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Detecting Shapes in Raven's Matrices

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April 30, 2010

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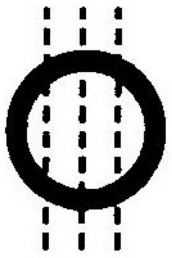
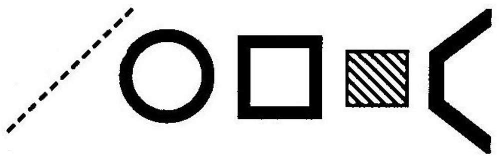
1.0 Introduction

Problem and Motivation: In Computer Vision, it is hard for computers to recognize and learn objects as humans do. For example, if humans learn that a four-sided figure with equal-length sides and four right angles is a square, then given another square rotated 30 degrees and scaled by 2, humans can easily recognize that that figure is still another square. However, for computers, the second object is completely different from the first one in pixel space, therefore most recognition methods today would fail horribly. This problem can be further complicated with images that do not represent common shapes. Being able to detect a similar feature in an image, given a model, is useful for object recognition and can be used to automate many processes, such as matching and classifying figures from a databank.

The problem this research addresses is being able to determine what figures an image contains given a databank of possible figures. For example, Figure 1a contains three dashed lines and a circle. Given a databank containing a dashed line, circle, square, patterns, and other non-conventional figures (Fig. 1b), this research would be able to determine that Figure 1a contains a circle and three dashed lines. The scope of this research is on selected images taken from a set of Raven's Matrices (Fig. 1c).


(a) Circle with three dashed lines (Raven, 1962)


(b) Databank of figures

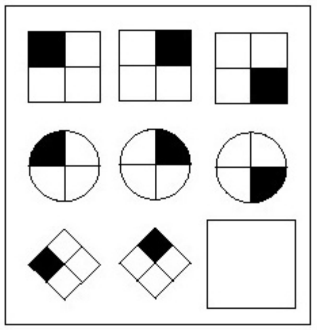

(c) Sample Raven's Matrix (Jirah, 2007)

Figure 1: Sample Figures from Raven's Matrices

2.0 Background and Related Work

This research uses the Scale-Invariant Feature Transform (SIFT) (Lowe, 2004) technique to match keypoints from a model to an image by providing the location, scale, and orientation of the matching keypoints. E.g., in a square, the main keypoints detected would include the four corners. Using an implementation of SIFT by Vedaldi (2006), the matched keypoints can be obtained (as in Fig. 2). The figures from each image in Raven's Matrices can then be extracted using additional techniques proposed in this work.

This research uses the SIFT approach because SIFT is a very robust technique that can detect key features regardless of its orientation, scale, or location.

3.0 Results

3.1 Overview

The SIFT implementation detects and matches keypoint between a test and a model image, but it does not determine which model from the databank is best for a particular Raven image. This research applies the Hough transform (Ballard, 1981) on the results of the keypoint matches between a Raven image and a model. The Hough transform is based on a voting procedure, where each keypoint match in the Raven image goes through the entire databank and votes for the possible models that it could contain. The most popular candidate from the databank would be declared the winner, indicating that the model is present in the image. Afterwards, an affine transformation is applied to find the best fit for the model onto the image. This method would be able to determine where, in a particular image, the model is located. Furthermore, the scale and orientation will also be known. In some cases, there may be more than one figure from the databank that is present in the image (refer to Fig. 1a). In these situations, several candidates from the databank would be very popular, and hence multiple winners would be declared. In other cases, the model may appear more than once in the image, so a clustering technique would be used to detect that the model appears more than once.

Afterwards, an affine transformation is applied to find the best fit for the model onto the image. This method would be able to determine where, in a particular image, the model is located. Furthermore, the scale and orientation will also be known. In some cases, there may be more than one figure from the databank that is present in the image (refer to Fig. 1a and Fig. 2). In these situations, several candidates from the databank would be very popular, and hence multiple winners would be declared.

3.2 Code Details

The given set of Raven's Matrices set is separated into 36 different folders named 'ravenx', where x is the number of each matrix. Each of the 8 cells in each matrix is cropped and put in their corresponding folder.

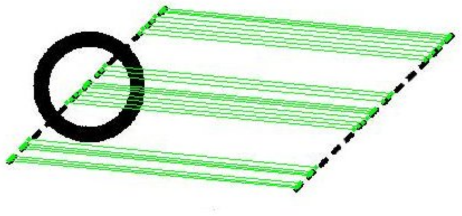


Figure 2: Matched keypoints from image to dashed line.

The training set is created by extracting specific figures from existing cells (e.g. from Fig. 1a, one training model is a circle, another is a dashed line). It was later discovered that having images too close to the border impacts SIFT's ability to extract keypoint descriptors, so an abundance of space was left between each image or model and its boundary.

3.3 Sift_raven.m

In this Matlab file, the script runs through each of the eight cell images (test images) from every Raven matrix and applies SIFT and the Hough transform on each test and model pair. To apply the SIFT technique, the function sift() is called twice, once for the test image and once for the model, given the following parameters:

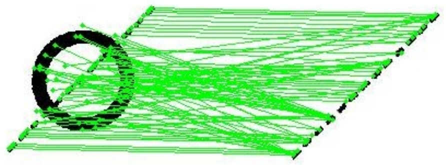
- image - the image on which sift() will extract keypoint descriptors
- threshold - value such that the maxima of the Difference of Gaussian scale space below this threshold are ignored (Vedaldi, 2006)
- edge threshold - localization threshold
- boundary point - remove points whose descriptor intersects the boundary

sift() returns two vectors. The first vector contains the image's frames, representing the location, scale, and orientation of the keypoint descriptor. The second vector is a 128-dimensional vector representing the descriptors. More information can be found in Vedaldi's SIFT documentation.

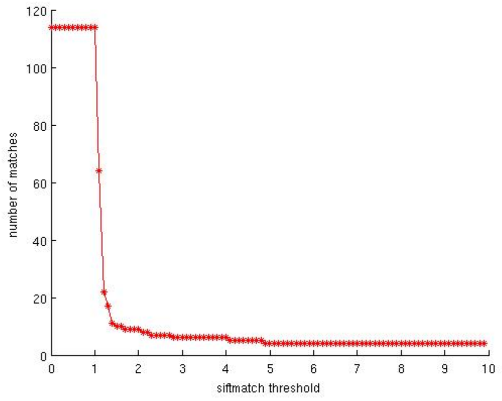
Once the descriptors are determined, siftmatch() is called to match the descriptors from the test and model images. A descriptor D1 is matched to a descriptor D2 only if the distance d(D1,D2) multiplied by the threshold is not greater than the distance of D1 to all other descriptors (Vedaldi, 2006). The default value of this threshold is 1.5, but setting the threshold to 0 provides better results (explained below).

siftmatch() returns a 2xM dimensional vector matching the index of each test descriptor to each model descriptor, where M is the number of descriptors in D1 (Vedaldi, 2006).

The results of siftmatch() are shown in Figure 3.



(a) Results of siftmatch() on test (left) and model (right) images.



(b) Plot of the siftmatch threshold versus the number of matches.

Figure 3: Siftmatch results and threshold

Determining the Thresholds for sift() and siftmatch()

The threshold used for sift() is set to 0 and edge threshold is also 0, so that the maximum number of descriptors will be returned. These results were determined by plotting the threshold and edge threshold versus the number of frames found. The boundary point is also to 0 so that it will not discard descriptors that intersect the boundary because those keypoints may be important later on.

The siftmatch threshold was also determined by plotting the it versus the number of matches. (See Fig. 3b). Usually this threshold is set to 1.5, however, that only returns values with very good keypoint matches, leaving very little data for the Hough transform to work. When the threshold is set to 0, siftmatch() returns the maximum number of matches possible (the number of matches is actually equal to the number of descriptors in the test image), and the Hough transform provides better matches for the training models.

After SIFT has been applied, hough() is called to apply the Hough transform on the keypoint matches.

3.4 Hough.m

The Hough transform is a feature extraction technique used in image analysis, computer vision, and digital image processing (Shapiro and Stockman, 2001), and it is based on a voting procedure. For example, given a circle (test image), and a databank containing a square, circle, and semi-circle (model images), each keypoint descriptor on the circle would vote for the possible model images from the databank. Most likely the circle model, and not the semi circle or square, would acquire the most votes from all the descriptors, and so it would be declared the "winner", meaning a circle exists in the test image. More information about the Hough transform can also be found in David Lowe's article, *Distinctive Image Features from Scale-Invariant Keypoints.*

In the hough() function, the Hough transform is applied in a similar way. Given a set of keypoint matches between the test and model images in the image space, each match will vote for a certain bin in the Hough space (a bin describes the (x,y) location, scale, and orientation of the descriptor). After all the keypoints have voted, the bin with the greatest number of votes will provide the most accurate information about the location, scale, and orientation of the model relative to the test image.

hough() takes the following parameters:

- matches - keypoint matches between the image and model produced by siftmatch()
- test_frames, model_frames - the test and model frames containing the (x,y) location, scale, and orientation of the descriptors
- model_name - name of the model, for convenience
- cell, model - the test and model images used for plotting

The output of hough() contains the following:

- (x,y) location of where the model is located on the test image,
- scale of model relative to the test image,
- orientation of the model relative to the test image,
- a number of figures or plots that will be described below, OR
- 'no matches' if there are no matches between the test and model image

Variables

- distinct_indices - stores the indices of each bin in a hash table

Each bin describes four dimensions, listed below:

- BW_x: x-bin width
- BW_y: y-bin width
- BW_scale: each partition is the range between two consecutive numbers in this vector
- BW_theta: bin width for orientation in radians

- test_uv, model_xy - vectors used for affine fitting
- best_count: bin with the greatest count
- winning_bin: bin containing the most votes

Explanation of Code

For each pair of matches passed in, the test and model frames are extracted into test_params and model_params. Then a transformation is applied to determine the transformation from the center of the model to the test image. The change in scale and orientation is calculated as follows:

$$\Delta scale = \frac{test\_scale}{model\_scale}$$

$$\Delta\theta = test\_orientation - model\_orientation$$

The transformation is calculated as follows:

$$\begin{bmatrix} x \\ y \\ 1 \end{bmatrix} = \begin{bmatrix} \Delta scale \times cos(\Delta\theta) & -sin(\Delta\theta) & x_t \\ sin(\Delta\theta) & \Delta scale \times cos(\Delta\theta) & y_t \\ 0 & 0 & 1 \end{bmatrix} \times \begin{bmatrix} -x_m + \frac{model\_width}{2} \\ -y_m + \frac{model\_height}{2} \\ 1 \end{bmatrix}$$

x and y represent where the center of the model image is mapped on the test image, and the subscripts t and m refer to the test and model descriptors.

The bins for the each dimension (bin_x, bin_y, bin_scale, bin_theta) are determined using the above information. Checks were made to ensure that there are no negative values for orientation, since negative values would be a duplicate other values (periodic property).

According to Lowes *Distinctive Image Features from Scale-Invariant Keypoints*, every descriptor should vote for the two closest bins in each dimension, resulting in 16 votes per descriptor. To do this, the floor and ceiling are taken from each dimension, and the bin values for each of the 16 votes are stored in permut.

Next the hash index for each bin is computed using serialization by calling get_hash_ind(), and the indices of the matches are stored in the hash table. For example, if 100 matches are passed in as a parameter to hough(), and the 10th pair matched the 4th test descripter with the 9th model descriptor, then the index 10 would be stored in the hash table at the computed index. This is considered one vote in the hash table. The bin with the greatest number of votes is tracked using best_count and winning_bin.

Clustering Section

This section determines if clustering should be performed. If the bin with the greatest number of votes (the first bin) contains at least three keypoint matches (i.e. the model is found in the test image), then the model could exist multiples times in the test image (see Fig. 1a). In that case, this section will proceed with clustering. However, if the first bin has too few keypoint matches (i.e. the model does not exist in the test image), then the clustering function, cluster(), will not be called.

Variables

- X, Y, S, and T are vectors that store the mean (x,y) values, scale, and orientation (radians) taken from the keypoints found in each bin. Tx and Ty represent the orientation on the unit circle.
- allX and allY store all the x and y values mapped from the model to the test image (these values are a collection from all 30 bins) - it is helpful later on as a diagnostic test to visualize where the clusters may lie.
- firsthasmatch - this is a flag that determines if the first bin found a match between the model and the test image

Explanation of Code

If there exists some keypoint matches between the test and model image, the size of each bin is stored in vec, and sorted in descending order to find out which bin has the most tallies. The number of votes in each bin is stored in sorted_bin_size, and the index into vec is stored in sorted_bin_size_ind.

The code runs through the top 30 bins (NBin), and for each bin it retrieves the index of the nth bin, the indices representing the matches in that bin, and stores all the x and y values from the test and model frames into test_uv and model_xy. These two vectors are used for affine fitting to determine accurate parameters for mapping the model points to the test points.

The equation used for affine fitting is the following (Lowe, 2004):

$$\begin{bmatrix} x & y & 0 & 0 & 1 & 0 \\ 0 & 0 & x & y & 0 & 1 \\ & & \cdots & & & \\ & & \cdots & & & \end{bmatrix} \times \begin{bmatrix} m_1 \\ m_2 \\ m_3 \\ m_4 \\ l_x \\ l_y \end{bmatrix} = \begin{bmatrix} u \\ v \\ \vdots \end{bmatrix}, m = \begin{bmatrix} m_1 \\ m_2 \\ m_3 \\ m_4 \\ l_x \\ l_y \end{bmatrix}$$

x and y represent the location for each model point, and u and v represent the test points. m_i represent the parameters that rotate, scale, and stretch the model points. l_x and l_y represent the model translation (Lowe, 2004).

The vector m is calculated using Matlab's pinv function instead of the backslash operator because the backslash operator often produced unpredictable results for m.

If the parameters in m are valid, then we perform a check to see where the model points are translated.

If there are more than three distinct model points and this is the first of the 30 bins, then the translation from the model point to the image point is plotted. The center of the model is plotted as a green square. Only the results for the first bin are plotted; since it contains the most votes, it would be the best bin to determine if the model is found in the image. This is also done for simplicity, but the results for the top 30 bins can be viewed if this restriction is removed. An example of the model points mapped to the image points shown in Figure 4.

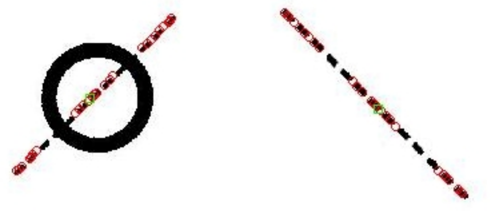
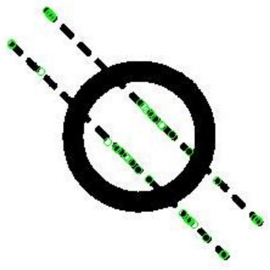


Figure 4: Translation of model points (right) to image points (left).

The next part stores all the x, y, scale, and orientation values in X, Y, S, T. X and Y store the x and y values


(a) Plot of all model points from a dashed line to the image points

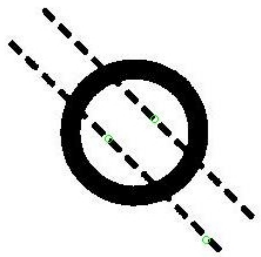

(b) Sample showing 2 clusters found in the image (green dots in the center)

Figure 5: Results for clustering

mapped from the middle of the model to the test image. S stores the mean scale between the test and the model image, calculated over all the points relative to the center of the images. T stores the mean of the difference in orientation between the test and model.

Finally, we print the location, scale, and orientation of the model that was found in the test image. The following is some sample output:

```
dashed_line2.jpg located at approximately (156.8097,156.8097)
scale: 1.0062 times the model
orientation: 3.1173 radians
```

If the first bin determines that the model exists in the test image, then we proceed with clustering. We map the orientation (in radians) to the unit circle to handle the periodic values.

We plot all the keypoints mapped onto the test image from the 30 bins. The sample in Figure 5a provides greater intuition as to where the clusters should belong.

Now we call cluster() given the following data and the test image: [X Y S Tx Ty], where X, Y, S, Tx, and Ty are column vectors. In this matrix, each row represents one data value containing the x and y location, scale, and orientation. Figure 5b shows the results of calling cluster().

If there are no matches, 'no matches' is printed.

3.5 Cluster.m

This function calls Matlab's subclust() function, which is a subtractive clustering technique using the Fuzzy Logic Toolbox. subclust() returns one vector containing the cluster centers, and another vector representing the sigma values that specify the range of influence of a cluster center in each dimension. More details can be found in Matlab's help documentation.

Variables

- X - the data passed in, containing the x and y values, scale, and orientation (each row is a data point)
- clust_radii - a vector storing the x and y radii threshold and the number of clusters found (used for plotting)
- XBounds - a matrix that specifies the minimum and maximum values for each dimension. It is used to normalize the data.

The subclust() function allows the user to specify the radii (a value between 0 and 1) for each dimension, indicating the cluster centers range of influence in that dimension. The x and y radii values are graphed against the number of clusters found, while the scale and theta radii are preset to 0.4 and 0.3. In the future, these thresholds can be further adjusted to find the optimal thresholds.

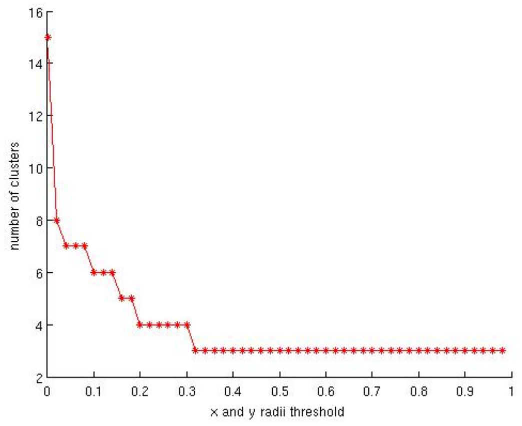


Figure 6: Plot of x and y radii versus number of clusters

Plotting the x and y radii against the number of clusters in an image shows that the fewest clusters occur when the x and y radii are set to 1. See Figure 6 for an example.

In some cases, the number of clusters found is not perfect:

In Figure 7a, there are three clusters detected for the left square, when there only exists one cluster. The reason for this is that the orientations of the data are oriented in different directions, so the subclust() function considers these data points to belong to different clusters. In Figure 7b, the top left cluster was not found. One possible reason is that SIFT provided too few keypoint matches between the model and the top left square (Fig. 8c) (See also Future Problems.)

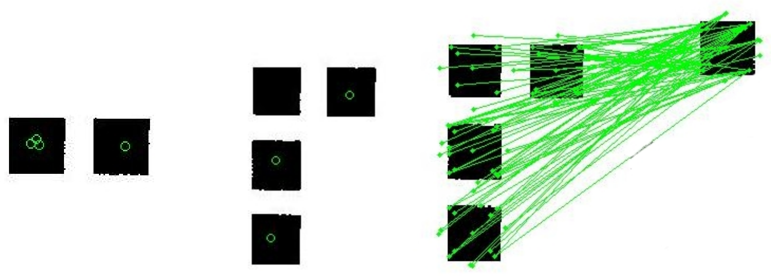

(a) Three clusters found in the left square **(b)** Top left cluster missing **(c)** siftmatch() results between Fig. 8b and the model

Figure 7: Errors from clustering

Now we print the information describing where the clusters were found:

```
There are clusters located at (format: [a b c d e]):
  156.8772  166.8502    1.0053   -0.9998    0.0211
  196.0512  149.6497    1.0226    0.0021   -1.0000
  240.3024  252.6831    0.8730    0.9999   -0.0109


where a and b represent the x-y location, c represents
the relative scale from the model to the test image,
and d and e represent the angle on a unit circle.
(cos(theta), sin(theta)) = (d,e)
```

4.0 Examples and Theoretical Adaptation to Rasmussen's Model

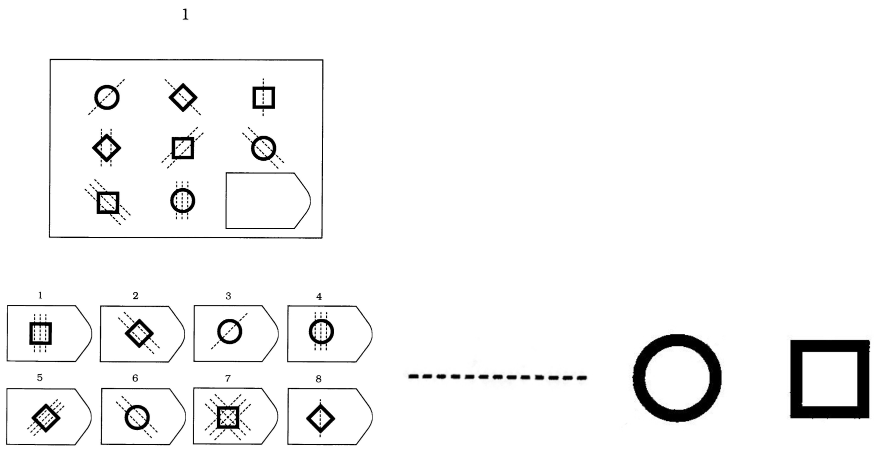
The Rasmussen Model, created by Daniel Rasmussen, is a model that provides an algorithm to solve Raven's Matrices. The following is a modified version of the Rasmussen input and output, that illustrates how this research can be adapted to the Rasmussen Model.

4.1 Basic Idea

For each Raven image, apply SIFT and the Hough transform on each of the 8 cells with the models in the databank. The output would provide information on what models exist in the test cell, and the number of times that model occurs (clustering). Then a converter would map the Rasmussen input with the output above. If there is a match, this converter would take the corresponding Rasmussen solution, and apply SIFT and the Hough transform on the answer cells to determine the image containing the correct answer. This method shows how solving Raven's Matrices can be automated using SIFT and the Hough transform to detect the figures in the Raven image.

The following examples assume that the output from the Hough transform (including clustering) do not contain the problems discussed above or in the Future Problems section. For example, if there are multiple clusters found in an image due to a difference in orientation, only one of those clusters would be considered for the purposes of these examples.

4.2 Example 1



(a) Raven Matrix 1 **(b)** Databank of figures

Figure 8: Raven Matrix 1 and Databank

Cell 1's output from the Hough transform:

```
HOUGH IMPLEMENTATION
================================
dashed_line_horizontal.jpg located at approximately (173.7823,173.7823)
scale: 0.99973 times the model
orientation: 5.4982 radians

There are clusters located at (format: [a b c d e]):
  173.6544  157.8504    1.0045    0.7079   -0.7063

where a and b represent the x-y location, c represents
the relative scale from the model to the test image,
and d and e represent the angle on a unit circle.
(cos(theta), sin(theta)) = (d,e)
HOUGH IMPLEMENTATION
================================
circle.jpg located at approximately (179.9844,179.9844)
scale: 1.0154 times the model
orientation: 6.2147 radians

There are clusters located at (format: [a b c d e]):
  180.5672  155.7880    1.0035    0.5597   -0.8287
where a and b ...
HOUGH IMPLEMENTATION
================================
no match for square.jpg
```

Cell 2's output from the Hough transform:

```
HOUGH IMPLEMENTATION
================================
dashed_line_horizontal.jpg located at approximately (98.3411,98.3411)
scale: 0.99012 times the model
orientation: 0.789 radians

There are clusters located at (format: [a b c d e]):
  135.9893  126.1805    0.9763    0.7136    0.7005
where a and b ...
HOUGH IMPLEMENTATION
================================
no matches for circle.jpg

HOUGH IMPLEMENTATION
================================
square.jpg located at approximately (176.2785,176.2785)
scale: 1.0809 times the model
orientation: 2.3588 radians

There are clusters located at (format: [a b c d e]):
  176.0277  166.0052    1.0769   -0.6971    0.7170
where a and b ...
```

Repeat until Cell 8.

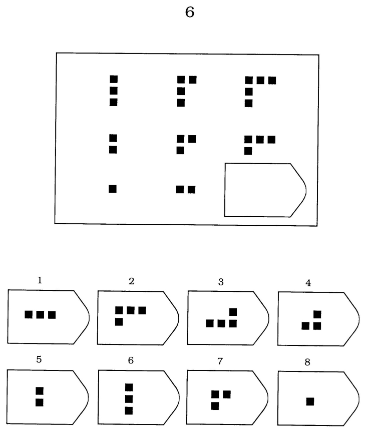
The converter would take the above output as well as the Rasmussen input for this matrix:

```
#matrix
circle; 1; 45deg
diamond; 1; 135deg
square; 1; 90deg
diamond; 2; 90deg
square; 2; 45deg
circle; 2; 135deg
square; 3; 135deg
circle; 3; 90deg

#answers
square; 3; 90deg
diamond; 2; 135deg
circle; 1; 45deg
circle; 3; 90deg
diamond; 3; 45deg
circle; 2; 135deg
square; 3; 45deg
diamond; 1; 90deg

#solution
diamond; 3; 45deg
```

The converter would use the following logic:

```
if cell 1 contains a circle and 1 dashed line at 45deg &&
   cell 2 contains a diamond and 1 dashed line at 135deg &&
   cell 3 contains a square and 1 dashed line at 90deg &&
   ... &&
   cell 8 contains a square and 3 dashed line at 90deg
then
   apply the Hough transform on the answer cells
   if Answer 1 contains a diamond and 3 dashed lines at 45deg
      then output Answer 1
   else if Answer 2 contains a diamond and 3 dashed lines at 45deg
      then output Answer 2
   ...
   else if Answer 8 contains a diamond and 3 dashed lines at 45deg
      then output Answer 8
end
```

4.3 Example 2



(a) Raven Matrix 6

(b) Databank of figures

Figure 9: Raven Matrix 6 and Databank

Cell 1's output from the Hough transform:

```
HOUGH IMPLEMENTATION
===============================
dot.jpg located at approximately (138.5898,138.5898)
scale: 1.0021 times the model
orientation: 1.0574 radians
There are clusters located at (format: [a b c d e]):
  136.6779   90.8459    0.9839   -0.0179   -0.9998
  138.5898  154.9850    1.0021    0.4911    0.8711
  138.8572  216.1572    0.9853    0.9987    0.0500
where a and b...
```

Cell 2's output from the Hough transform:

```
HOUGH IMPLEMENTATION
===============================
dot.jpg located at approximately (198.91,198.91)
scale: 0.99389 times the model
orientation: 1.5926 radians
There are clusters located at (format: [a b c d e]):
  198.9100   89.2979    0.9939   -0.0218    0.9998
  140.8672  85.2642     1.0182   -0.9878   -0.0230
  139.0668  142.0829    0.9590   -0.0237   -0.9997
  134.9845  204.9490    1.0071   -0.9998   -0.0214
where a and b...
```

Cell 3's output from the Hough transform:

```
HOUGH IMPLEMENTATION
================================
dot.jpg located at approximately (102.3028,102.3028)
scale: 0.99602 times the model
orientation: 0.0309 radians
There are clusters located at (format: [a b c d e]):
  162.6272   72.9363    1.0117   -0.8096    0.5869
  216.6745   72.6565    1.0213   -0.9997   -0.0228
  102.1979   72.2020    1.0024    0.9995    0.0324
  99.2356   131.1557    1.0093   -0.0115    0.9999
  98.1655   188.9925    1.0134    0.0255   -0.9997
where a and b...
```

Repeat until Cell 8.

The converter would take the above output as well as the Rasmussen input for this matrix:

```
#horizontal dots(number);#vertical dots(number)
#matrix
1;3
2;3
3;3
1;2
2;2
3;2
1;1
2;1

#answers
3; 1
3; 2
3; 2
2; 2
1; 2
1; 3
2; 2
1; 1

#solution
3; 1
```

The converter would use the following logic:

```
if cell 1 contains 1 horizontal dot(s) and 3 vertical dot(s) &&
   cell 2 contains 2 horizontal dot(s) and 3 vertical dot(s) &&
   cell 3 contains 3 horizontal dot(s) and 3 vertical dot(s) &&
   ... &&
   cell 8 contains 2 horizontal dot(s) and 1 vertical dot(s)
then
   apply Hough transform on the answer cells
   if Answer 1 contains 3 horizontal dot(s) and 1 vertical dot(s)
      then output Answer 1
   else if Answer 2 contains 3 horizontal dot(s) and 1 vertical dot(s)
      then output Answer 2
   ...
   else if Answer 8 contains 3 horizontal dot(s) and 1 vertical dot(s)
      then output Answer 8
end
```

5.0 Conclusion

The problem we are trying to address is whether or not it is possible to determine the existence of a model in a given test image. Using SIFT to determine the matching keypoints between the test and model image, then applying the Hough transform, it is definitely possible to determine whether or not a model is found in the test image. This method is able to determine the best possible match, in terms of the (x,y) location, scale, and orientation, from the model to the test image. Furthermore, it is also possible to determine how many times a particular model occurs in the image using a clustering technique.

5.1 Summary of Contributions

- demonstrated the ability to detect figures in an image using the SIFT technique and Hough transform
- illustrated the ability to determine multiple occurrences of a figure in an image
- developed a theoretical approach to adapt the above methods with the Rasmussen model

5.2 Future Problems

This research is just the beginning of one method to automate solving Raven's Matrices. It is by no means complete, and there are many things that can be improved.

SIFT has Limitations

Firstly, SIFT is not perfect in detecting all the keypoint matches between the test and model image. For example, if there is a dashed line in the image that is occluded by another figure, SIFT may not be able to detect the feature descriptors of the dashed line. Also, if the test or model image contains a lot of noise, SIFT would also have difficulty detecting keypoints. These factors directly affect the results of the Hough transform because it influences the number and quality of matches detected.

Another limitation of SIFT is that this technique cannot handle images with non-detectable features, meaning images that are pixel based. For instance, the keypoints for the small triangle in the left image of Figure 10 are the corners and the middle of the triangle. However, given the image on the right, SIFT will not be able to detect features pertaining to two small triangles because no features are detectable where the two smaller triangles are joined. As a result, the Hough transform and clustering will be ineffective for these types of images.

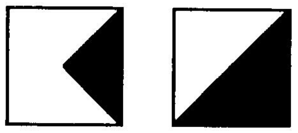


Figure 10: Image with one small triangle (left) and two small triangles combined (right).

One method to handle the above problems would be to use an alternative technique that detects figures based on the way the pixels are arranged in the image space.

Design of the Scale Bin

In the Hough transform, a descriptor often votes for the same bin out of the 16 votes. This is due to how the bin for the scale was created. For example, if the scale was very close to 1, two of the 16 votes would go to the same scale bin (refer to permut). However, every descriptor should vote for 16 distinct bins. This method of storing the scale can be refined to give a more accurate representation of the scale bin.

Clustering Improvements

One problem mentioned earlier with clustering is that sometimes several clusters are found in the same area when there should only be one cluster there. The reason for this is that when clustering based on the (x,y) location, scale, and orientation, the differences in orientation would indicate those data points belong to different clusters. But since a square rotated 90 degrees is still a square, this solution would be redundant. One way to resolve this issue would be to use a similarity transform or prior information, such as determining that the model will not be rotated 90 degrees when mapped to the image. These methods would provide more accurate numbers of clusters.

In this research, clustering was used only when the first bin found a match between the test and model image. It is unknown whether or not this method provides optimal results. Further investigation into this area would be required.

This research only adjusted the x and y radii parameters for the subclust() function. However, in the future, all the parameters for subclust() should be compared and adjusted to find the values that provide the best results.

Selection of Training Models

All the models in this research were taken directly from the test image. Although some models were resized and rotated, the next step in this field of research would be to use training models that have never been presented before. To be able to detect the presence of new figures in an image would have widespread applications.

References

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Appendix A - Sift_raven.m

```
% IMPLEMENT SIFT ON RAVEN'S IMAGE
% Purpose: This script will siftmatch each cell in Raven's images with the
% training set and then apply the hough transform to determine if there are
% matching figures
% By: Jacqueline Mok
% Acknowledgements: Charlie Tang
% Date: January 25, 2010

% This script assumes that the directories 'raven1' through to 'raven36'
% have been created in
% /home/jkmok/workspace/trunk/sift/Ravens_Vision/results/

clear;

disp('BEGINNING');
EDGE_THRESHOLD = 0; % the smaller this threshold, the more frames we get
THRESHOLD = 0;      % Maxima of the Difference Of Gaussian scale space below
                    % this threshold are ignored. Smaller values accept more features.
SIFTMATCH_THRES = 0;

% i determines the raven folder
for i=1:36
    IMG_PATH = ['/home/jkmok/workspace/trunk/sift/Ravens_Vision/raven_images/raven' num2str(i) '/'];
    imgDir = dir( IMG_PATH );
    TRAINING_PATH = '/home/jkmok/workspace/trunk/sift/Ravens_Vision/training_set/';
    trainingDir = dir(TRAINING_PATH);
    SAVING_PATH = '/home/jkmok/workspace/trunk/sift/Ravens_Vision/results/';
    savingDir = dir(SAVING_PATH);

    % j determines the test image
    for j=1:8
        img_name = [IMG_PATH imgDir(j+3).name];
        test = double ( imread (img_name) );
        % apply sift on test image, returns frames and descriptors
        [frames_test, test_desc] = sift(test, 'Threshold', THRESHOLD, ...
            'EdgeThreshold', EDGE_THRESHOLD, 'BoundaryPoint', 0);

        % k determines the traning image
        for k = 1:length(trainingDir) - 3
            model_name = [TRAINING_PATH trainingDir(k+3).name];
            model = double ( rgb2gray( imread (model_name) ) );
            [frames_model, model_desc] = sift(model, 'Threshold', THRESHOLD,...
                'EdgeThreshold', EDGE_THRESHOLD, 'BoundaryPoint', 0);

            % example showing a plot of the threshold values versus the number
            % of matches when calling siftmatch()
            plot_thresholds(test_desc, model_desc);
            % siftmatch matches two sets of SIFT descriptors
            matches = siftmatch(test_desc, model_desc, SIFTMATCH_THRES);
            figure(1); clf;
            plotmatches(test, model, frames_test, frames_model, matches);

            % apply hough transform for each test/model pair
            hough(matches, frames_test, frames_model, trainingDir(k+3).name, test, model);
        end
        fprintf('\n');
    end
end
disp('END');
```

Appendix B - Hough.m

```
function [ output_args ] = hough( my_matches, frames_test, frames_model,
 model_name, cell, model )
% this function applies the Hough transform to a set of frames from a test
% and model image. If there is more than one occurrence of the model on the
% test image, the a cluster function is called (cluster()). hough() takes
% the following parameters:
%
% my_matches    - the indices representing the matches between the test and
%               model descriptors produced by siftmatch()
% frames_test, frames_model - the test and model frames containing the
%               (x,y) location, scale, and orientation of the descriptors
% model_name    - name of the model
% cell, model   - the test and model images

disp('HOUGH IMPLEMENTATION');
distinct_indices=[];
hashtable = java.util.Properties; % stores the bin indices

BW_x = 10; % x-bin width
BW_y = 10; % y-bin width
BW_scale = [0.05 .75 1.5 2.5 4]; % bin is the range inbetween these numbers
BW_theta = 2*pi/12; %theta bin size
test_uv = []; % used for affine fitting
model_xy = []; % used for affine fitting
bestcount = 0;
winning_bin = NaN;

%figure that displays 'NO MATCH'
nomatch= double(imread ('/home/jkmok/workspace/trunk/sift/Ravens_Vision/no_match.jpg'));

%for each match
for i=1:size(my_matches, 2)
    s = my_matches(1,i);
    t = my_matches(2,i);
    test_params = frames_test(:,s);
    model_params = frames_model(:,t);

    % apply a transformation to determine where the center of the model
    % is mapped to on the test image
    delta_scale = test_params(3)/model_params(3);
    delta_theta = test_params(4) - model_params(4);

    rotation = [delta_scale*cos(delta_theta) -sin(delta_theta) test_params(1); ...
     sin(delta_theta) delta_scale*cos(delta_theta) test_params(2); 0 0 1];
    transform = rotation * [-model_params(1)+.5*size(model,2); ...
     -model_params(2)+.5*size(model,1); 1];
    % determine which bin the location, scale, and orientation belong to
    bin_x = (transform(1) - 0.5*BW_x)/BW_x;
    bin_y = (transform(2) - 0.5*BW_y)/BW_y;
    inds = find( BW_scale > delta_scale);
    if size(inds, 2) == 0
        bin_scale = 5;
    else
        bin_scale = inds(1)-1;
    end
    bin_theta = (delta_theta - 0.5*BW_theta)/BW_theta;

    % we want the 2 closest bins in each dimension, so we take the
    % floor and ceiling of the above bins. should get a total of 16
    params = [floor(bin_x) ceil(bin_x) floor(bin_y) ceil(bin_y) floor(bin_scale)...
     ceil(bin_scale) floor(bin_theta) ceil(bin_theta)];
    x1 = params(1); x2 = params(2); y1 = params(3); y2 = params(4);
    s1 = params(5); s2 = params(6); t1 = params(7); t2 = params(8);

    %check for negative bins for orientation
    %12 is the number of bins;
    while t1 < 0
        t1 = t1 + 12;
    end
    while t1 > 11
        t1 = t1 - 12;
    end
    while t2 < 0
        t2 = t2 + 12;
    end
    while t2 > 11
        t2 = t2 - 12;
    end

    assert(t1 >= 0); assert(t2 >= 0); assert(t1 < 2*pi/(BW_theta));
    assert(t2 < 2*pi/(BW_theta));
    % store the 16 permutations of the parameters in permut
    permut = [x1 y1 s1 t1; x1 y1 s1 t2; x1 y1 s2 t1; x1 y1 s2 t2; ...
     x1 y2 s1 t1; x1 y2 s1 t2; x1 y2 s2 t1; x1 y2 s2 t2; ...
x2 y1 s1 t1; x2 y1 s1 t2; x2 y1 s2 t1; x2 y1 s2 t2; ...
x2 y2 s1 t1; x2 y2 s1 t2; x2 y2 s2 t1; x2 y2 s2 t2];
    assert(size(permut,1) == 16);

    %compute hash index
    for j = 1: 16
        ind = get_hash_ind( permut(j,:), 30, 4, 12);

        % stores all distinct indices
        if(isempty(distinct_indices(distinct_indices == ind)))
            distinct_indices = [distinct_indices ind];
        end
        % store indices of match is stored in the hash table
        if(hashtable.containsKey(ind))
            info = hashtable.get(ind);
            info = [info; i];
            hashtable.put(ind, info);
        else
            store=i;
            hashtable.put(ind, store);
        end

        retrieve_info = hashtable.get(ind);
        current_bin_count = size(retrieve_info, 1);
        if current_bin_count > bestcount
            bestcount = current_bin_count;
            winning_bin = ind;
        end
    end
end

%==============================clustering section==========================

% X, Y, S, T store the mean (x,y) location, scale, and orientation
% of the keypoints found in each bin. Tx and Ty represent the orientation
% on the unit circle. allX and allY store all the (x,y) points that were
% mapped to the test image. This is just used for convenience to see where
% all the keypoints mapped to (plotted in figure 4).
X=[];
Y=[];
S=[];
T=[];
Tx=[];
Ty=[];
allX=[];
allY=[];
firsthasmatch = 1; %assume there is a match, this is just a flag

%check if there were any matches to begin with
if bestcount ~= 0

    % store size of each bin in vec
    vec=[];
    for k=1:size(distinct_indices,2)
        vec(k) = size(hashtable.get(distinct_indices(k)),1);
    end
    %sort descending order into sorted_bin_sizes
    %sorted_bin_sizes_ind stores the index of the corresponding bin in the
    %hash table
    [sorted_bin_sizes sorted_bin_sizes_ind]=sort(vec,2,'descend');

    % take the top 30 bins, used for clustering. NBin is the nth bin
    for NBin=1:min(size(distinct_indices,2), 30)
```

```
if (size(sorted_bin_sizes,1) ~= 0) && (size(sorted_bin_sizes_ind, 1) ~= 0)
    winning_bin = distinct_indices(sorted_bin_sizes_ind(NBin));
end

use = unique(hashtable.get(winning_bin));
size_t = size(use,1);

%reset variables used for affine fitting
test_uv = [];
model_xy = [];

% store all the test and model frame parameters
for i=1:size_t
    testind = my_matches(1, use(i));
    modelind = my_matches(2, use(i));

    test_uv = [test_uv frames_test(:, testind)];
    model_xy = [model_xy frames_model(:, modelind)];
end

model_xy = model_xy(1:2,:)'; % only take the x and y values
test_uv = test_uv(1:2,:)'; % only take the x and y values
affine = zeros(size_t*2, 6);
affine(int32(1:2:size_t*2),:) = [model_xy zeros(size_t, 2) repmat([1 0], size_t, 1)];
affine(int32(2:2:size_t*2),:) = [zeros(size_t, 2) model_xy repmat([0 1], size_t, 1)];
b = reshape(test_uv',size_t*2,1);

m = pinv(affine)*b;

%if m does not contain any NaN
if max(isnan(m)) ~= 1
    %check to see where the keypoints mapped to on the test image
    first = [m(1) m(2) m(5); m(3) m(4) m(6); 0 0 1];
    %the last column is for the midpoint of model
    %remove duplicates
    model_xy = unique(model_xy, 'rows');
    sec = model_xy';
    sec = [sec [size(model,2)/2; size(model,1)/2]]; %point for the center
    sec(3,:) = ones(1, size(model_xy,1)+1); %row of ones
    checked = first*sec;


    %if there are more than 3 distinct keypoints to be mapped
    if( size(sec,2) - 1 >= 3)
        %only plot the first bin, can change this if you want to
        %see all 30 bins
        if NBin == 1
            figure(3); clf;
            subplot(1,2,1); imshow(cell, [0 255]); hold on;
            subplot(1,2,2); imshow(model, [0 255]); hold on;
            subplot(1,2,1); plot( checked(1,1:end-1), checked(2,1:end-1), 'ro')
            subplot(1,2,2); plot( sec(1,1:end-1), sec(2,1:end-1), 'ro');
            subplot(1,2,1); plot( checked(1,end), checked(2,end), 'gs')
            subplot(1,2,2); plot( sec(1,end), sec(2,end), 'gs')
        end

        allX=[allX checked(1,1:end-1)];
        allY=[allY checked(2,1:end-1)];
        X=[X checked(1,end)];
        Y=[Y checked(2,end)];

        tempScale=[];
        for a = 1:size(sec,2) - 1 %don't want to include the midpoint
            ss = norm(sec(1:2, a) - sec(1:2, end))/norm(checked(1:2, a)
             - checked(1:2, end));
            if ~isnan(ss)
                tempScale=[tempScale ss];
            end
        end

        tempTheta=[];
        for a = 1:size(sec,2) - 1 %don't want the midpoint that was added
            tt = atan2(checked(2, a) - checked(2, end), checked(1, a) - ...
            checked(1, end)) - atan2(sec(2, a) - sec(2, end), sec(1, a) ...
            - sec(1, end));
            if ~isnan(tt)
                while tt < 0
                    tt = tt + 2*pi;
                end
                tempTheta=[tempTheta tt];
            end
        end

        if(size(tempScale,1) ~= 0 && size(tempTheta,1) ~= 0)
            S=[S mean(tempScale)];
            T=[T mean(tempTheta)];
        end

        %display answer only for the first bin
        if NBin == 1
            disp('==============================');
            disp([model_name ' located at approximately (' ...
                num2str(checked(1,end)) ',' ...
                num2str(checked(1,end)) ')']);
            disp(['scale: ' num2str(mean(tempScale)) ' times the model']);
            disp(['orientation: ' num2str(mean(tempTheta)) ' radians']);
        end
    else
        if NBin == 1
            disp('==============================');
            figure(3); clf;
            subplot(1,2,1); imshow(cell, [0 255]); hold on;
```

```
                    subplot(1,2,2); imshow(model, [0 255]); hold on;
                    disp(['no matches for ' model_name]);
                    subplot(1,2,1);
                    imshow(nomatch, [0 255]);
                    firsthasmatch = 0;
                end
            end
        end
    end

    if firsthasmatch ==1
        %now want to plot the theta values on the unit circle
        %take the remainder after division by 2*pi, shouldn't have any
        %values over 2*pi, but do this as a safety check
        T = rem(T(1,1:end), 2*pi);
        Tx = cos(T(1,1:end));
        Ty = sin(T(1,1:end));

        figure(4); clf;
        imshow(cell, [0 255]); hold on;
        plot(allX, allY, 'go')

        cluster([X' Y' S' Tx' Ty'], cell);
    end
    pause(5);
else
    figure(3); clf;
    subplot(1,2,1); imshow(cell, [0 255]); hold on;
    subplot(1,2,2); imshow(model, [0 255]); hold on;
    disp('no matches!');
    subplot(1,2,1);
    imshow(nomatch, [0 255]);

end
end % function

% returns serialized index
function [hash_ind] = get_hash_ind( vect, num_bins_y, num_bins_scale, num_bins_theta)
hash_ind = vect(1)*num_bins_y*num_bins_scale*num_bins_theta + ...
    vect(2)*num_bins_scale*num_bins_theta + vect(3)*num_bins_theta+vect(4);
end
```

Appendix C - Cluster.m

```
function [ output_args ] = clust(X, cell)
% this function calls Matlab's subclust() function, which is a subtractive
% clustering technique, plots a graph of the x and y radii threshold versus
% the number of clusters found

%if there are unreasonably large values or if there are negative
%x and y values, remove them
X = X( ~any(X(:,1:2)>500, 2), :);
X = X( ~any(X(:,1:2)<0, 2), :);

howmany = 100; % cap the number of times subclust is called
% used to plot the x and y radii versus the number of clusters found
clust_radii = [];
Xbounds = [0 0 0 -1 -1; 500 500 5 1 1];
num_pixels = 0.01;
incr = 10;
c=1;
for i=1:howmany
    xy_radii = num_pixels/Xbounds(2,1);
    if xy_radii  > 0 && xy_radii <= 1
        [C S] = subclust(X, [xy_radii xy_radii 0.4 0.3 0.3], Xbounds);
        clust_radii=[clust_radii [xy_radii; size(C, 1)]];
        c = c + 1;
    end
    num_pixels = num_pixels + incr;
end

% plot the clusters from the last subclust() call because
% this usually gives the fewest number of clusters (after
% analyzing all the graphs
figure(5); clf;
imshow(cell, [0 255]); hold on;
plot(C(:,1), C(:,2), 'go');
% print out where the clusters are located
disp('There are clusters located at (format: [a b c d e]):');
disp(C);
fprintf('where a and b represent the x-y location, c represents \n...
the relative scale from the model to the test image, \nand...
d and e represent the angle on a unit circle. \n(cos(theta), sin(theta)) = (d,e)\n');

figure(6);clf;hold on;
plot(clust_radii(1,:), clust_radii(2,:), 'r*-');
xlabel('x and y radii threshold');
ylabel('number of clusters');
end
```

Appendix D - Plot_thresholds.m

```
function [ output_args ] = plot_thresholds( test_desc, model_desc )
% plot the thresholds to find out what threshold value results
% in the greatest number of matches

howmany = 100;
edge_thres=zeros(2, howmany);
temp = 0;
for m=1:howmany
    matches = siftmatch(test_desc, model_desc, temp);
    edge_thres(1, m) = temp;
    edge_thres(2, m) = size(matches,2);
    temp = temp + 0.1;
end

figure(2); clf; hold on;
plot(edge_thres(1,:), edge_thres(2,:), 'r*-');
xlabel('siftmatch threshold');
ylabel('number of matches');
end
```