# Assigment 1 Computer Vision

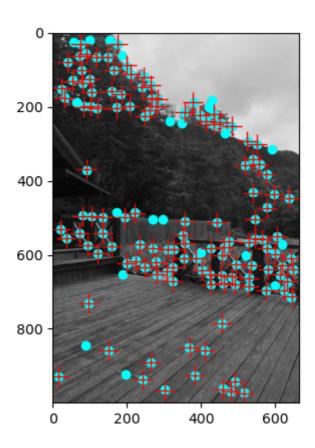
### Giulio Zani

### Testing the code

Please check the README.md in order to run the code on new images.

### **Computing Corner Harris**

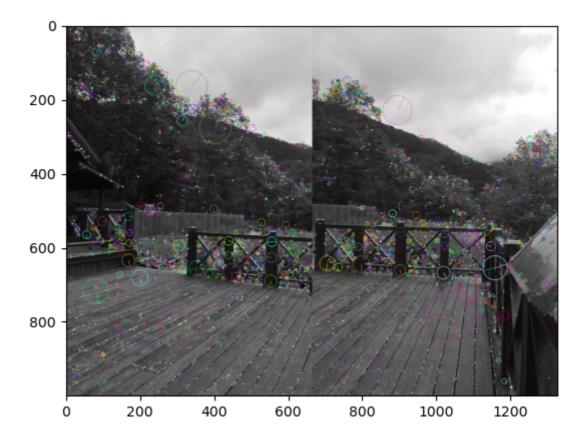
The Corner Harris are computed as described in the assignment detail using skimage. feature. Afterwards the peaks and the corner subpix are computes using the same library and applied in this sample image.



## **Selecting Descriptors**

To select the descriptors and keypoints, I have used the cv2.SIFT\_create() function.

#### Resulting in the following image:

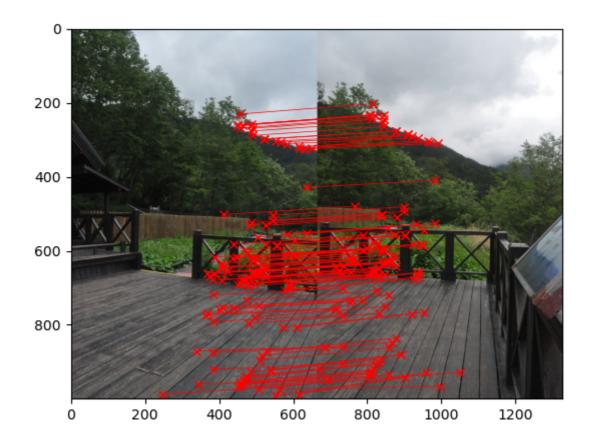


After

the descriptors are extracted, they are selected based on their distance between all of the descriptors of the other image. This will yield a NxM matrix, where N is the number of descriptors found in the left image and M in the right. The minimum for each row is found and then the descriptors are selected usign a threshold that is *relative*. So if t is the threshold, and k is the number of descriptors:

$$k = tN$$

As mentioned in the assignment description, there are two ways to compute the distance between two descriptors: \*eucledian\* and \*normalized correlation\*. The results of both techniques are reported in the following subsections. These results are based on the sensitivity analysis described in its corresponding section.



### Normalized Correlation

### Hyperparameters

ransac	ransac	ransac distance	ransac accepted	distance	top
iters	sample size	threshold	threshold	method	matches
10000	0.2	0.1	0.01	correlation	0.04

### Results

accuracy	error	
0.07895	0.03056	

### **Euclidian Distance**

### Hyperparameters

ransac	ransac	ransac distance	ransac accepted	distance	top
iters	sample size	threshold	threshold	method	matches
10000	0.2	0.1	0.01	euclidean	0.04

### Results

accuracy	error	
0.07895	0.06185	

As we can see the error is lower for the normalized correlation.

#### Ransac

While implementing the Ransac algorithm, I have tried as much as possible to use *relative* thresholds. This is because the number of descriptors and the sample size are not known in advance and thus using relative thresholds makes the algorithm more robust. At every iteration, the ransac computes the ratio inliers/outliers and the mean error. At the end of the iteration process, models are selected first on basis of the ratio and then on basis of the mean error. Both these selections use relative thresholds.

### Sensitivity Analisys

As requested, I have performed a sensitivity analysis on the Ransac algorithm using the ratio number of inliers/number of outliers. This is one of the two metrics presented. The other one is the error on the remaining sample of the model seleted by the Ransac algorithm. The error is thus based on MSE (mean squared error). The error is computed as follows:

$$||f1' - f2||_2^2$$

Where f1 and f2 are the matching keypoints of the two images, and f1' are the keypoints after applying a model.

The accuracy is given by:

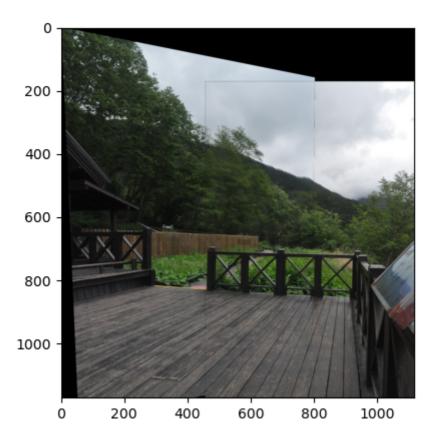
$$\frac{i}{i+o}$$

Where  $\mathbf{i}$  is the number of inliers and  $\mathbf{o}$  is the number of outliers (which are also selected on the basis of the euclidian distance).

### Stitching images

To stitch the images, we first compute the corners of the left image. Then we apply the model selected by Ransac to them and get a translation matrix which we can use to warp our image using the cv2.warpPerspective function. Then we create a new model based on this translation matrix and apply it the right image to get also the right warped image. Once we have both images warped we can stitch

them together by looping through every pixel. We will select non-black pixel of each image (if any).

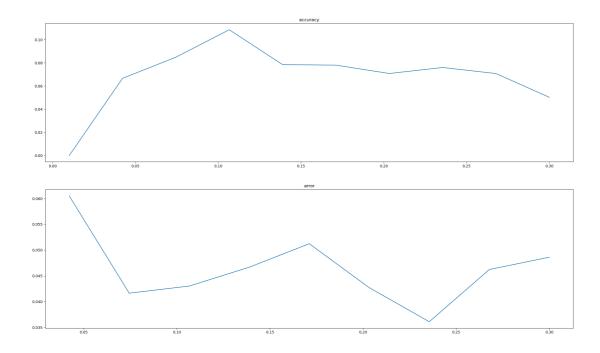


### Experiments

To find out the optimal hyperparameters, I have created a loop that evalues the error of the model for different values given by a range.

#### **Top Matches**

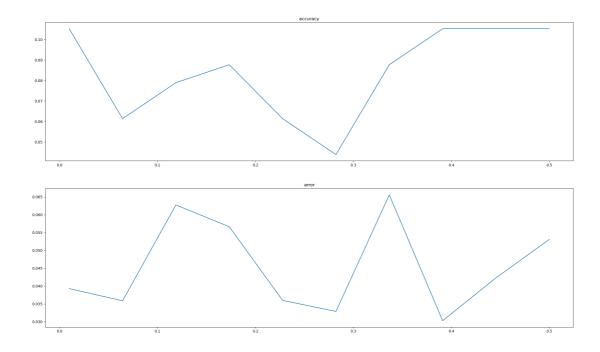
Top matches is a hyperparameter that defines a relative threshold for the number of matches. The higher the value, the more matches are selected. Its possible maximum value is 1, but in practice even for values higher than 0.3, the algorithm becomes very slow. Below are shown results for 10 values between 0.01 and 0.3.



Interestingly, the two metrics don't seem to be proportional to each others.

### **Accuracy Threshold**

Given the accuracies of all the models, the accuracy threshold selects the top percentage of the models that will subsequently be selected according to error.



### Other images

# Image 2

### Hyperparameters

ransac	ransac	ransac distance	ransac accuracy	distance	top
iters	sample size	threshold	threshold	method	matches
10000	0.2	0.1	0.01	euclidean	0.04

### Results

ассигасу	еггог		
0.03614	0.03401		

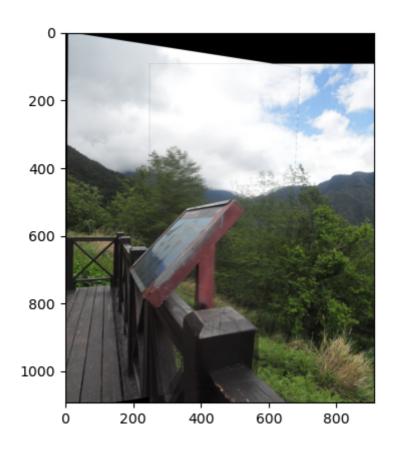
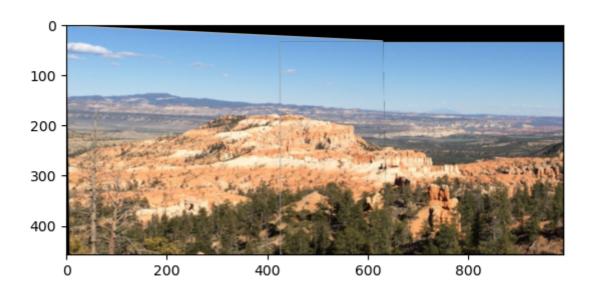


Image 3
Hyperparameters

ransac	ransac	ransac distance	ransac accuracy	distance	top
iters	sample size	threshold	threshold	method	matches
10000	0.2	0.1	0.01	euclidean	0.04



# Results

accuracy	error	
0.11404	0.04336	