CSE 573 HW 3

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1. Homography estimation:

(a) Describe your solution, including any interesting parameters or implementation choices for feature extraction, putative matching, RANSAC, etc.

Approach:

Intitally after detecting the corner from both images using the given harris detector. Descriptors for all the key points in both the images were generated by selecting a neighborhood size of 5 and flattening was done to format each descriptor as an array.

The pair wise distance between each descriptor in both the images were estimated using given Dist2.m function.

Out of this Dist2 result, the distance matrix was sorted based on distances between descriptors in increasing order and then top 100 matches were selected based on the sorted rows.

Ransac:

For ransac part I chose the number of iteration as 10000, then after selecting four points at random from the putative matches from both descriptors. A homography matrix is generated in each iteration. Based on the highest no.of inliers best fit of homography matrix is generated.

A canvas big enough to hold both the images is created.

 Then images are stitched together using the maketform() and imtransform() methods. Thus resulting in stitched image.

Way to run:

Just pass IM_left and IM_left images as parameters to panaroma_stitching(IM_left, IM_right).

(b) For the uttower pair provided, report the number of homography 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). Also, display the locations of inlier matches in both images.

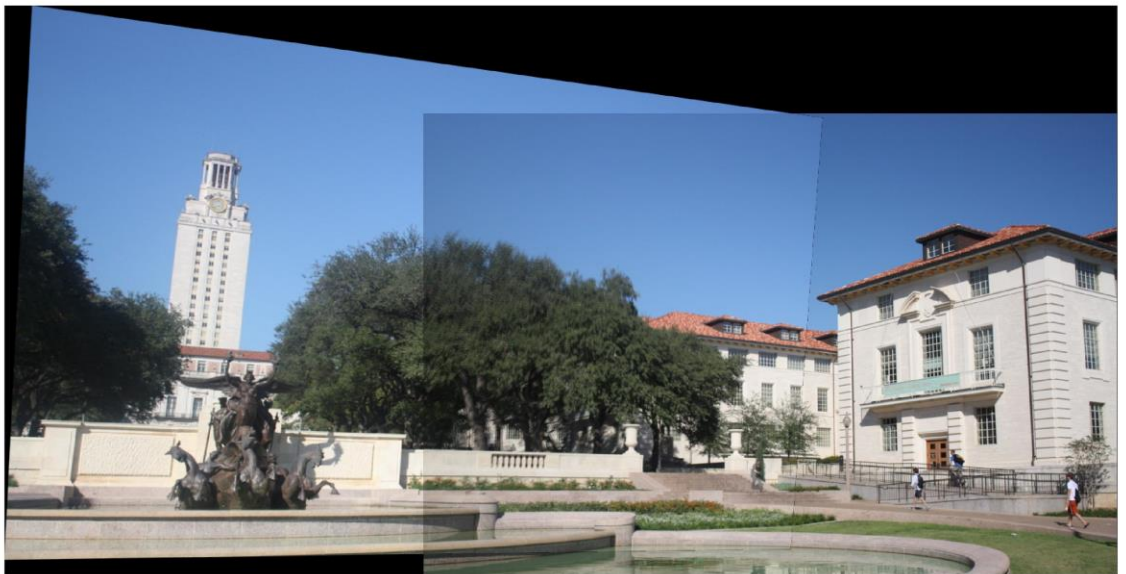The no. of inliers for the provided uttower pair were 22.

Inlier_number = 22.

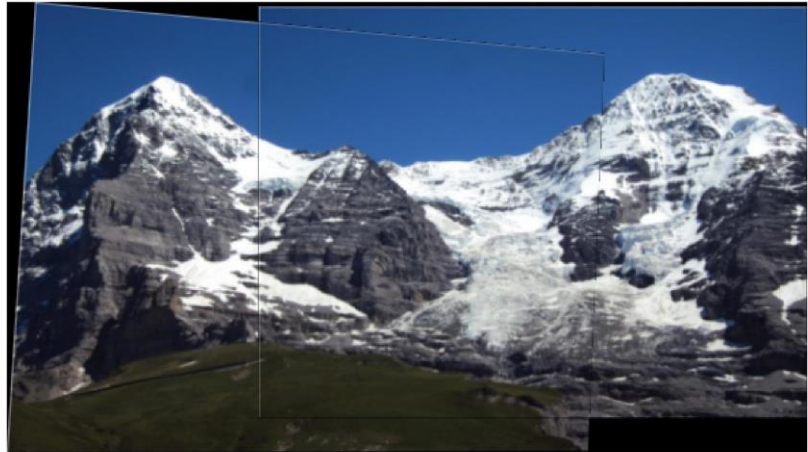The residual for the inliers is 3.157e+05.

Homography matrix for ut_tower.

H =   1.6840   0.0135 -821.1464

       0.2931   1.6270 -330.1916

       0.0005   0.0003   1.0000

(c) Display the final result of your stitching.

2. Fundamental matrix estimation:

(a) For both image pairs, for both unnormalized and normalized estimation using ground truth matches, display your result and report your residual.

For unnormalized and normalized approaches, initially the matches were loaded. Then in each iteration of RANSAC eight points were selected at random from both the descriptors.

Then they are passed to getFundamentalMatrix(), it returns a Fundamental Matrix for that iteration of RANSAC.

Finally the best fit of fundamental matrix is calculated based on the iterations where maximum number of matches occur using the particular fundamental matrix.

using fit_fundamental() by passing the matches loaded from the given text files as parameters returns a F matrix which is the best fit fundamental matrix.

For House Matches

F =   0.0000   0.0001 -0.0171

-0.0001   0.0000   0.0220

0.0103 -0.0265   1.0000

For this part, pass the matches as parameter to fit_fundamental(matches) ->This calls getFundamentalMatrix().

fit_fundamental(m) will return best fundamental matrix given matches (m).

Way to run:

Just run the fit_fundamental.m passing matches as parameter. This will return best fundamental matrix fit.