

Assignment 2

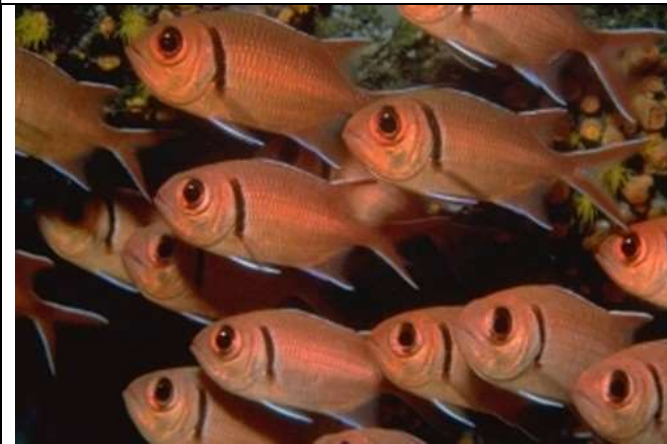
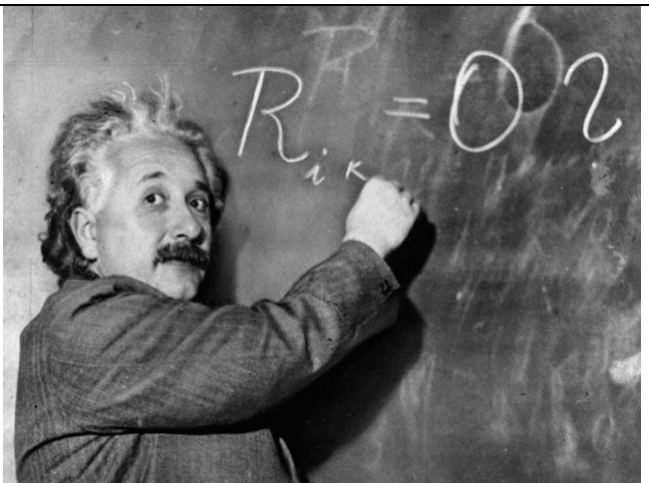
ECE 736: 3D Image Processing and Computer Vision

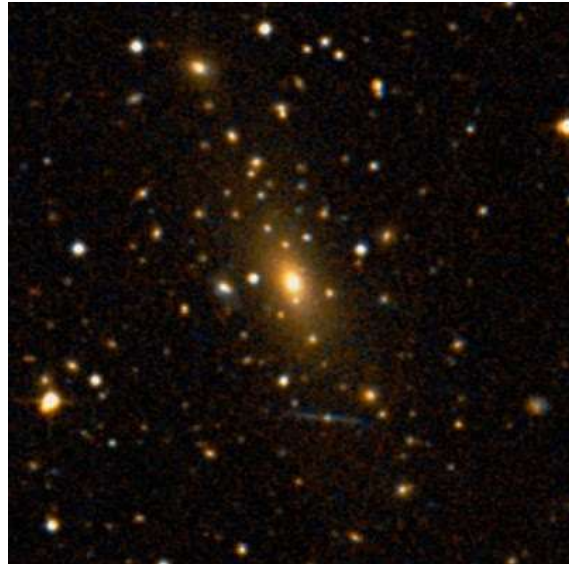
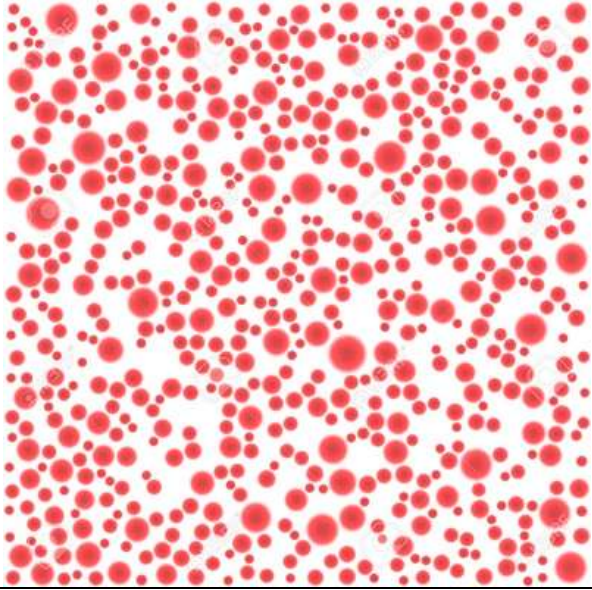
Pranav Rawal

Department of Electrical & Computer Engineering, McMaster University

**Question 1: Scale-Space Blob Detection**

The script **scaleSpaceBlobDetection.m** located in input\_blob folder can be run to detect the top 100 detections for the input images, found in the same folder, shown below.

**Input Images:**

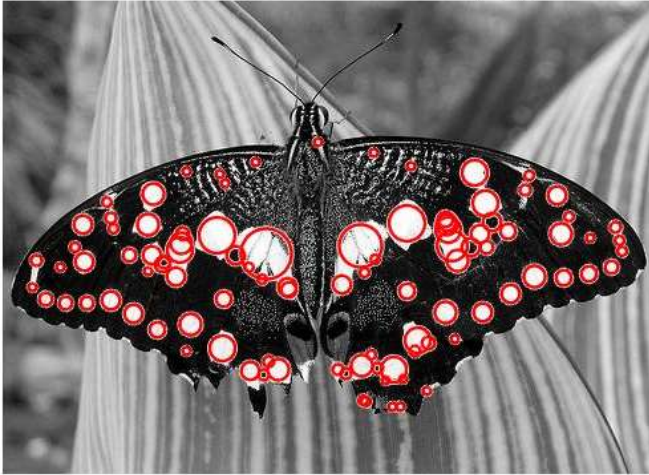




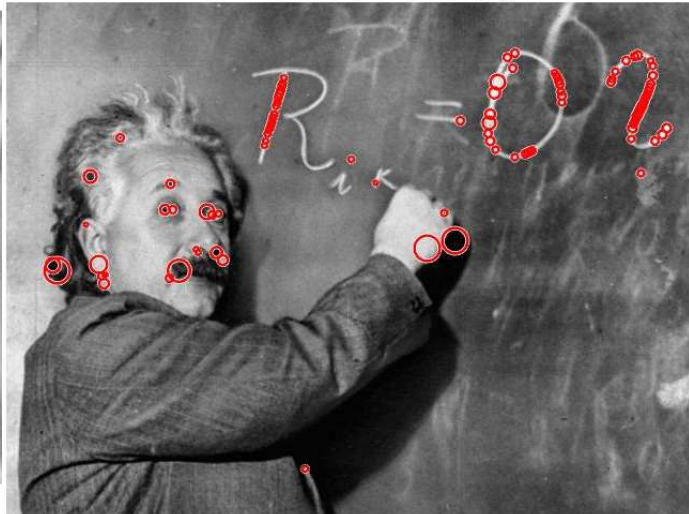
The output images are saved in the output\_blob\_PR folder but they are also shown below. For some images I felt it was necessary to show more than 100 detections. The script is thoroughly documented and will provide more details on the algorithm itself.

### Output Images:

Top 100 detections for butterfly.jpg



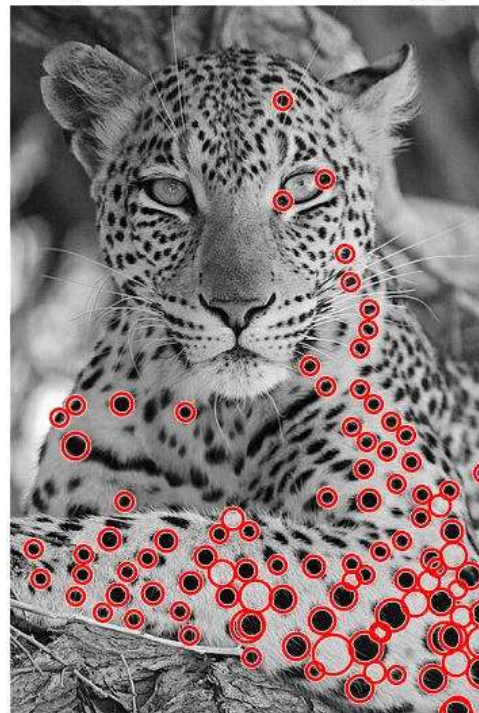
Top 100 detections for einstein.jpg



Top 100 detections for fishes.jpg

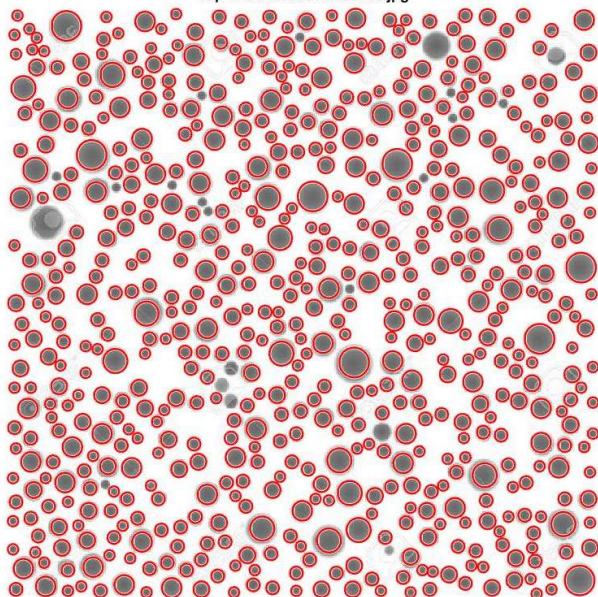


Top 100 detections for leopard.jpg





Top 625 detections for rbc.jpg



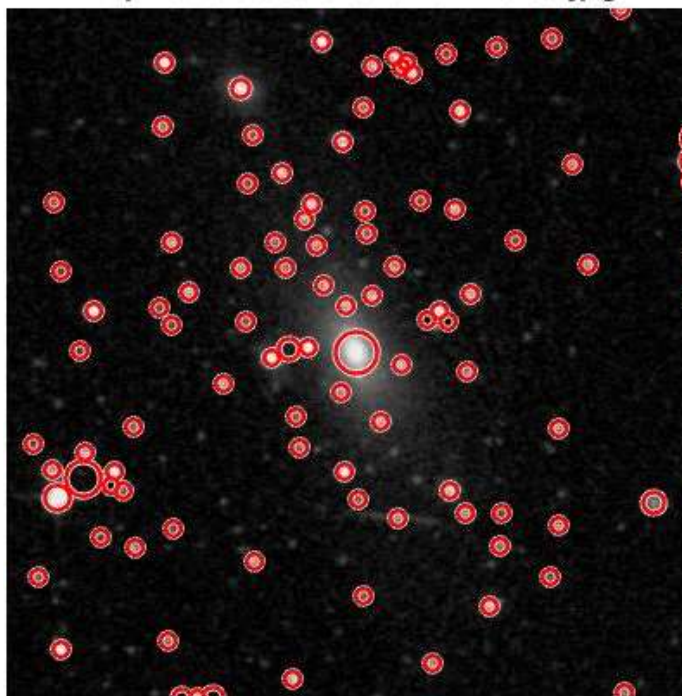
Top 300 detections for spottedEagleRay.jpg



Top 100 detections for sunflowers.jpg



Top 100 detections for universe.jpg



## Question 2: Stitching pairs of images

The following plots and explanation on the **imageStitching.m** script found in the hw2q2 folder. Only the highlights of the script are discussed here, the details of the script are well documented and the specifics can be found in the script.

First, the **harris.m** function is run on **uttower\_left.jpg** and **uttower\_right.jpg** individually to collect the coordinates of the key features in both images. Then **SIFT descriptors** for each of the Harris key features are computed. The putative matches between the images are determined by computing the Euclidean distances between all the SIFT descriptors for the two images using the provided **dist2.m** function. Distance values below 0.05 are classified as matches. **Figure 1** is plot of the two images and the corresponding putative matches between the image.



**Figure 1:** Putative Matches

Then using the RANSAC algorithm a homography matrix estimation is done to generate the panorama. The number of RANSAC trials are determined using the following equation from the lectures:

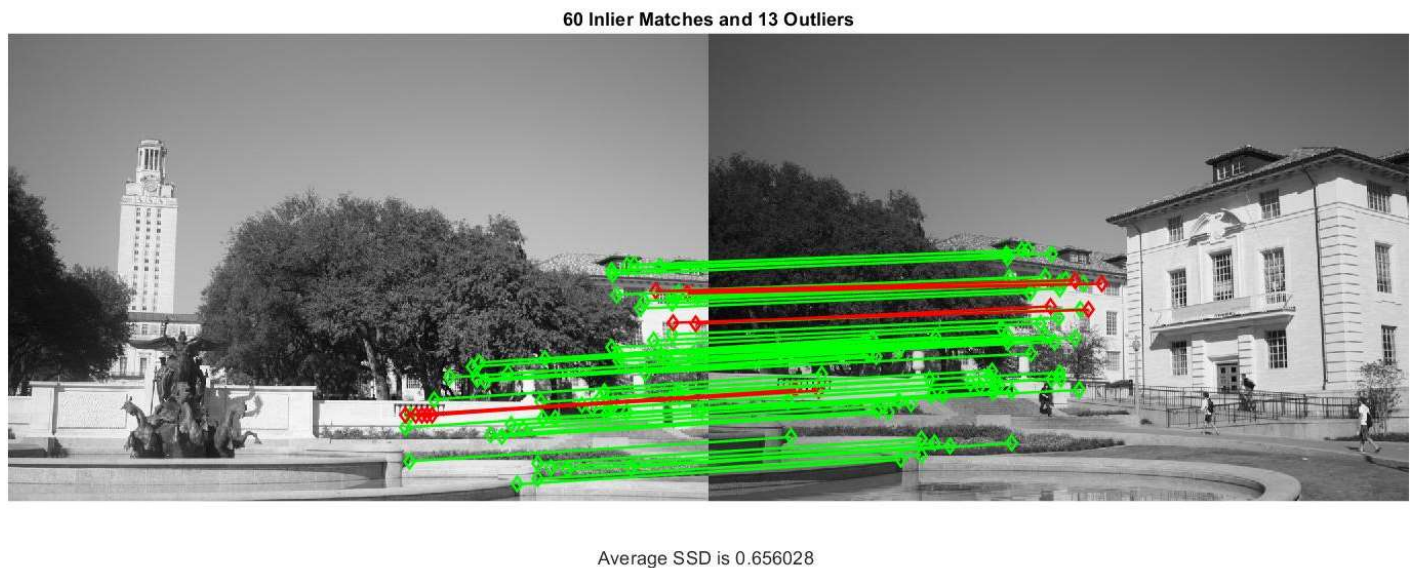
$$S = \log(1-P) / \log(1-p^k)$$

Where  $P = 0.99$ ,  $p = 0.6$ ,  $k = 8$ , therefore  $S = 272$  RANSAC trials.



Every iteration of the RANSAC algorithm will randomly sample 8 of the 73 putative matches and estimate a homography matrix for those 8 randomly sampled matches. Using the estimated homography matrix and the coordinates of the 73 putative matches of the left image, corresponding 73 projections of the right image are computed. Then using the actual coordinates of the right image, the squared sum differences are computed. Inliers and Outliers for the 73 matches are determined using thresholding, where difference above 5 are considered outliers.

This process is repeated for 272 RANSAC trials and the number of inliers for each of the trials along with the average squared sum difference for the inliers. Then the best homography matrix from the 272 trials is determined by two conditions: 1) largest number of inliers and 2) lowest average squared sum difference for the inliers. **Figure 2** below is a plot of the inliers (green), outliers (red) and the average SSD ( $\sim 0.656$ ) for the best homography matrix.



**Figure 2:** *Inliers and Outliers from the Putative Matches*

Then using **projective2d** function, a projective transformation matrix object is constructed which will be used in conjunction with the **imwarp** function to transform the left image according to the specifications of the homography matrix. Figure 3 and 4 are the transformed images ready for stitching.



*Figure 3: Transformed left image*



UT Tower Right Transformed Image



Figure 4: Transformed right image

Finally, the composite image is formed by taking the average of the intensity values for overlapping regions. Figure 5 shows the final stitched image.



*Figure 5: Final Sticked Image*