CVIP Homework-3

Part1: Stitching pairs of Images

a) I have used the provided harris function for feature detection and to get proper match points in both the images I used below parameter for harris corner detector:
sigma = 2, thresh = .05, This gives me good number of features.
I took neighborhood size of 19 around the matched points, to get the matching feature in other image.
I am selecting top 200 putative matches from the matched points using dist2 function provided. Then, In RANSAC algorithm selecting random 4 points to calculate the homography. Apply this homography to check number of point(inliers) satisfying this homography based on threshold value of 10. Keep track of inlier counts in each iteration for a particular homography. Repeating this steps for 300 time selecting the Homography which gives maximum number of inliers. Then stitching the images using best homography.
Below are the files for part 1 with brief explanation.

1. MainScript_part1.m: This is main script file from where other methods are get called. reading the two images, displaying the matched inliers and final output image.
2. neighborhood_features.m: This method is returning neighborhood features around all the coordinates of a given size.
3. ransac_inliers.m: Implementation of RANSAC algorithm. It returns best homography and all the inliers and residual of all the inliers.
4. stich_images.m: Stitching the both the images using the best homography
5. computeHomography.m: compute the homography using 4 pairs of points
6. harris.m: Provided with code.
7. dist2.m: Provided with code.
8. find_sift.m: Provided with code. [Not used by me in this implementation]

b) Calculation and results for uttower:

By taking parameters taken as described above:
number of homography inliers : 105
Average residual for inliers: 1.6226

```
>> MainScript_part1
No of inliers: 105
Average residual for the inliers: 1.6226
Warning: Image is too big to fit on screen; displaying at 67%
> In images.internal.initSize (line 71)
  In imshow (line 328)
  In MainScript_part1 (line 44)

homography =

    1.1706   -0.0905 -496.3530
    0.1321    1.1147 -128.6766
    0.0002   -0.0000    1.0000
```

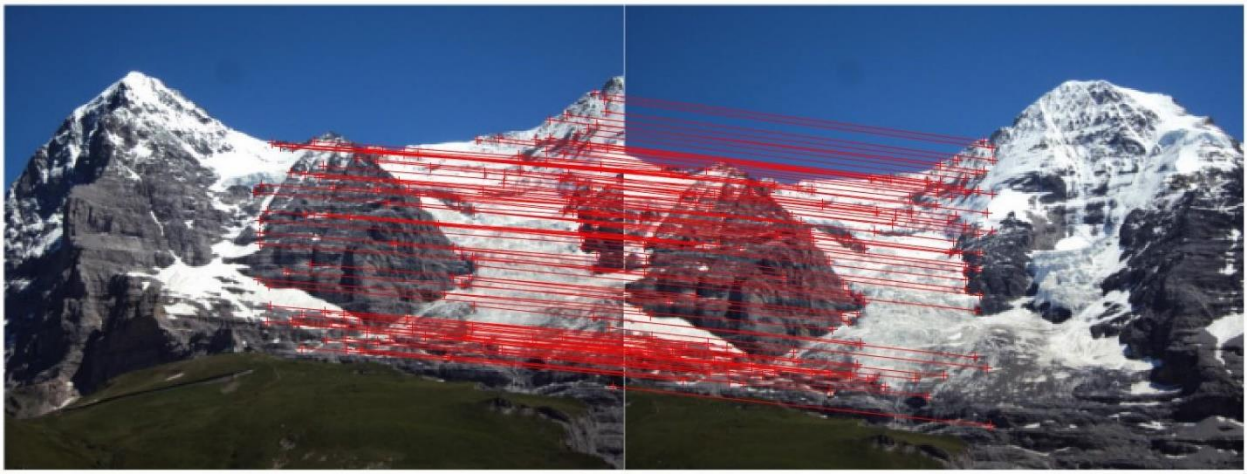
Inliers match points for uttower image:

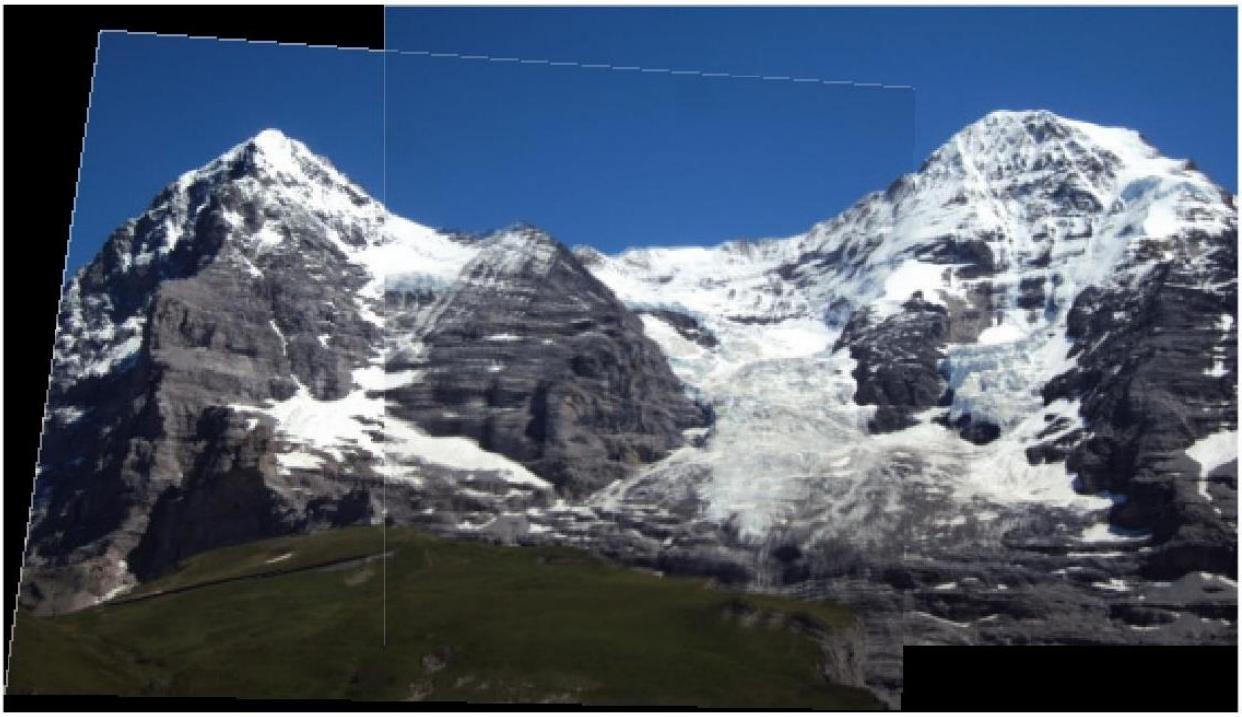
c)

1. Hill

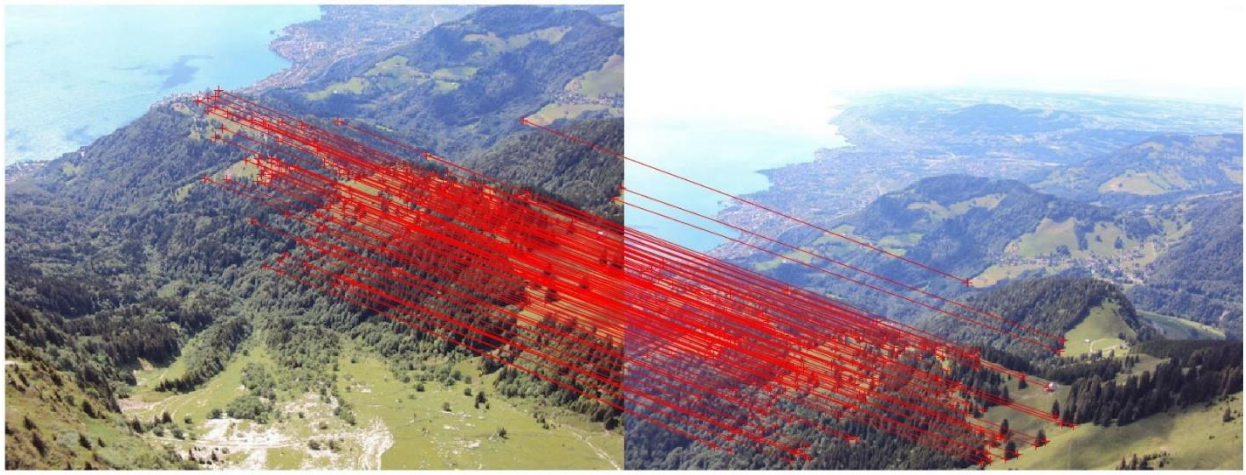
No of inliers: 128

Average residual for the inliers: 1.7648

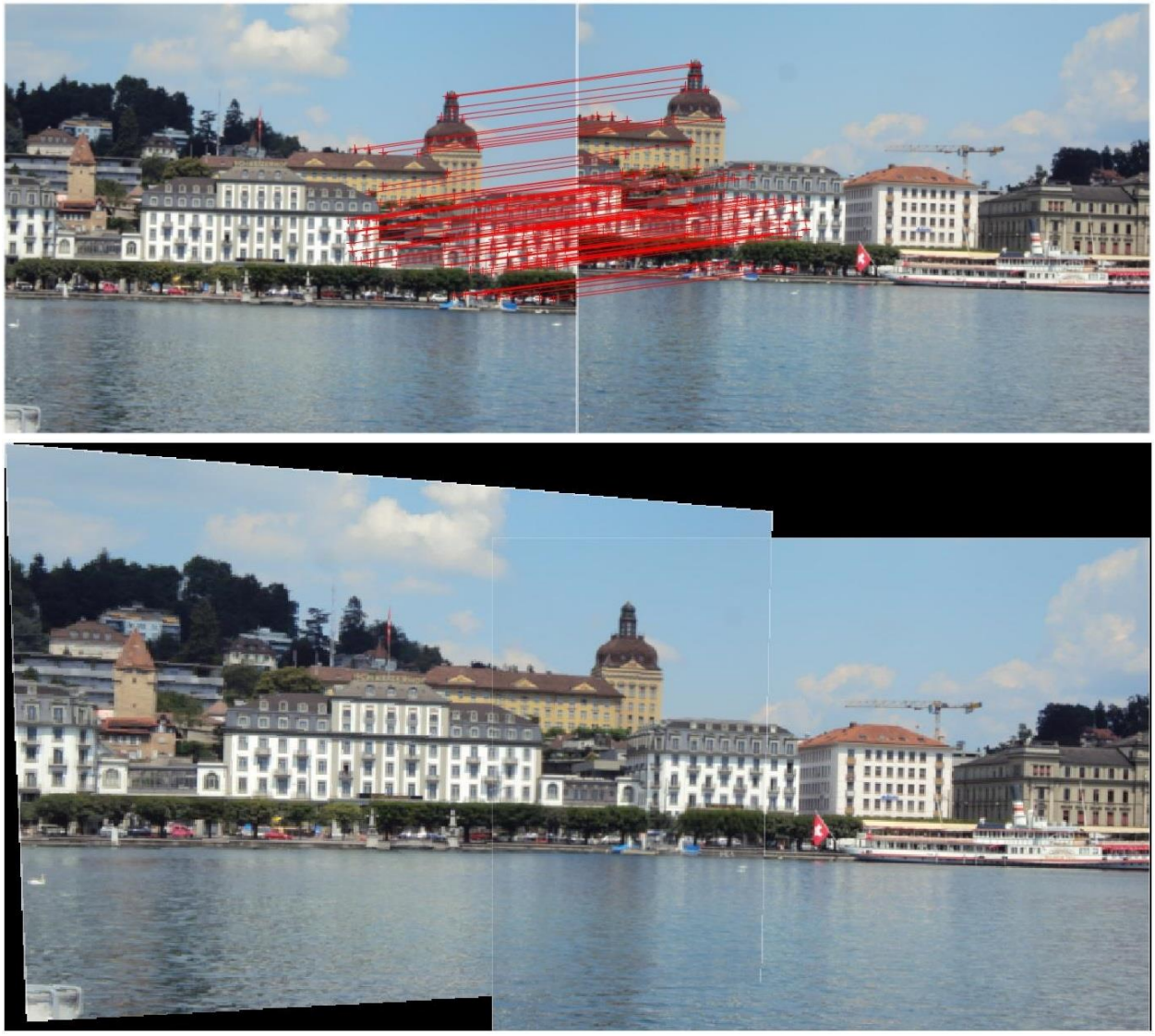




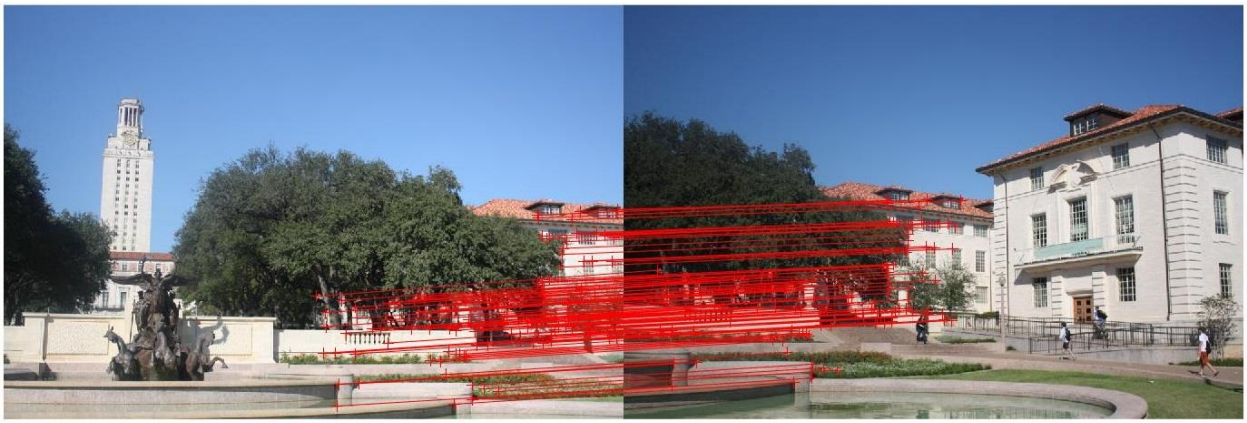
2: ledge
No of inliers: 152
Average residual for the inliers: 1.7681

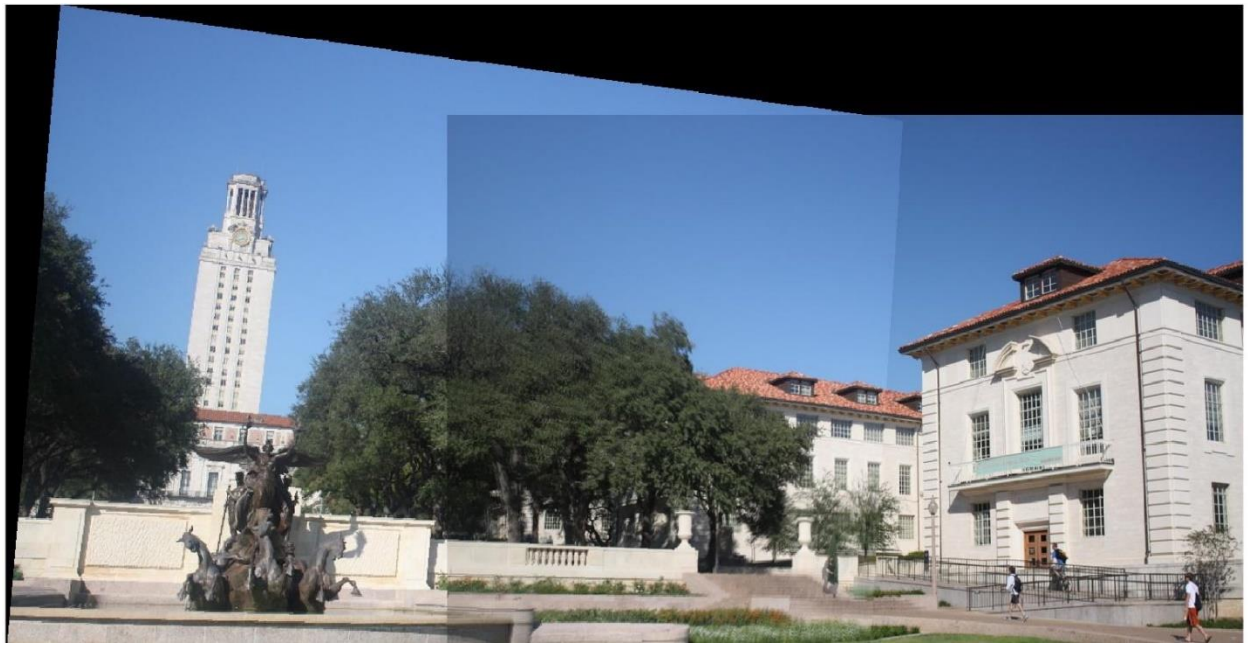


3.pier
No of inliers: 99
Average residual for the inliers: 1.0098



4. uttower
number of homography inliers : 105
Average residual for inliers: 1.6226





2) Fundamental Matrix Estimation and Triangulation

Implemented fundamental matrix using both the normalized and the unnormalized algorithms.

1. MainScript_part2.m: Main script , from here all the fucntion get called

2. display_results.m: display the inlier results (snippet from sample_code)

3. dist2.m: already provided

4. fit_fundamental.m: calculation of fundamental matrix using match points

5. fundamental_normalized_cord.m: Calculation of fundamental matrix after normalization

6. ransac_inliers.m: RANSAC implementation for fundamental matrix. Almost similar Implementation as part1.

7. residuals_for_givenF.m: Calculation of residual (Code snippet from sample_code)

8. sample_code.m: Already provided

9. Traingulation.m: code for triangulation, and plotting using plot3 method as given in hint.

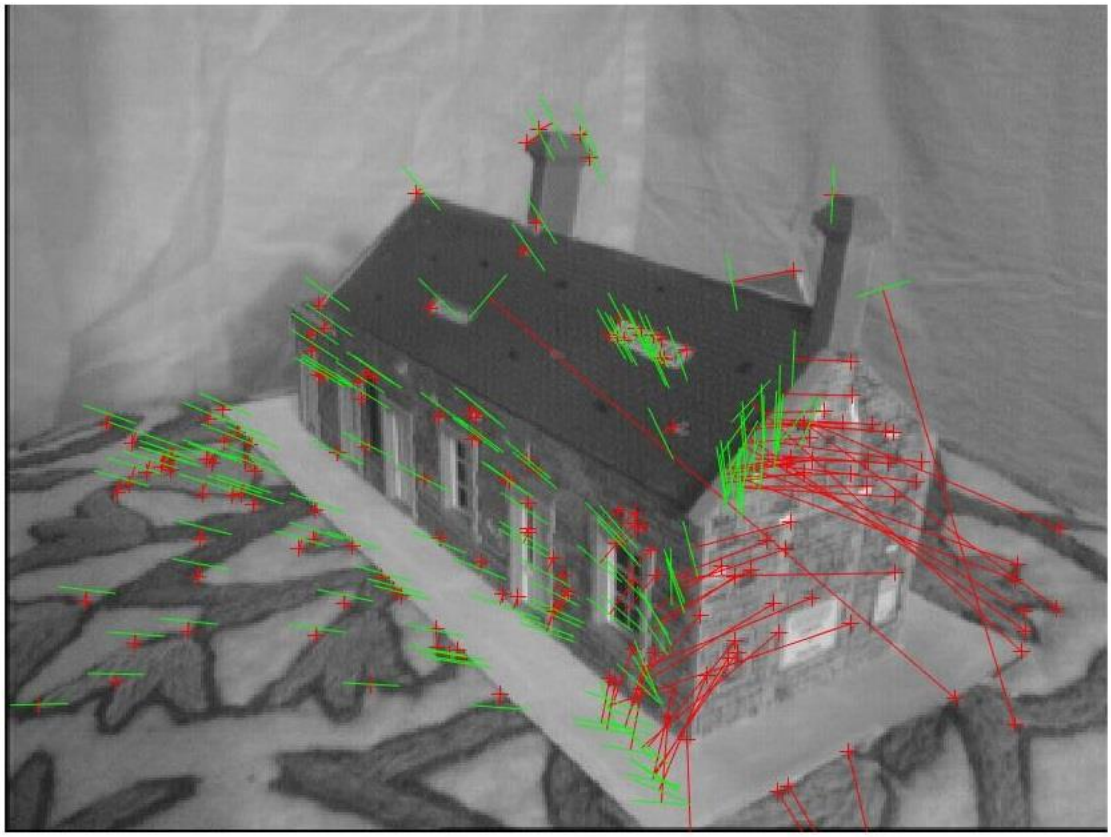
a)

1. house

```
mean residual for unnormalized algorithm :
   22.3353

43   F_norm = fundamental_normalized_cord(matches);
mean residual for normalized algorithm :
    0.2157
```

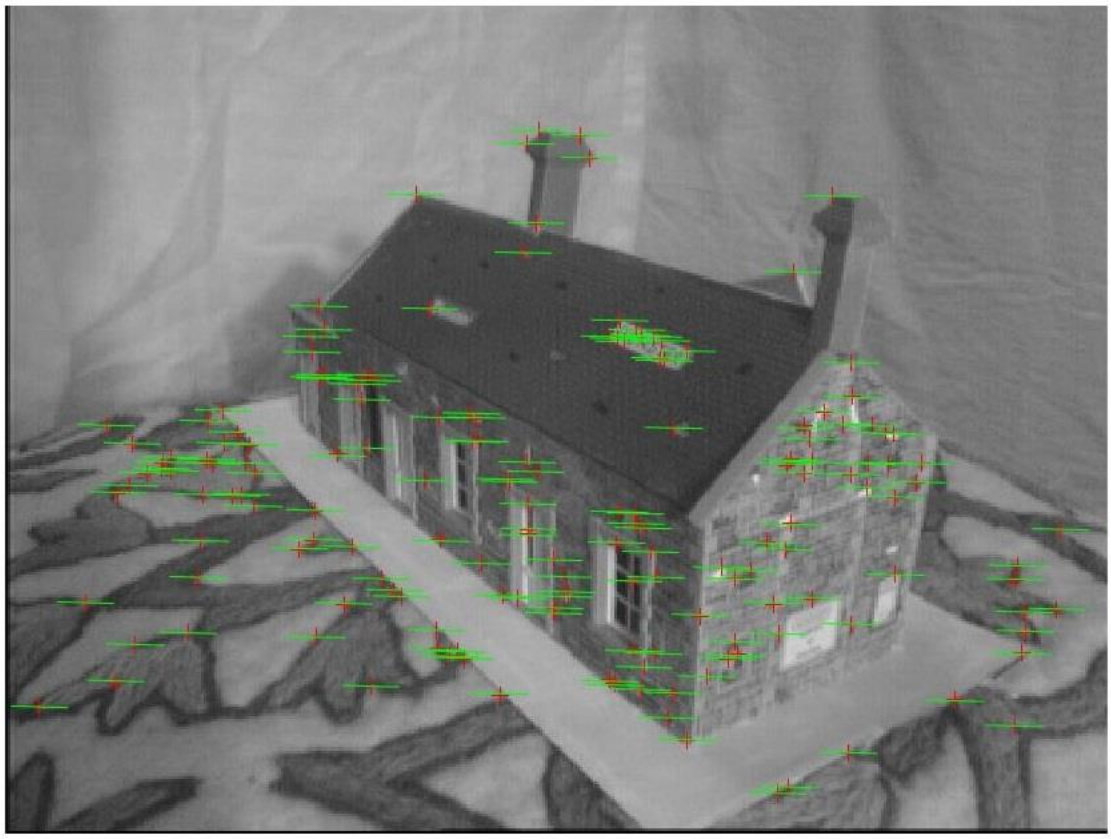
Un-normalized:

mean residual for un-normalized algorithm: 22.3353



Normalized:

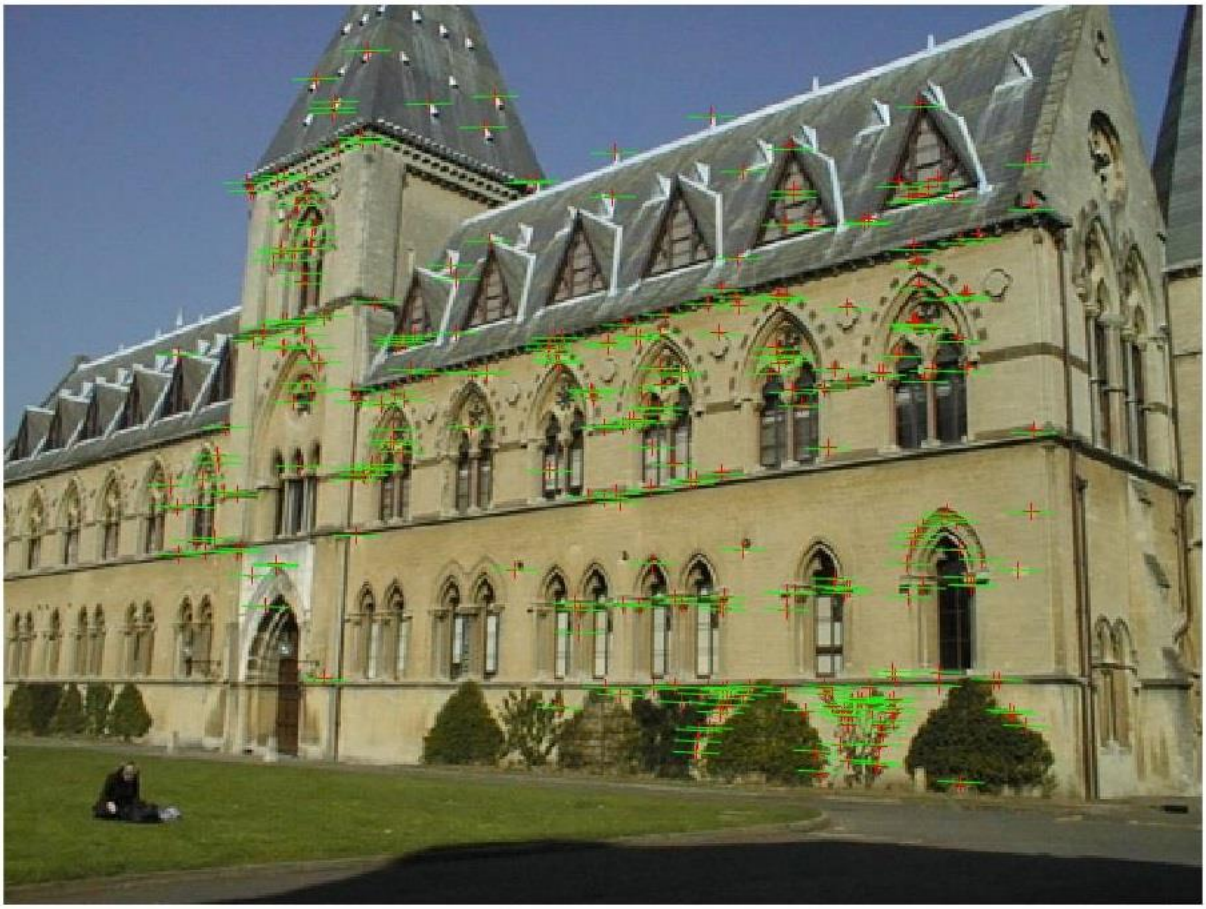
mean residual for normalized algorithm: 0.2157



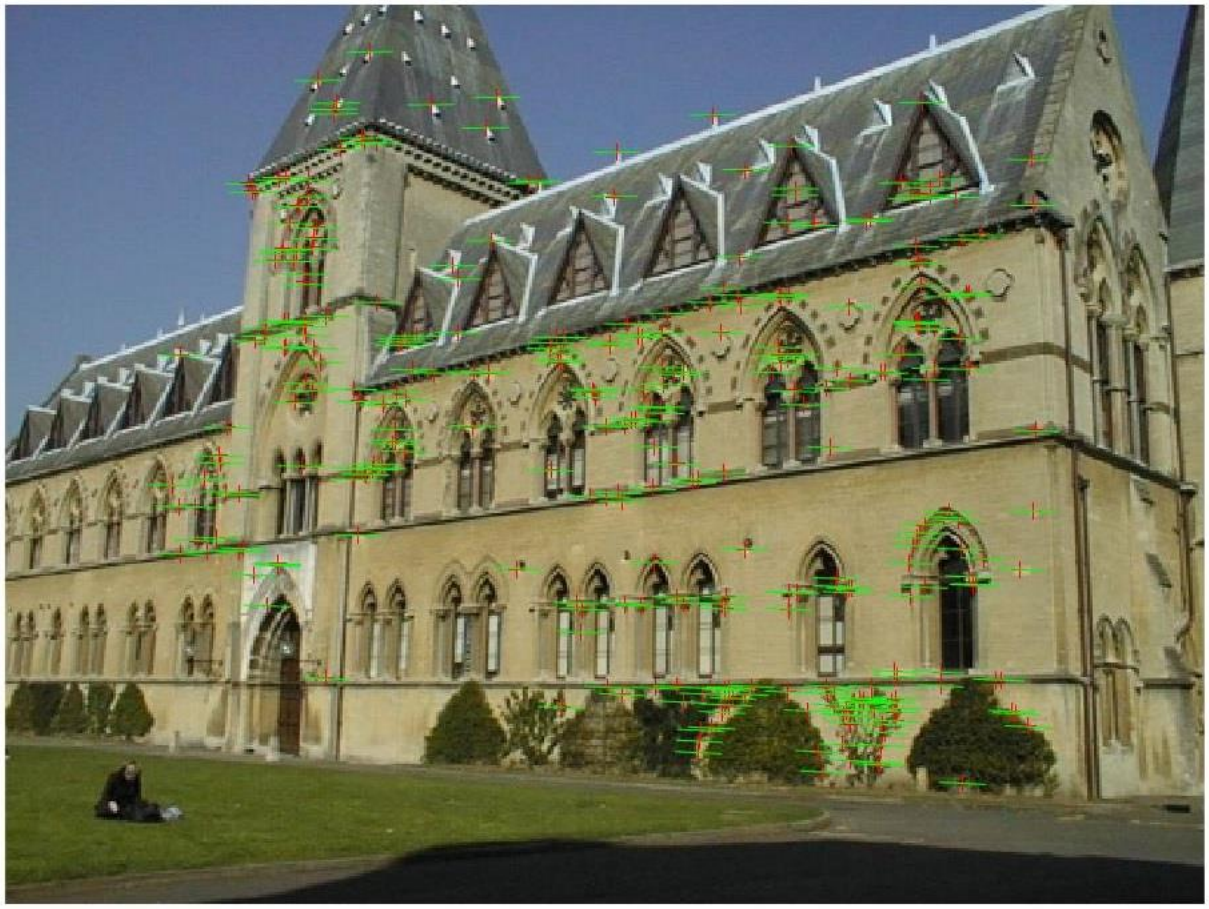
2. library

```
35    F = fit_fundamental(matches); % this is a function that you should write
mean residual for unnormalized algorithm:
    0.4651

43    F_norm = fundamental_normalized_cord(matches);
mean residual for normalized algorithm:
    0.2236
```

mean residual for un-normalized algorithm: 0.4651



mean residual for normalized algorithm: 0.2236



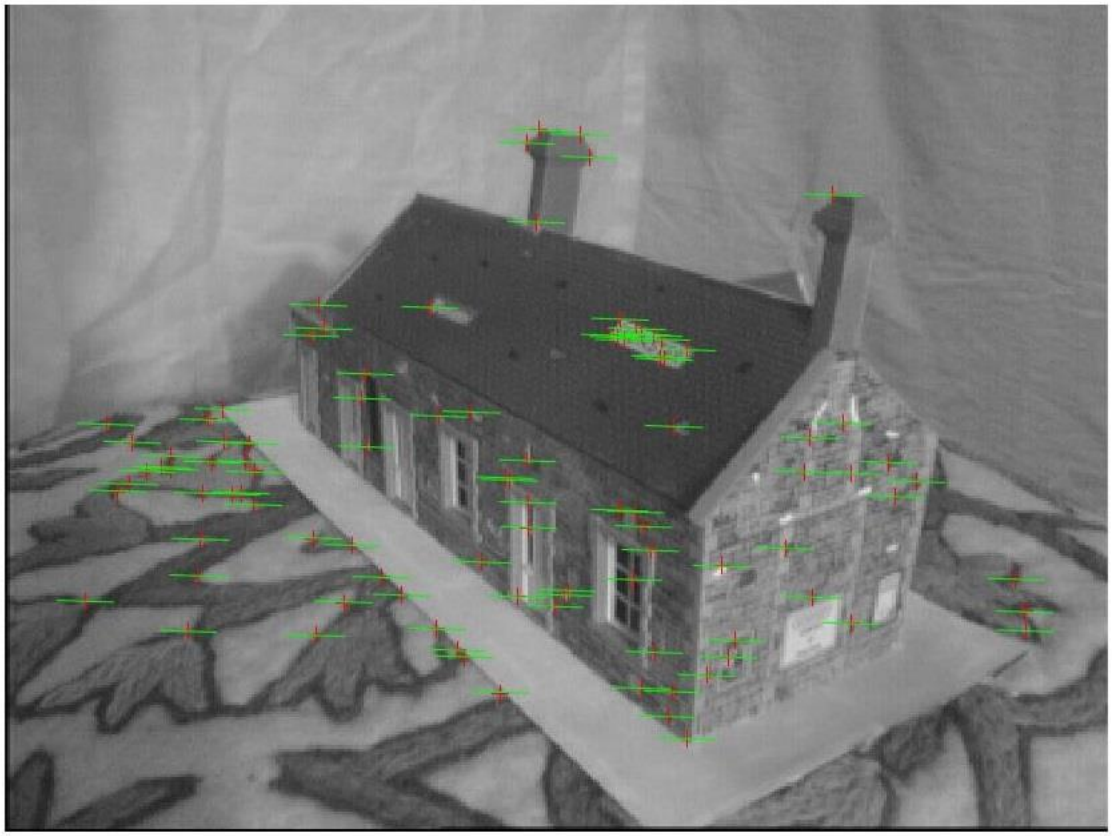
B) normalized estimation without ground truth matches

1.House:

```
43   F_norm = fundamental_normalized_cord(matches);
mean residual for normalized algorithm:
    0.2157

52   [ inliermatches , F, res] = ransac_inliers( matches );
Using RANSAC and Normalized,mean residual for Inliers:
    0.0983

no of inliers:
    97
```

Using RANSAC and Normalized, mean residual for Inliers: 0.0983

no of inliers: 97

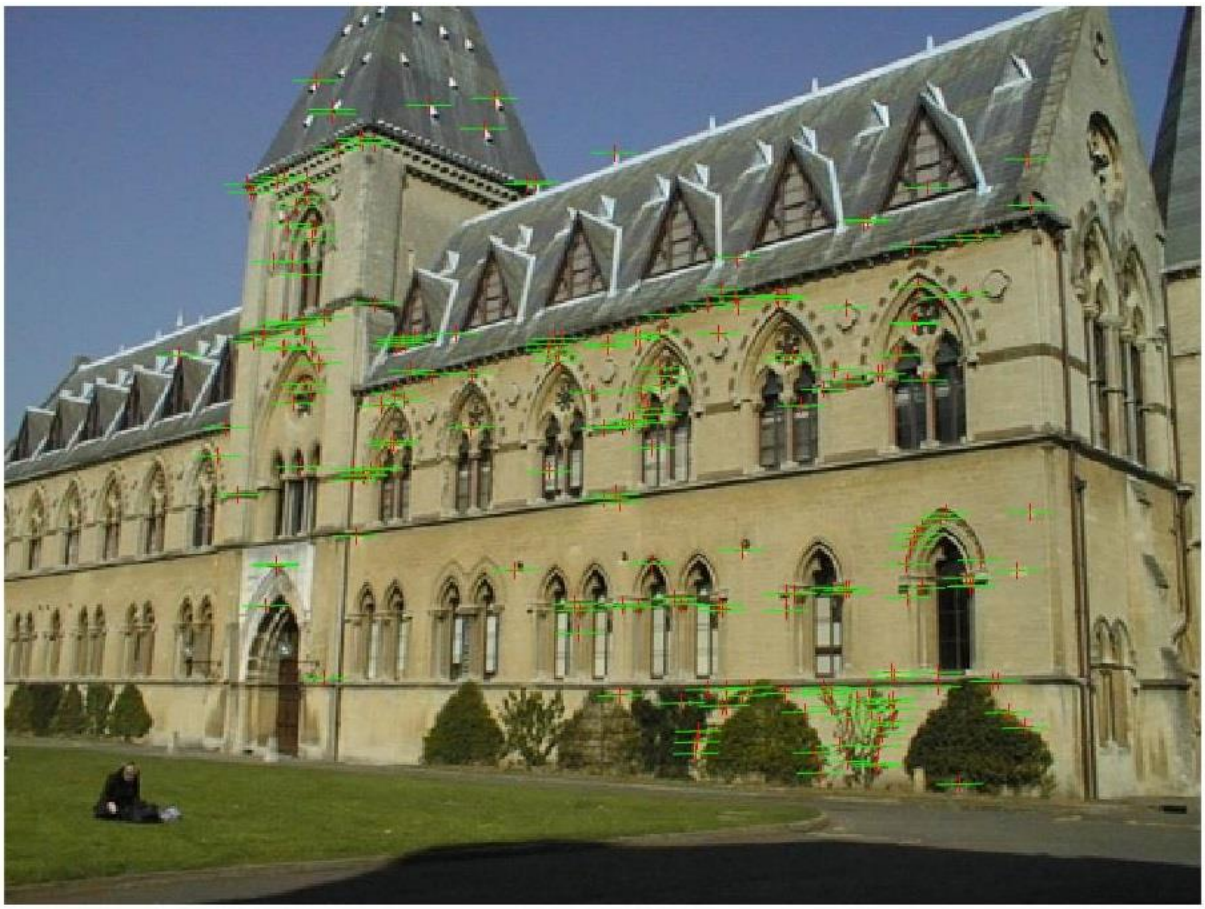


2. library:

```
43   F_norm = fundamental_normalized_cord(matches);
mean residual for normalized algorithm:
    0.2236

52   [ inliermatches , F, res] = ransac_inliers( matches );
Using RANSAC and Normalized,mean residual for Inliers:
    0.1039

no of inliers:
   216
```

Using RANSAC and Normalized, mean residual for Inliers: 0.1039

no of inliers: 216



Comparison for Ground truth matches vs without Ground Truth matches (Using RANSAC)

Image	Ground Truth(Mean Residual)	Without Ground Truth(Mean Residual)
house	.2157	.0983
library	.2236	.1039

C)

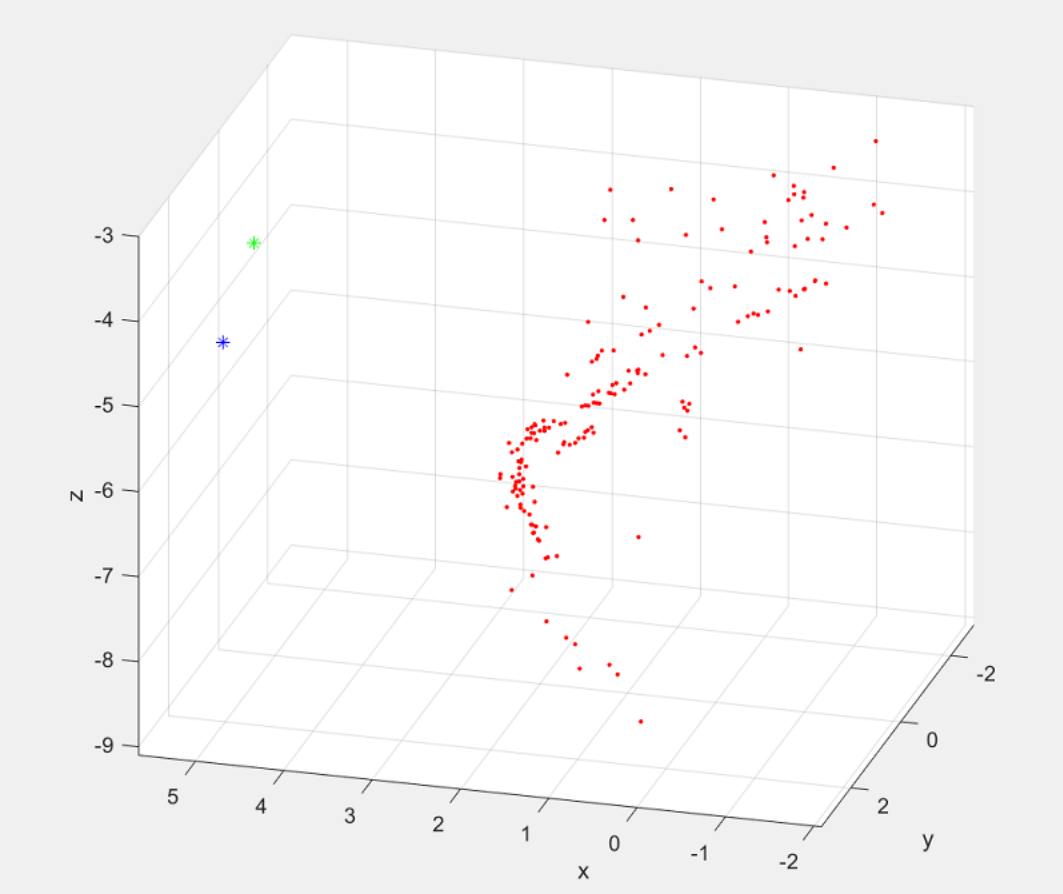
House:

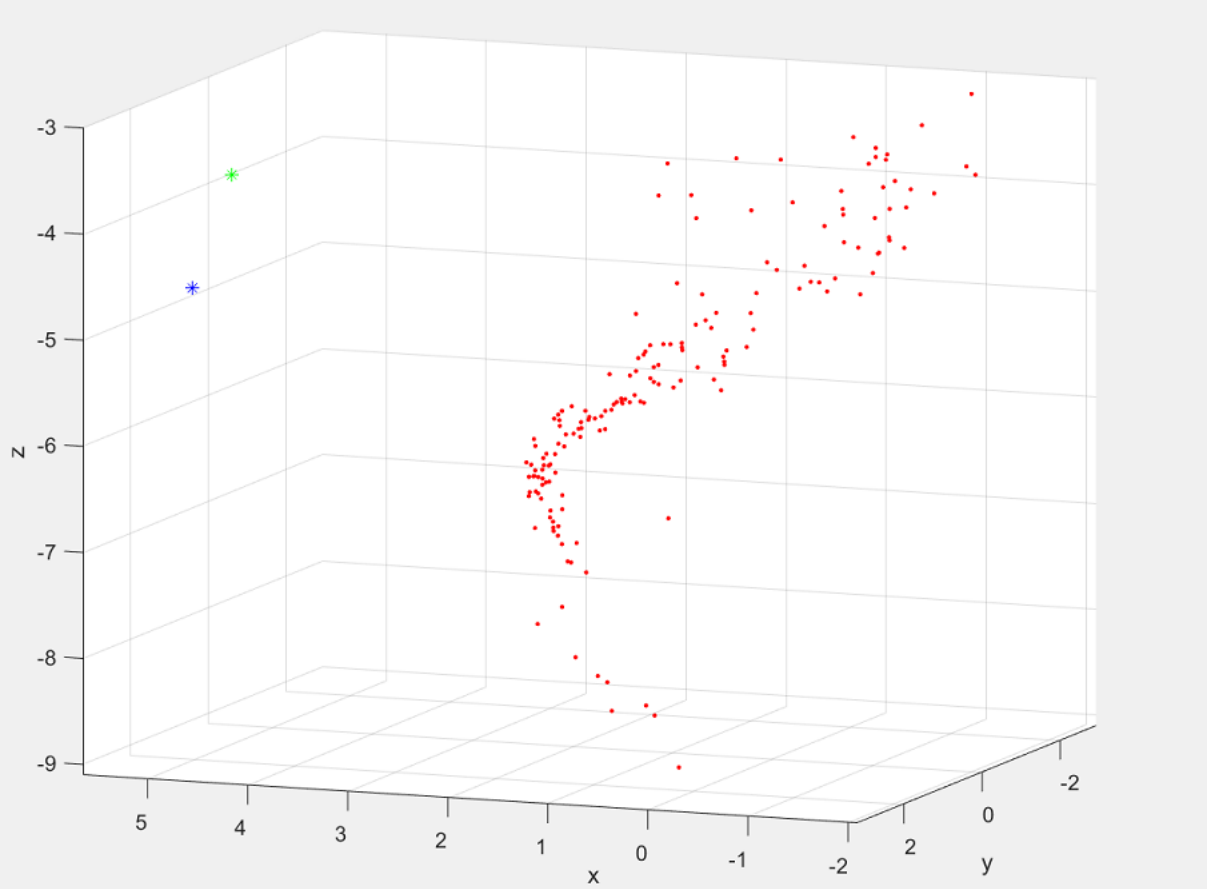
```
residuals between the observed 2D points and the projected 3D points Image 1
    0.0025

residuals between the observed 2D points and the projected 3D points Image 2
    0.1566

fx >>
```

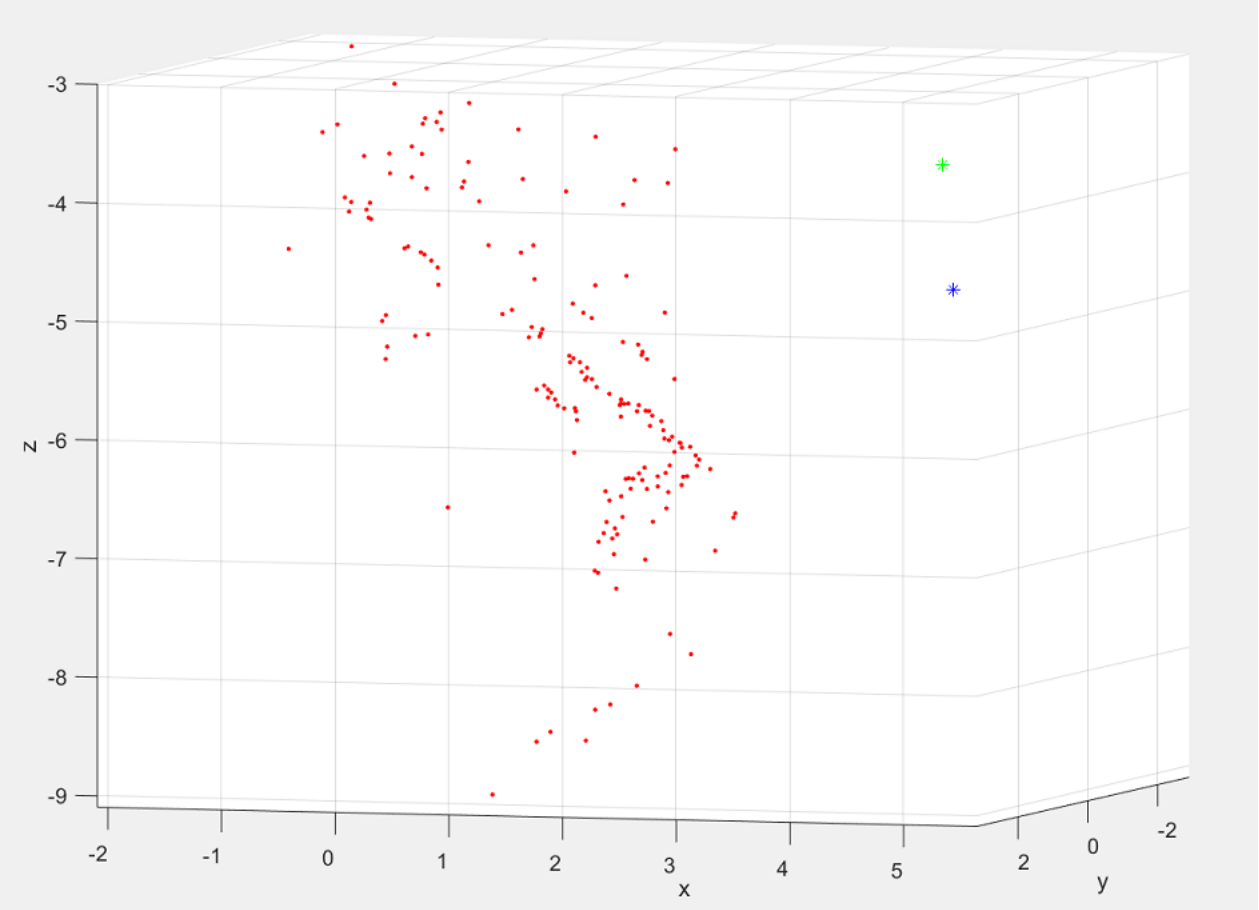
residuals between the observed 2D points and the projected 3D points Image 1: 0.0025

residuals between the observed 2D points and the projected 3D points Image 2: 0.1566

snapshots from several viewpoints:




-3
-4
-5
-6
-7
-8
-9
z
5
4
3
2
1
0
-1
-2
x
2
0
-2
y



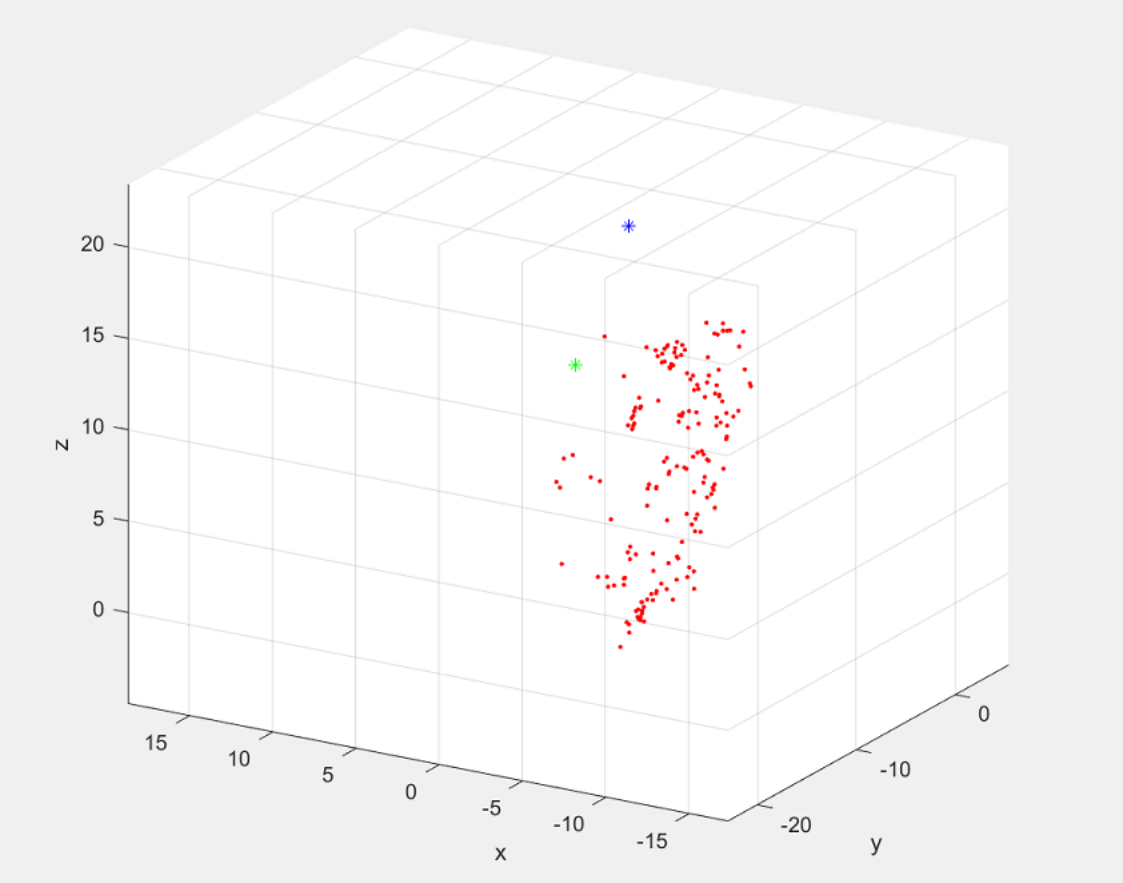
Library:

```
residuals between the observed 2D points and the projected 3D points Image 1
  112.2827

residuals between the observed 2D points and the projected 3D points Image 2
  158.0115

fx >>
```

residuals between the observed 2D points and the projected 3D points Image 1: 112.2827

residuals between the observed 2D points and the projected 3D points Image 2: 158.0115

snapshots from several viewpoints:


20
15
10
5
0
z
15
10
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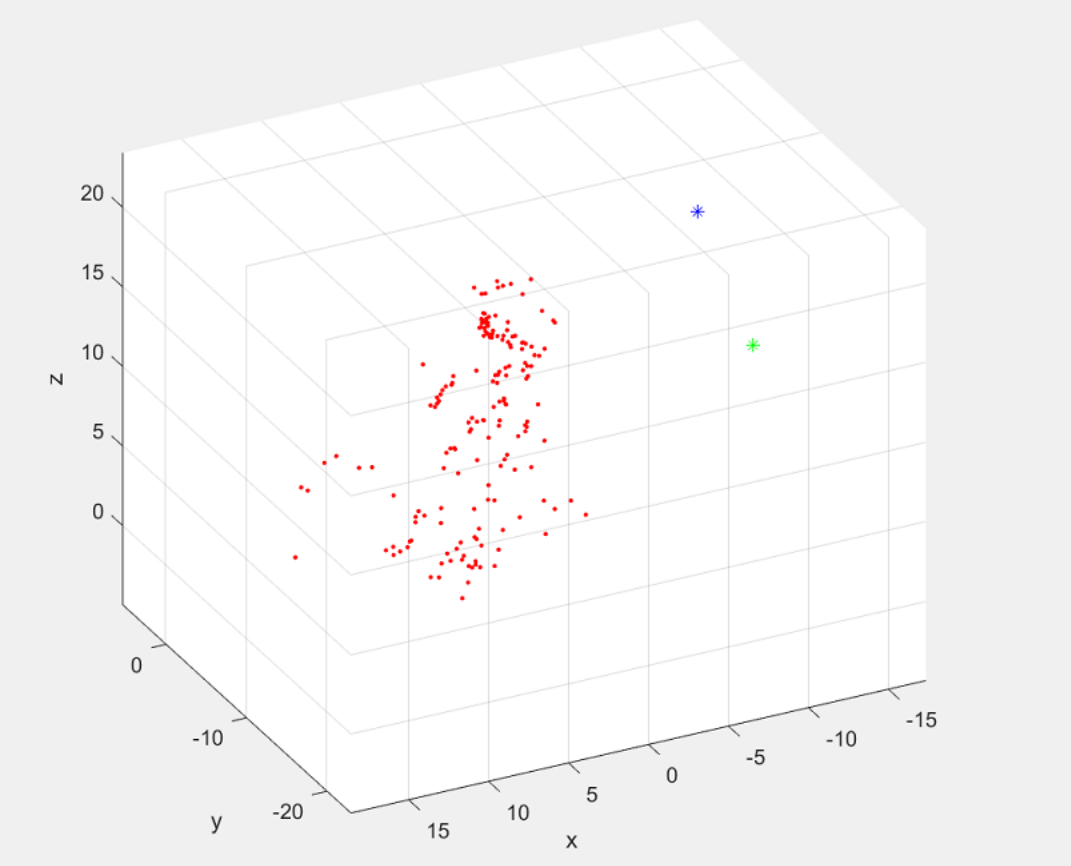
-5
-10
-15
x
0
-10
-20
y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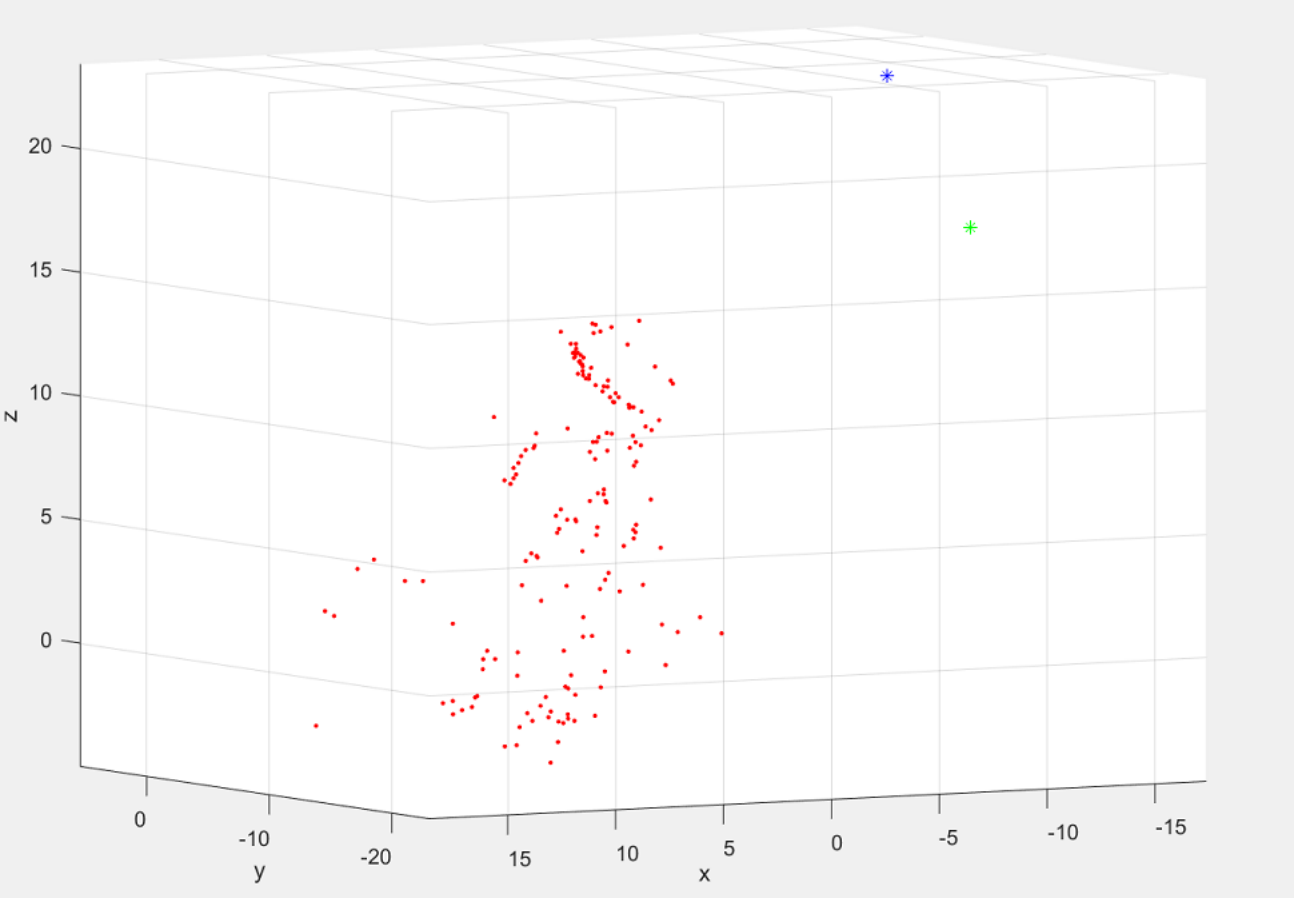
-15
x


20
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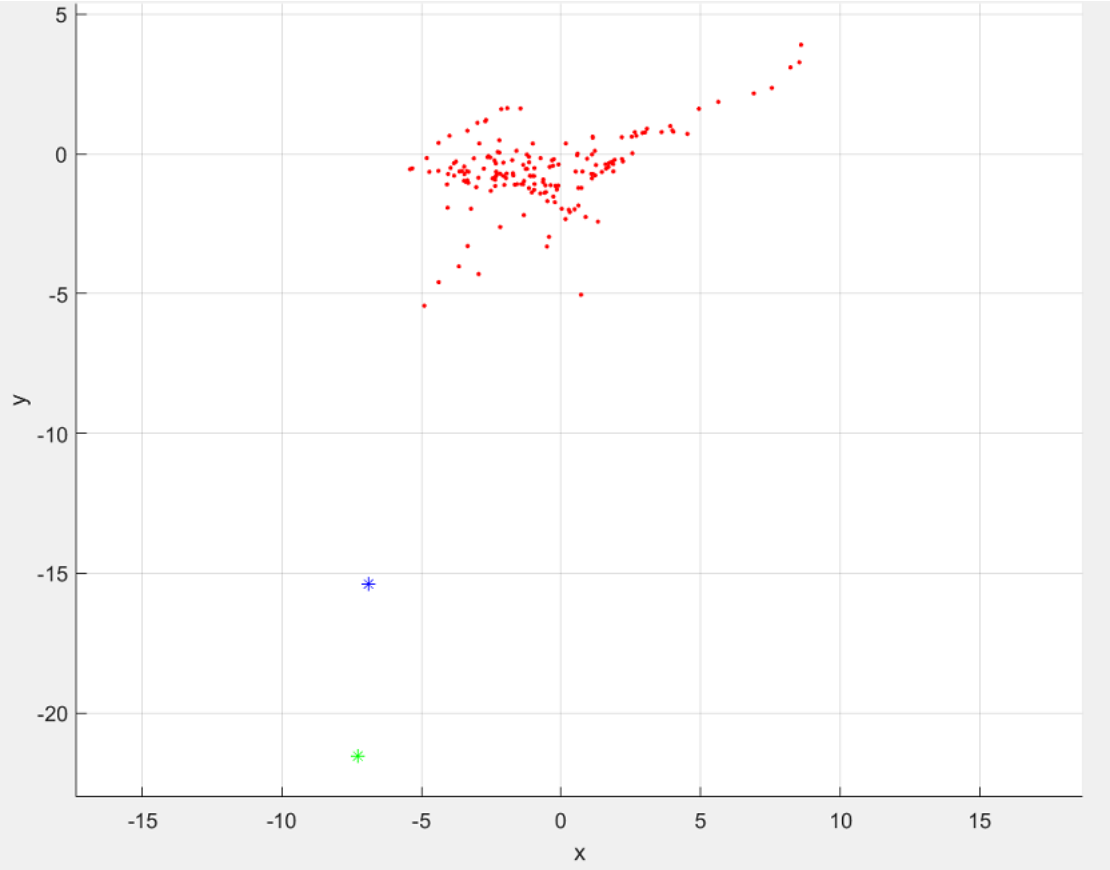
-10
-20
y
15
10
5
0
-5
-10
-15
x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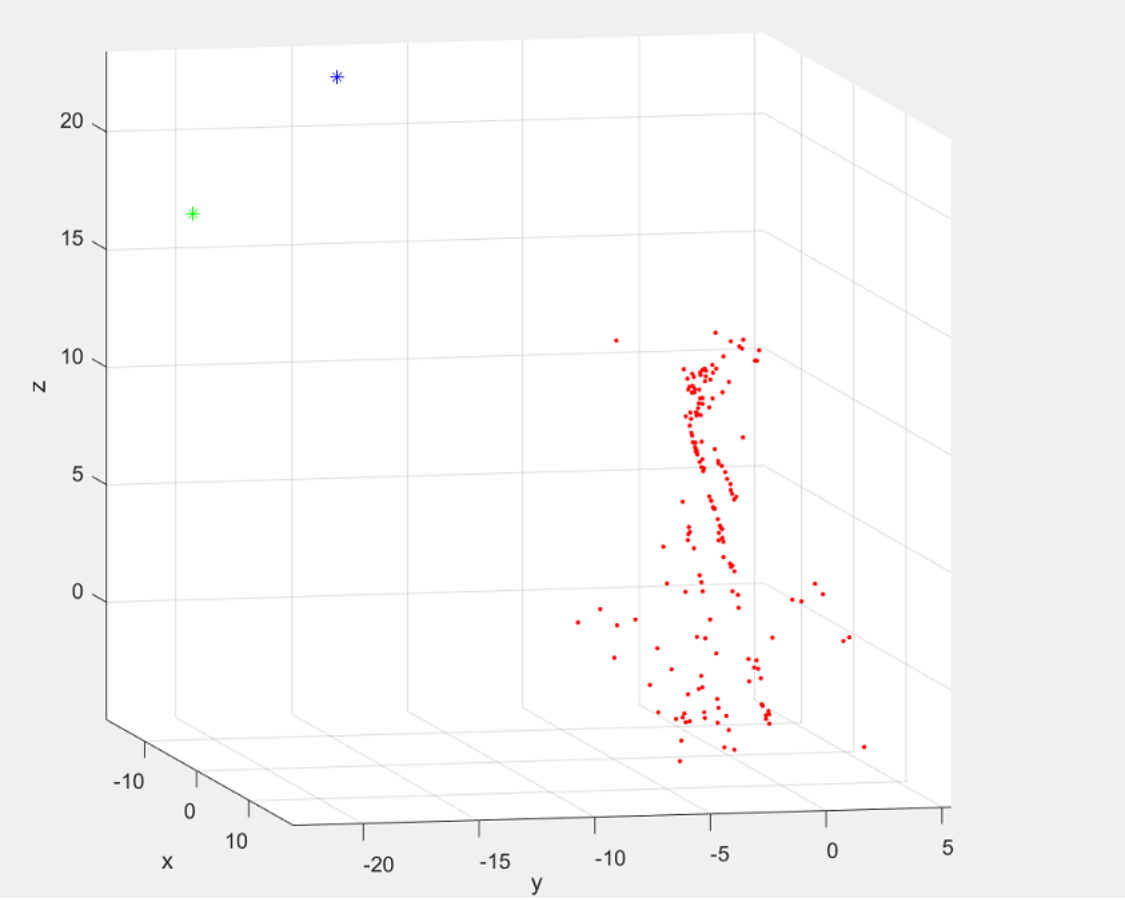
-5
-10
-15
-20
y
-15
-10
-5
0
5
10
15
x



Reference: Apart from lecture slides and Piazza, I referred below recitation slides for Part2 Fundamental Matrix Calculation and Triangulation part

http://www-users.cs.umn.edu/~hspark/CSci5980/recitation.pdf