Image_Mosaicing

Pulkit Gera-20171035

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```
In [1]: import numpy as np
        import cv2
        import os
        import matplotlib.pyplot as plt
        %matplotlib inline
In [2]: def readImages(index):
            1 = []
            diry = 'image_mosaicing/'
            for img in os.listdir(diry):
                if img[3] == str(index):
                    i = cv2.imread(diry+img)
                    i = cv2.cvtColor(i,cv2.COLOR_BGR2RGB)
                    1.append(i)
            return np.asarray(1)
In [3]: def resize(images,scale_percent):
            new = []
            for img in images:
                width = int(img.shape[1] * scale_percent / 100)
                height = int(img.shape[0] * scale_percent / 100)
                dim = (width, height)
                resized = cv2.resize(img, dim, interpolation = cv2.INTER_AREA)
                new.append(resized)
            return np.asarray(new)
```

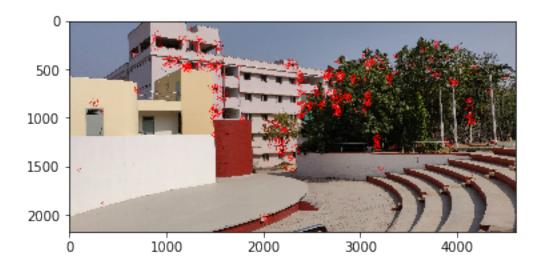
0.1 Feature Matching

We make keypoints using ORB and then match features using both flann and brute force., FLANN builds an efficient data structure (KD-Tree) that will be used to search for an approximate neighbour, while cv::BFMatcher does an exhaustive search and is guaranteed to find the best neighbour. The real benefit of FLANN is seen with large data sets.

```
In [4]: def keypoints(image,disp=False):
    orb = cv2.ORB_create(nfeatures=1000)
    gray = cv2.cvtColor(image,cv2.COLOR_RGB2GRAY)
    keypoints,descriptors = orb.detectAndCompute(gray, None)
    key = np.int32([kp.pt for kp in keypoints])
```

```
if disp:
    return keypoints,key,descriptors
else:
    return key,descriptors
```

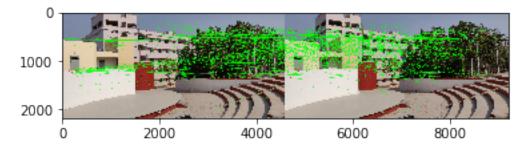
Out[7]: <matplotlib.image.AxesImage at 0x7fd57167a8d0>



```
In [19]: # Flann Matching
         def feature_matching(kp1,kp2,ds1,ds2,test_ratio=0.3):
             FLANN_INDEX_LSH = 6
             index_params= dict(algorithm = FLANN_INDEX_LSH,
                            table_number = 6, # 12
                            key_size = 12,
                                              # 20
                            multi_probe_level = 1) #2
             search_params = dict(checks=200)
             flann = cv2.FlannBasedMatcher(index_params, search_params)
             matches = flann.knnMatch(ds1,ds2,k=2)
                 As per Lowe's paper
             refined_matches = []
             for i,m in enumerate(matches):
                 if m[0].distance < test_ratio*m[1].distance and len(m)==2:</pre>
                     refined_matches.append((m[0].queryIdx, m[0].trainIdx))
```

```
match1, match2 = [], []
             for id1, id2 in refined_matches:
                 match1.append(kp1[id1])
                 match2.append(kp2[id2])
             return np.int32(match1),np.int32(match2)
In [38]: def match_keypoints(keypoints_A, keypoints_B, features_A, features_B, test_ratio):
             matcher = cv2.DescriptorMatcher_create("BruteForce")
             matches = matcher.knnMatch(features_A, features_B, 2)
             refined_matches = []
             for m in matches:
                 if len(m) == 2 and m[0].distance < m[1].distance * test_ratio:
                     refined_matches.append((m[0].queryIdx, m[0].trainIdx))
             match_A, match_B = [], []
             for idA, idB in refined_matches:
                 match_A.append(keypoints_A[idA])
                 match_B.append(keypoints_B[idB])
             return np.int32(match_A), np.int32(match_B)
In [10]: \# m, img = feature\_matching(l1, kp1, ds1, 0)
         # plt.imshow(imq)
Out[10]: <matplotlib.image.AxesImage at 0x7efd013dbac8>
```





0.2 Homography Matrix

We have keypoints between images and we want to calculate the homography matrix. In order to do that we take any 4 points, compute the homography matrix, project the points from image A onto image B and then calculate the reprojection error. We do this using RANSAC algorithm where in we perform this operation for N times to make it robust. N is chosen such that the probability of having atleast one inlier is 0.99.

```
In [66]: def DLT(match1, match2):
             assert match1.shape[0] == match2.shape[0]
```

```
A = np.zeros((match1.shape[0]*2, 9))
             i = 0
             total = zip(match1, match2)
             for ip, wp in total:
                 u, v = ip
                 x, y = wp
                 A[2*i] = [0, 0, 0, -u, -v, -1, u*y, v*y, y]
                 A[2*i+1] = [u, v, 1, 0, 0, 0, -u*x, -v*x, -x]
                 i += 1
             # Solving using SVD
             u_{,} D, v_{T} = np.linalg.svd(A)
             v_T[-1] = v_T[-1]/v_T[-1, -1]
             H = np.reshape(v_T[-1], (3, 3))
             return H
In [102]: def projectError(H, matches_A, matches_B):
              errors = []
              matches_A = np.pad(matches_A, ((0, 0), (0, 1)), 'constant', constant_values=1)
              matches_B = np.pad(matches_B, ((0, 0), (0, 1)), 'constant', constant_values=1)
              try:
                  H_inv = np.linalg.inv(H)
              except np.linalg.LinAlgError:
                  return False, 0
              A_{-} = (H@matches_A.T).T
              A_{-} = A_{-}[:, :2] / A_{-}[:, -1].reshape(matches_A.shape[0], 1)
              d1 = np.linalg.norm(A_[:, :2] - matches_B[:, :2], ord=2, axis=1)
              B_{-} = (H_{inv@matches_B.T}).T
              B_{-} = B_{-} / B_{-}[:, -1].reshape(matches_B.shape[0], 1)
              d2 = np.linalg.norm(B_[:, :2] - matches_A[:, :2], ord=2, axis=1)
              outliers = np.nonzero(d1+d2 > 0.5)[0]
              return True, len(outliers)
In [97]: def makeHomography(matches_A, matches_B, ransac_iters):
             n_points = matches_A.shape[0]
             best_Homo = None
             min_error = np.inf
             for i in range(ransac_iters):
                 indices = np.int32(np.random.permutation(n_points))
```

```
X, Y = matches_A[indices[0:4]], matches_B[indices[0:4]]
X_test, Y_test = matches_A[indices[4::]], matches_B[indices[4::]]
homography = DLT(X, Y)
res, error = projectError(homography, X_test, Y_test)
if not res:
    continue

if error < min_error:
    min_error = error
    best_Homo = homography

return best_Homo, min_error</pre>
```

0.3 Warping Images

Once we get homography matrix, we project the image onto the other images plane and stitch them together

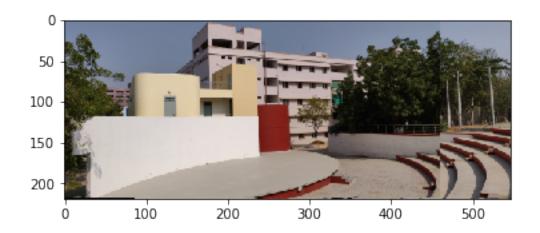
```
In [121]: def warp_project(imageA, imageB, homography):
             h1, w1, c1 = imageA.shape
              h2, w2,c2 = imageB.shape
              pts1 = np.float32([[0, 0], [0, h1], [w1, h1], [w1, 0]]).reshape(-1, 1, 2)
              pts2 = np.float32([[0, 0], [0, h2], [w2, h2], [w2, 0]]).reshape(-1, 1, 2)
              pts2_ = cv2.perspectiveTransform(pts2, homography)
              pts = np.concatenate((pts1, pts2_), axis=0)
              xmin, ymin = np.int32(pts.min(axis=0).reshape(-1) - 0.5)
              xmax, ymax = np.int32(pts.max(axis=0).reshape(-1) + 0.5)
              diff = (xmax-xmin, ymax-ymin)
              t = [-xmin, -ymin]
              Ht = np.array([[1, 0, t[0]], [0, 1, t[1]], [0, 0, 1]])
              result = cv2.warpPerspective(imageB, Ht@homography, diff)
              result[t[1]:h1+t[1], t[0]:w1+t[0]] = imageA
              return result
In [122]: def stitch(image1, image2, brute,test_ratio=0.75, N=10000,):
              k1,d1 = keypoints(image1)
              k2,d2 = keypoints(image2)
              if brute:
                  m1,m2 = match_keypoints(k1,k2,d1,d2,test_ratio)
              else:
                  m1,m2 = feature_matching(k1,k2,d1,d2,test_ratio)
              homography, error = makeHomography(m1,m2, N)
              stitched_image = warp_project(image2, image1, homography)
              return stitched_image
```

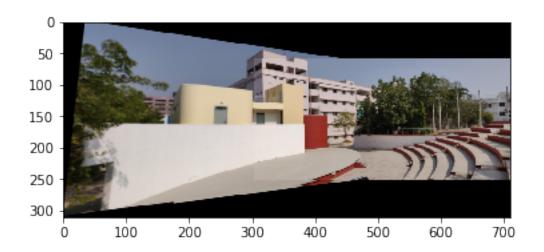
```
In [123]: def stitchAll(images,brute):
    res = images[0]
    i=0
    for img in images[1:]:
        plt.imshow(res)
        plt.show()
    res = stitch(res,img,brute)
        i +=1
    return res
```

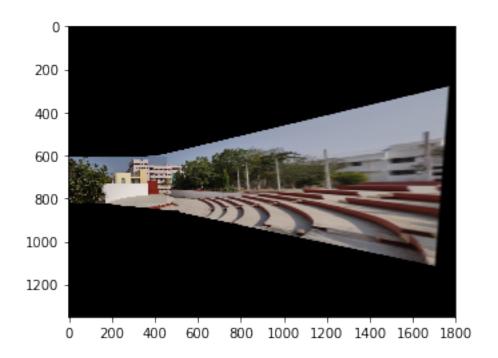
0.4 Experiments

```
In [134]: images = readImages(1)
    images = resize(images,10)
    s = stitchAll(images,False)
    plt.imshow(s)
    plt.show()
```

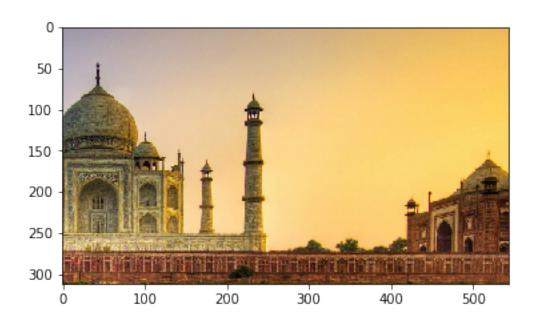


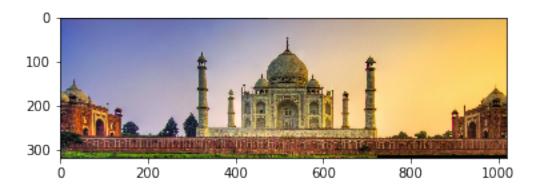


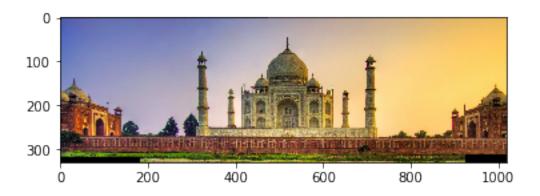


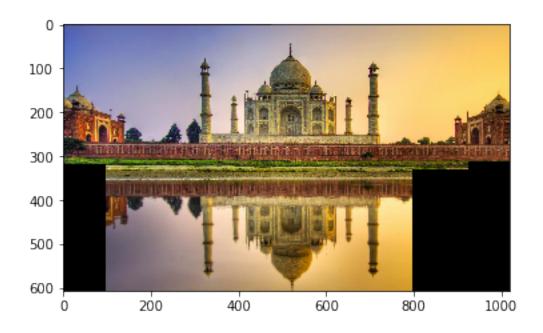


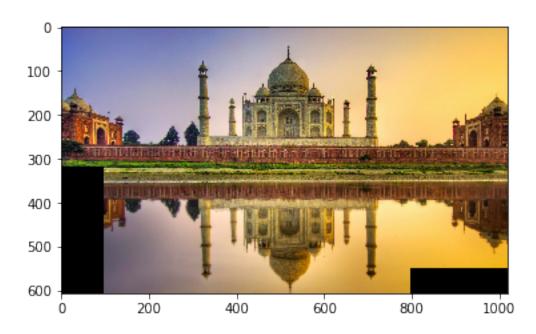
```
In [126]: images = readImages(2)
    # images = resize(images,10)
    s = stitchAll(images,True)
    plt.imshow(s)
    plt.show()
```

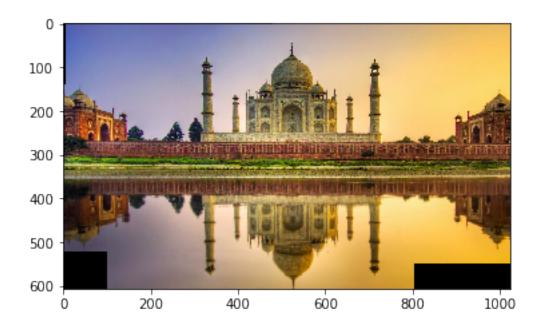






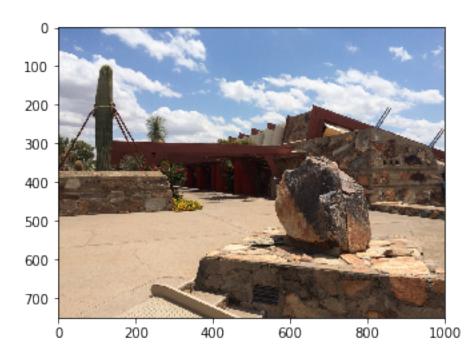


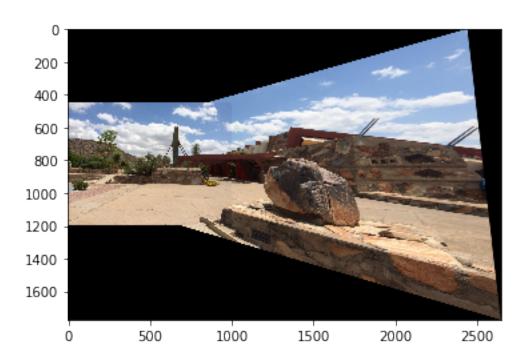




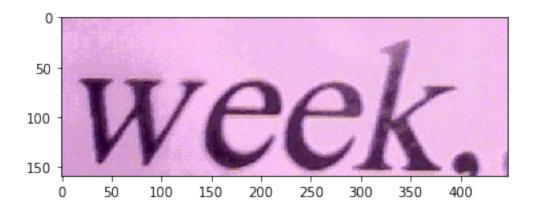
In this example we see that its able to stitch seamlessly due to no rotation between images so the homography matrix is a simple cut. For some reason flann is unable to work

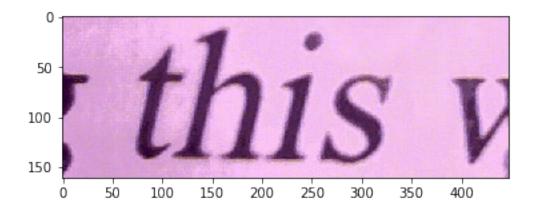
```
In [130]: images = readImages(3)
    # images = resize(images,10)
    s = stitchAll(images,False)
    plt.imshow(s)
    plt.show()
```





In [133]: images = readImages(4)
 # images = resize(images,10)
 s = stitchAll(images,False)
 plt.imshow(s)
 plt.show()



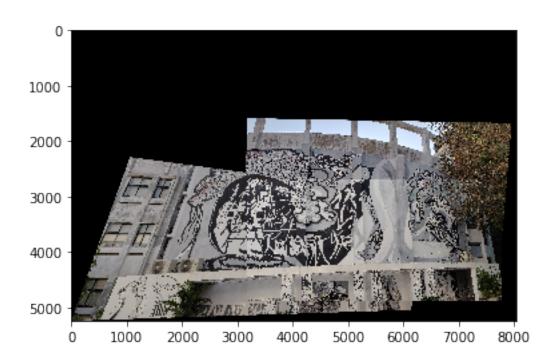


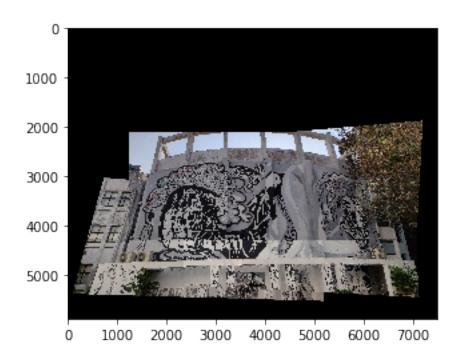
In the last example we observe that very few matches are there, thus its unable to stitch. If we lower the threshold then it maybe able to stitch.

```
In [137]: images = readImages(5)
    # images = resize(images,10)
    s = stitchAll(images,False)
    plt.imshow(s)
    plt.show()
```









```
In [138]: images = readImages(6)
    # images = resize(images, 10)
    s = stitchAll(images, False)
    plt.imshow(s)
    plt.show()
```



