

Write Up

Feature points are detected by using Harris detector and points are extracted.

The following parameters were used with Harris detector $\sigma = 2$; $\text{thresh} = .005$;

Local neighborhood:-

We extract local neighborhood around every keypoint, kernel size is taken as 20. Image is padded with kernel size to get detection from the corners. Putative matches are selected by comparing distance with the threshold distance (taken as 200).

Ransac: -

Ransac parameters are $\text{iterations} = 200$; $\text{initial_match} = 4$; $\text{inlier_threshold} = 10$;

Random indices are selected from initial match by using function `randsample`. These 4 points are sent to homography matrix. Transformation is done on the first image and compared with the second image. We see how close the points are. If they are close by they are inliers else they are treated as outliers. The best model is taken with matches having more number of inliers. Threshold is used here to separate inliers from outliers. These iterations are carried out for 200 times and best matching result is taken.

Stitching: -

The first image is warped. Second image has been transformed. Size of the image has been scaled to overlap. The average is done to find out whether image has been stitched correctly.

Results and observation

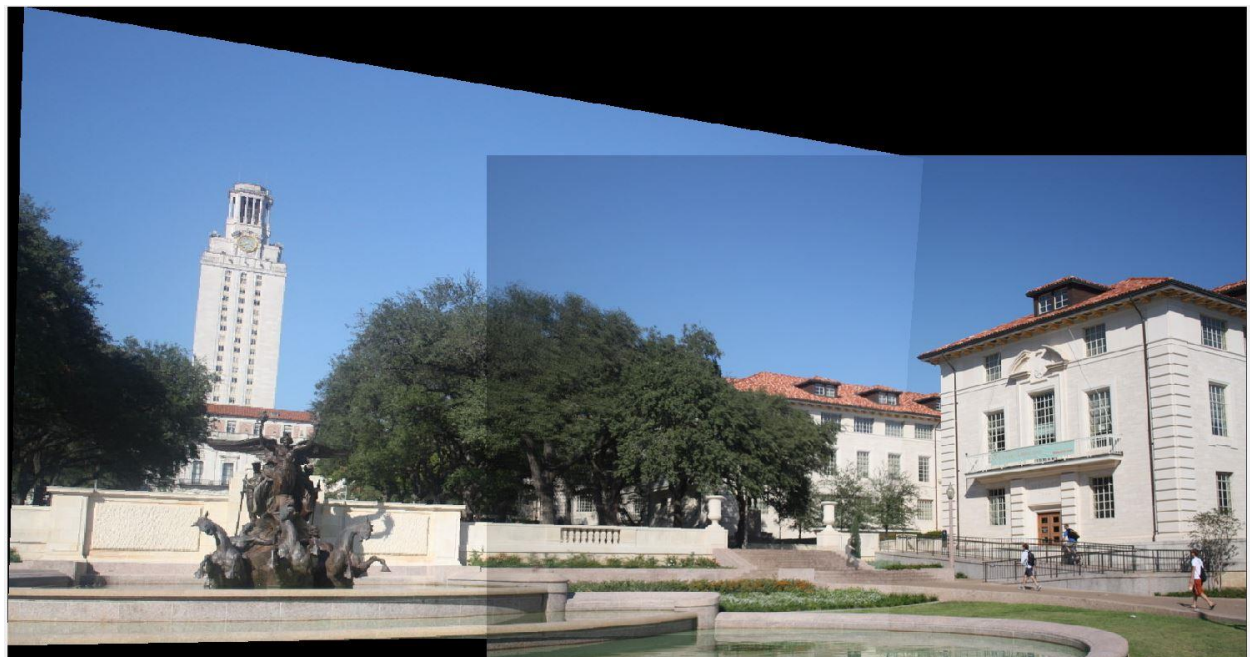
Number of homography inliers = 65

best average residual = 1.003161

Location of indices matching



Stitched Image

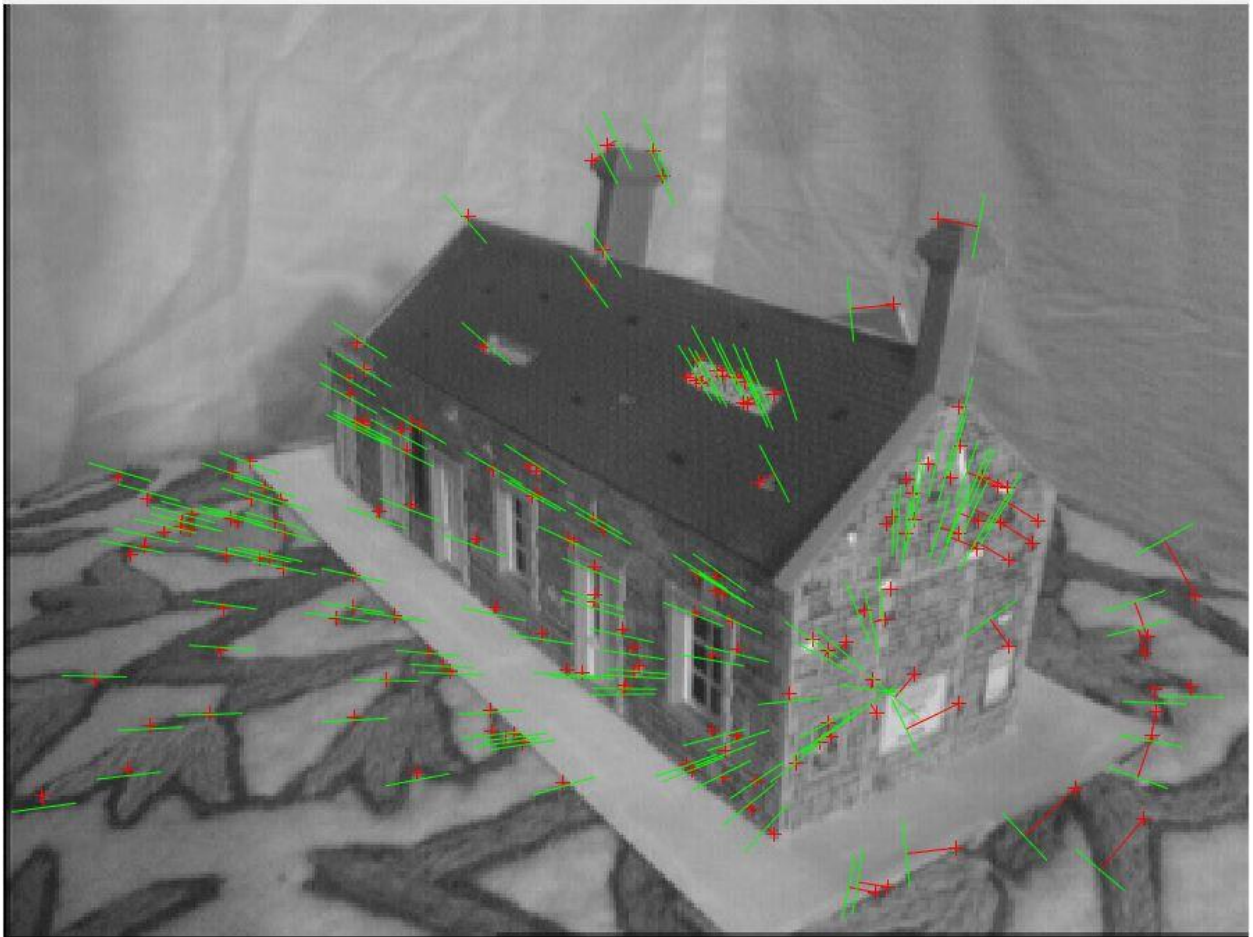


Warped Image



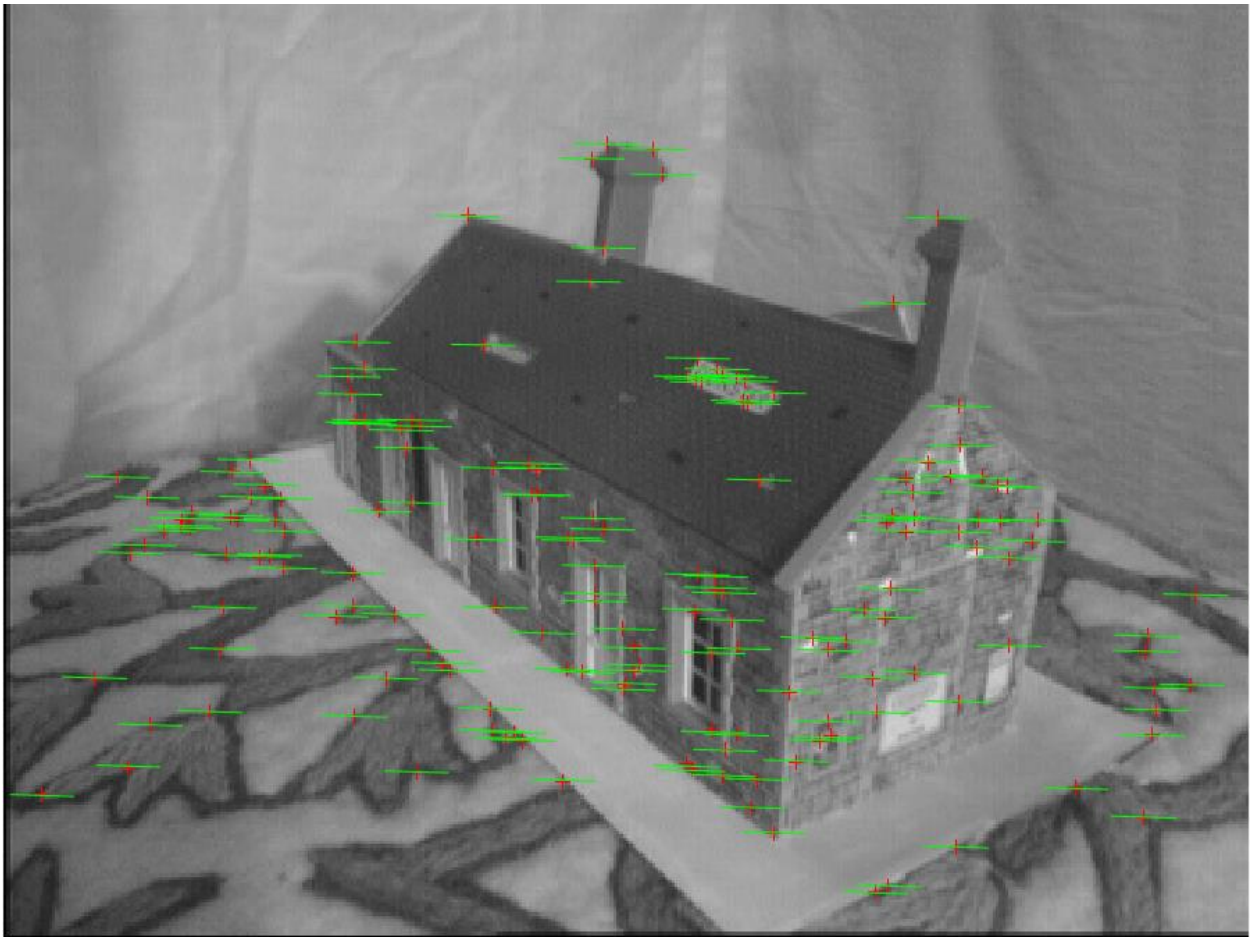
Unnormalized

Average residual error = 3.0342



Normalised (ground truth matching)

Average residual error =0.2103



Ransac normalized(without ground truth matching)

Parameters :-

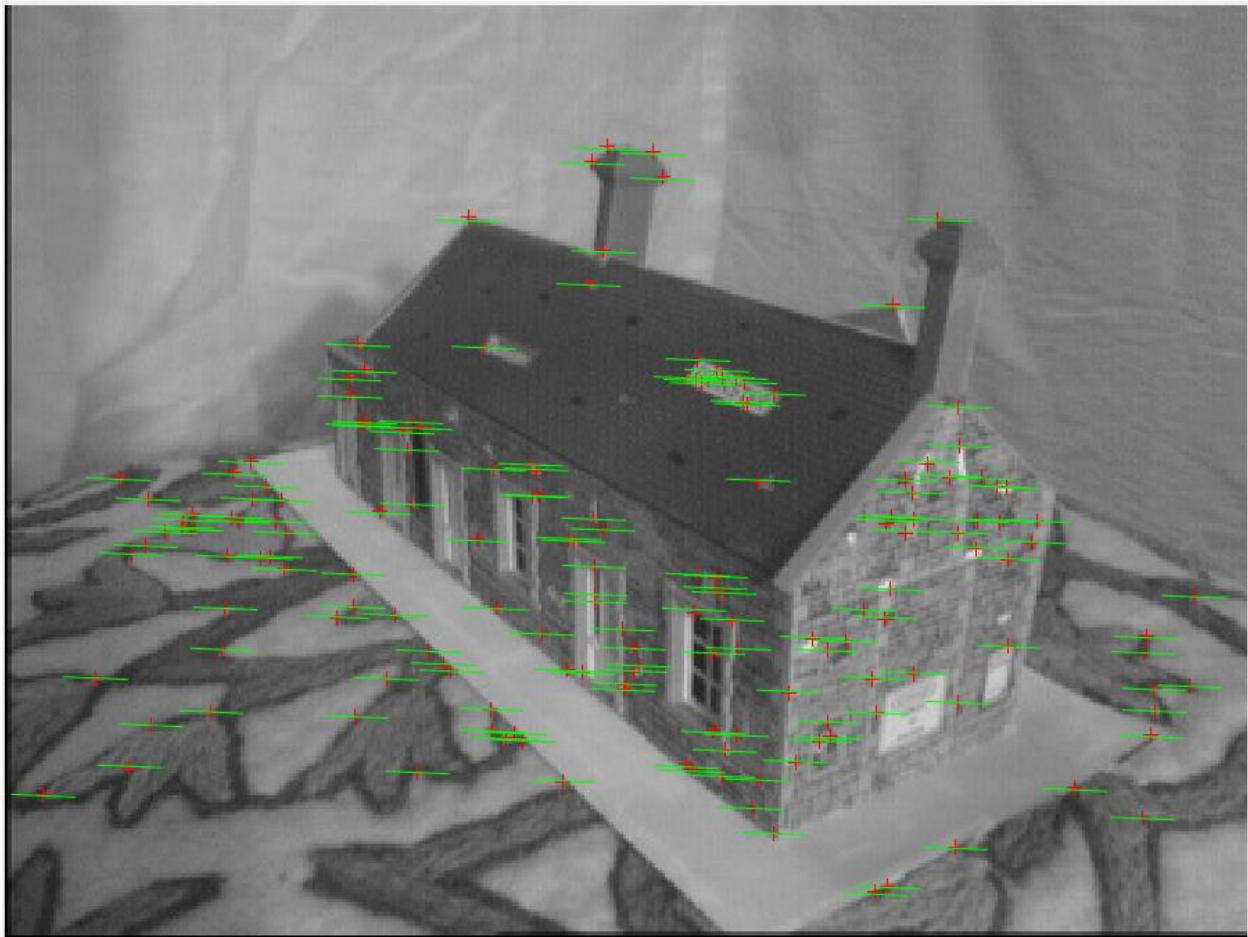
iterations = 200;

initial_match = 8;

inlier_threshold = 0.1;

Average residual error = 0.0444

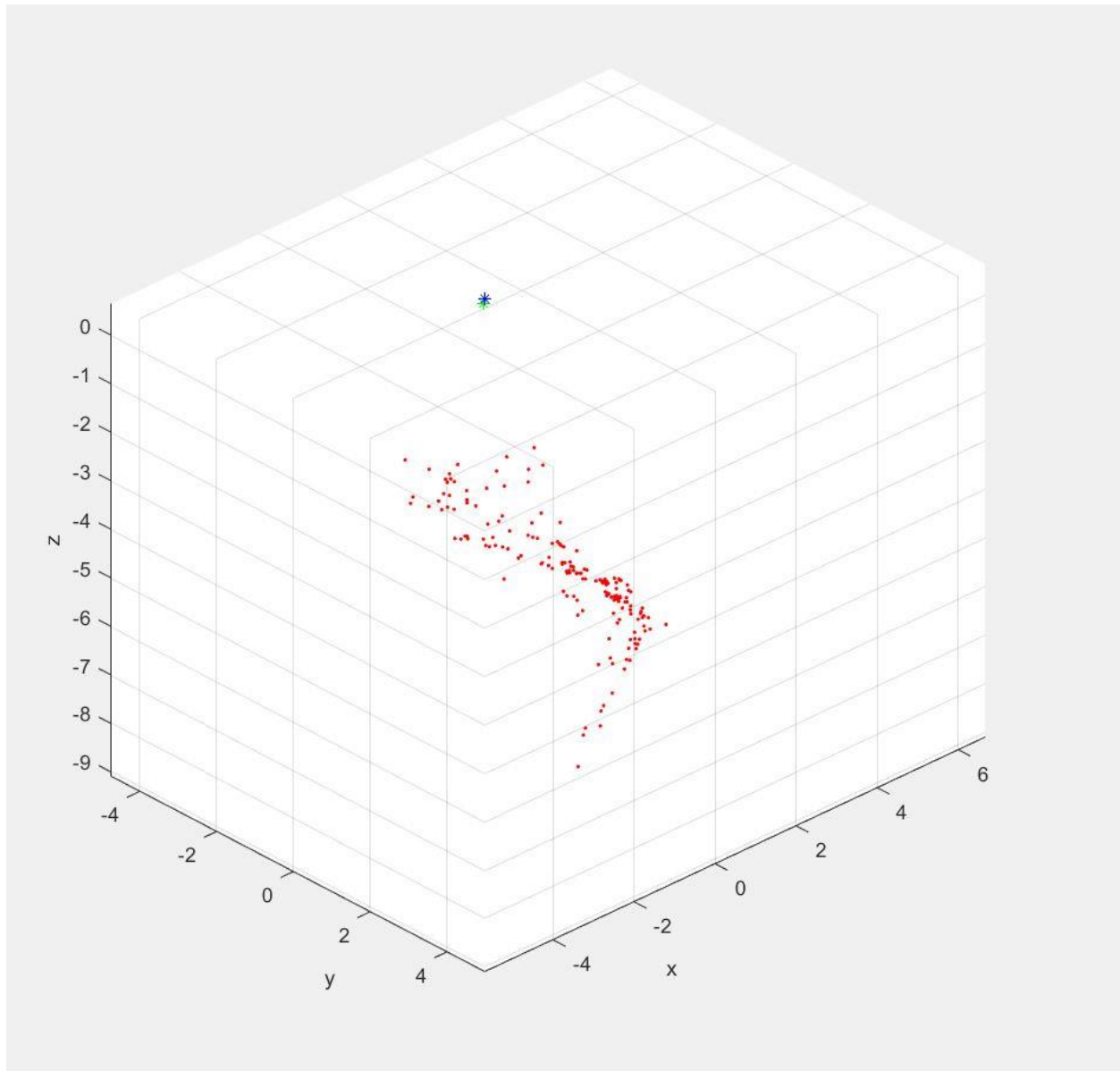
Number of inliers = 49



Triangulation

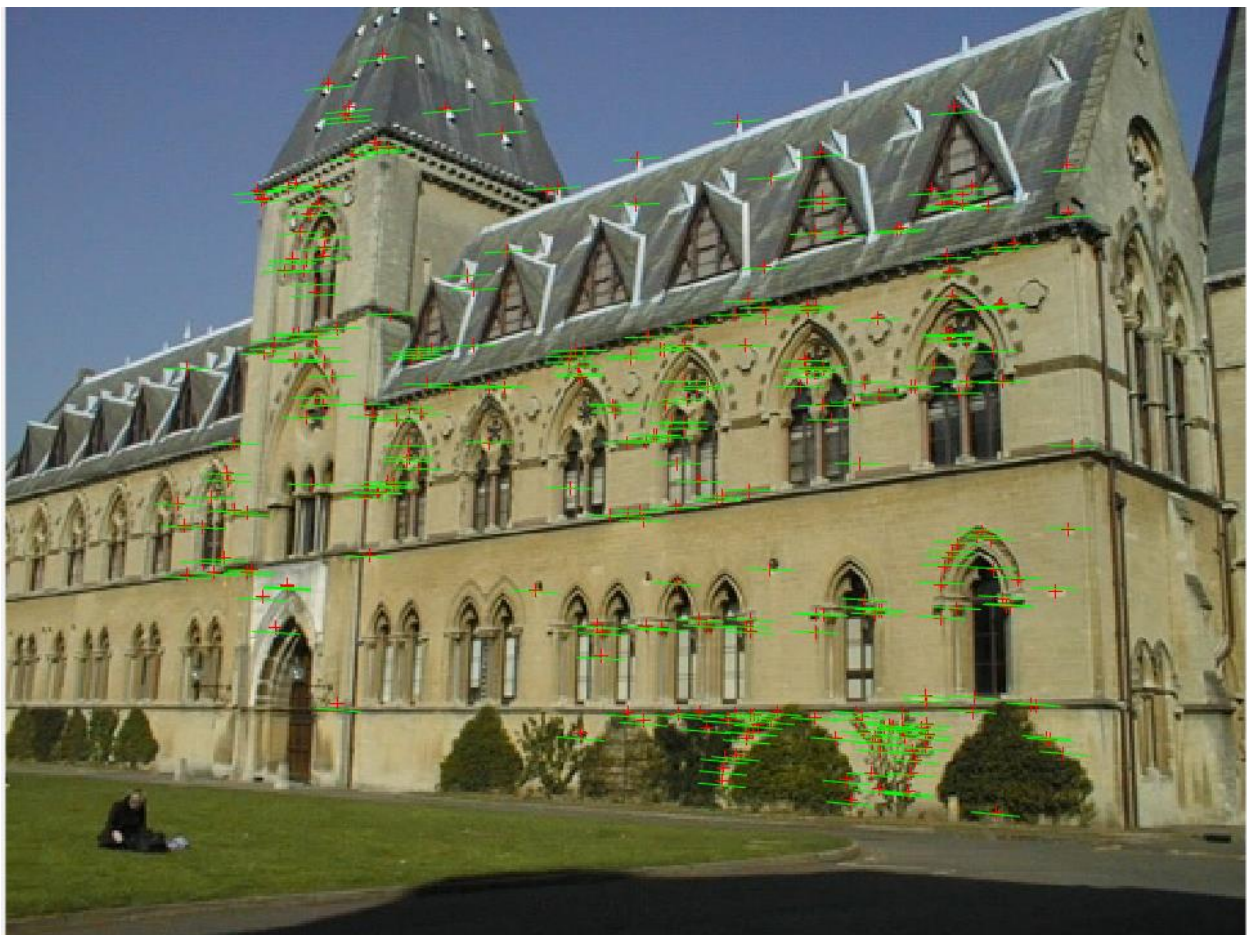
average residual1 = 0.002522

average residual2 = 0.156552



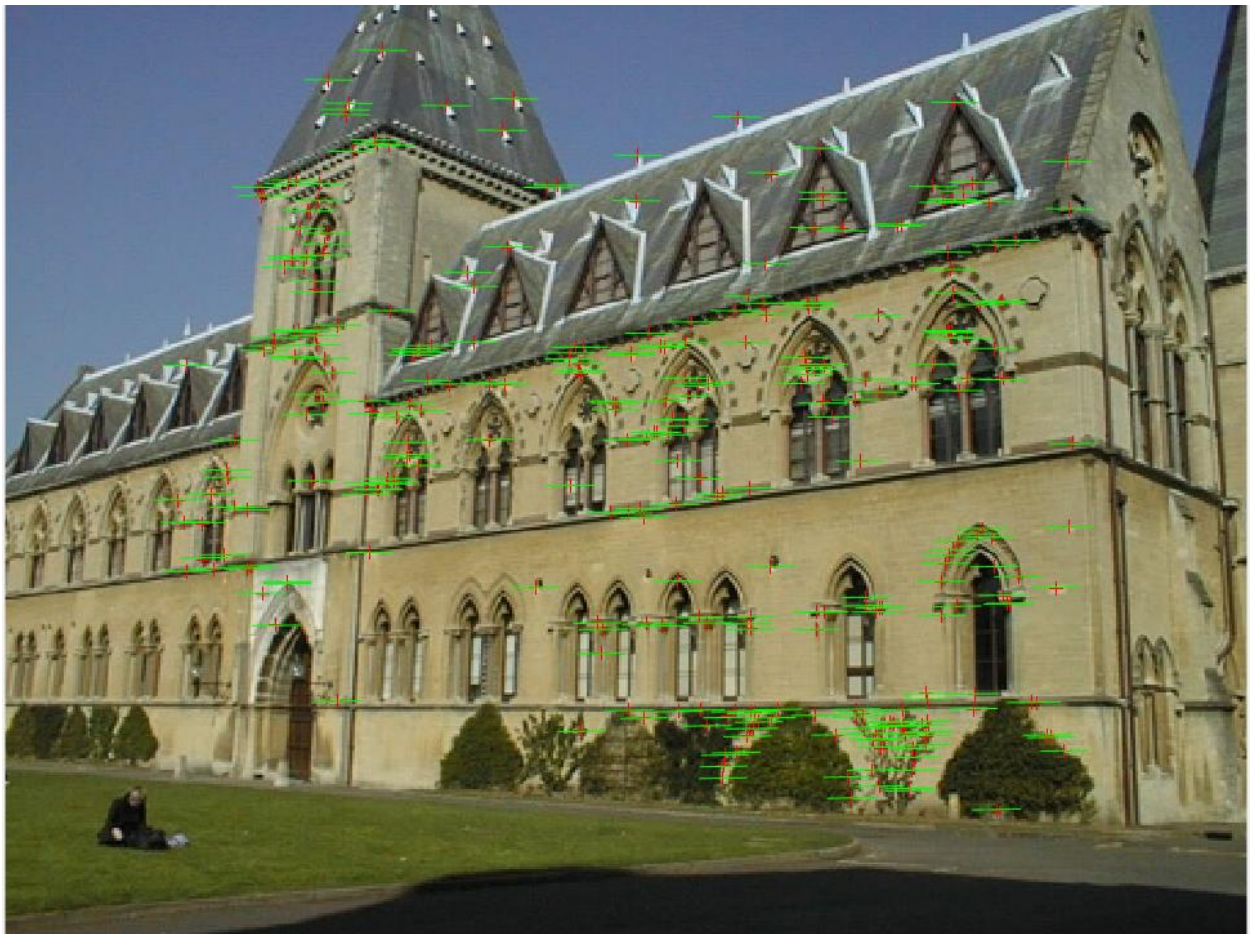
Unnormalised

Average residual error = 0.3385



Normalised (ground truth matching)

Average residual error = 0.1836



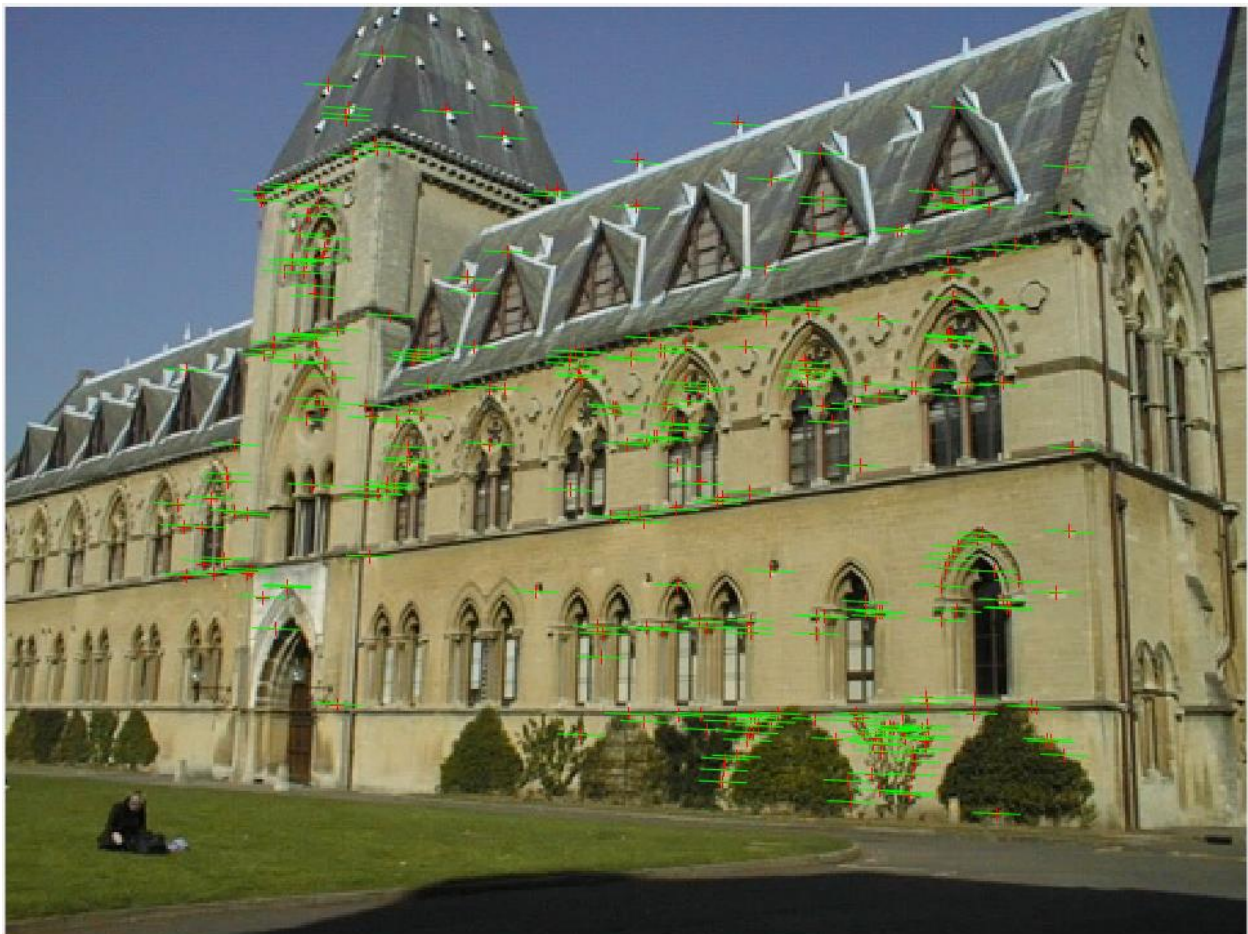
Ransac normalized (without ground truth matching)

Parameters :-

iterations = 200;
initial_match = 8;
inlier_threshold = 0.1;

Average residual error = 0.0470

Number of inliers = 103



Triangulation

average residual1 = 0.073128

average residual2 = 0.267680

