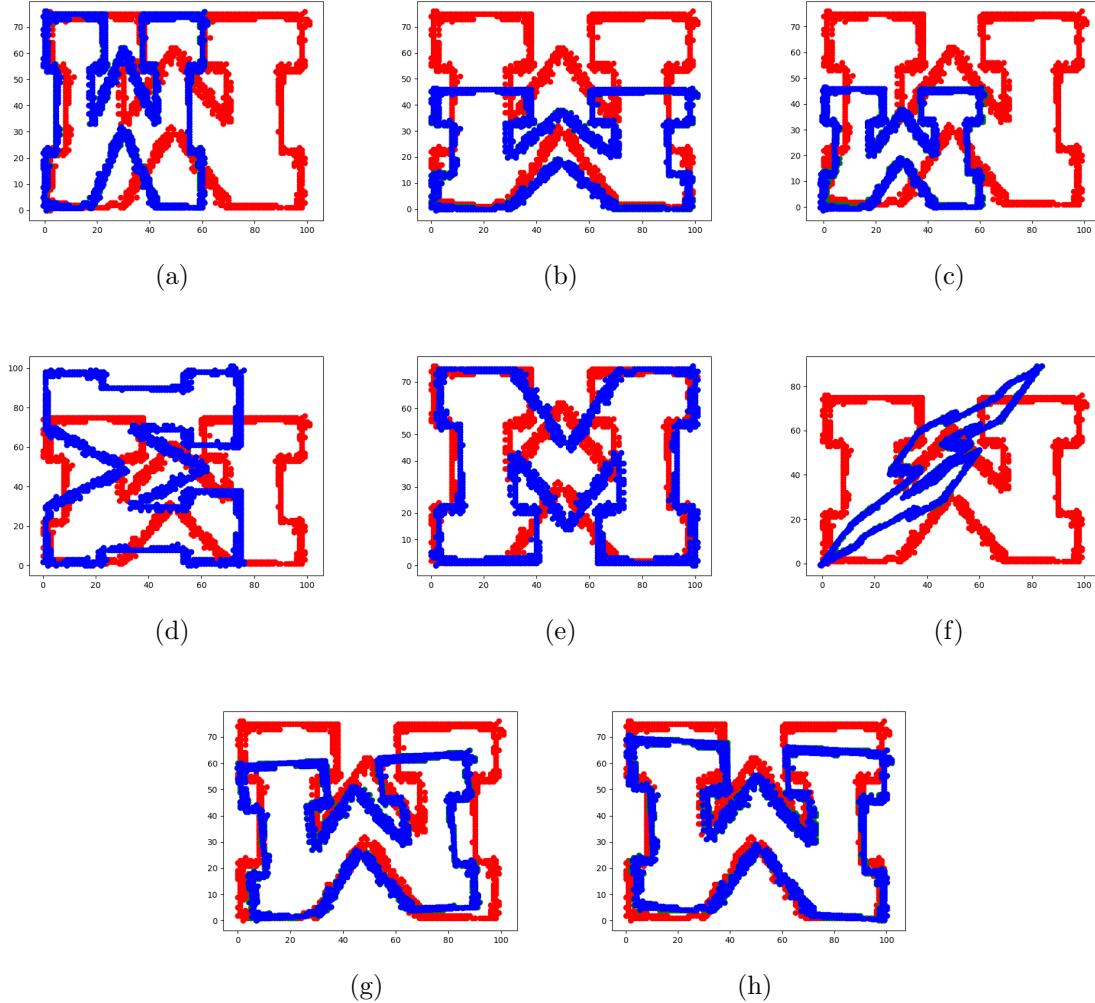


Figure 3: Visualize the original points, the target points and the points after homography transformation in one figure

8. Yes, they do make sense to me:

The green image Y and the blue image \hat{Y} align with each other really well in each figure, both of them can be regarded as being homography transformed from the red image X .

2 Image Stitching

1. I display the grayscale images

Homework 3



(a) Left (b) Right

Figure 4: Display the grayscale images

2. I display both the images along with the feature points

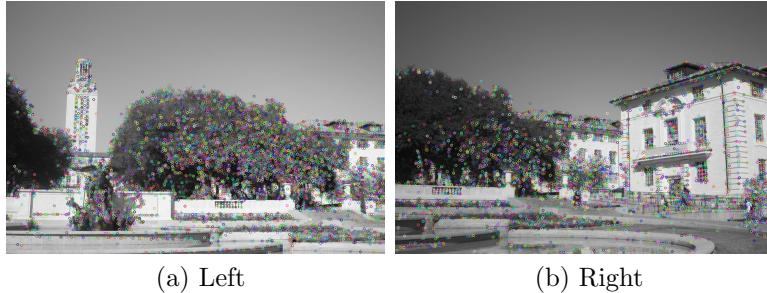


Figure 5: Display both the images along with the feature points

- I chose Euclidean distance after normalizing all descriptors to have zero mean and unit standard deviation.
 - I select all pairs whose descriptor distances are below a specified threshold, which is 3 in my settings. Finally, there are 362 pairs of key points.
 - After RANSAC, there are 324 inliers and the average residual for the inliers (squared distance between the point coordinates in one image and the transformed coordinates of the matching point in the other image) is 1.20. I show the matched image results as below:



Figure 6: Match left and right

6. I warp the left image to align with the right one.



Figure 7: Warp left to right

7. I stitch the left image with the right one.

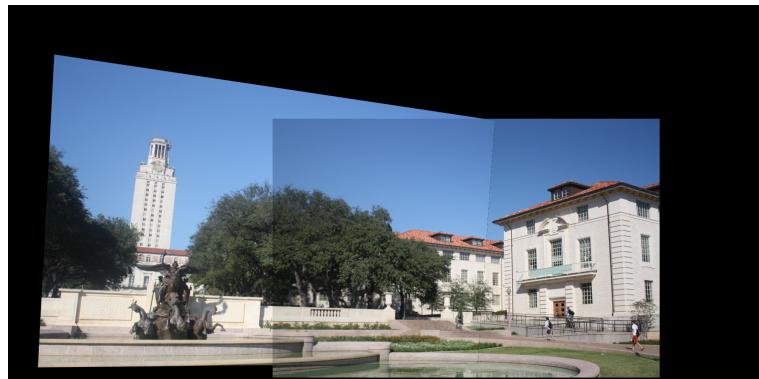
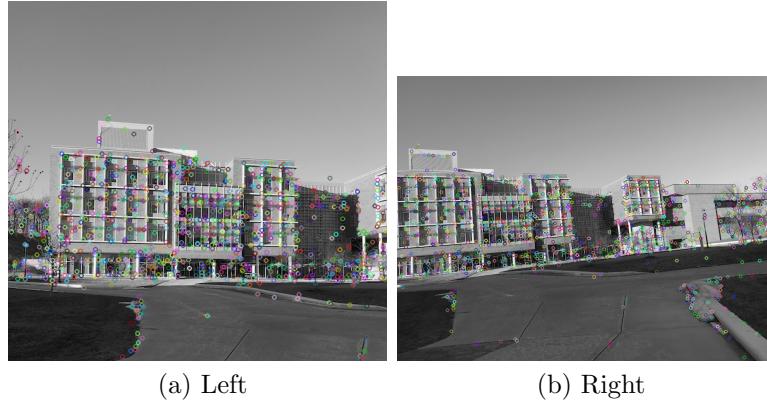


Figure 8: Stitch

8. Detected feature points:



(a) Left

(b) Right

Figure 9: Display both the images along with the feature points

Match:

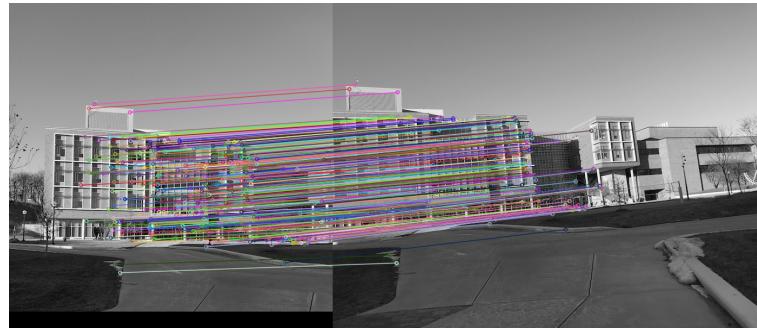


Figure 10: Match left and right

The inliers: After RANSAC, there are 299 inliers and the average residual for the inliers (squared distance between the point coordinates in one image and the transformed coordinates of the matching point in the other image) is 1.17.

I stitch the left image with the right one.

Homework 3

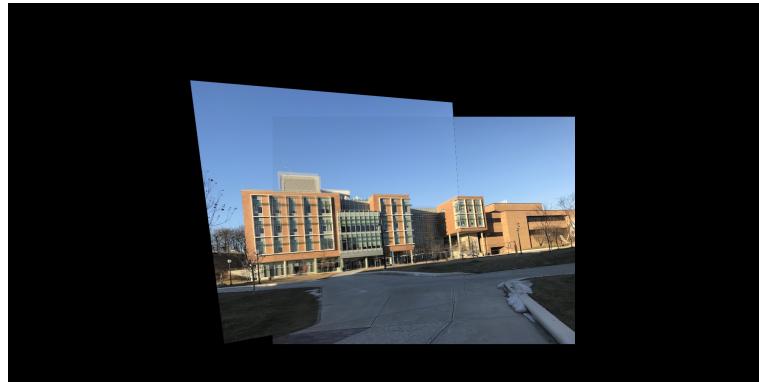


Figure 11: Stitch