COSC 342 Assignment 1 – Image Mosaicing

Report for Beckham Wilson ID #7564267

Introduction

n this assignment you will need to conduct some experiments to see the effects of

different choices in the image stitching pipeline

The aim of this report is to perform experiments on parts of the image stitching process specifcally the feature matching and homography estimation. First experiment we will compare two feature matchers used by OpenCV and second experiment vary the choice of RANSAC threshold used in homogrpahy estimation. Both experiemtn will be measuring the accuracy of the homography via the reprojection error.

Reprojection Error, calculates the euclidean distance between transformed points in source image to points in destination image. It measures how well the homography aligns the source and destination points. The same reprojection error used by OpenCV findHomography() for filtering by the ransacThreshold.

$\mathbf{d}$ point in the image we want to align to

$\mathbf{s}$ point in the image we want to transform using homography H

Projection error = $||\mathbf{d} - H\mathbf{s}||$

Image Dataset:

Both experiments used the same image dataset, it contains a mix of 3 scene types: Outdoor/Natural greenery, Exteriror of buildings, Interior of buildings. Image pairs differ by camera rotations or translation of camera for planar scenes

Image Number	Resolution/Image type	Source
1-40	1000x750 / JPG	https://github.com/tlliao/Single-perspective-warps/tree/master [1]
41-59	3000x4000 / JPG	Myself
60-104	1500x2000 / JPG	Myself

Images 1-40 scene type is all Exterior of buildings with a mix of Outdoor/Natural greenery

Images 41-104 scene types: Interior scenes 40, Exterior scenes 16, Greenery scenes 8.

Experiment Process:

For each image pair:

1. Generate SIFT features from both images.
2. Use a feature matcher like Brute-Force or FLANN to find corresponding features between the images.
3. Apply Lowe's ratio test to remove unreliable matches.
4. Use RANSAC to estimate the homography between the images.
5. Compute the reprojection error for both inlier and outlier points.

Data Filtering:

Reprojection error data was filtered where all data points must be between LQ − 1.5 IQR and UQ + 1.5 IQR.

LQ (Lower Quartile)

UQ (Upper Quartile)

IQR (InterQuartile Range)

Experiment 1: Feature Matching

Hypothesis/Question:

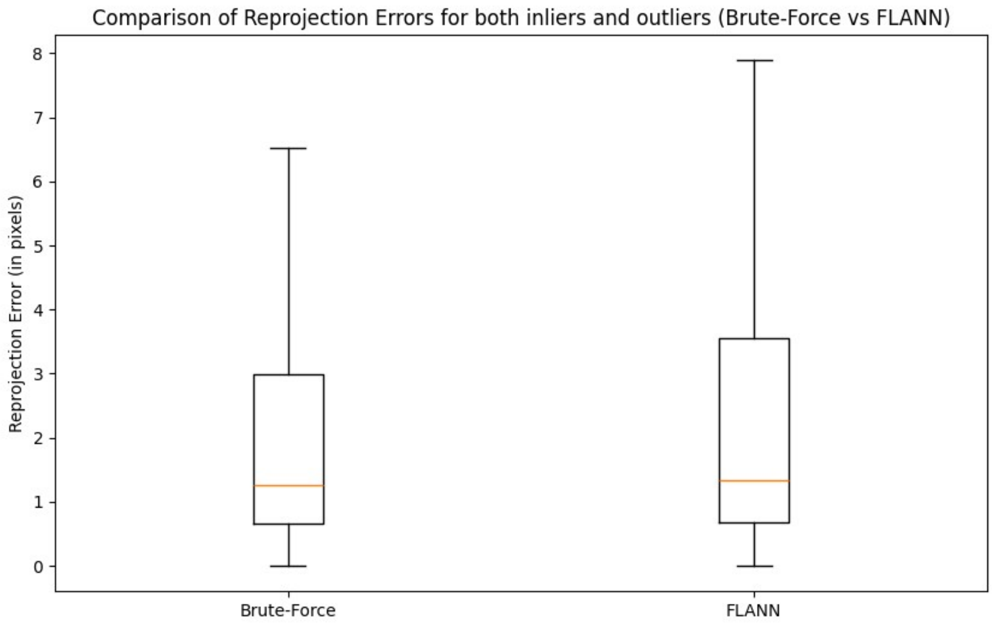
Brute-Force feature matcher results in a more accurate homography than FLANN feature matcher.

Experimental Design:

We will follow the Experiment Process above, but vary the feature matcher between Brute-Force and FLANN.

Results:

Below boxplot shows the distributions for the Reprojection error for both inlier and outlier points for the Brute-Force and FLANN feature matcher.



Below is the summary statistics for reprojection errors for both inliers and outliers

Feature Matcher:	Brute-Force	FLANN
Count before data filtering	172242	181106
Couunt after data filtering	140447	140495
Mean	2.93	4.59
Standard Deviation	4.15	9.07
Min	0.01	0
Lower Quartile (25%)	0.65	0.67
Median (50%)	1.26	1.33
Upper Quartle (75%)	3	3.56
Max	22.54	67.65

Standard Deviation: Brute-Force's standard deviation stands at 4.15, slightly lower than FLANN's 4.59, indicating FLANN's higher variability in reprojection errors.

Quartiles: Brute-Force and FLANN have similar lower quartile and median values. However, FLANN's upper quartile is higher at 3.56 compared to Brute-Force's 3, suggesting FLANN's tendency for higher reprojection errors at the upper end. This, along with the standard deviation, explains FLANN's higher mean of 4.59 compared to Brute-Force's 2.93.

Overall, Brute-Force matching generally exhibits lower reprojection errors across all summary statistic metrics. The difference is more evident at the higher end of the distribution, with FLANN showing higher variability. FLANN tends to have slightly higher maximum errors and higher reprojection errors in the upper quartile range, indicating more significant errors from its outliers compared to Brute-Force. However, for inlier points (below threshold of 3), the reprojection error difference between the two methods is minimal.

Discussion/Conclusions:

The results support our hypothesis that the Brute-Force feature matcher generates a more accurate homography compared to FLANN due to it's lower reprojection error. This aligns with expectations as FLANN employs an approximate method, resulting in less precise matches. Hence this is why we see a very noticeable difference in the reprojection error for outliers as the matching wasn't accurate.

Experiment 2: RANSAC for Homography Estimation

Hypothesis/Question:

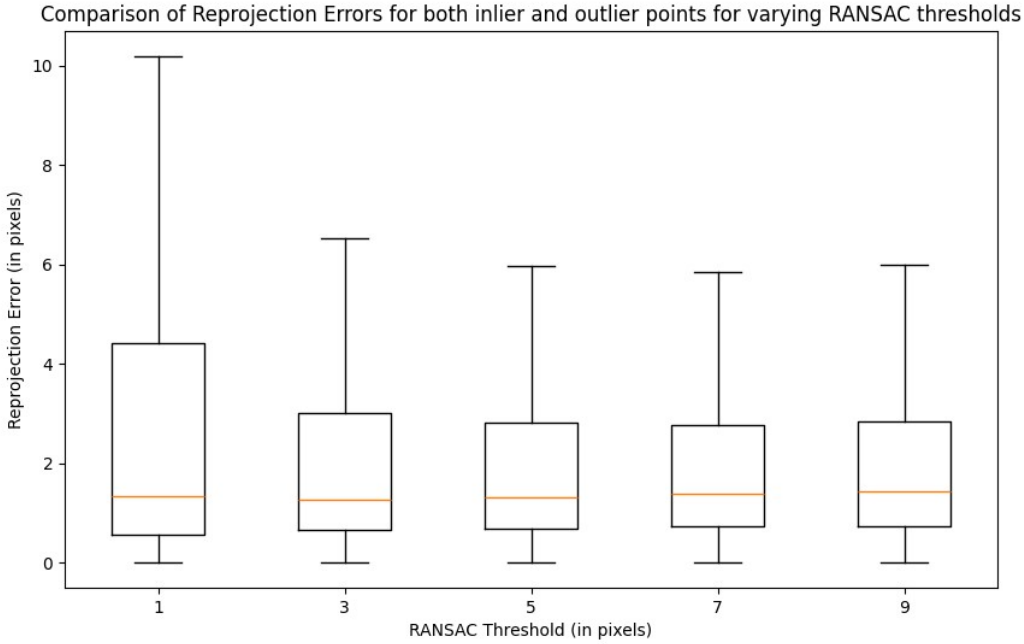
How does the choice of RANSAC threshold affect the accuracy of the homography?

Experimental Design:

We will follow the Experiment Process mentionedat the start, but only use the Brute-Force feature matcher and then only vary the RANSAC threshold.

Results:

Below boxplot shows the distributions for the Reprojection error for both inlier and outlier points for the varying RANSAC thresholds.



Below is the summary statistics for reprojection errors for both inliers and outliers (Number of feature matches before data filtering was 172242)

RANSAC Threshold:	1	3	5	7	9
Count after data filtering	142468	140447	138779	138698	138704
Mean	4.14	2.93	2.55	2.42	2.38
Standard Deviation	6.35	4.15	3.32	2.93	2.74
Min	0	0	0	0	0
Lower Quartile (25%)	0.56	0.65	0.68	0.72	0.73
Median (50%)	1.32	1.26	1.32	1.39	1.43
Upper Quartle (75%)	4.41	3	2.8	2.77	2.83
Max	33.17	22.54	19.87	17.75	16.44

Lower Quartile (LQ) Increase: As the RANSAC threshold increases, the Lower Quartile (LQ) for reprojection error also increases. This suggests that points closer to inlier points exhibit higher reprojection errors. The largest increase in LQ occurs from a RANSAC threshold of 1 to 3.

Upper Quartile (UQ), Mean, and Standard Deviation Decrease: Increasing the RANSAC threshold leads to a decrease in the Upper Quartile (UQ), Mean, and Standard Deviation of the reprojection error. This indicates that as the threshold increases, points closer to outlier points show decreased reprojection errors. The most significant decrease occurs from a RANSAC threshold of 1 to 3.

Median RANSAC Threshold: The median RANSAC threshold exhibits a decreasing trend from 1.32 for a threshold of 1 to 1.26 for a threshold of 3. However, there is a consistent increase in the median RANSAC threshold for threshold values of 5, 7, and 9, reaching 1.32, 1.39, and 1.43 respectively.

Discussion/Conclusions:

As the RANSAC threshold increases, errors tend to rise for points closer to inliers but decrease for those closer to outliers. The median RANSAC threshold reaches its lowest value at a threshold of 3. This implies that while errors for inliers tend to rise and errors for outliers tend to decrease with higher thresholds, there's an optimal balance at a threshold of 3 where the median reprojection error is minimised evenly for both inliers and outliers. Therefore we notice that the choice of RANSAC threshold does play a noticeable part in the accuracy of the homogrpahy.

Final Remarks

Draw together the two experiments and tell us what you've found from them in general. This is also a good place to suggest what the next steps will be. It is good to be honest about the limitations of your work, especially if you can see how to improve things in the future.

Some limitations: Only 3 scene types although due to time constraints and not balalnced and not balanced within the pixel reoslutions.

Also I resized alot of images to smaller reoslutiosn since the processing time was rather long with the 3000x4000 images with some images returning 100,000+ features

Would be interesting to see the distributions for just the outliers or just the inlier although this would make the report rather long and time consuming.

Interesting to analyse both inlier and outlier points seprately … for part 2

References

[1] Liao, T., & Li, N. (2020). Single-Perspective Warps in Natural Image Stitching. *IEEE Transactions on Image Processing*, *29*, 724–735. https://doi.org/10.1109/TIP.2019.2934344