EN-2550 Assignment 2

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GitHub Repository: https://github.com/sasdil/EN-2550-Computer-Vision

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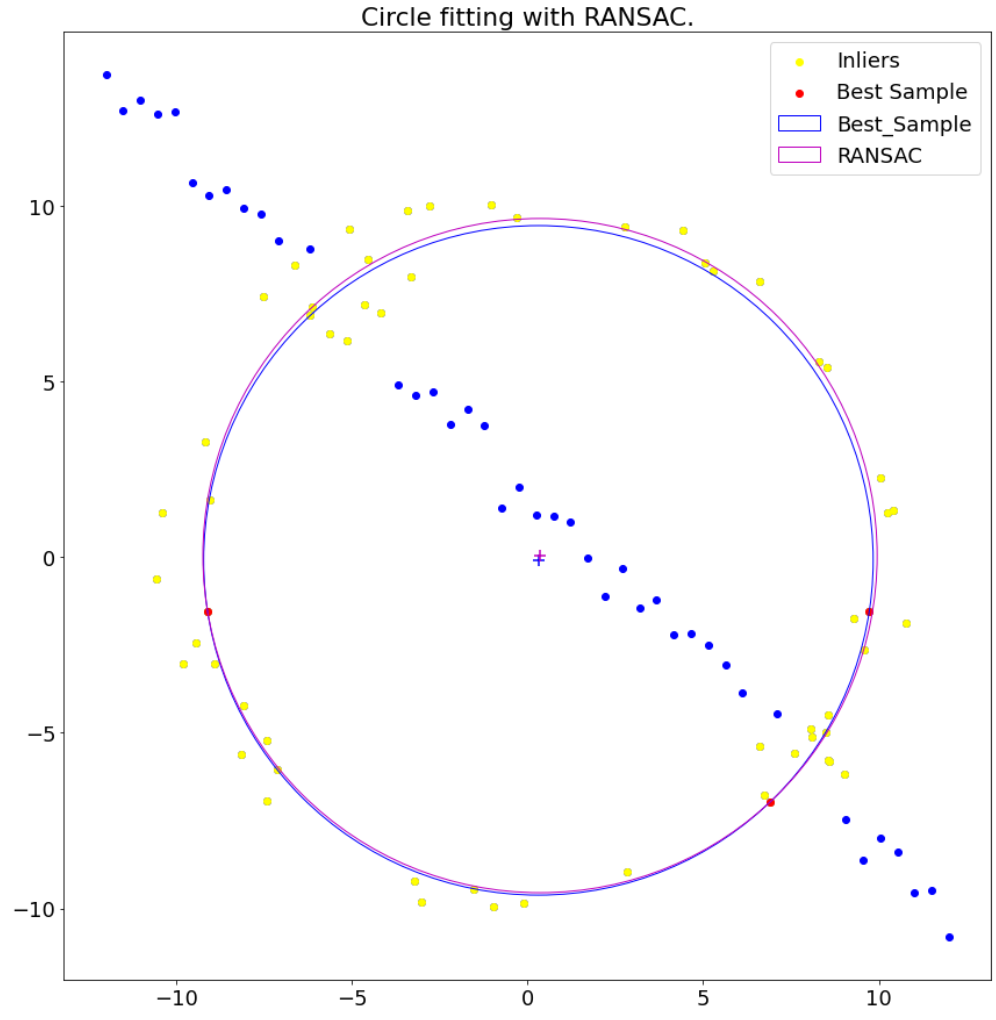
Question 1

In below code, I implementing the RANSAC algorithm for Circle fitting. So we get randomly choosed sample which consist with 3 point coordinates, we estimate the circle which go through those points using geometry. Then set a threshold value for check which circle is consist with most inliers.That belongs to best sample and then we put those inliers and best sample coordinates to get the RANSAC circle, So it is little bit deviate from best sample circle. Because RANSAC circle is genarated by using the inliers which belongs to best sample. In this case i set the threshold as '1.4' and i got '59' as most inliers votes. According to that the Resulting fitted cirlce is shown below with the best sample.

In the code 'sampling' function returns the random three points, According to that points we get corresponding circle using 'make_model' function.'Calc_inliers' function is used for get the inlier voting and 'ransac' function is used to combine the whole functions according to required operations.

In [6]:

```
#Class Object for Generating All required functions for RANSAC
class RANSAC_gen:
    def __init__(self, src, dst, n):
        self.src = src
        self.dst = dst
        self.n = n
        self.d_max=15
        self.best_model = None
        self.point= None
        self.mod = None
        self.inliers = None
    #Function for Randomly take 3 points sample
    def sampling(self):
        sample = []
        save_ran = []
        count = 0

        # get three points from data
        while True:
            ran = np.random.randint(len(self.src))
            if ran not in save_ran:
                sample.append((self.src[ran], self.dst[ran]))
                save_ran.append(ran)
                count += 1
                if count == 3:
                    break
        return sample
    #Function for genarate respective model
    def make_model(self, sample):

        pt1 = sample[0]
        pt2 = sample[1]
        pt3 = sample[2]

        A = np.array([[pt2[0] - pt1[0], pt2[1] - pt1[1]], [pt3[0] - pt2[0], pt3[1] - pt2[1]]])
        B = np.array([[pt2[0]**2 - pt1[0]**2 + pt2[1]**2 - pt1[1]**2], [pt3[0]**2 - pt2[0]**2 + pt3[1]**2 - pt2[1]**2]])
        inv_A = inv(A)

        c_x, c_y = np.dot(inv_A, B) / 2

        c_x, c_y = c_x[0], c_y[0]
        r = np.sqrt((c_x - pt1[0])**2 + (c_y - pt1[1])**2)
        return c_x, c_y, r
    #Function for filter out inliers
    def Calc_inliers(self,cx,cy,r):
        P=[]
        t=1.4
        xd=self.src
        yd=self.dst
        for i in range(len(xd)):
            dis = np.sqrt((xd[i]-cx)**2 + (yd[i]-cy)**2)
            if (r-t<=abs(dis)<=r+t):
                P.append([xd[i],yd[i]])
        return (P)
    def execute_model(self, model):
        c_x, c_y, r = model
        P = self.Calc_inliers(c_x,c_y,r)
        return P
    #Find the best model by excuting functions
    def ransac(self):
        # find best model
        for i in range(self.n):
            mod=self.sampling()
            model = self.execute_model(mod)
            c_x, c_y, r = model
            d_temp = self.eval_model(model)
            if self.d_max < len(d_temp):
                self.best_model = model
                self.d_max = len(d_temp)
                self.mode = mod
                self.inliers = d_temp
```



59

Question 2

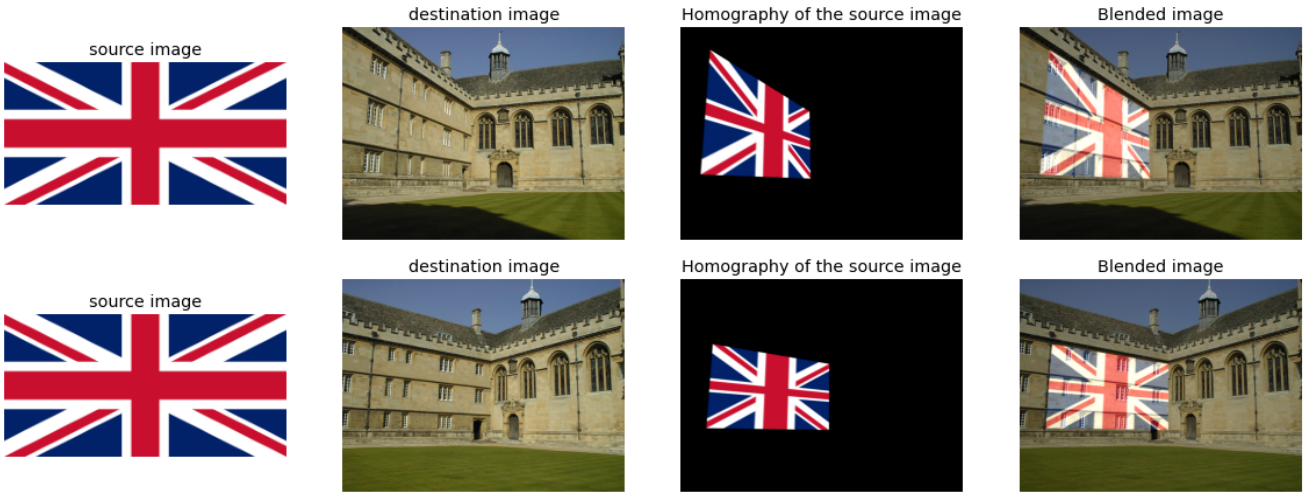
In here first we take 4 point coordinates given by user.(In class object 'Click' function is belongs to that task). These points refer to destination points which use to compute homography later. Afterwards we take vertices of source image as source points and then calculate the homography using 'cv.findHomography()' inbuilt function. Resulting images are shown in the below.

The blending of the image is done by using "cv2.addWeighted()" inBuilt fuction to make necessary adjustments of the final stitched image. The Important code parts are given below.

Resulting images are shown in the below according to the order.

In [3]:

```
#Class object for genarate warpped image
class warp_gen:
    def __init__(self,im1,im2,count,Points):
        self.im1 = im1
        self.im2 = im2
        self.count = count
        self.Points = Points
    #function for get coordinates according to mouse clicks
    def Click(self,event,x,y,flags,param):
        if event == cv2.EVENT_LBUTTONDOWN:
            self.Points.append([x,y])
            self.count+=1
    #Function for homography calcultions and warpping/ Blending of the image
    def process(self):
        wname = "Image"
        cv2.namedWindow(winname=wname)
        cv2.setMouseCallback(wname, self.Click)
        while self.count<4 :
            cv2.imshow(wname,self.im2)
            cv2.waitKey(1)
        cv2.destroyAllWindows()
        if (len(self.Points)==4):
            im_src = self.im1
            h, w, c = im_src.shape
            pts_src = np.array([[0,0],[w-1, 0],[w-1, h-1],[0,h-1]])
            im_dst =self.im2
            pts_dst = np.array(self.Points)
            h, status = cv2.findHomography(pts_src, pts_dst)
            im_out = cv2.warpPerspective(im_src, h, (im_dst.shape[1],im_dst.shape[0]))

            #Blend the image to get finale proper image
            result = cv2.addWeighted(im_dst,0.8,im_out ,0.6, 0)
```



Question 3

Part (A)

SIFT features of two images matched using following code. Mainly this function returns the matches and keypoints as outputs.

In [6]:
```
def siftmatch(img1,img2):
    sift = cv.SIFT_create()
    kp1, descriptors_1 = sift.detectAndCompute(img1, None)
    kp2, descriptors_2 = sift.detectAndCompute(img2, None)
    bf1 = cv.BFMatcher(cv.NORM_L1, crossCheck = True)
    matches1 = bf1.match(descriptors_1, descriptors_2)
    sortmatches1 = sorted(matches1, key = lambda x:x.distance)

    return matches1,[kp1,kp2]
```

Part (B) & Part (C)

In here basically I calculate homography of image 1 to 5 using saperate homograpies of imagea 1 to 2 , 2 to 3, 3 to 4, 4 to 5.Then we multiply those homography matrices reversely to obtain the 1 to 5 image homography. It is very hard to calculate the homography of the image 1 to 5 directly. Because the homography of those two images is very high. So using Homography function, we can calculate homography matrix according to the RANSAC algorithm. The main code parts are given below.

In following case 'SSD' function returns the geometric distance between the destination points and the resulting points corresponds to homography matrix. The 'Homography' function returns the homography matrix, which corresponds to given four random four points.The 'ransac' function is consist with ransac algorithm to genarate the most suitable homography matrix among all possible homography matrices.

So in here i set the threshold value as '5' and get the most inliers according to that and then calculated the homograpies separately.

The mathematical procedure to get the homography matrix is we put source and destination points according to a linear system(matrix). Then we get the Transpose of the matrix and multiply it with the previous version and take the eigen vector corresponds to the minimum eigen value. The required calculations are done in the 'Homography function'.

In [9]:
```
def SSD(corres, h):
    pts1 = np.transpose(np.matrix([corres[0].item(0), corres[0].item(1), 1]))
    estimatep1 = np.dot(h, pts1)
    estimatep2 = (1/estimatep1.item(2))*estimatep1
    pts2 = np.transpose(np.matrix([corres[0].item(2), corres[0].item(3), 1]))
    error = pts2 - estimatep2
    return np.linalg.norm(error)
def Homography(correspondences):
    #Loop through correspondences and create assemble matrix
    Lst = []
```

```
    for corr in correspondences:
        p1 = np.matrix([corr.item(0), corr.item(1), 1])
        p2 = np.matrix([corr.item(2), corr.item(3), 1])

        a2 = [0, 0, 0, -p2.item(2) * p1.item(0), -p2.item(2) * p1.item(1), -p2.item(2) * p1.item(2),
              p2.item(1) * p1.item(0), p2.item(1) * p1.item(1), p2.item(1) * p1.item(2)]
        a1 = [-p2.item(2) * p1.item(0), -p2.item(2) * p1.item(1), -p2.item(2) * p1.item(2), 0, 0, 0,
              p2.item(0) * p1.item(0), p2.item(0) * p1.item(1), p2.item(0) * p1.item(2)]
        Lst.append(a1)
        Lst.append(a2)
    matrixA = np.matrix(Lst)
    #svd composition
    u, s, v = np.linalg.svd(matrixA)
    #reshape the min singular value into a 3 by 3 matrix
    h = np.reshape(v[8], (3, 3))
    #normalize and now we have h
    h = (1/h.item(8)) * h
    return h
def ransac(corr, thresh):
    maxInliers = []
    finalH = None
    for i in range(1000):
        #find 4 random points to calculate a homography
        corr1 = corr[random.randrange(0, len(corr))]
        corr2 = corr[random.randrange(0, len(corr))]
        randomFour = np.vstack((corr1, corr2))
        corr3 = corr[random.randrange(0, len(corr))]
        randomFour = np.vstack((randomFour, corr3))
        corr4 = corr[random.randrange(0, len(corr))]
        randomFour = np.vstack((randomFour, corr4))
        #call the homography function on those points
        h = Homography(randomFour)
        inliers = []
        for i in range(len(corr)):
            d = SSD(corr[i], h)
            if d < 5:
                inliers.append(corr[i])
        if len(inliers) > len(maxInliers):
            maxInliers = inliers
            finalH = h
        if len(maxInliers) > (len(corr)*thresh):
            break
    return finalH, maxInliers
def corr_list(matches1,key):
    correspondenceList1 = []
    keypoints1 = [key[0],key[1]]
    for match in matches1:
        (x1, y1) = keypoints1[0][match.queryIdx].pt
        (x2, y2) = keypoints1[1][match.trainIdx].pt
        correspondenceList1.append([x1, y1, x2, y2])
    return correspondenceList1
#calculate homographies
match1,ky1=siftmatch(img1,img2)
correspondenceList1=corr_list(match1,ky1)
corrs1 = np.matrix(correspondenceList1)
finalH1, inliers1 = ransac(corrs1, 0.6)
match2,ky2=siftmatch(img2,img3)
correspondenceList2=corr_list(match2,ky2)
corrs2 = np.matrix(correspondenceList2)
finalH2, inliers2 = ransac(corrs2, 0.6)
match3,ky3=siftmatch(img3,img4)
correspondenceList3=corr_list(match3,ky3)
corrs3 = np.matrix(correspondenceList3)
finalH3, inliers3 = ransac(corrs3, 0.6)
match4,ky4=siftmatch(img4,img5)
correspondenceList4=corr_list(match4,ky4)
corrs4 = np.matrix(correspondenceList4)
finalH4, inliers4 = ransac(corrs4, 0.6)
#Obtaining the homography matrix of 1 to 5
H = finalH4 @ finalH3 @ finalH2 @ finalH1
print(H)
```

```
[[ 6.04345394e-01 -1.47445713e-02  2.26355740e+02]
 [ 2.12269414e-01  1.02437998e+00 -4.20289643e+00]
 [ 4.80594964e-04 -2.10740505e-04  9.92345796e-01]]
```

After calculating the homography using above RANSAC algorithm, in here we campare it with the actual homography matrix to observe the accuracy of the above code. For that we get the Sum of Square Difference between those two matrix.So we achieve reasonable value for it.

The resulting stitched image is shown above.

In [13]:

```
Original_Homography = [ [6.2544644e-01,5.7759174e-02,2.2201217e+02],
   [2.2240536e-01,1.1652147e+00,-2.5605611e+01],
   [4.9212545e-04,-3.6542424e-05,1.0000000e+00]]
Calculated_Homography = [[ 6.51222636e-01 , 7.03255113e-02 , 2.20540605e+02],
 [ 2.31063212e-01 , 1.19780873e+00, -2.55386339e+01],
 [ 5.43289009e-04, -4.18605266e-06 , 1.00140169e+00]]
Original_Homography =np.array(Original_Homography)
Calculated_Homography = np.array(Calculated_Homography)

SSD_Calc= np.sum(np.sum((Original_Homography-Calculated_Homography)*(Original_Homography-Calculated_Homography)))
print("SSD Value =",SSD_Calc)
```

```
SSD Value = 2.171951103855168
```