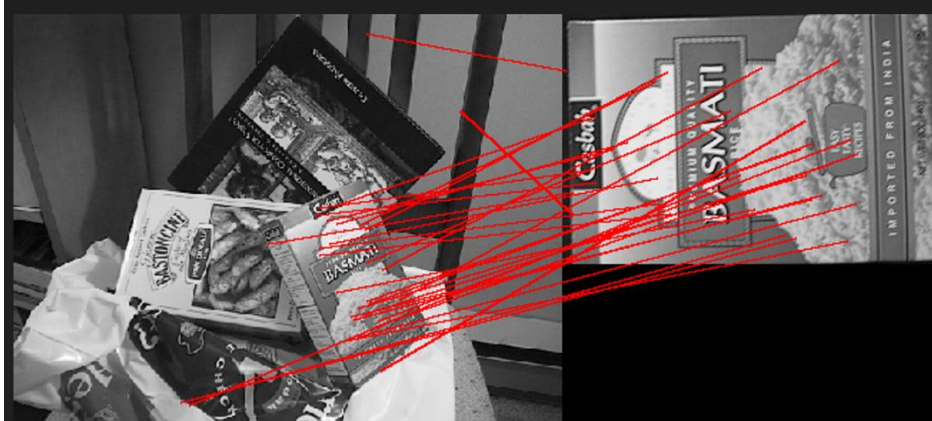


**** I took one late day for this Assignment****

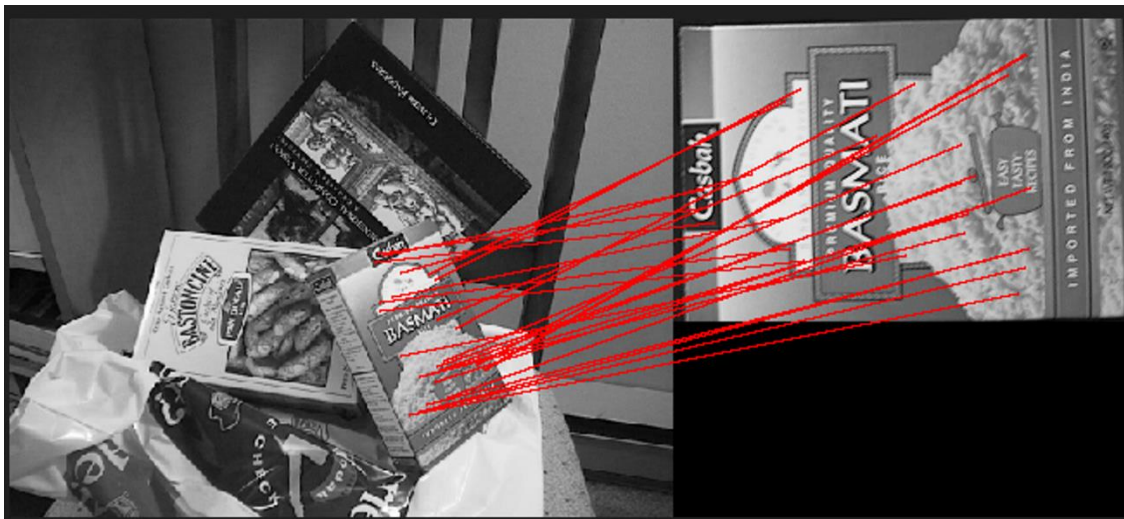
Q1.

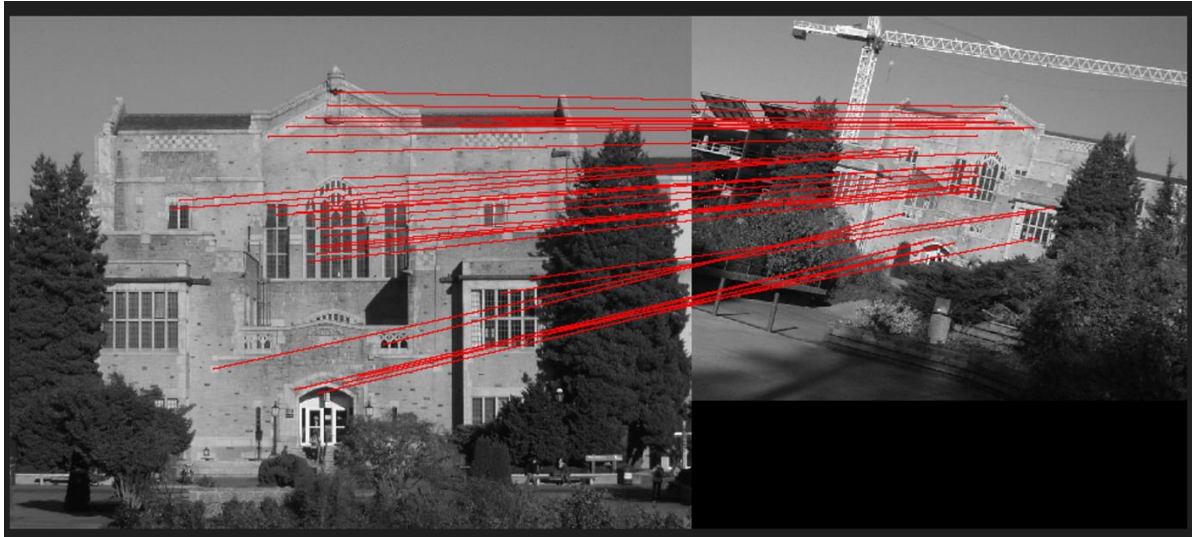
3.



This is the result of my code when I use the threshold 0.75. I chose this value because it seemed to be the happy medium between having a few outliers present, while still being mostly right. It was important to get the value correct because if I select too small of a threshold then it could be too strict which would lead to missing non-outlier matches. While if I pick too high of a threshold then it will likely have far too many outliers present. 0.75 seemed to be the happy medium in this regard.

4.

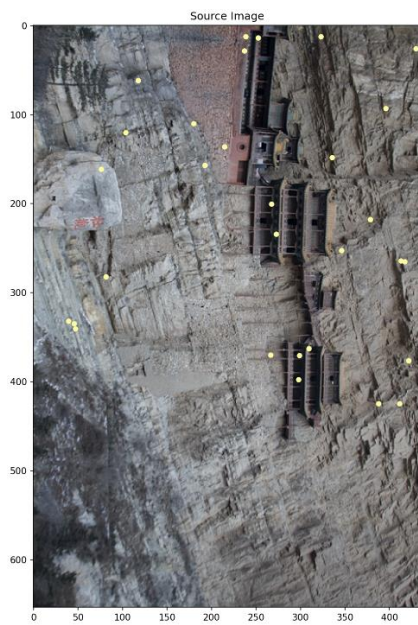




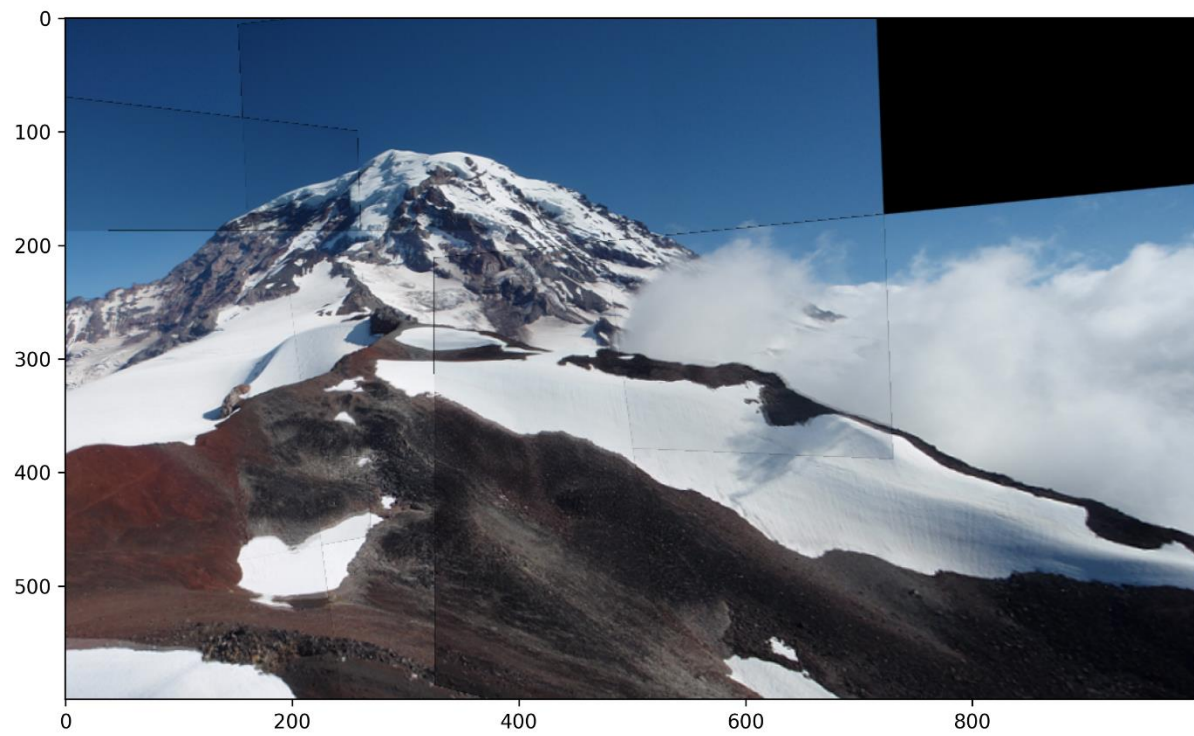
Consistency checking is a very powerful tool to tighten up your output and get better results. What it does is look at the difference in scale as well as the difference in orientation between a pair of points, and compares it to other pairs. If two pairs are similar in these values then they are more likely to be inliers. So if the set with the most inliers is taken, it will more likely reduce the outliers and only keep good results that are similar to each other. Since it does a good job of detecting outliers it also allows you to increase the threshold higher than you normally would. This will give you more key points to work with and may mean will find more inliers. For instance, in the basmati example, the initial image with some outliers was with a threshold of 0.75. In the version with RANSAC I was able to increase the threshold up to 0.9 which is quite significant. If I did not use RANSAC and had a threshold of 0.9, the picture would be riddled with red lines scattered everywhere throughout the image, and most of it would be wrong, but with RANSAC you can see the result above is quite good.

Q2.

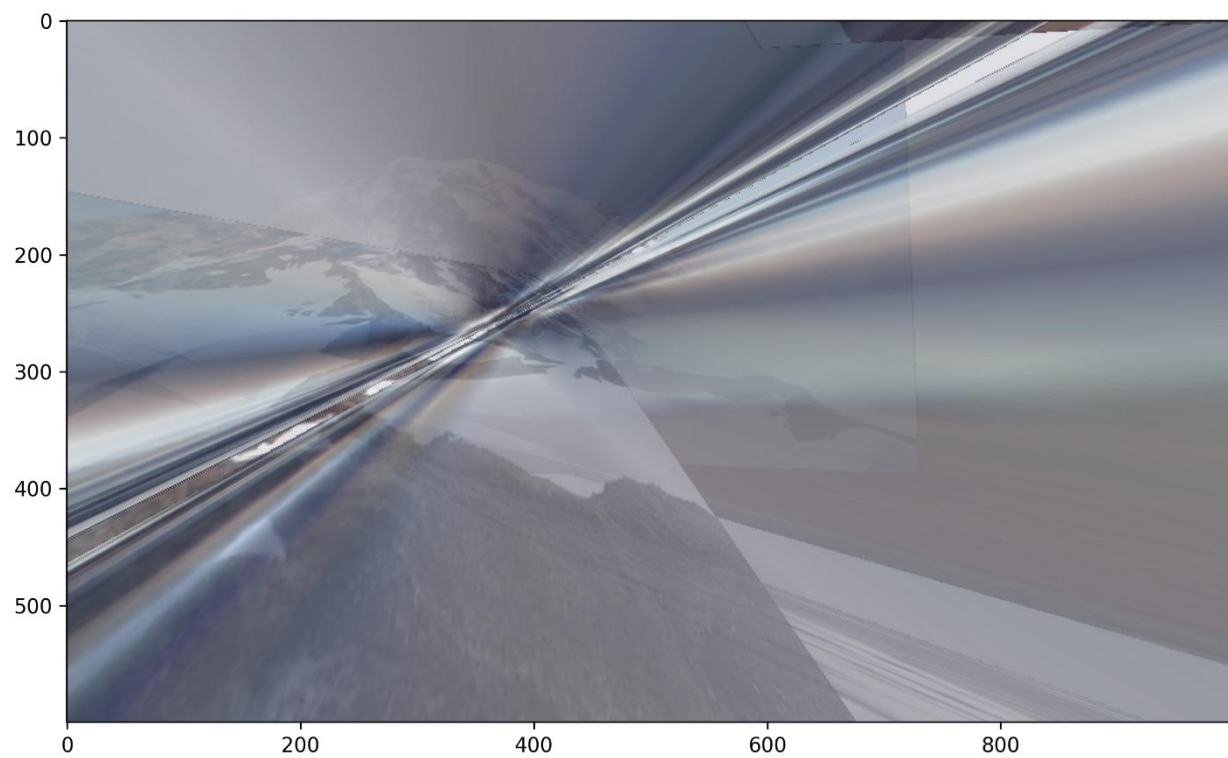
3.



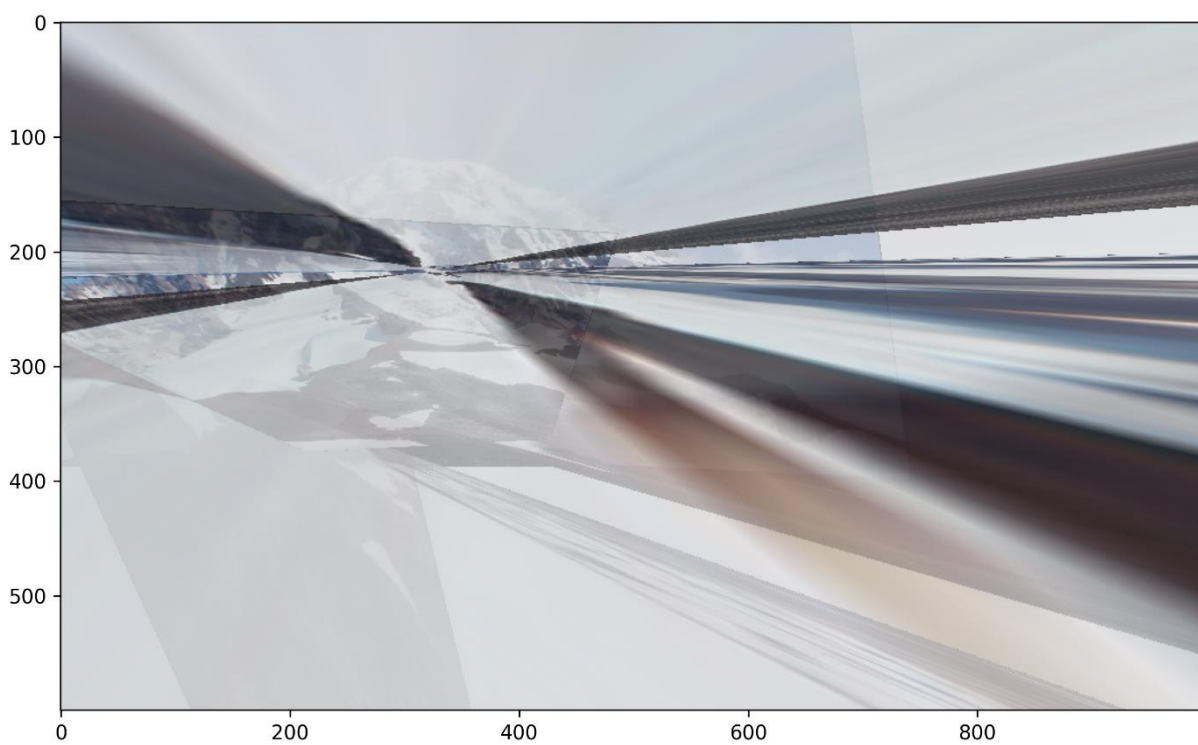
4.



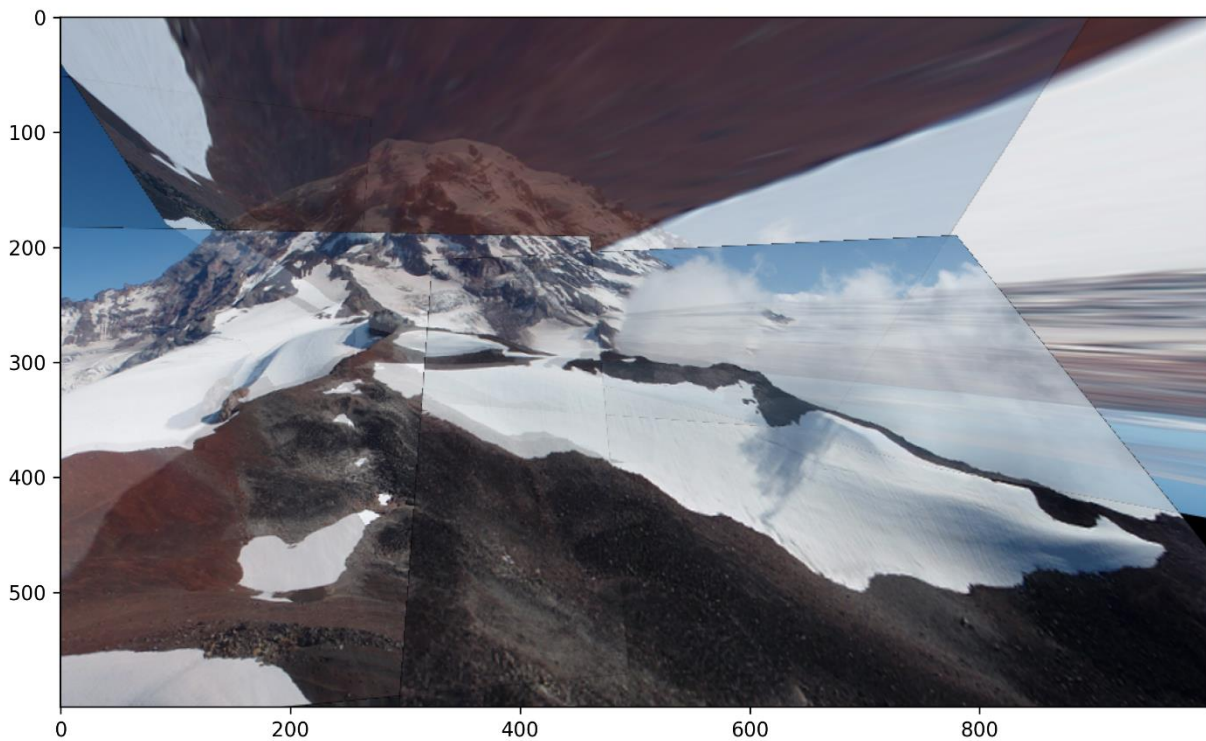
Num_iter = 75, tol = 5



Num_iter = 5, tol = 5



Num_iter = 5, tol = 15



Num_iter = 50, tol = 50

The number of iterations parameter will determine how many separate homography matrices will be tested before returning the result. Too few iterations will increase the likelihood of potentially getting a homography matrix that doesn't work very well with many of the points, which will give a worse result. Too many iterations may be too computationally unnecessarily costly as you would be able to get a very similar result in less iterations. For the tol parameter it will determine how close the projected point will have to be to the reference point to be considered a good point. If it is too big then it will deem points that aren't good as good points, leading to the algorithm potentially selecting a homography matrix that doesn't actually perform well to be used. If it is too small, then it will unnecessarily strict in choosing the points and may not have enough data to select a good matrix to be used.

5.

