

## Objective:

In this task we are combining two images into a single larger image. In order to do so, we need to do certain image transformations on the image so that we can warp and align it with the other image.

## Steps:

The transformation should be projective transformations and to calculate this we need to find the homography matrix.

So as a first step, we need to find the homography matrix which is the set of matching points in two images. This will help us align the two images into one coordinate system.

There is a problem in matching the points in two images. It might happen that the points two images would appear to match but are not valid matches. So we need to find the good matches that are valid and match the corresponding points in both the images. To do so we need to find the inliers and outliers. This can be achieved using RANSAC.

### 1. Key Matches

As a first step, we need to locate the keypoints and corresponding descriptors. We are doing this using SIFT detector.

```
sift = cv2.xfeatures2d.SIFT_create()
kp, des = sift.detectAndCompute(img, None)
```

SIFT is used for detecting the blobs, its size and orientation.

So we get the interest points for matching the images

To match the two SIFT descriptors we use the 2-norm distance. Lower the distance it is a good match.

Here we are computing the the L2 distance for each point in left image to each point in right image and getting the two lowest distances.

In order to remove the disambiguity in matches we are using the ratio test.

If  $d(p,m) < \text{Eta} * d(p,n)$  then it is good match.

Here  $\text{Eta}=0.75$

After this step we have the good matches.

### 2. Estimating Homography.

Homography is estimated for two images if they are taken from the same view point.

It is a matrix which when multiplied with one image can give its corresponding points in another image.

$p' = hp$

here  $h$  is the matrix which is unknown to us. To solve this, we find the Eigen values and Eigen vectors

So applying SVD to this matrix we find the homography matrix.

As we know, there could be matches which are invalid that is they do not match in the 3d view. Such points are called the outliers.

To do so we use RANSAC algorithm. ( $k=1000$ ,  $t=4.5$ )

Here we randomly select 4 pairs of points and compute the homography matrix. Using this homography we get the matching points in second image.

We calculate the distance between the predicted value by the model using homography and the actual value.

We consider it as an outlier, if this distance is greater than a threshold.

This process is repeated for  $k$  iterations. After every iteration we get the number inliers and outliers. We take the homography matrix that give the maximum inliers.

### 3. Warping

Now that we have the best homography matrix, we do the warping of the images

Using the homography, we find the bounds for one image in the coordinates of another.

To do so we take the corners of one image, take its corners. Using homography matrix transform it to second image's coordinate system.

After we have the bounds for final image, we fill in the gaps with the two images to get the stitched image