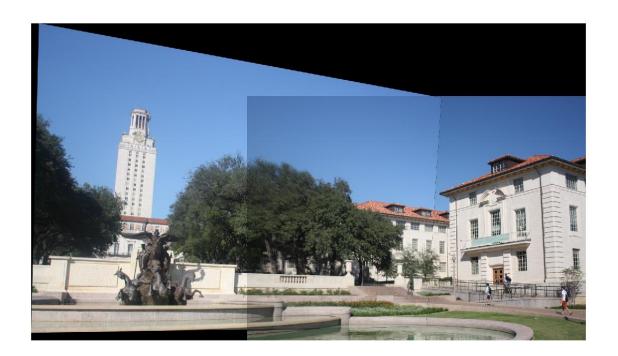
CSE 573: Computer Vision and Image Processing Homework 3_ Homography and fundamental matrix estimation

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Stitching pairs of images

- a. For stitching pairs of images, I performed the following steps:
 - i. First, I calculated features (corners) in both the images using Harris detector (The script 'harris.m' was provided with the initial code).
 - ii. For these feature points, I extracted a neighborhood of all the points. To calculate the neighborhood, I a basically setting the boundaries to 1 (for left) and width of imaged (for right). So, while calculating any position whose left neighbor cannot be calculated will be kept as zero. For extracting the neighborhoods, I have written the 'extractNeighboorHood.m'.
 - iii. After calculating the neighborhoods, using the dist() function, I got the distance between the descriptors. I then selected the points where the descriptors from both the images have a lower distance than threshold (0.7). These are the point pairs.
 - iv. I then sent these points (from both images) to RANSAC function which computes the homography matrix and also return inlier indices and residual. In the RANSAC function for each iteration I calculated homography matrix and number of inliers obtained after projecting this homography matrix onto the points from image1. I have considered the maximum value of inliers and return thee homography matrix and inlier indices corresponding to this number of inliers. Based on these indices the corresponding points can be fetched from both the images. The inliers between both the images can be viewed as:



v. After computing the homography matrix, we can stitch the images. I have transformed the first image, according to the homography matrix, using 'imtransform'. The transformation is 'maketform' and projective transformation is applied. After This I have added the two images, by calculating the bounds and transforming both the images based on the bounds calculated. For overlapping region, I have simply calculated the average values of the pixels and set them in the overlapped pixel region.

b. Parameters used:

iterations - 10000

Minimum Threshold Distance - 15

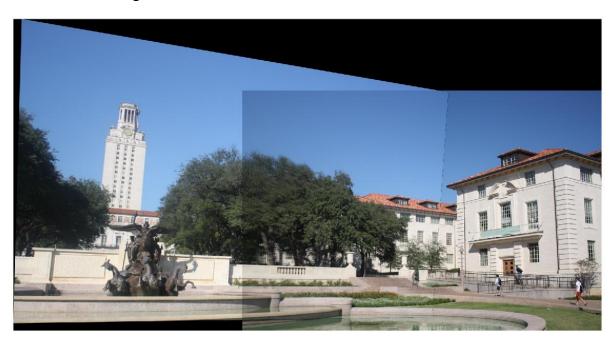
Using these parameters, the number of inliers I got is 25. The average residual error is 510.0988.

The indices of the inliers and the corresponding point co-ordinates in both the images is given in the below table.

Inlier indices	img1_x	img1_y	img2_x	img2_y
15	623	535	166	498
20	748	537	293	503
24	783	562	326	529
27	829	482	376	451
28	840	543	384	511

29 854 548 397 516 31 879 547 420 515 34 893 469 438 441 35 905 554 443 523 36 905 540 444 509 38 905 547 444 516 43 910 412 457 387 44 906 339 458 317 46 923 433 468 408 47 933 496 472 468 49 931 391 478 368 55 947 377 493 356 64 970 540 503 511 66 973 573 504 542 71 998 539 528 511 72 1001 549 531 520 79 994 342 538 326 80 995 350 538 333					
34 893 469 438 441 35 905 554 443 523 36 905 540 444 509 38 905 547 444 516 43 910 412 457 387 44 906 339 458 317 46 923 433 468 408 47 933 496 472 468 49 931 391 478 368 55 947 377 493 356 64 970 540 503 511 66 973 573 504 542 71 998 539 528 511 72 1001 549 531 520 79 994 342 538 326 80 995 350 538 333 84 1021 477 553 453	29	854	548	397	516
35 905 554 443 523 36 905 540 444 509 38 905 547 444 516 43 910 412 457 387 44 906 339 458 317 46 923 433 468 408 47 933 496 472 468 49 931 391 478 368 55 947 377 493 356 64 970 540 503 511 66 973 573 504 542 71 998 539 528 511 72 1001 549 531 520 79 994 342 538 326 80 995 350 538 333 84 1021 477 553 453	31	879	547	420	515
36 905 540 444 509 38 905 547 444 516 43 910 412 457 387 44 906 339 458 317 46 923 433 468 408 47 933 496 472 468 49 931 391 478 368 55 947 377 493 356 64 970 540 503 511 66 973 573 504 542 71 998 539 528 511 72 1001 549 531 520 79 994 342 538 326 80 995 350 538 333 84 1021 477 553 453	34	893	469	438	441
38 905 547 444 516 43 910 412 457 387 44 906 339 458 317 46 923 433 468 408 47 933 496 472 468 49 931 391 478 368 55 947 377 493 356 64 970 540 503 511 66 973 573 504 542 71 998 539 528 511 72 1001 549 531 520 79 994 342 538 326 80 995 350 538 333 84 1021 477 553 453	35	905	554	443	523
43 910 412 457 387 44 906 339 458 317 46 923 433 468 408 47 933 496 472 468 49 931 391 478 368 55 947 377 493 356 64 970 540 503 511 66 973 573 504 542 71 998 539 528 511 72 1001 549 531 520 79 994 342 538 326 80 995 350 538 333 84 1021 477 553 453	36	905	540	444	509
44 906 339 458 317 46 923 433 468 408 47 933 496 472 468 49 931 391 478 368 55 947 377 493 356 64 970 540 503 511 66 973 573 504 542 71 998 539 528 511 72 1001 549 531 520 79 994 342 538 326 80 995 350 538 333 84 1021 477 553 453	38	905	547	444	516
46 923 433 468 408 47 933 496 472 468 49 931 391 478 368 55 947 377 493 356 64 970 540 503 511 66 973 573 504 542 71 998 539 528 511 72 1001 549 531 520 79 994 342 538 326 80 995 350 538 333 84 1021 477 553 453	43	910	412	457	387
47 933 496 472 468 49 931 391 478 368 55 947 377 493 356 64 970 540 503 511 66 973 573 504 542 71 998 539 528 511 72 1001 549 531 520 79 994 342 538 326 80 995 350 538 333 84 1021 477 553 453	44	906	339	458	317
49 931 391 478 368 55 947 377 493 356 64 970 540 503 511 66 973 573 504 542 71 998 539 528 511 72 1001 549 531 520 79 994 342 538 326 80 995 350 538 333 84 1021 477 553 453	46	923	433	468	408
55 947 377 493 356 64 970 540 503 511 66 973 573 504 542 71 998 539 528 511 72 1001 549 531 520 79 994 342 538 326 80 995 350 538 333 84 1021 477 553 453	47	933	496	472	468
64 970 540 503 511 66 973 573 504 542 71 998 539 528 511 72 1001 549 531 520 79 994 342 538 326 80 995 350 538 333 84 1021 477 553 453	49	931	391	478	368
66 973 573 504 542 71 998 539 528 511 72 1001 549 531 520 79 994 342 538 326 80 995 350 538 333 84 1021 477 553 453	55	947	377	493	356
71 998 539 528 511 72 1001 549 531 520 79 994 342 538 326 80 995 350 538 333 84 1021 477 553 453	64	970	540	503	511
72 1001 549 531 520 79 994 342 538 326 80 995 350 538 333 84 1021 477 553 453	66	973	573	504	542
79 994 342 538 326 80 995 350 538 333 84 1021 477 553 453	71	998	539	528	511
80 995 350 538 333 84 1021 477 553 453	72	1001	549	531	520
84 1021 477 553 453	79	994	342	538	326
	80	995	350	538	333
86 1015 338 557 323	84	1021	477	553	453
	86	1015	338	557	323

c. Final Stitched image



a.

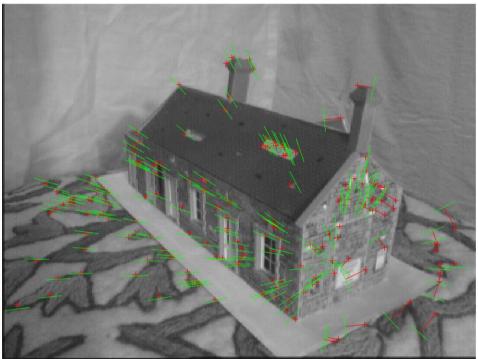


Figure 1Un-normalized output for image 2



Figure 2Un-normalized output for image 1



Figure 3 Normalized output for image 2



Figure 4 Normalized output for image 1

Residual Estimation for both the images using normalized and un-normalized approach of calculation of Fundamental Matrix

Residual	Un-normalized	Normalized
lmg1	18.0501	16.0765
Img2	26.4013	16.4980

b.

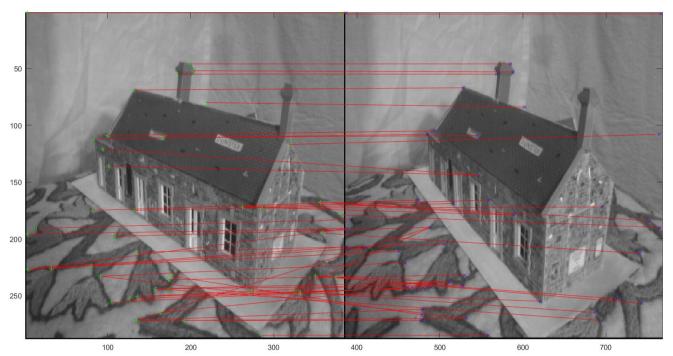
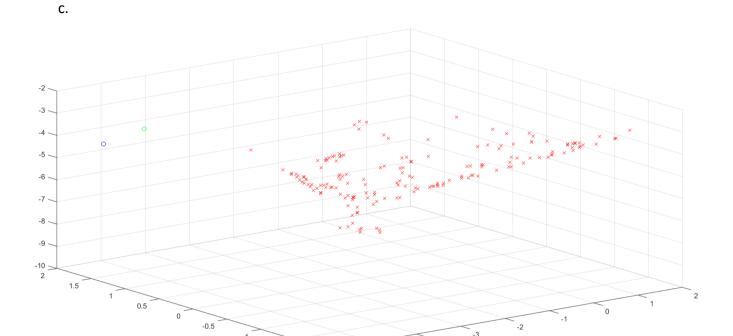


Figure 5 Inlier matches between 2 images

Number of inliers: 53

Residual Estimation: 1.7724e+03

(Number of inliers obtained using ground truth correspondences provided was 168 and residual is 16.0765)



- Scripts in the 'code' directory Part1
- **main.m** main function to call for part1 image stitching
- extracNeighborHood.m- returns the distance calculated between the feature descriptors of both the images
- > ransac.m- calculates the homography matrix using RANSAC implementation and also returns inlier indices and residual
- > solveH.m calculates Homography matrix when passed a set of points from 2 images
- **harris.m** sample Harris detector (already given)
- find_sift.m (already given)
- dist2.m (already given)

Part2

- ➤ main_part2.m main function to call for part2 to obtain inliers between both images
- sample_code.m (already given)
- fit_fundamental.m calculates the fundamental matrix (un-normalized)
- fit_normalized.m calculates normalized fundamental matrix
- **fransac.m** implements RANSAC for calculating fundamental matrix
- > triangulate1.m to calculate the corresponding 3 D points and calculate triangulation.

• References:

- https://inside.mines.edu/~whoff/courses/EENG512/lectures/24-EpipolarAndEssential.pdf
- http://www.cs.cmu.edu/~16385/Slides/11.4 Triangulation.pdf
- http://www.cse.psu.edu/~rtc12/CSE486/lecture20.pdf
- http://www.cse.psu.edu/~rtc12/CSE486/lecture19.pdf