

Computer Vision
Mini-project 4
CS 670, Fall 2019

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Contents

1 Problem 1: Scale-space blob detection	3
1.1 Building a Laplacian Scale Space	5
1.2 Perform Non-Maximum Suppression in Scale Space	6
1.3 Storing the Blobs	8
1.4 Results and Conclusions	9
2 Problem 2: Image Stitching	12
2.1 Detect Keypoints in Each Image	12
2.2 Extract SIFT Features at Each Detected Keypoints	12
2.3 Match Features Based on Pairwise Distance	13
2.4 Intermediate Results: Matching the SIFT features	15
2.5 RANSAC to estimate the best affine transformation	23
2.5.1 Extracting all the matches between SIFT features	23
2.5.2 Affine Transform	24
2.5.3 RANSAC Initial Structures	25
2.5.4 Running RANSAC	26
2.6 Two Stitched images using the Estimated Transformation	28
3 Extensions for Extra Credit	38
3.1 Downsample Image and Filter it with Fixed Kernel Size	38
3.2 Homography Transformation in RANSAC	40
A	
Matlab code for Problem 1: Scale-space blob detection	52
A.1 Implementation of <code>detectBlobs.m</code>	52
B	
Matlab code for Problem 2: Image Stitching	57
B.1 Implementation of <code>computeMatches.m</code>	57
B.2 Implementation of <code>ransac.m</code>	59

1 Problem 1: Scale-space blob detection

Let's look at some definitions which might be useful in understanding the blob detection:

- **BLOB DETECTION** methods are aimed at detecting regions in a digital image that differ in properties, such as brightness or color, compared to surrounding regions.[1]
- **SCALE-SPACE BLOB DETECTION** extract features with characteristic scale that matches the image transformation such as scaling and translation.
- **THE LAPLACIAN OF GAUSSIAN** is a circularly symmetric operator for blob detection in 2D. Given an input image $f(x, y)$, this image is convolved by a Gaussian kernel

$$g(x, y, \sigma) = \frac{1}{2\pi\sigma} e^{-\frac{x^2+y^2}{2\sigma}}$$

at a certain scale σ to give a scale space representation

$$L(x, y; \sigma) = g(x, y, \sigma) * f(x, y)$$

Then, the result of applying the **LAPLACIAN OPERATOR**

$$\nabla^2 L = L_{xx} + L_{yy}$$

is computed, which usually results in strong positive responses for dark blobs of radius $r = \sqrt{2\sigma}$ (for a two-dimensional image) and strong negative responses for bright blobs of similar size.

- **SPATIAL SELECTION** The magnitude of the Laplacian response will achieve a maximum at the center of the blob, provided the scale of the Laplacian is “matched” to the scale of the blob.
- **HOWEVER, THE LAPLACIAN RESPONSE DECAYS AS SCALE INCREASES**
- **SCALE NORMALIZATION** The response of a derivative of Gaussian filter to a perfect step edge decreases as σ increases. To keep response the same (scale-invariant), must multiply Gaussian derivative by σ . Laplacian is the second Gaussian derivative, so it must be multiplied by σ^2 :

$$\nabla_{norm}^2 L = \sigma^2 (L_{xx} + L_{yy})$$

- **MAXIMUM RESPONSE** The Laplacian achieves a maximum response to a binary circle of radius r at $\sigma = r/\sqrt{2}$
- **CHARACTERISTIC SCALE** The scale that produces peak of Laplacian response in the blob center.

We start with converting images to grayscale (to deal with only one channel as blob locations aren't affected by RGB color intensity) and then to double (as further processing with gaussian kernels is in double data type).

```

1 % Convert image to grayscale and convert it to double
  [0 1].
2 if size(im, 3) > 1
3   im = rgb2gray(im);
4 end
5 if ~isfloat(im)
6   im = im2double(im);
7 end

```

Then, we initialize some parameters which are needed for creating Laplacian Space and its response:

```

1 %% Compute the scale space representation
2 sigma = 1.6; % Initial Scale
3 k = sqrt(2); % Factor by which the scale is
               mulitplied each time
4 sigma_final = power(k,16); % Last Scale
5 % Dynamically decide the interation levels from the
  first and last scale values and multiplication
  factor
6 n = ceil((log(sigma_final) - log(sigma))/log(k)); %
  Iterations of Laplacian scale space
7 [h, w] = size(im);
8 scaleSpace = zeros(h, w, n); % [h,w] – Dimensions of
  Image, n – Number of Levels in Scale Space
9
10 % Generate the Laplacian of Gaussian for the First
    Scale Level
11 filt_size = 2 * ceil(3*sigma) + 1;
12 LoG = fspecial('log', filt_size, sigma);

```

Note that;

- We are setting σ from 0 to 3 and experimenting with the results.
- Scaling factor k is $\sqrt{2}$.
- We chose first and last σ values, each scales previous value by factor $\sqrt{2}$, and then calculated number of iterations/levels; because, the multiplication factor should depend on the largest scale at which we want regions to be detected.
- We use 3d array to represent the scale space. $scaleSpace(:,:,i)$ will give the i 'th level of the scale space.

1.1 Building a Laplacian Scale Space

We start with `sigma` and go through n levels of iterations to `sigma_final`; and at level, we filter image with scale-normalized Laplacian with that level's σ value. We save the square of Laplace Response for each level in `scaleSpace(:,:,i)` and increase the σ for the next level by the factor k .

```
1 %% Compute the blob response
2 % Increase filter size, keep image the same
3
4 for i = 1:n
5     sigma_next = sigma * k^(i-1); % Increment sigma
6         for next level
7     filt_size = 2*ceil(3*sigma_next)+1; % Compute the
8         filter kernel size in the same way as
9             previously
10    LoG = sigma_next^2 * fspecial('log', filt_size,
11        sigma_next); % Making a custom LoG filter
12            with trial and error
13    filter_next = imfilter(im, LoG, 'same', 'replicate
14        '); % Create a replica of the previous filter
15    filter_next = filter_next.^ 2; % Multiply it
16        by itself
17    scaleSpace(:,:,:,i) = filter_next; % Store filter
18        of each level
19
20 end
```

As shown in code snippet, we created Laplacian of Gaussian filter with `fspecial('log', hsize, sigma)` function available in Matlab.

The first option, '*log*' stands for a rotationally symmetric Laplacian of Gaussian. The second option, is filter size which we compute with the formula

$$2\lceil 3\sigma \rceil + 1$$

$+1$ is to make the value odd, because $x2$ (for half above/left, other half below/right) will make it even and generally, kernel sizes are always odd to maintain symmetry around the center. $\lceil \rceil$ makes sure we are getting an integer for the filter size, multiplying it by almost $\times 6$ is proportional to increase in σ .

Then we apply the filter on our grayscale image with `imfilter`, square the result and save it in `scaleSpace` at appropriate level. We used '*same*' as a filter option because we want the output size to be the same and '*replicate*' as the padding option.

1.2 Perform Non-Maximum Suppression in Scale Space

NON-MAXIMUM SUPPRESSION If we think about the value of corner response R for all the points in a patch that contains a corner: it is likely that more than one cell value $>$ threshold (intuition: moving the window by one pixel will not change the image much). Thus for each candidate point $>$ threshold, we detect if it is the absolute maximum within its territory, if not then we discard it.

First, we evaluate the functions are available for NMS:

- For each pixel location in our image, `nfilter` processes a neighborhood surrounding this pixel and a single output pixel is produced. For this reason, `nfilter` cannot be used.
- `colfilt` operates the same way, but it takes pixel neighborhoods, reshapes them into single columns, and we filter each column separately. The output for each column is a single pixel, and `colfilt` then reshapes the output so that it is an image again and that's the output.

- `ordfilt2` replaces each element in filtered image by the $order^{th}$ element in the sorted set of neighbors specified by the nonzero elements in domain.

We used `ordfilt2` with 3x3 neighborhood domain (there are 8 neighbors at most for a pixel in 2D), and we choose order as $3 * 3 = 9^{th}$ order to make it a maximum filter (because we want a filter which suppresses all non-maximums).

```

1 % Perform Non-Maximum Suppression for each Scale-Space
2 % Slice
3 suppression_size = 3; % To make it Maximum Filter
4 max_space = zeros(h, w, n); % NMS output for each
5 % level
6 for i = 1:n
7     max_space(:,:,i) = ordfilt2(scaleSpace(:,:,i),
8         suppression_size^2, ones(suppression_size));
9 end

```

And save each level's result in `max_space(:,:,i)`.

Next, we set a threshold on the squared Laplacian response above which to report region detections. We played around with different threshold and σ values for each image, we report the values which produces the best result; with the output images in later sections.

Then, we zero out all positions that are not the Local Maxima of the score (if the value is not greater than all its neighbors).

```

1 % Non-Maximum Suppression between Scales and Threshold
2 % For scales, compare the current one with the
3 % previous and next ones, choose the maximum of the
4 % three
5 for i = 1:n
6     max_space(:,:,i) = max(max_space(:,:,max(i-1,1):
7         min(i+1,n)),[],3);
8 end
9 % Zero Out All Positions that are not the Local Maxima
10 % of the score (if the Value is not Greater than all
11 % its Neighbors)
12 max_space = max_space .* (max_space == scaleSpace);

```

1.3 Storing the Blobs

We need to store the x-y co-ordinates of the blob, the radius of the blob and the score associated with it, which is just the level of the scale space.

We will look for all the maxima which are higher than some arbitrary threshold (we experimented between 0.005 to 0.03). The blobs having larger squared Laplacian than the threshold will be stored with their x-y co-ordinates and the level score.

We compute the radius from the level of the scale space where maxima is, the initial σ value and the scaling factor.

```
1 x = []; % X – axis of blob's center
2 y = []; % Y – axis of blob's center
3 radius = []; % Radius of the blob
4 score = [];

5
6 % For each level
7 for i=1:n
8     % Set a Threshold on the Squared Laplacian
         Response above which to report Region
         Detections
9     [rows, cols, value] = find(max_space(:,:,i) .*(
10        max_space(:,:,i) >= 0.01));
11    numBlobs = length(rows);
12    % Create Lists of each tuple fields separately
13    if (numBlobs > 0)
14        radii = sigma * k^(i-1) * sqrt(2);
15        radii = repmat(radii, numBlobs, 1);
16        x = [x; rows];
17        y = [y; cols];
18        score = [score; value];
19        radius = [radius; radii];
end
```

```
20 end  
21  
22 blobs = [y, x, radius, score];
```

We now have all 4 attributes for every blob whose maxima passes the threshold.

1.4 Results and Conclusions

The [FULL CODE](#) for `detectBlob.m` is in Appendix A.1.

Now, we show the results we produced and the parameter values which produces the best results, see Figures 1, 2, 3 and 4:

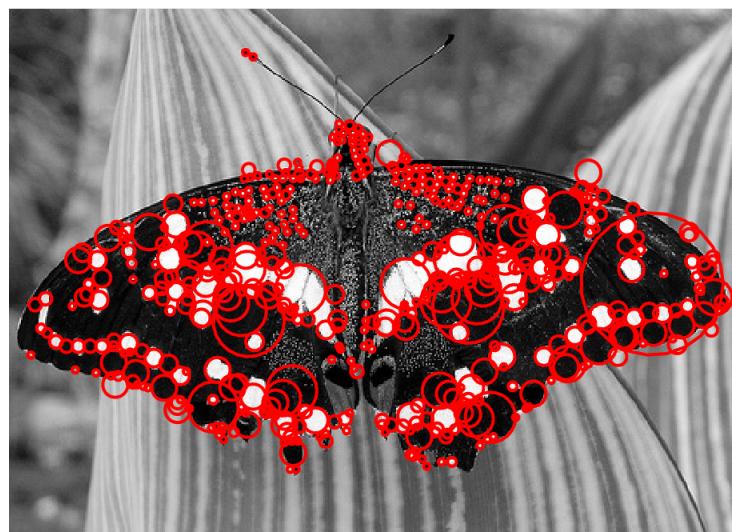


Figure 1: butterfly.jpg: Initial Sigma - 2.0; Threshold - 0.02



Figure 2: einstein.jpg: Initial Sigma - 2.3; Threshold - 0.025



Figure 3: fishes.jpg: Initial Sigma - 1.0; Threshold - 0.019

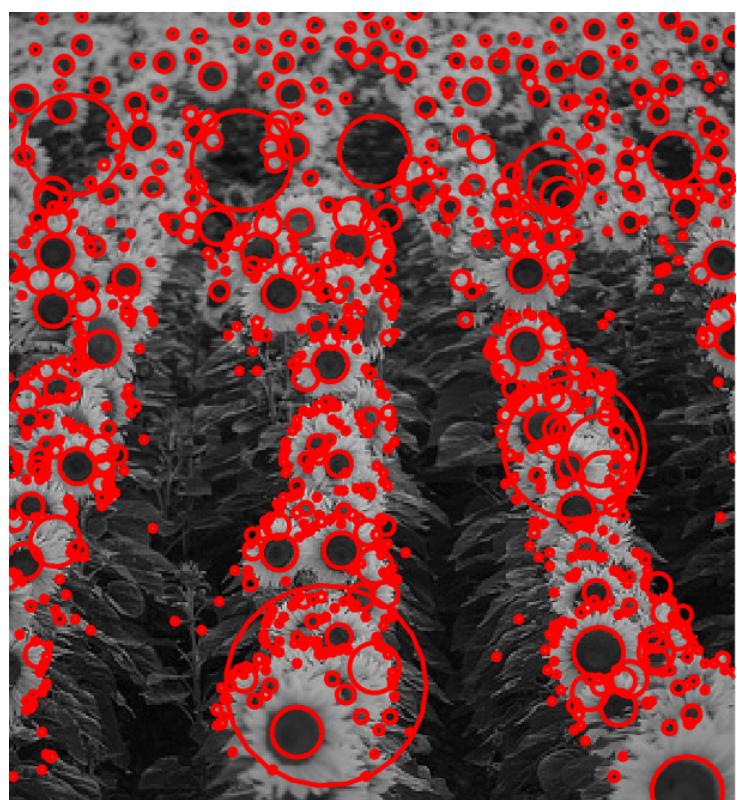


Figure 4: sunflowers.jpg: Initial Sigma - 1.0; Threshold - 0.019

2 Problem 2: Image Stitching

In this section, we will implement RANSAC to stitch two images. We will use our blob detector from Problem 1, to extract keypoints and extract feature descriptors on them. Our goal is to estimate an affine transformation using feature matching and RANSAC to produce a combined image.

We step-by-step go through alignment algorithm.

2.1 Detect Keypoints in Each Image

We already implemented this in the first section. We set initial scale $\sigma = 2$ and threshold at 0.02.

We will get blobs for both images by calling `detectBlob.m`.

2.2 Extract SIFT Features at Each Detected Keypoints

SIFT Feature Descriptors transforms an image into a large collection of feature vectors, each of which is invariant to image translation, scaling, and rotation, partially invariant to illumination changes and robust to local geometric distortion.

In this method[2]:

- We divide each blob in 4x4 grid.
- Inside each sub-patch, compute histogram of gradient orientations (8 reference angles).
- We normalize the vector to a unit length.
- Resulting descriptor will be $4 \times 4 \times 8 = 128$ dimensions for each blob.

This step is already implemented; at the end of this step, we will get SIFT features for both of our images.

2.3 Match Features Based on Pairwise Distance

Here, we compute matches between the two sets of SIFT features. We find the best match of each feature f_1 from image1 to f_2 of image2 using the smallest sum-of-squared-differences.

If we find a match for $f_1(i)$ where $i \in [0, 1, \dots, N]$, from $f_2[0, 1, \dots, M]$; we will say $\text{matches}(i)$ is the closest feature in f_2 to the i^{th} feature $f_1(:, i)$. All other entries will be $\text{matches}(i) = 0$, which indicates no matches.

We initialize $\text{matches}()$ to all zeros and then loop through all SIFT features of image2, for each feature of image1, to find the pairs where SSD is the least and store that f_2 for i^{th} feature in f_1 . Code snippet for this logic is presented here:

```
1 %% Computing Matches using SSD
2 matches = zeros(f1_size, 1);
3 % Start Stopwatch Timer
4 tic
5 if 0
6     fprintf('Computing matching using SSD: \n');
7     % For each feature from image 1
8     for i = 1 : f1_size
9         % Find its nearest match image 2
10        bestMatch = inf;
11        for j = 1 : f2_size
12            % SSD
13            match = sum(sum((f1(i,:) - f2(j,:)).^2));
14            % Store the lowest SSD feature
15            if (match < bestMatch)
16                matches(i) = j;
17                bestMatch = match;
18            end
19        end
20    end
21 % Stop Stopwatch Timer
22 toc
23 end
```

There is a shortcoming of this method where we must deal with am-

biguous putative matches. We can compare distance of NEAREST NEIGHBOR to that of SECOND NEAREST NEIGHBOR.

The ratio of closest distance to second-closest distance will be HIGH FOR FEATURES THAT ARE NOT DISTINCTIVE. Threshold of 0.8 provides a good separation.

We set `matches(i)=0` if i^{th} feature $f1(:,i)$ fails on the ratio test.

```
1 %% Computing Matches using ratio
2
3 % For each Descriptor in the First Image, Select its
4 % Match to Second Image
5 for i = 1 : f1_size
6     % The most likely match
7     bestMatch = inf;
8     % The next most likely match after the best one
9     secondMatch = inf;
10    index = inf;
11    for j = 1:f2_size
12        % Compute SSD
13        match = sum(sum((f1(i ,:)-f2(j ,:)).^2));
14        % compare it with the best match
15        if (match < bestMatch)
16            secondMatch = bestMatch;
17            bestMatch = match;
18            index = j;
19            % compare it with the second best match
20            elseif (match < secondMatch && match ~= bestMatch)
21                secondMatch = match;
22            end
23        end
24    % Now we have determined best and second best
25    % match
26
27    % Computer Ratio
28    ratio = bestMatch/secondMatch;
29    % Compare it with a threshold
30    if (~isequal(index,inf) && ratio < 0.8)
31        matches(i)= index;
```

```

30     else
31         matches( i ) = 0;
32     end
33 end

```

Here, we have just fount out the best and second best matches by SSD and then if the ratio is above the threshold, we enter the index of best match into out `matches(i)`, otherwise it is 0.

2.4 Intermediate Results: Matching the SIFT features

Here we show the output of `showMatches(im1, im2, c1, c2, matches)`. We changed the initial σ to 1.0 and Region Detection threshold to 0.01 to get the best results. See Figures 5, 7, 9, 11, 13, 15, 17 and 19 for SIFT features. See Figures 6, 8, 10, 12, 14, 16, 18 and 20 for macthes between the SIFT features of two images.

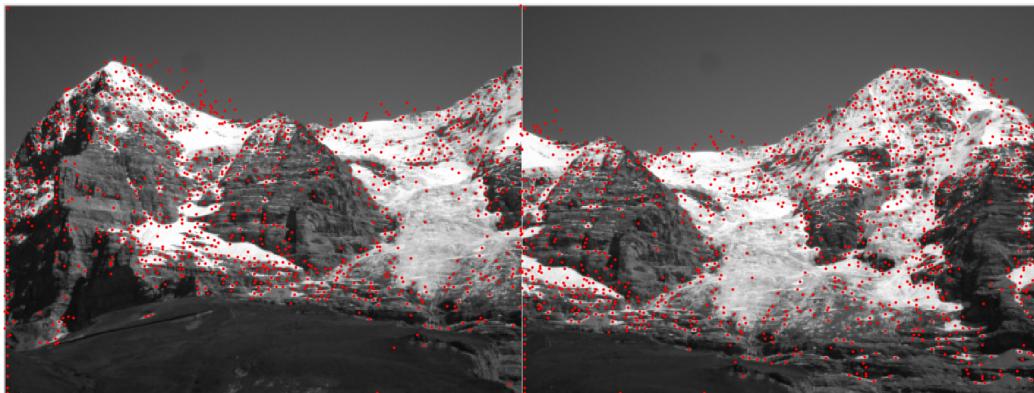


Figure 5: SIFT features of Hill images

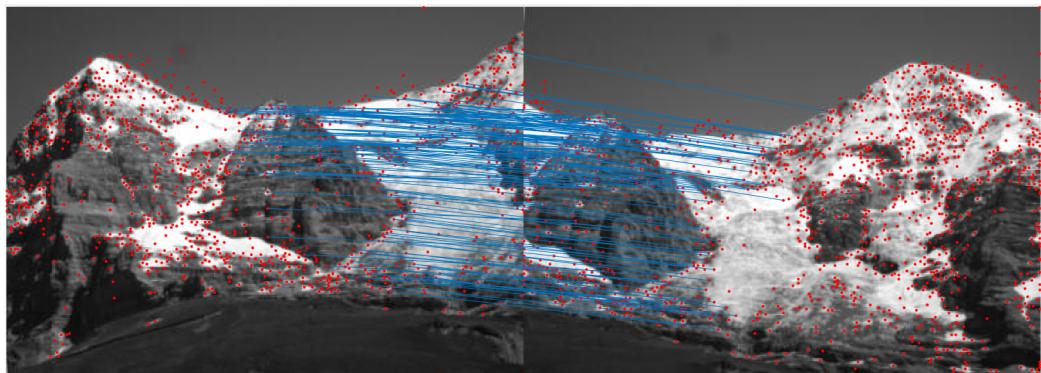


Figure 6: Matches between SIFT features of Hill images

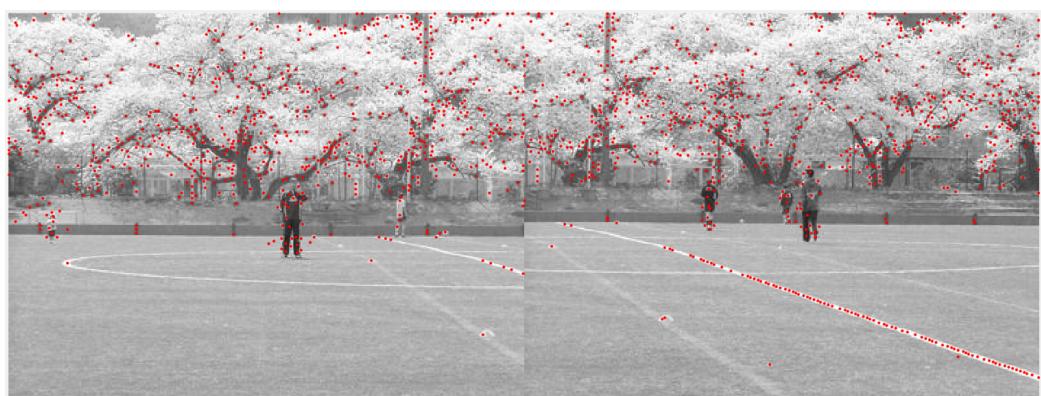


Figure 7: SIFT features of Field images

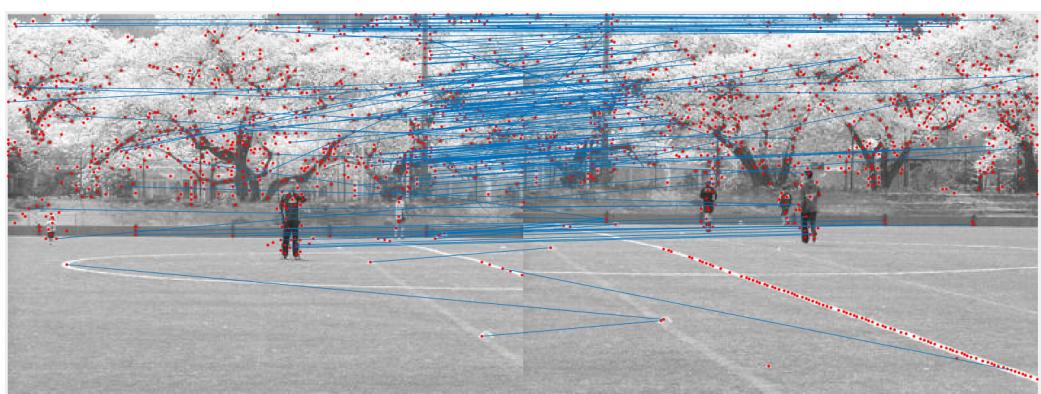


Figure 8: Matches between SIFT features of Field images

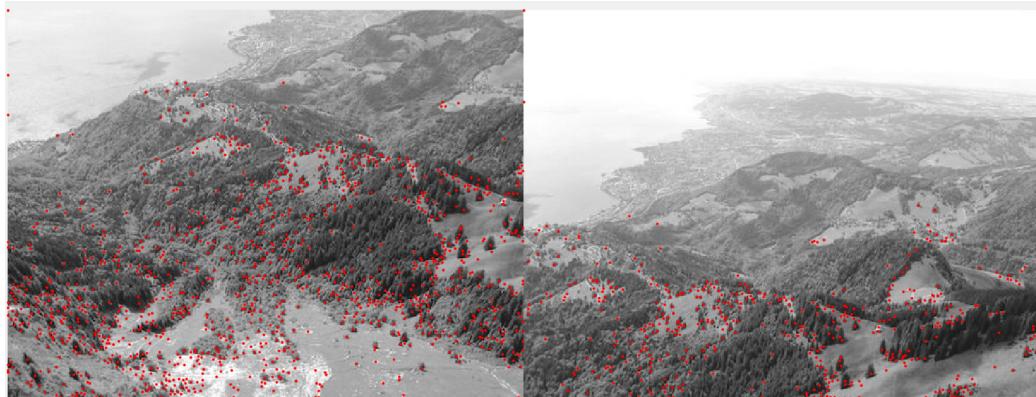


Figure 9: SIFT features of Ledge images

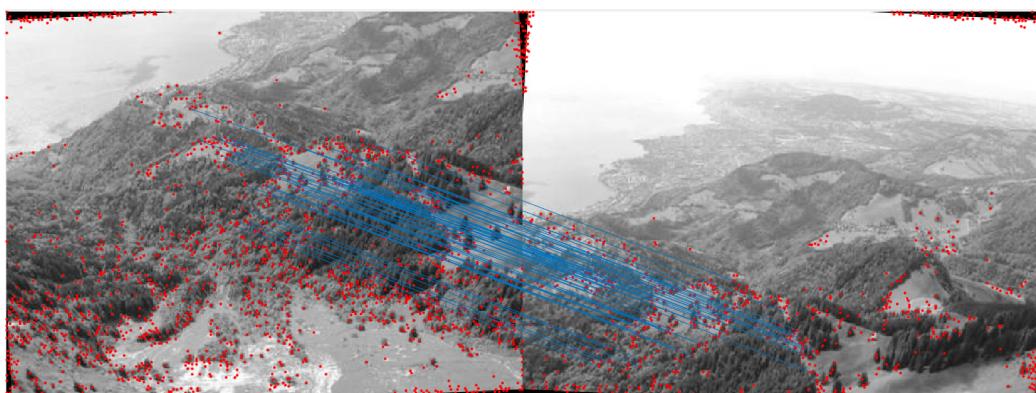


Figure 10: Matches between SIFT features of Ledge images



Figure 11: SIFT features of Pier images

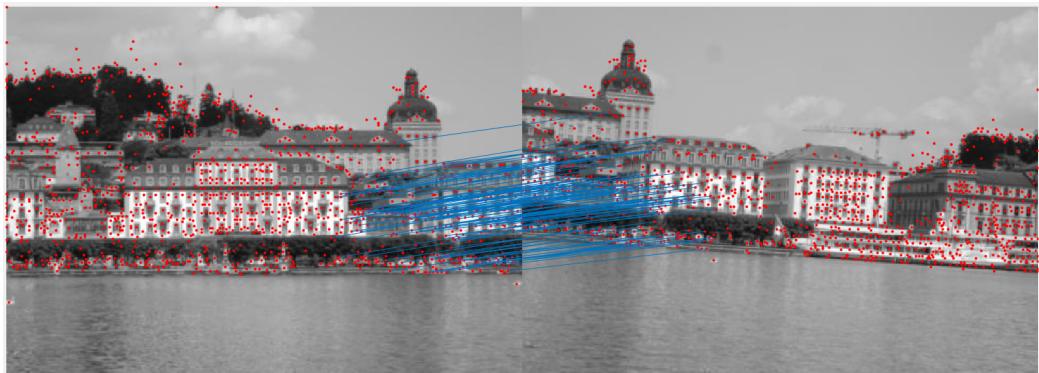


Figure 12: Matches between SIFT features of Pier images

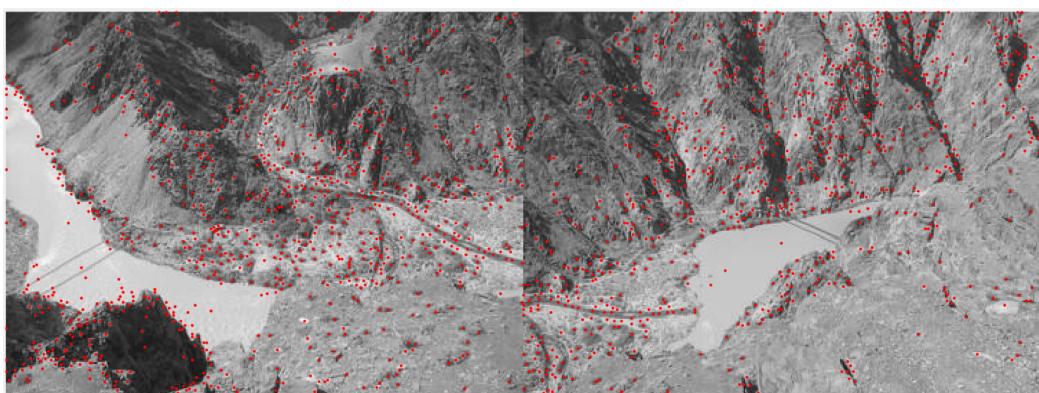


Figure 13: SIFT features of River images

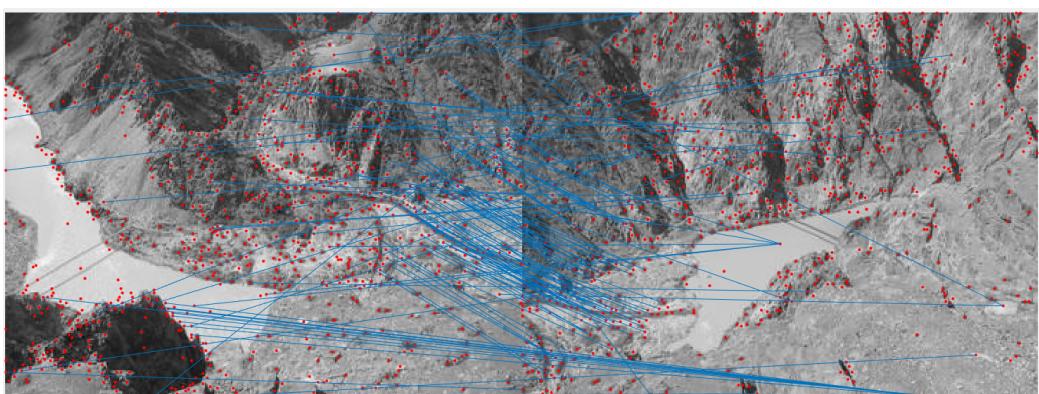


Figure 14: Matches between SIFT features of River images

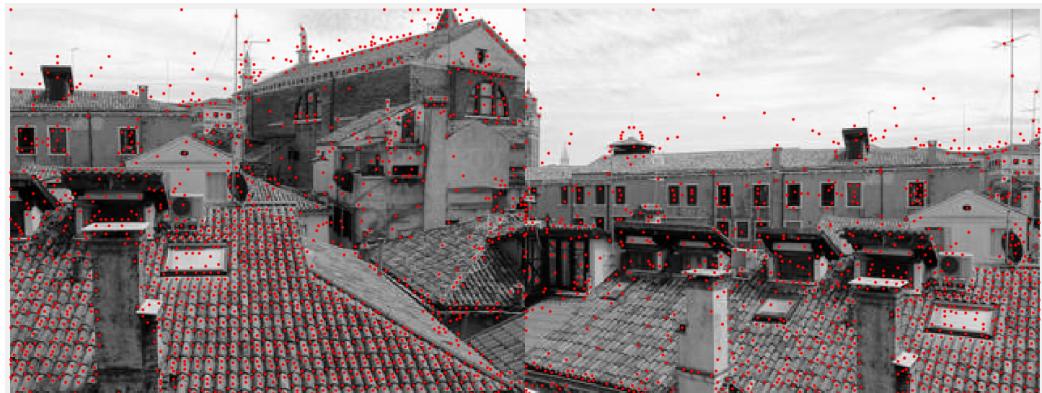


Figure 15: SIFT features of Roofs images

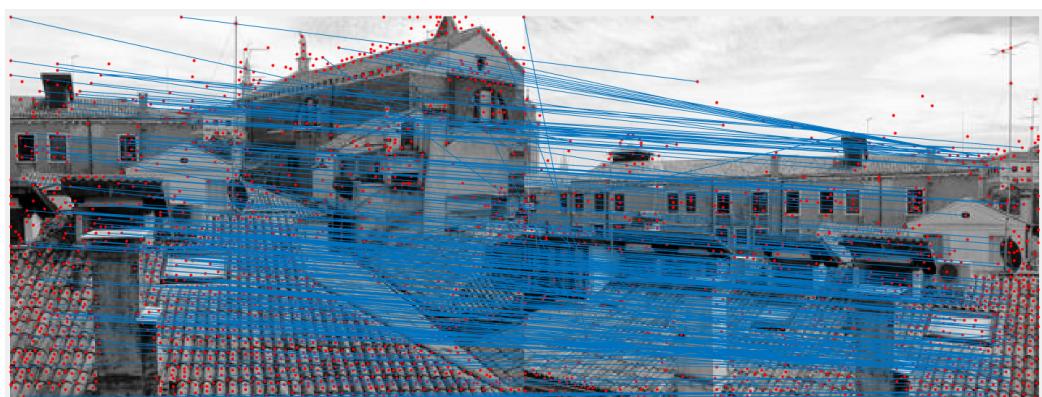


Figure 16: Matches between SIFT features of Roofs images

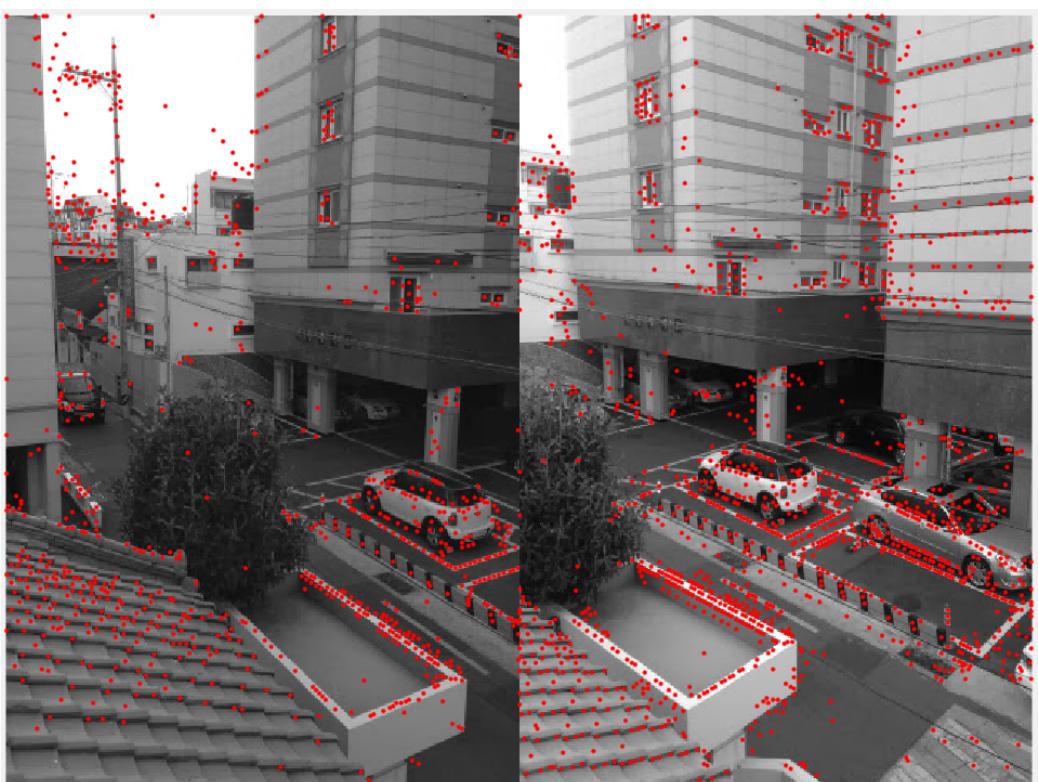


Figure 17: SIFT features of Building images

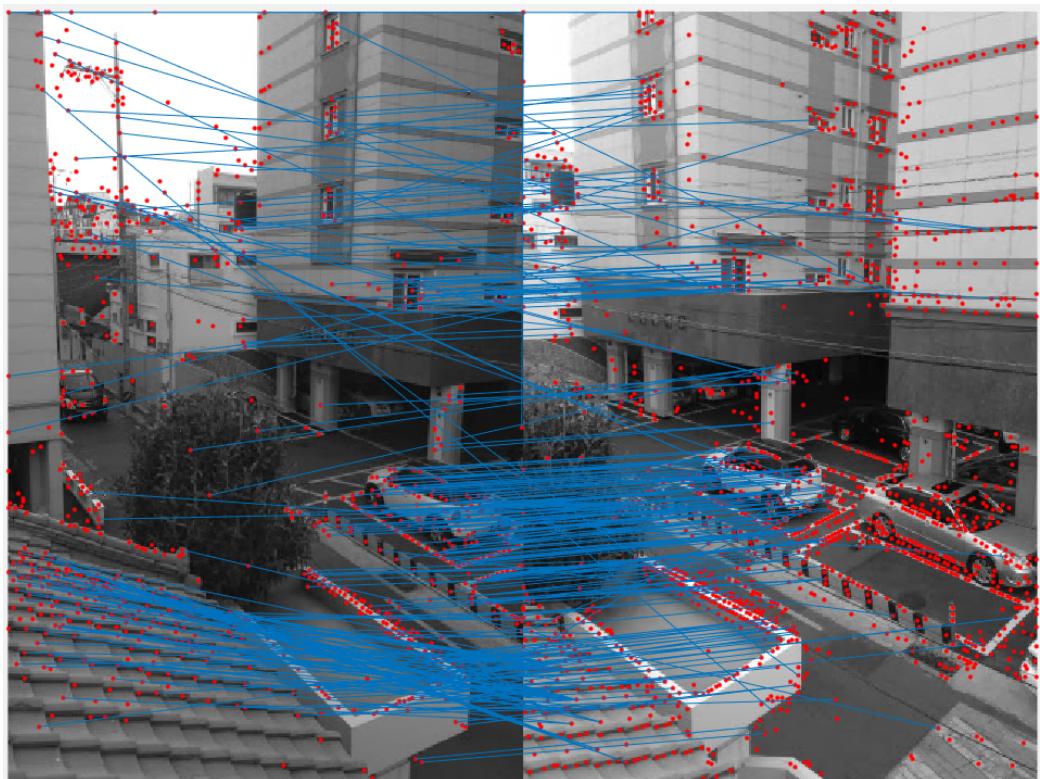


Figure 18: Matches between SIFT features of Building images



Figure 19: SIFT features of Tower images

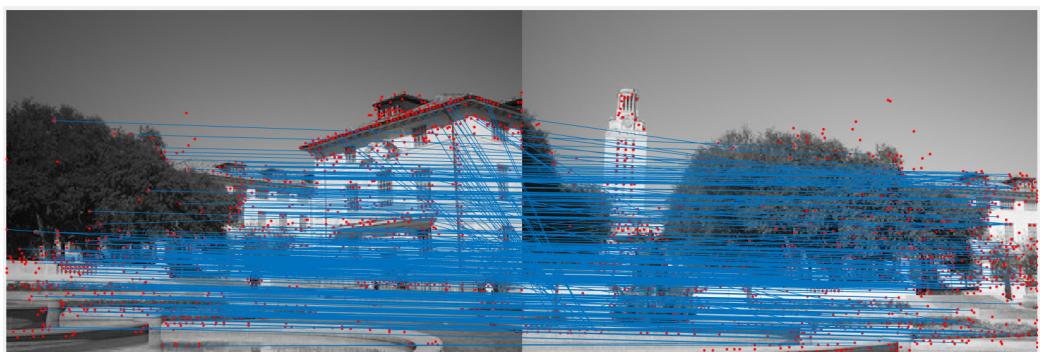


Figure 20: Matches between SIFT features of Tower images

2.5 RANSAC to estimate the best affine transformation

Using RANSAC, we will estimate the [AFFINE TRANSLATION](#) that agrees with most matches (inliers).

An affine transformation is any transformation that preserves collinearity (i.e., all points lying on a line initially still lie on a line after transformation) and ratios of distances (e.g., the midpoint of a line segment remains the midpoint after transformation).

The affine transformation of a model point $[x, y]^T$ to an image point $[x', y']^T$ can be written as below

$$\begin{bmatrix} x' \\ y' \end{bmatrix} = \begin{bmatrix} m1 & m2 \\ m3 & m4 \end{bmatrix} \begin{bmatrix} x \\ y \end{bmatrix} + \begin{bmatrix} tx \\ ty \end{bmatrix}$$

To solve for the transformation parameters the equation above can be rewritten to gather the unknowns into a column vector;

$$\begin{bmatrix} x & y & 0 & 0 & 1 & 0 \\ 0 & 0 & x & y & 0 & 1 \\ \dots & & & & & \\ \dots & & & & & \end{bmatrix} \begin{bmatrix} m1 \\ m2 \\ m3 \\ m4 \\ tx \\ ty \end{bmatrix} = \begin{bmatrix} u \\ v \\ \cdot \\ \cdot \\ \cdot \\ \cdot \end{bmatrix}$$

This is a linear system with six unknowns. [2]

Each match gives us two linearly independent equations, we need at least three to solve for the transformation parameters.

We implement [RANDOM SAMPLE CONSENSUS](#) - RANSAC as follows:

2.5.1 Extracting all the matches between SIFT features

We have been given blobs for `image1` and `image2` & the matches of SIFT features between them.

So first task will be to find all the non-empty matches from the `matches` list, because some of them are assigned to 0, which are of no use in this context.

We also store the original indices of the feature comparison entries

is that doesn't get lost in compaction, and the size of the non-zero entries to run a loop.

The code for that is shown in the snippet below:

```

1 %% Get all the non-empty feature matches
2 [inputs, cols, bases] = find(matches);
3 % Reset max inliers counter
4 maxInliers = 0;
5 % Store the original indices of matches so that
      removing the 0 index entries doesn't change the
      actual indices
6 originalIndices = find(matches);
7 % Get the non-zero entries size
8 inputs_size = size(inputs,1);
```

2.5.2 Affine Transform

We arrange the base and transform points according to the matrix forms shown in above equation. Then we just do

$$AffineTransformation = \frac{BasePoints}{TransformedPoints}$$

```

1 function [Transform] = computeAffine(basePoints,
2 transPoints)
3     baseP = zeros(6,6); % input points
4     transP = zeros(6,1); % points after transformation
        of input points.
5     for j = 1:3
6         index = ceil(rand*(size(basePoints,1)-1))+1;
        % Prepare base matrix with points before
        transformation; put them in the position
        shown in affine transform matrix equation
7         baseP(2*j-1,:) = [basePoints(index,1),
        basePoints(index,2),1,0,0,0];
8         baseP(2*j,: ) = [0,0,0,basePoints(index,1),
        basePoints(index,2),1];
```

```

9      % Set transformed points matrix; put them in
10     % the position shown in affine transform
11     % matrix equation
12     transP(2*j - 1,:) = transPoints(index,1);
13     transP(2*j ,:) = transPoints(index,2);
14   end
15 % Matrix Division
16 Transform = baseP\transP;
17 end

```

2.5.3 RANSAC Initial Structures

The structures and matrices which we are using for RANSAC iterations are as shown in the snippet below, the explanation is in comments:

```

1 % This structure stores current point co-ordinates
2 inputPoints = zeros(inputs_size,2);
3 % This structure stores the points whose co-ordinates
4 % are getting transformed
5 basePoints = zeros(inputs_size,2);
6 % Number of points whose distance from the line is
7 % less than some constant threshold
8 threshold = 4;
9 iterations = 35;
10 % Store the best affine transformation (with the least
11 % error)
12 best_model = zeros(2,3);
13 % Store the points who are inlier
14 inliersInfo = zeros(inputs_size,2);
15 % Store the affine transformation for a particular
16 % iteration
17 transInfo = zeros(2,3,inputs_size);
18
19 % Store all features and locations in inputPoints for
20 % 1st image and in basePoints for 2nd image
21 for ind= 1:inputs_size
22     basePoints(ind,1) = blobs1(bases(ind),1);
23     basePoints(ind,2) = blobs1(bases(ind),2);

```

```

19      inputPoints(ind,1) = blobs2(inputs(ind),1);
20      inputPoints(ind,2) = blobs2(inputs(ind),2);
21 end

```

2.5.4 Running RANSAC

Now we can run the actual RANSAC algorithm.

The pseudocode:

- Randomly select minimal subset of points.
- Compute Affine Transformation for the base and transformed point matrices.
- Reshape the Affine Transform and the Base Point matrices so they can be multiplied to get the Transformed Point matrix **HYPOTHE-SIZING THE MODEL**.
- Calculate the error between actual transformed points and the ones which we computed by getting an Affine Transform **COMPUTING THE ERROR FUNCTION**.
- If the inlier count is more than the 10% of the input size; it counts as a valid model.
- And if the inlier count is more than the previous best, the current Affine Transform is the best now. Store the best transform, the SSD error and the input and transformed points that produce that transform.
- Iterate this procedure arbitrary times.

The code snippet for RANSAC:

```

1 % Try RANSAC for 'iterations' number of times
2 for itr = 1:iterations
3     % Affine Transform for the current iteration
4     T = computeAffine(inputPoints,basePoints);
5     % Reshape the transform matrix in [3x3] for
6     % tranformed_points = tranform x base_points
7     trans = [reshape(T,[3,2])';0,0,1];

```

```

8 % Reshape base_points to [3x1] for
9 % tranformed_points = transform x base_points
10 inputPt = [inputPoints';ones(1,inputs_size)];
11 % Compute tranformed_points = transform x
12 % base_points
13 inputptF = trans*inputPt;
14 % Take the x-y co-ordinates of every tranformed
15 % point
16 calPoints = inputptF(1:2,:);
17
18 % Calculate Error between Expected Tranformed
19 % point co-ordinates and actual Transformed
20 % points
21 dist = calculateError(calPoints,basePoints');
22 % Only take the points whose distance is lower
23 % than threshold
24 [rows,cols,error] = find(dist.*(dist < threshold));
25 ;
26 % Count the number of inliers
27 inliersCount = size(cols,2);
28 total_error = sum(error,2);
29
30 % Find the best model by inlier count and error
31 % values
32 if inliersCount > round(0.10*inputs_size) &&
33 inliersCount >= maxInliers && inliersCount ~= inputs_size
34
35 best_model = reshape(T,[3,2])';
36 if(inliersCount == maxInliers)
37     maxIndex = find(inliersInfo(:,1) ==
38         maxInliers);
39     if(total_error < inliersInfo(maxIndex,2))
40         best_model = reshape(T,[3,2])';
41     end
42 end
43
44 inliersC = cols';
45 maxInliers= inliersCount;
46 inliersInfo(itr,1)=maxInliers ;
47 inliersInfo(itr,2)= total_error;
48 transInfo(:,:,itr) = best_model;

```

```
39      end  
40 end
```

2.6 Two Stitched images using the Estimated Transformation

THE CODE FOR `computeMatches.m` AND `ransac.m` ARE IN APPENDIX **B.1** AND **B.2**.

Figures 5 to 20 shows intermediate results.

In this section, we show the final output and the affine transforms computed to stitch the two images.

See Figures 21, 22, 23, 24, 25, 26, 27 and 28 & their corresponding Affine Transforms.

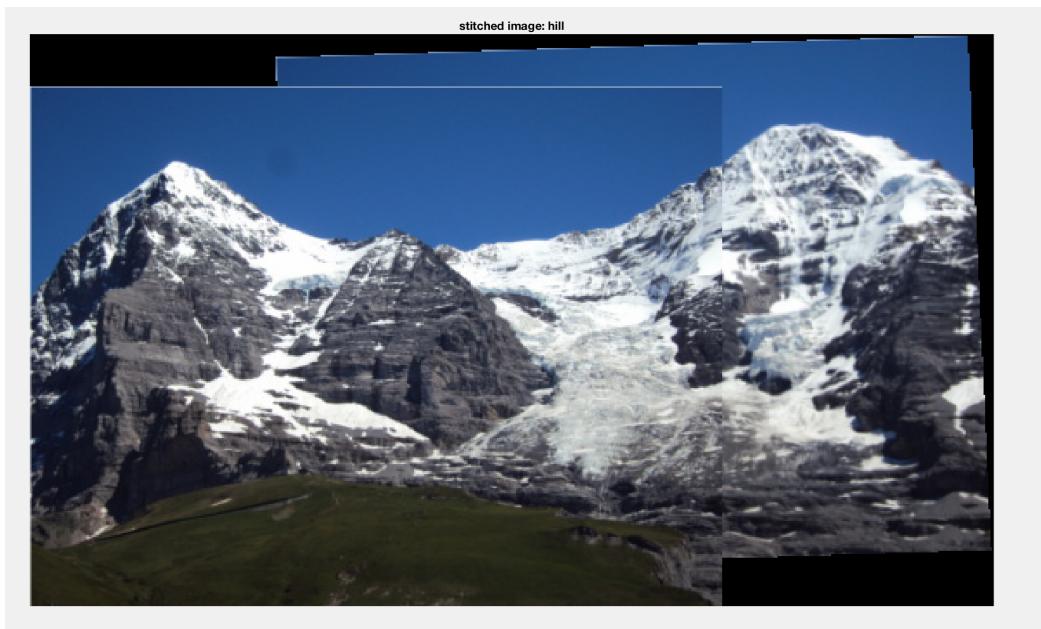


Figure 21: Panoramic Stitching of Hill images

Hill.jpg

Maximum Inliers 226 and Msize is 460

Affine Transformation is:

1.0169	0.0341	139.5263
-0.0597	1.0177	-9.4434



Figure 22: Panoramic Stitching of Field images

Field.jpg

Maximum Inliers 89 and Msize is 186

Affine Transformation is:

1.0000	0.0000	257.0000
-0.0103	1.0147	11.3895

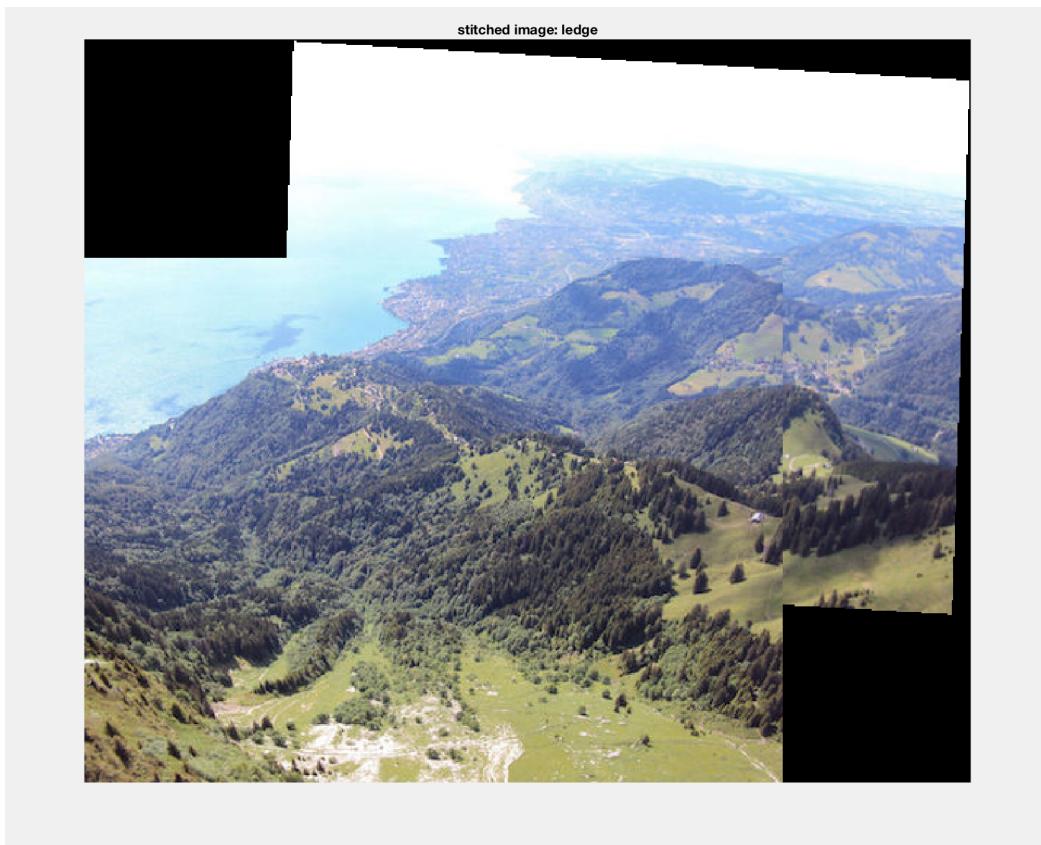


Figure 23: Panoramic Stitching of Ledge images

Ledge.jpg

Maximum Inliers 92 and Msize is 217

Affine Transformation is:

0.9748	-0.0556	144.7856
0.0553	0.9680	-142.8991



Figure 24: Panoramic Stitching of Pier images

Pier.jpg

Maximum Inliers 207 and Msize is 469

Affine Transformation is:

0.9905	0.0237	287.4163
0.0000	1.0000	27.0000



Figure 25: Panoramic Stitching of River images

River.jpg

Maximum Inliers 51 and Msize is 138

Affine Transformation is:

$$\begin{array}{ccc} 0.9628 & -0.3282 & 273.7572 \\ 0.3540 & 0.9889 & -169.4819 \end{array}$$



Figure 26: Panoramic Stitching of Roofs images

Roofs.jpg

Maximum Inliers 59 and Msize is 316

Affine Transformation is:

0.9649	0.0504	-160.9132
-0.1228	0.9890	-21.7032

Building.jpg

Maximum Inliers 75 and Msize is 340

Affine Transformation is:

1.1428	-0.0590	93.0511
0.1105	1.0511	-25.1110

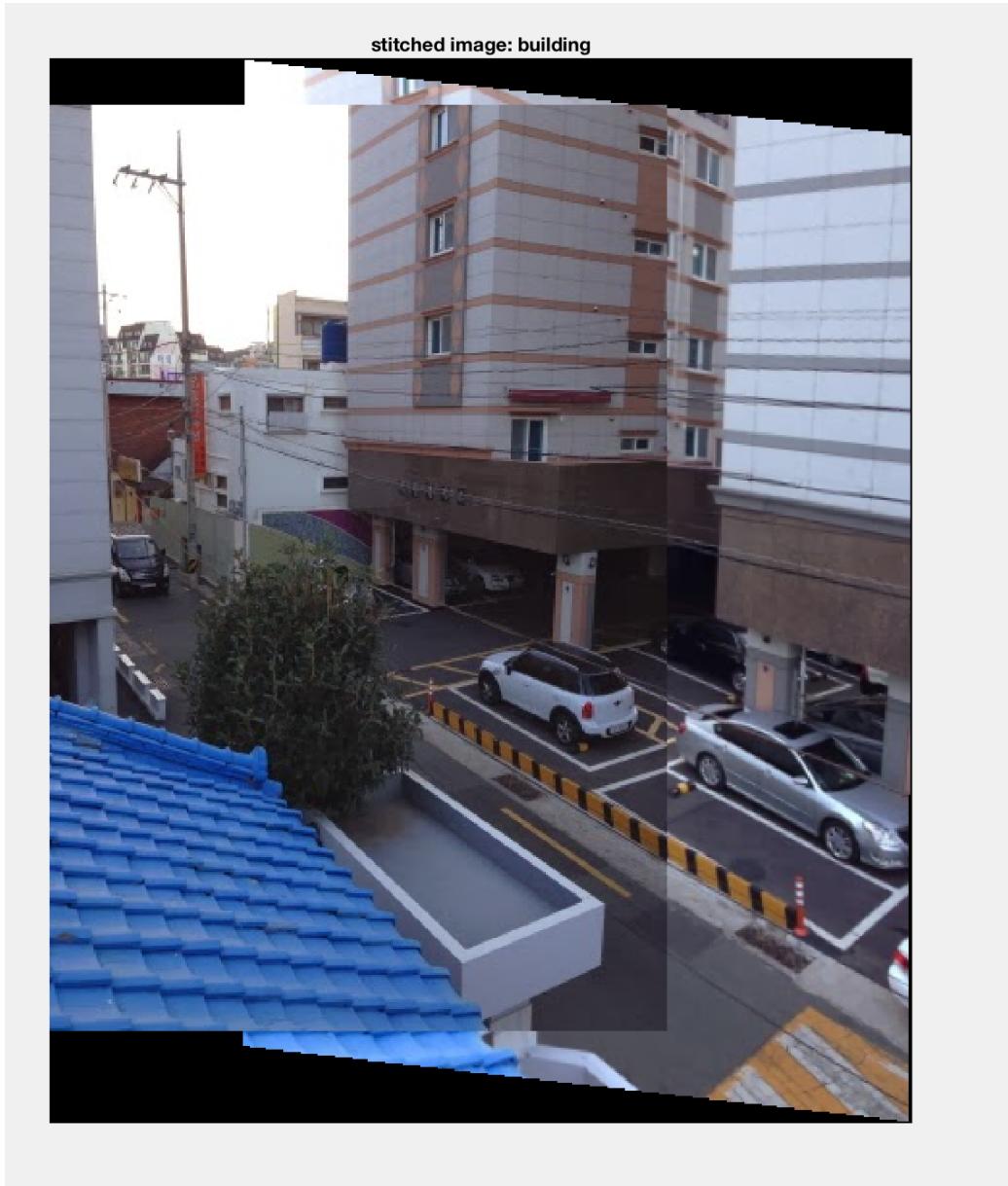


Figure 27: Panoramic Stitching of Building images

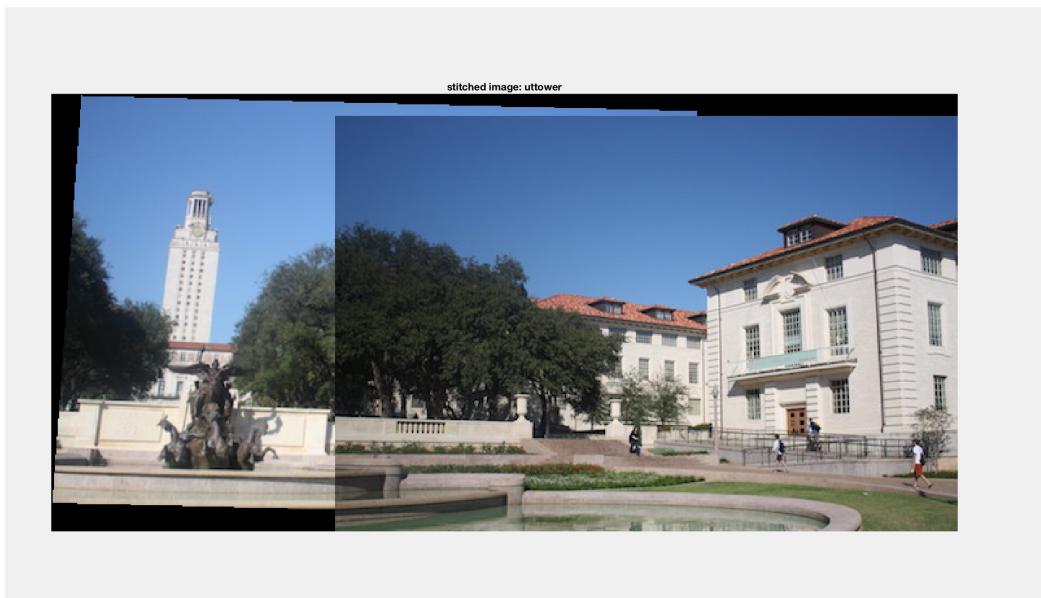


Figure 28: Panoramic Stitching of Tower images

Tower.jpg

Maximum Inliers 98 and Msize is 383

Affine Transformation is:

1.0377	-0.0680	-203.9290
0.0071	1.0284	-24.6143

3 Extensions for Extra Credit

3.1 Downsample Image and Filter it with Fixed Kernel Size

In this section, we compare the results of first approach “iteratively filter the image with kernel of increasing size” [Problem 1], with a second approach where we iteratively downsample the image and filter it with the kernel of fixed size.

At each level, we downsample(resize) the image by factor k .

Filter it with fixed sized LoG already made in the previous section.

Resize it to its original size with **BICUBIC INTERPOLATION**. The code snippet is as shown below:

```
1 imRes = im; % Create a copy of the image
2 for i = 1:n
3     imFiltered = imfilter(imRes, LoG, 'same', '
4         replicate'); % Apply the Laplacian of Gaussian
5         filter here, the filter is already created in
6         the above section
7     imFiltered = imFiltered .^ 2; % Square of the LoG
8     scaleSpace(:,:,:i) = imresize(imFiltered, size(im),
9         'bicubic'); % Resize the image to original
          size with bicubic interpolation
10    if i < n
11        imRes = imresize(im, 1/(k^i), 'bicubic'); %
12            Decrease the image size for next iteration
13    end
14 end
```

See the blobs for both technique along with the parameter values used in Figures 29, 30, 31 and 32. The timing results are shown in Table 1.

Full code is in Appendix A.1.

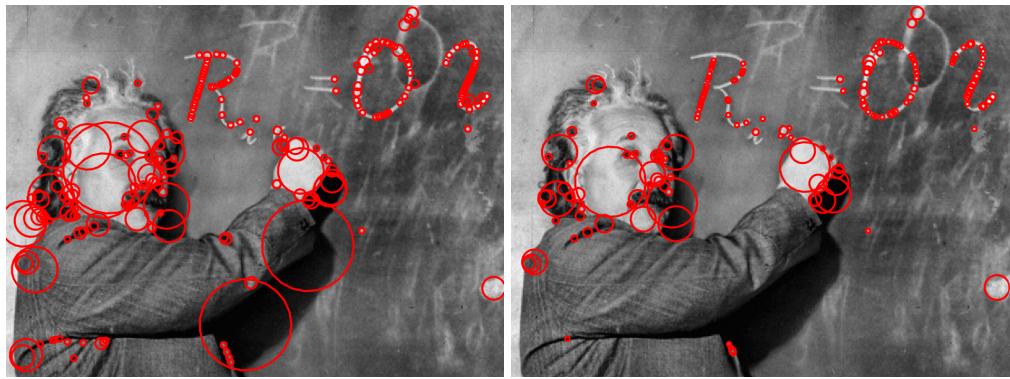
From the results shown, we can conclude that downsampling and then interpolating the results to original size is much more time-wise



(a) Increasing Kernel Size

(b) Downsampling the Image

Figure 29: Blob Detection on butterfly.jpg with both LoG filtering techniques, at initial $\sigma = 1.6$ and Threshold = 0.009



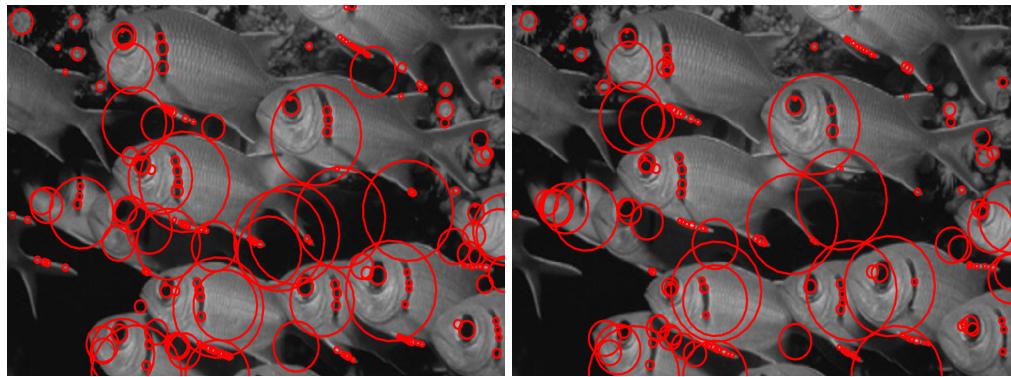
(a) Increasing Kernel Size

(b) Downsampling the Image

Figure 30: Blob Detection on einstein.jpg with both LoG filtering techniques, at initial $\sigma = 1.6$ and Threshold = 0.02

efficient over increasing the kernel size.

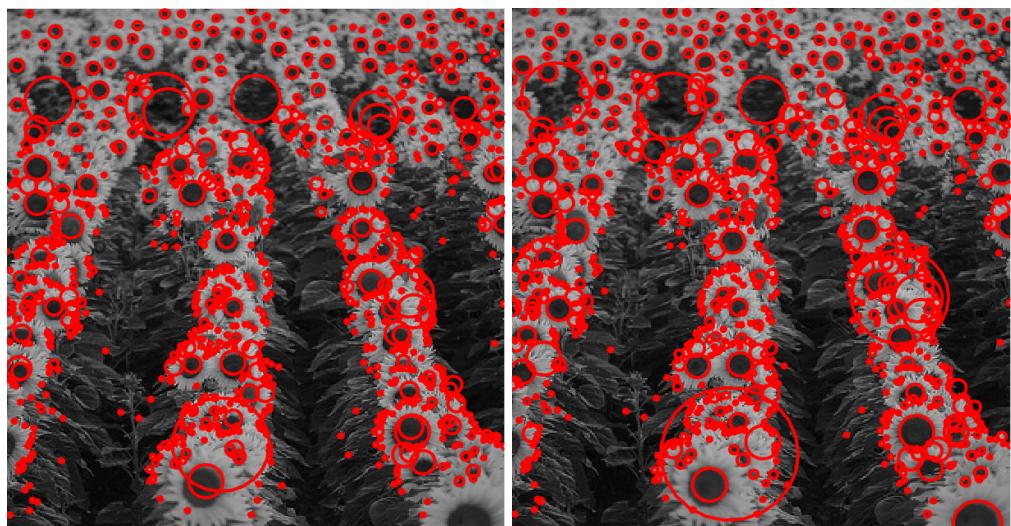
Naturally, the convolution is faster when we do it for smaller resolutions. But we might lose some tiny blob details in doing that.



(a) Increasing Kernel Size

(b) DownSampling the Image

Figure 31: Blob Detection on fishes.jpg with both LoG filtering techniques, at initial $\sigma = 1.0$ and Threshold = 0.019



(a) Increasing Kernel Size

(b) DownSampling the Image

Figure 32: Blob Detection on sunflowers.jpg with both LoG filtering techniques, at initial $\sigma = 1.0$ and Threshold = 0.019

Method →	Increasing Filter Size		Downsampling the Image	
Elapsed Time→	Computing		Computing	
Name↓	Whole Process	Blob Response	Whole Process	Blob Response
butterfly.jpg	102.383 s	98.629974 s	2.037 s	0.268332 s
einstein.jpg	134.837 s	132.56010 s	1.692 s	0.318100 s
fishes.jpg	85.5053 s	82.286573 s	1.206 s	0.194998 s
sunflowers.jpg	61.0202 s	57.543230 s	1.279 s	0.264452 s

Table 1: Elapsed Times for each process using both techniques: Increasing Kernel Size and Downsampling the Image, for whole process and only the blob response computation

3.2 Homography Transformation in RANSAC

We will get base points and transformed points just like before but now we will present them in this form:

$$\begin{bmatrix} x_i & y_i & 1 & 0 & 0 & 0 & -x'_i x_i & -x'_i y_i & -x'_i \\ 0 & 0 & 0 & x_i & y_i & 1 & -y'_i x_i & -y'_i y_i & -y'_i \end{bmatrix} \begin{bmatrix} h_{00} \\ h_{01} \\ h_{02} \\ h_{10} \\ h_{11} \\ h_{12} \\ h_{20} \\ h_{21} \\ h_{22} \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}$$

The code for finding the h parameters is as follows:

```

1 function [H] = computeHomography(x1,y1,x2,y2)
2     num = numel(x1);
3     H = ones(3);
4     eq = zeros(num*2, 8);
5     sol = zeros(num*2,1);
6     for i =1:num
7
8         pts1 = [x1(i),y1(i),1];
9         z = [0, 0, 0];
10        rem = (-1 * [x2(i);y2(i)]) * [x1(i),y1(i)];
11        sol((i-1)*2+1:(i-1)*2+2) = [x2(i); y2(i)];
12        eq ((i-1)*2+1:(i-1)*2+2,:) = [[pts1, z;z, pts1
13            ] rem];
14    end
15 H = eq\sol;
16
17 H(9) = 1;
18 H = reshape(H,3,3)';
19 end

```

Now we have got

$$\begin{bmatrix} h_{00} & h_{01} & h_{02} \\ h_{10} & h_{11} & h_{12} \\ h_{20} & h_{21} & h_{22} \end{bmatrix}$$

we can compute Transformed points from the Base point and Homography Transform and calculate the error between that and the actual Transformed co-ordinate.

```
1 function [x2, y2] = applyHomography(H, x1,y1)
2     p(1,:) = x1(:);
3     p(2,:) = y1(:);
4     p(3,:) = 1; % Homogenous co-ordinate
5
6     % Compute Transformed Point
7     x2 = H(1,:)*p;
8     y2 = H(2,:)*p;
9     thd = H(3,:)*p;
10
11    x2 = x2 ./ thd;
12    y2 = y2 ./ thd;
13 end
```

Then we choose the best model which has the least error just like we did in Affine Transform case.

The results are as shown below. See Figures 33, 34, 35, 36, 37, 38, 39 and 40 & their corresponding Homography Transforms.

Full code is in Appendix B.1.

Hill.jpg

. Maximum Inliers 413
Homography Transformation is:
0.9967 0.1063 136.7116
-0.0368 1.0539 -23.7154
-0.0001 0.0002 1.0000

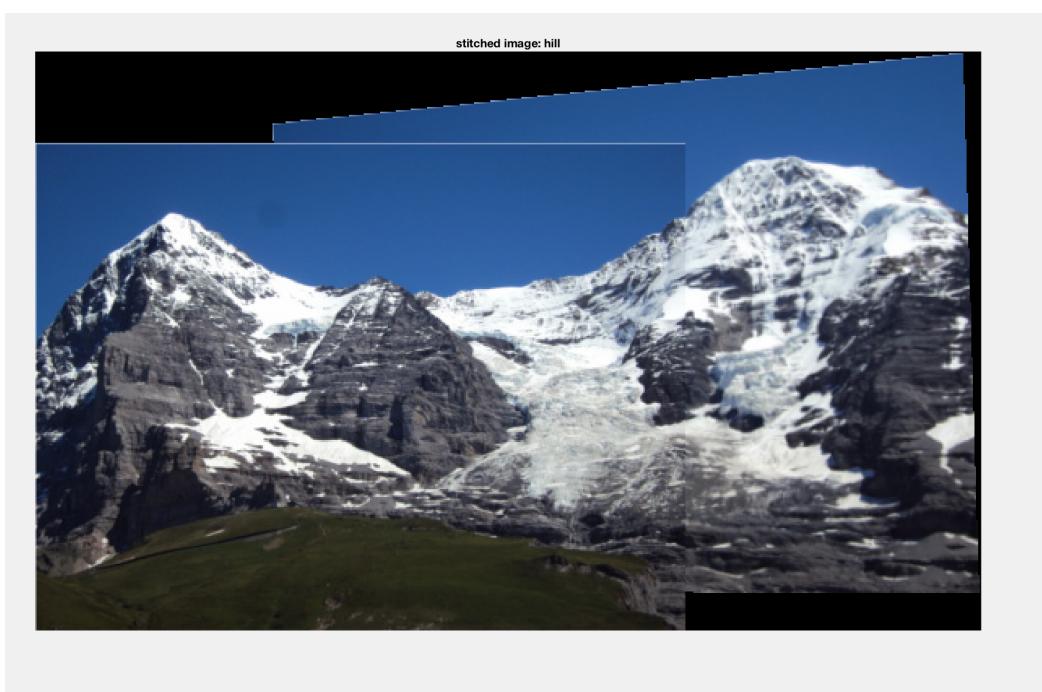


Figure 33: Panoramic Stitching of Hill images with Homography



Figure 34: Panoramic Stitching of Field images with Homography

Field.jpg

Maximum Inliers 116

Homography Transformation is:

0.9068	0.1104	255.2360
-0.0415	1.0482	8.7926
-0.0003	0.0003	1.0000



Figure 35: Panoramic Stitching of Ledge images with Homography

Ledge.jpg

Maximum Inliers 169

Homography Transformation is:

1.0004	0.2301	110.6853
-0.0265	1.2457	-170.1197
-0.0005	0.0009	1.0000

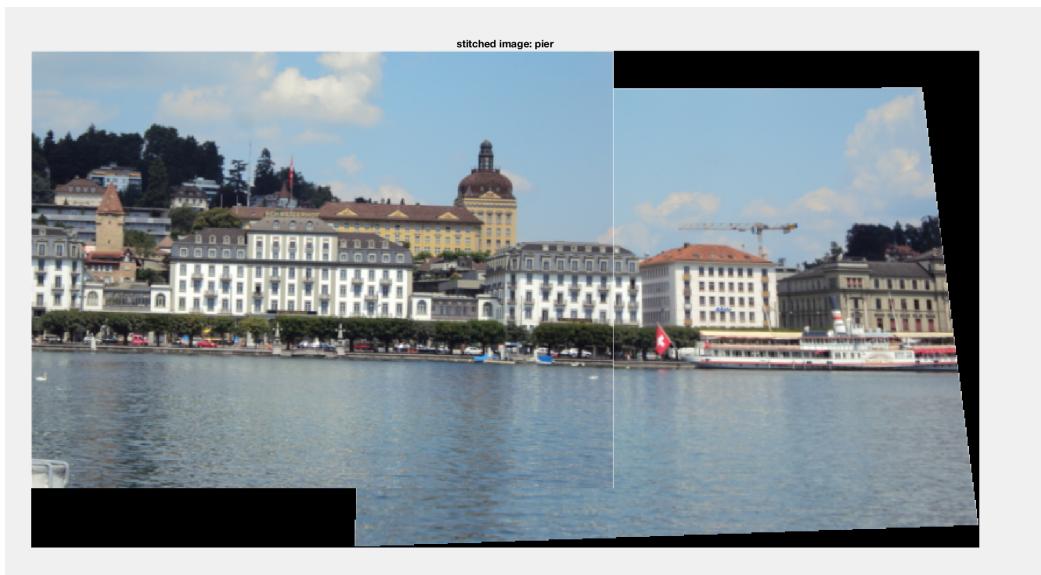


Figure 36: Panoramic Stitching of Pier images with Homography

Pier.jpg

Maximum Inliers 275

Homography Transformation is:

1.0908	-0.0536	285.5045
0.0061	0.9795	28.4132
0.0001	-0.0001	1.0000



Figure 37: Panoramic Stitching of River images with Homography

River.jpg

Maximum Inliers 87

Homography Transformation is:

0.8239	-0.1951	324.8764
0.3001	1.0629	-72.2569
-0.0005	0.0005	1.0000

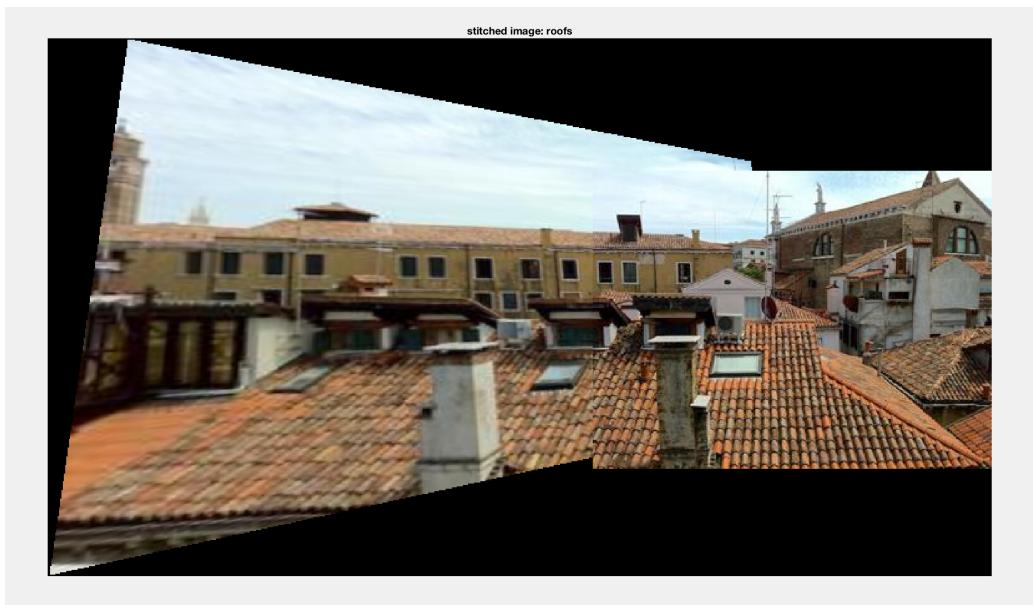


Figure 38: Panoramic Stitching of Roofs images with Homography

Roofs.jpg

Maximum Inliers 215

Homography Transformation is:

2.7722	0.3423	-538.9436
0.4573	2.2519	-183.8534
0.0052	-0.0001	1.0000

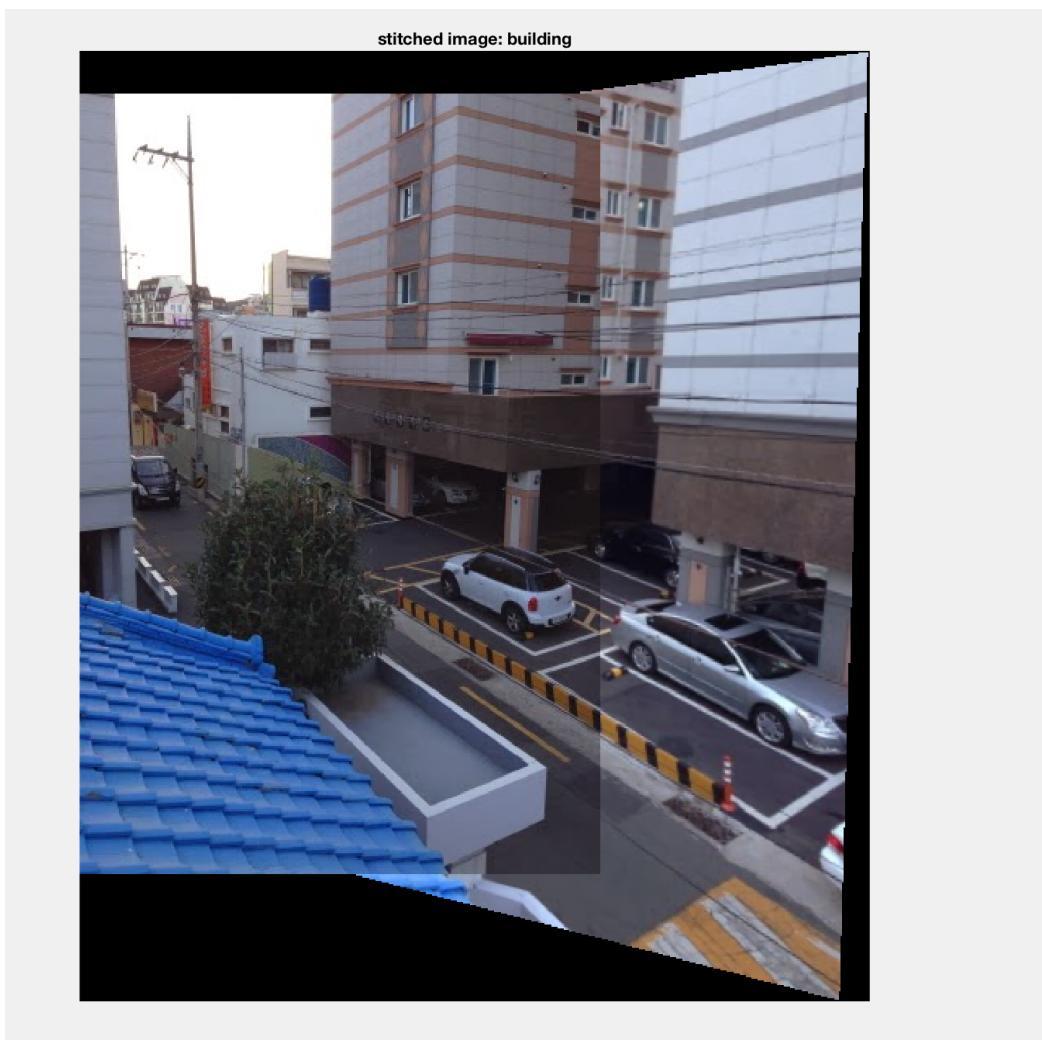


Figure 39: Panoramic Stitching of Building images with Homography

Building.jpg

Maximum Inliers 218

Homography Transformation is:

0.7735	-0.0161	125.7620
-0.0940	0.9434	16.2253
-0.0006	0.0000	1.0000



Figure 40: Panoramic Stitching of Tower images with Homography

Tower.jpg

Maximum Inliers 273

Homography Transformation is:

1.0793	-0.0891	-212.6703
0.0701	1.0257	-35.4482
0.0002	-0.0001	1.0000

References

- [1] Blob Detection, https://en.wikipedia.org/wiki/Blob_detection
- [2] Subhransu Maji, *Image Alignment* https://www.dropbox.com/s/5flemuwc73wv7o9/lec11\%2B12\%2B13_image_alignment.pdf?dl=0
- [3] Richard Szeliski, *Computer Vision: Algorithms and Applications*
ISBN: 978-1-848-82934-3

A

Matlab code for Problem 1: Scale-space blob detection

A.1 Implementation of detectBlobs.m

```
1 function blobs = detectBlobs(im, param)
2 % DETECTBLOBS detects blobs in an image
3 % BLOBS = DETECTBLOBS(IMAGE, PARAM) detects
4 % multi-scale blobs in IM.
5 % The method uses the Laplacian of Gaussian filter
6 % to find blobs across
7 % scale space.
8 %
9 % Input:
10 % IM – input image
11 % PARAM – struct containing the following fields
12 %     PARAM.SIGMA – sigma of the LoG filter (smallest blob desired)
13 %     PARAM.INTERVAL – number of intervals in an octave
14 %     PARAM.THRESHOLD – threshold for blob detection
15 %     PARAM.DISPLAY – if true then shows intermediate results
16 %
17 % Output:
18 % BLOBS – n x 4 array with blob in each row in (x, y, radius, score)
19 %
20 % Convert image to grayscale and convert it to double [0 1].
21 if size(im, 3) > 1
22     im = rgb2gray(im);
23 end
24 if ~isfloat(im)
25     im = im2double(im);
26 end
```

```

27 % If param is not specified use default
28 if nargin < 2
29     param.sigma = 2;
30     param.interval = 12;
31     param.threshold = 1e-2;
32     param.display = false;
33 end
34
35 % dummy blob
36 % blobs = [size(im, 2)/2, size(im, 1)/2, 100, 1.0];
37
38
39 %% Implement these:
40
41 %% Compute the scale space representation
42 sigma      = 1.6;      % Initial Scale
43 k          = sqrt(2);  % Factor by which the scale is
                           mulitplied each time
44 sigma_final = power(k,16);    % Last Scale
45 % Dynamically decide the interation levels from the
                           first and last scale values and multiplication
                           factor
46 n          = ceil((log(sigma_final) - log(sigma))/log
                           (k)); % Iterations of Laplacian scale space
47 [h, w]      = size(im);
48 scaleSpace  = zeros(h, w, n);  % [h,w] – Dimensions
                           of Image, n – Number of Levels in Scale Space
49
50 % Generate the Laplacian of Gaussian for the First
                           Scale Level
51 filt_size   = 2 * ceil(3*sigma) + 1;
52 LoG         = fspecial('log', filt_size, sigma);
53
54 %% Compute the blob response
55 % Increase filter size, keep image the same
56 if 0
57     tic
58     for i = 1:n
59         sigma_next = sigma * k^(i-1); % Increment
                           sigma for next level
60         filt_size = 2*ceil(3*sigma_next)+1; % Compute

```

```

    the filter kernel size in the same way as
    previously
61 LoG      = sigma_next^2 * fspecial('log',
62     filt_size, sigma_next); % Making a custom
63     LoG filter with trial and error
64 filter_next = imfilter(im, LoG, 'same', '
65     replicate'); % Create a replica of the
66     previous filter
67 filter_next = filter_next .^ 2; % Multiply
68     it by itself
69 scaleSpace(:,:,i) = filter_next; % Store
70     filter of each level
71 end
72 toc
73 end
74
75 % Faster version: keep the filter size, downsample the
76 % image
77 if 1
78     tic
79     imRes = im; % Create a copy of the image
80     for i = 1:n
81         imFiltered = imfilter(imRes, LoG, 'same', '
82             replicate'); % Apply the Laplacian of
83             Gaussian filter here, the filter is already
84             created in the above section
85         imFiltered = imFiltered .^ 2; % Square of the
86             LoG
87         scaleSpace(:,:,i) = imresize(imFiltered, size(
88             im), 'bicubic'); % Resize the image to
89             original size with bicubic interpolation
90         if i < n
91             imRes = imresize(im, 1/(k^i), 'bicubic');
92                 % Decrease the image size for next
93                 iteration
94             end
95         end
96     toc
97 end
98
99 %% Perform NMS (spatial and scale space)

```

```

85 % Perform Non-Maximum Suppression for each Scale-Space
86 % Slice
87 suppression_size = 3; % To make it Maximum Filter
88 max_space = zeros(h, w, n); % NMS output for each
89 % level
90 for i = 1:n
91     max_space(:,:,:i) = ordfilt2(scaleSpace(:,:,:i),
92         suppression_size^2, ones(suppression_size));
93 end
94
95 % Non-Maximum Suppression between Scales and Threshold
96 % For scales, compare the current one with the
97 % previous and next ones, choose the maximum of the
98 % three
99 for i = 1:n
100    max_space(:,:,:i) = max(max_space(:,:,max(i-1,1):
101        min(i+1,n)),[],3);
102 end
103
104 % Zero Out All Positions that are not the Local Maxima
105 % of the score (if the Value is not Greater than all
106 % its Neighbors)
107 max_space = max_space .* (max_space == scaleSpace);
108
109 x = []; % X - axis of blob's center
110 y = []; % Y - axis of blob's center
111 radius = []; % Radius of the blob
112 score = [];
113
114 % For each level
115 for i=1:n
116     % Set a Threshold on the Squared Laplacian
117     % Response above which to report Region
118     % Detections
119     [rows, cols, value] = find(max_space(:,:,:i).*(
120         max_space(:,:,:i) >= 0.01));
121     numBlobs = length(rows);
122     % Create Lists of each tuple fields separately
123     if (numBlobs > 0)
124         radii = sigma * k^(i-1) * sqrt(2);
125         radii = repmat(radii, numBlobs, 1);
126         x = [x; rows];

```

```
115     y = [y; cols];
116     score = [score; value];
117     radius = [radius; radii];
118 end
119 end
120
121 blobs = [y, x, radius, score];
```

B

Matlab code for Problem 2: Image Stitching

B.1 Implementation of computeMatches.m

```
1 function matches = computeMatches(f1,f2)
2 % COMPUTEMATCHES Match two sets of SIFT features f1
3 % and f2
4 % This code is part of:
5 %
6 % CMPSCI 670: Computer Vision , Fall 2019
7 % University of Massachusetts, Amherst
8 % Instructor: Subhransu Maji
9 %
10 % Mini project 4
11 % Implement this
12 f1_size = size(f1, 1);
13 f2_size = size(f2, 1);
14
15 %% Computing Matches using SSD
16 matches = zeros(f1_size, 1);
17 % Start Stopwatch Timer
18 tic
19 if 0
20     fprintf('Computing matching using SSD: \n');
21     % For each feature from image 1
22     for i = 1 : f1_size
23         % Find its nearest match image 2
24         bestMatch = inf;
25         for j = 1 : f2_size
26             % SSD
27             match = sum(sum((f1(i,:)-f2(j,:)).^2));
28             % Store the lowest SSD feature
29             if (match<bestMatch)
30                 matches(i) = j;
31                 bestMatch = match;
32             end
33         end
34     end
```

```

35 % Stop Stopwatch Timer
36 toc
37 end
38
39 %% Computing Matches using ratio
40 if 1
41     % For each Descriptor in the First Image, Select
        its Match to Second Image
42     for i = 1 : f1_size
43         % The most likely match
44         bestMatch = inf;
45         % The next most likely match after the best
            one
46         secondMatch = inf;
47         index = inf;
48         for j = 1:f2_size
49             % Compute SSD
50             match = sum(sum((f1(i,:)-f2(j,:)).^2));
51             % compare it with the best match
52             if(match < bestMatch)
53                 secondMatch = bestMatch;
54                 bestMatch = match;
55                 index = j;
56                 % compare it with the second best match
57                 elseif(match < secondMatch && match ~= bestMatch)
58                     secondMatch = match;
59                 end
60             end
61             % Now we have determined best and second best
                match
62
63             % Computer Ratio
64             ratio = bestMatch/secondMatch;
65             % Compare it with a threshold
66             if(~isequal(index,inf) && ratio < 0.8)
67                 matches(i)= index;
68             else
69                 matches(i) = 0;
70             end
71         end

```

```
72 end
```

B.2 Implementation of ransac.m

```
1 function [inliers, transf] = ransac(matches, blobs1,
2     blobs2)
3 % This code is part of:
4 %
5 % CMPSCI 670: Computer Vision, Fall 2019
6 % University of Massachusetts, Amherst
7 % Instructor: Subhransu Maji
8 %
9 % Homework 4
10 %
11 % implement this
12 %
13 %% Get all the non-empty feature matches
14 [inputs, cols, bases] = find(matches);
15 % Reset max inliers counter
16 maxInliers = 0;
17 % Store the original indices of matches so that
18 % removing the 0 index entries doesn't change the
19 % actual indices
20 originalIndices = find(matches);
21 % Get the non-zero entries size
22 inputs_size = size(inputs,1);
23 if nargin < 4
24     method = 'affine';
25 end
26 %
27 if strcmp(method, 'affine')
28     % This structure stores current point co-ordinates
29     inputPoints = zeros(inputs_size,2);
30     % This structure stores the points whose co-
31     % ordinates are getting transformed
32     basePoints = zeros(inputs_size,2);
33     % Number of points whose distance from the line is
34     % less than some constant threshold
35     threshold = 4;
36     iterations = 35;
37     % Store the best affine transformation (with the
```

```

    least error)
33 best_model = zeros(2,3);
34 % Store the points who are inlier
35 inliersInfo = zeros(inputs_size,2);
36 % Store the affine transformation for a particular
   iteration
37 transInfo = zeros(2,3,inputs_size);

38
39 % Store all features and locations in inputPoints
   for 1st image and in basePoints for 2nd image
40 for ind= 1:inputs_size
41     basePoints(ind,1) = blobs1(bases(ind),1);
42     basePoints(ind,2) = blobs1(bases(ind),2);
43     inputPoints(ind,1) = blobs2(inputs(ind),1);
44     inputPoints(ind,2) = blobs2(inputs(ind),2);
45 end
46
47 % Try RANSAC for 'iterations' number of times
48 for itr = 1:iterations
49     % Affine Transform for the current iteration
50     T = computeAffine(inputPoints,basePoints);
51     % Reshape the transform matrix in [3x3] for
52     % tranformed_points = tranform x base_points
53     trans = [reshape(T,[3,2])';0,0,1];
54     % Reshape base_points to [3x1] for
55     % tranformed_points = tranform x base_points
56     inputPt = [inputPoints';ones(1,inputs_size)];
57     % Compute tranformed_points = tranform x
       base_points
58     inputptF = trans*inputPt;
59     % Take the x-y co-ordinates of every
       transformed point
60     calPoints = inputptF(1:2,:);

61
62     % Calculate Error between Expected Tranformed
       point co-ordinates and actual Transformed
       points
63     dist = calculateError(calPoints,basePoints');
64     % Only take the points whose distance is lower
       than threshold
65     [rows,cols,error] = find(dist.*(dist <

```

```

        threshold));
66 % Count the number of inliers
67 inliersCount = size(cols,2);
68 total_error = sum(error,2);
69
70 % Find the best model by inlier count and
71 % error values
71 if inliersCount > round(0.10*inputs_size) &&
72 inliersCount >= maxInliers && inliersCount
73 ~= inputs_size
74
75 best_model = reshape(T,[3,2])';
76 if(inliersCount == maxInliers)
77     maxIndex = find(inliersInfo(:,1) ==
78         maxInliers);
79     if(total_error < inliersInfo(maxIndex,
80         2))
81         best_model = reshape(T,[3,2])';
82     end
83 end
84 inliersC = cols';
85 maxInliers= inliersCount;
86 inliersInfo(itr,1)=maxInliers ;
87 inliersInfo(itr,2)= total_error;
88 transInfo(:,:,itr) = best_model;
89
90 end
91
92 end
93
94 fprintf('Maximum Inliers %d and Msize is %d\n',
95     maxInliers ,inputs_size);
96 transf = [inv(best_model(:,1:2)), -1*best_model
97     (:,3)];
98 inliers = originalIndices(inliersC);
99 disp('Affine Transformation is:')
100 disp(transf)
101
102 end
103
104 if strcmp(method, 'homography')
105     % X co-ordinates of base points
106     xBase = zeros(inputs_size,1);
107     % Y co-ordinates of base points
108     yBase = zeros(inputs_size,1);

```

```

99      % X co-ordinates of transformed points
100      xInput = zeros(inputs_size,1);
101      % Y co-ordinates of transformed points
102      yInput = zeros(inputs_size,1);

103
104      % Blobs of Image 1 are Base Points
105      for i= 1:inputs_size
106          xBase(i,1) = blobs1(inputs(i),1);
107          yBase(i,1) = blobs1(inputs(i),2);
108      end

109
110      % Blobs of Image 2 are Transformed Points
111      for i= 1:inputs_size
112          xInput(i,1) = blobs2(bases(i),1);
113          yInput(i,1) = blobs2(bases(i),2);
114      end

115
116
117      for i = 1:10000

118
119          randBase = zeros(4,2);
120          randInput = zeros(4,2);

121
122          % Picking up random base points for first step
123          % of RANSAC
124          for j = 1:4
125              index = ceil(rand*(inputs_size-1))+1;
126              randBase(j,1) = xBase(index);
127              randBase(j,2) = yBase(index);
128              randInput(j,1) = xInput(index);
129              randInput(j,2) = yInput(index);

130          end

131
132          h = computeHomography(randInput(:,1),randInput
133          (:,2),randBase(:,1),randBase(:,2));

134          [x,y] = applyHomography(inv(h),xBase,yBase);
135          total = 0;
136          for j = 1:numel(x)
137              sigma = 100;

```

```

138         error = sum(sum(([xInput(j) yInput(j)] - [
139             x(j) y(j)]).2));
140
141         if error < sigma
142             total = total + 1;
143         end
144     end
145
146     if total > maxInliers
147
148         maxInliers = total;
149         H = h;
150
151     end
152 end
153 transf = H;
154 inliers = [];
155 end
156 end
157
158 function [x2, y2] = applyHomography(H, x1, y1)
159     p(1, :) = x1(:);
160     p(2, :) = y1(:);
161     p(3, :) = 1;
162
163     x2 = H(1, :) * p;
164     y2 = H(2, :) * p;
165     thd = H(3, :) * p;
166
167     x2 = x2 ./ thd;
168     y2 = y2 ./ thd;
169 end
170
171 function [H] = computeHomography(x1, y1, x2, y2)
172     num = numel(x1);
173     H = ones(3);
174     eq = zeros(num*2, 8);
175     sol = zeros(num*2, 1);
176     for i = 1:num
177

```

```

178     pts1 = [x1(i),y1(i),1];
179     z = [0, 0, 0];
180     rem = (-1 * [x2(i);y2(i)]) * [x1(i),y1(i)];
181     sol((i-1)*2+1:(i-1)*2+2) = [x2(i); y2(i)];
182     eq ((i-1)*2+1:(i-1)*2+2,:) = [[pts1, z;z, pts1
183     ] rem];
184 end
185 H = eq\sol;
186
187 H(9) = 1;
188 H = reshape(H,3,3)';
189 end
190
191 function [dist]= calculateError(calPoints ,FinputPoints
192 )
193 dist = sum((calPoints-FinputPoints).^2);
194 end
195 function [Transform] = computeAffine(basePoints ,
196 transPoints)
197 baseP = zeros(6,6); % input points
198 transP = zeros(6,1); % points after transformation
199 % of input points.
200 for j = 1:3
201     index = ceil(rand*(size(basePoints,1)-1))+1;
202     % Prepare base matrix with points before
203     % transformation; put them in the position
204     % shown in affine transform matrix equation
205     baseP(2*j -1,:) = [basePoints(index,1),
206         basePoints(index,2),1,0,0,0];
207     baseP(2*j ,:) = [0,0,0,basePoints(index,1),
208         basePoints(index,2),1];
209     % Set transformed points matrice; put them in
210     % the position shown in affine transform
211     % matrix equation
212     transP(2*j -1,:) = transPoints(index,1);
213     transP(2*j ,:) = transPoints(index,2);
214 end
215 % Matrix Division
216 Transform = baseP\transP;

```

209 end