

Pattern Recognition Assignment 1

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Question 1

Part A

```
1 close all
2 clear all
3 clc
4
5 % 1 A
6 N = 10; % used throughout the script
7 % Generate distinct random points
8 r = randperm(25);
9 [x y] = ind2sub([5,5], r(1:N));
10 z = [x' y'];
11 figure
12 hold on
13 % have to increase marker size as it is
14 plot(z(:,1), z(:,2), 'k.', 'markersize', 30);
15 text(z(:,1) + 0.1, z(:,2) + 0.1, num2cell(1:N));
```

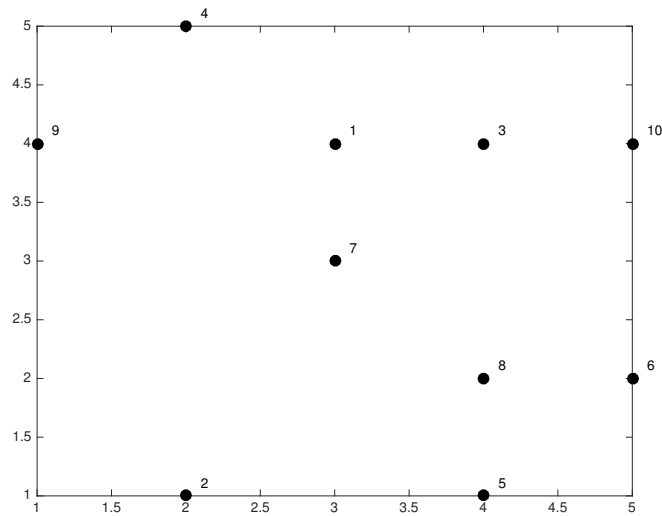


Figure 1: Random plots generated by Question 1 part A

Part B

```

1 % use repmat to create a matrix which contains the objects
2 % repeated in order
3 % use repelem to create a matrix containing the objects repeated
4 % in groups
5 % calculate distances between the matrices
6 % reshape the resulting vector to form an NxN matrix
7 d=reshape(sum((repmat(z,N,1)'-repelem(z,N,1)).^2),N,N);

```

Output

1	0	10	1	2	10	8	1	5	4	4
2	10	0	13	16	4	10	5	5	10	18
3	1	13	0	5	9	5	2	4	9	1
4	2	16	5	0	20	18	5	13	2	10
5	10	4	9	20	0	2	5	1	18	10
6	8	10	5	18	2	0	5	1	20	4
7	1	5	2	5	5	5	0	2	5	5
8	5	5	4	13	1	1	2	0	13	5
9	4	10	9	2	18	20	5	13	0	16
10	4	18	1	10	10	4	5	5	16	0

Part C

```

1 % Apply kruskals minimum spanning tree to the dataset and plot
2 % the clusters on the figure as coloured rings around the data
3 % values
4 a = kruskals_mst_with_comments(z, 3);
5 plot(z(a==1,1), z(a==1,2), 'ro', 'markersize', 10, 'linewidth', 10);
6 plot(z(a==2,1), z(a==2,2), 'go', 'markersize', 10, 'linewidth', 10);
7 plot(z(a==3,1), z(a==3,2), 'bo', 'markersize', 10, 'linewidth', 10);

```

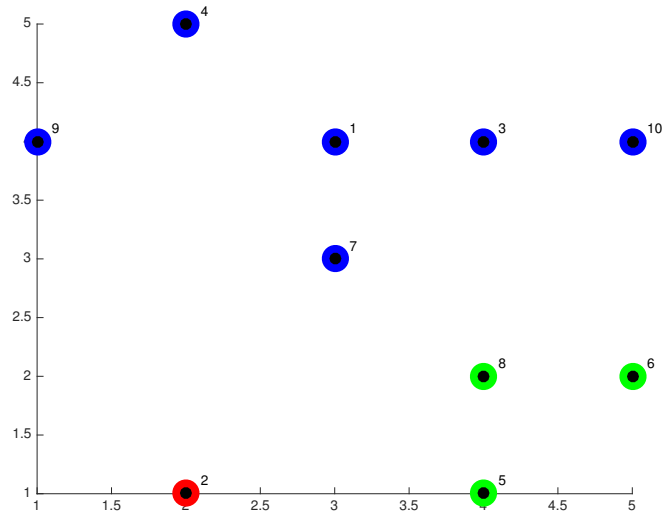


Figure 2: Clustered points

Part D

Kruskals Minimum Spanning Tree with Step Return

```
1 function [a, steps] = kruskals_mst_with_steps(b,c)
2 d = size(b,1);
3 e = nchoosek(1:d,2);
4 f = b(e(:,1),:) - b(e(:,2),:);
5 [~,g] = sort(sum(f.*f,2));
6 e = e(g,:);
7 % sort weights
8 f = sort(sum(f.*f,2));
9 % set the size of steps we will use the d+1 column to store the jump
10 steps = zeros(d, d+1);
11 a = 1:d;
12 i = 1;
13 % J will hold the jump length
14 J = 0;
15 p = 0;
16 while numel(unique(a)) > c
17     if a(e(1,1)) ~ a(e(1,2))
18         steps(i, :) = [a J];
19         a(a==a(e(1,1))) = a(e(1,2));
20         J = sqrt(f(1,:).^2);
21         i = i+1;
22         f(1,:) = []; % remove the shortest distance after use
23     end
24
25
26     e(1,:) = []; % remove the shortest edge after use
27 end
28 steps(i+1, :) = [a J]; % last step
29 steps(all(steps==0,2),:) = []; % remove rows of zeros
30 a = cmunique(a) + 1;
```

Using the above function we now output the steps to the console

```
1 % get the clusters and the steps from the new function
2 [a, steps] = kruskals_mst_with_steps(z, 3);
3 [N, n] = size(steps);
4 index = 1 : n - 1; % minus 1 as the last column is the Jump
5 % loop over the steps returned
6 for i = 1 : N
7     % get step array and Jump size
8     [x J] = deal(steps(i,1:10), steps(i,11));
9     u = unique(x);
10    % use arrayfun to build a cell array of the values in the clusters
11    line = arrayfun(@(a) sprintf('%s', sprintf('%d', index(x==a))), ...
12        u, 'uniformoutput', 0);
13    % print the current step
14    fprintf('Step %3i J = %3i, #Cl %3i: ( %s)\n', ...
15        i, J, numel(u), strjoin(line, ' ') ( ' '));
16 end
```

Output

```
1 Step 1 J = 0, #Cl 10: ( 1 ) ( 2 ) ( 3 ) ( 4 ) ( 5 ) ( 6 ) ( 7 ) ( 8 ) ( 9 ) ( 10 )
2 Step 2 J = 1, #Cl 9: ( 2 ) ( 1 3 ) ( 4 ) ( 5 ) ( 6 ) ( 7 ) ( 8 ) ( 9 ) ( 10 )
3 Step 3 J = 1, #Cl 8: ( 2 ) ( 4 ) ( 5 ) ( 6 ) ( 1 3 7 ) ( 8 ) ( 9 ) ( 10 )
4 Step 4 J = 1, #Cl 7: ( 2 ) ( 4 ) ( 5 ) ( 6 ) ( 8 ) ( 9 ) ( 1 3 7 10 )
5 Step 5 J = 1, #Cl 6: ( 2 ) ( 4 ) ( 6 ) ( 5 8 ) ( 9 ) ( 1 3 7 10 )
6 Step 6 J = 1, #Cl 5: ( 2 ) ( 4 ) ( 5 6 8 ) ( 9 ) ( 1 3 7 10 )
7 Step 7 J = 2, #Cl 4: ( 2 ) ( 1 3 4 7 10 ) ( 5 6 8 ) ( 9 )
8 Step 8 J = 2, #Cl 3: ( 2 ) ( 5 6 8 ) ( 1 3 4 7 9 10 )
```

Part E

```
1 % get the step before the largest jump
2 % rerun function but get all steps back
3 [a, steps] = kruskals_mst_with_steps(z, 1)
4 % sort the differences between the criterion values (must assign a 0
5 % column to get the first difference of 0)
6 [d, i] = sort(diff( [0 steps(:,11) ]));
7 % get the index of the largest jump with fewest clusters
8 S = i(end) - 1;
9
10 % get step array and Jump size
11 [x, J] = deal(steps(S,1:10), steps(S,11));
12 u = unique(x);
13 % use array fun to build a cell array of the values in the clusters
14 line = arrayfun(@(a) sprintf('%s', sprintf('%d ', index(x==a))), ...
15     u, 'uniformoutput', 0);
16 % print the current step
17 fprintf('Suggested Clustering:\nStep %3i J = %3i, #Cl %3i: ( %s)\n', ...
18     S, J, numel(u), strjoin(line, ' ) ( '));
```

Output

```
1 Suggested Clustering
2 Step 6 J = 1, #Cl 5: ( 2 ) ( 4 ) ( 5 6 8 ) ( 9 ) ( 1 3 7 10 )
```

Question 2

Part A

```
1 % functions to generate data and labels
2 f = @(x) randn(400,2) * randi(6) - 3;
3 l = @(a) ones(400,1) + a;
4 Z = [f(); f(); f(); f(); f()];
5 labs = [l(-1); l(0); l(1); l(2); l(3)];
6 figure
7 hold on
8 % plot data outlined
9 arrayfun(@(a) plot(Z(labs==a,1), Z(labs==a,2), '.', ...
10     'color', rand(1,3), 'markersize', 20), 0:4)
```

Output

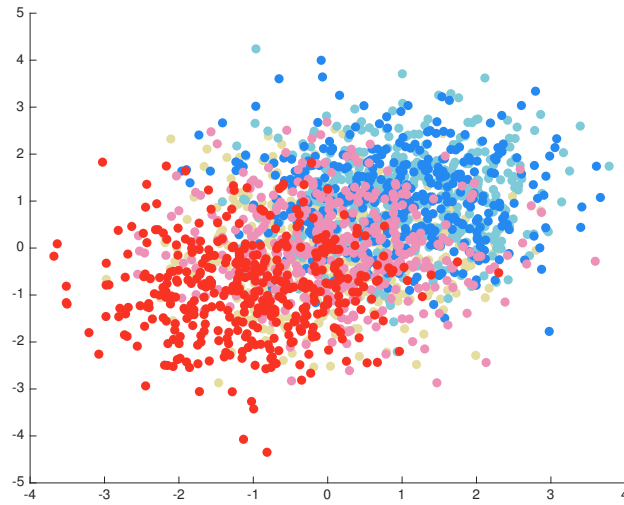


Figure 3: Data plotted from 2A

Part B

```

1 figure
2 for i = 2:7
3     c = kmeans_cg(Z, i);
4     subplot(2, 3, i-1), hold on, axis square off;
5     % Draw subplots
6     arrayfun(@(a) plot(Z(c==a,1), Z(c==a,2), '. ', ...
7         'color', rand(1,3), 'markersize', 20), 1:i)
8     title(i);
9 end

```

Output

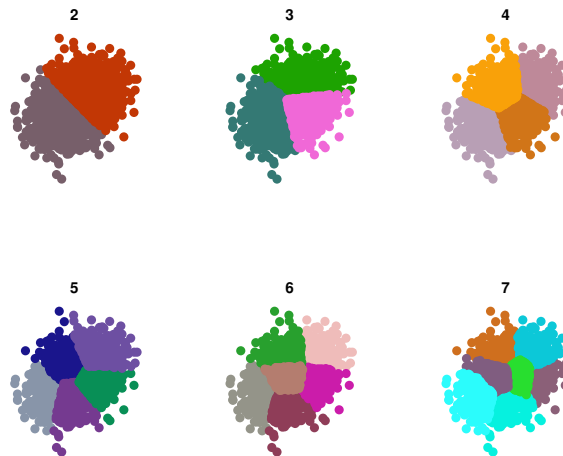


Figure 4: Clustered forms of data from 2a

Question 3

Part A

```
1 close all
2 clear all
3 clc
4
5 load('Example_MNIST_digits.mat');
6 D38 = b(labb==4 | labb==9, :);
7 % we are interested in 3 and 8 so minus one off labels to make for
8 % clearer code
9 l = labb(labb==4 | labb==9) - 1;
```

Part B

```
1 % we are doing 1 dimensional distance so only need the absolute
2 % distance between the means
3 d = abs(mean(D38(l==3,:))-mean(D38(l==8,:)));
4 % sort in descending order
5 [J, i] = sort(d, 'descend');
6 fprintf('Feature\t\tJ\n=====\t\t===\n');
7 fprintf('%i\t\t%.2f \n', [i(1: 10)' J(1: 10)']');
```

Output

```
1 Feature    J
2 =====
3 488        149.10
4 489        148.48
5 462        141.63
6 461        139.66
7 516        138.49
8 515        130.65
9 490        122.05
10 463        119.22
11 517        117.49
12 487        117.24
```

Part C

```
1 figure, hold on, axis square off, colormap jet
2 imagesc(reshape(d,28,28));
```

Output

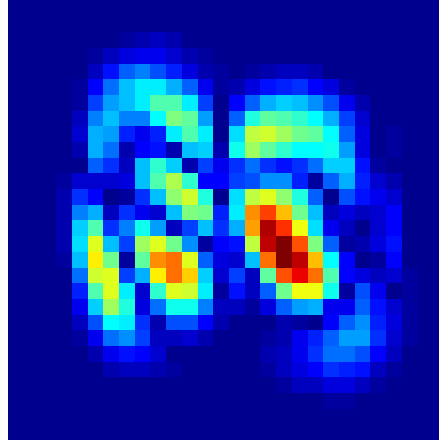


Figure 5: Image representation of criterion values

Part D

```
1 badF = sum(d==0)
2 figure
3 % flip the data set so that the 0's are at the beginning
4 % this will allow for better visualisation of 0s
5 plot(fliplr(J), '-','linewidth', 5);
6 D38_clean = D38(:, d~=0);
```

Output

```
1 badF =
2     235
```

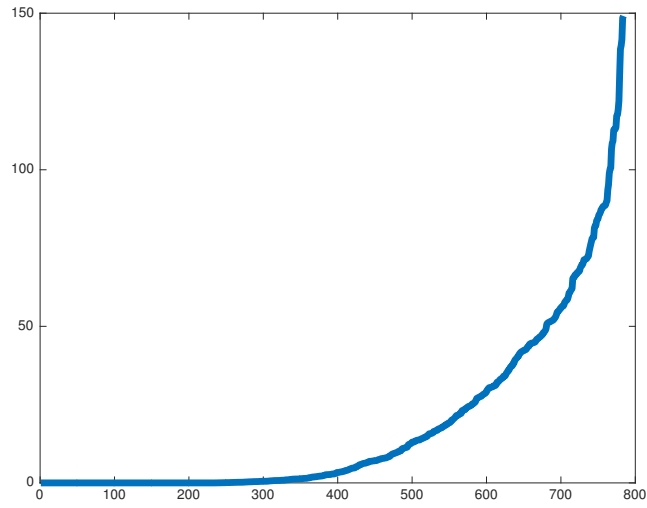


Figure 6: Plot of J values

Part E

```

1 [~,pc] = pca(D38_clean);
2 figure, hold on, axis square
3 plot(pc(l==3,1), pc(l==3,2), 'k.', 'markersize', 20);
4 plot(pc(l==8,1), pc(l==8,2), 'r.', 'markersize', 20);
5 legend('Digit 3', 'Digit 8');

```

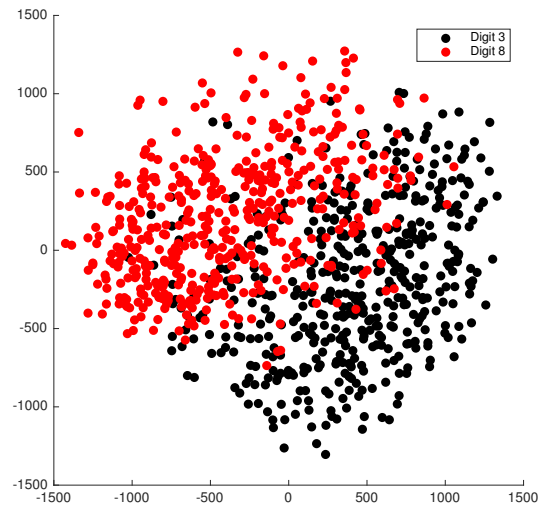


Figure 7: Plot of first two PC

Part F

```
1 % index for the top 8 features
2 ind = i(1: 8);
3 rE1 = 1 - mean(1 == MyNMC(D38(:, ind), 1, D38(:, ind)))
4 rE2 = 1 - mean(1 == MyNMC(pc(:, 1:8), 1, pc(:, 1:8)))
```

Output

```
1 rE1 =
2     0.1421
3 rE2 =
4     0.1285
```

The resubstitution errors between these two feature representations is very similar. In this case, selecting the top 8 features gives a marginally better result. Increasing the number of features selected continues the trend but closes the gap, for example. If we select the top 16 features and take the first 16 components our results are:

```
1 rE1 =
2     0.1181
3 rE2 =
4     0.1202
```

When we reduce the number to 4 there is still marginal difference between the two methods but PC performs better.

```
1 rE1 =
2     0.1755
3 rE2 =
4     0.1526
```

Principal component analysis analyses the variance between features and returns the highest to lowest in terms of this variance. For our 2D dataset the variance between features is the distance between them so our univariant feature selection is essentially applying the same method for ranking features which leads to the very similar outputs.

Question 4

```
1 function w = perceptron(d,l,epochs,E)
2     m = [min(d(:,1)) max(d(:,1))];
3     figure, hold on, axis square
4     axis([m(1) m(2) min(d(:,2)) max(d(:,2))])
5     u = unique(1);
6     % Get sizes of dataset
7     [p, q] = size(d);
8     % initialise weights with small random numbers
9     w = rand(q+1,1);
10    errors = 1;
11    count = 0;
12    % infinite loop
13    % while q*q'
14    % could use rand(1,3) but similar colors make it hard to read
15    c = [1 0 0; 0 1 0];
16    while errors > 0 && count < epochs
17        errors = 0;
18        count = count + 1;
19        % loop over objects
20        for i = 1:p
21            % get input for the perceptron including the bias
22            z = [1 d(i,:)];
23            % get output value which is the product of the inputs and
24            % the weights less than 0 (will return 1 or 0 (T or F))
25            v = z * w < 0;
26            % q(i) will be 1 or 0 depending on whether v is the same as l(i)
27            q(i) = v==l(i);
28            errors = ~q(i);
```

```

29         if errors
30             % adjust weights according to the formula
31             w = w + ( 2 * v - 1 ) * E * z';
32             y1 = -(w(1) + w(2) * m(1)) / w(3);
33             y2 = -(w(1) + w(2) * m(2)) / w(3);
34             y = [y1 y2];
35             plot(m,y, 'k-');
36         end
37     end
38 end
39 end
40 % plot points
41 % find y's based on max and min x's
42 y1 = -(w(1) + w(2) * m(1)) / w(3);
43 y2 = -(w(1) + w(2) * m(2)) / w(3);
44 y = [y1 y2];
45 % plot the line
46 plot(m,y, 'b-', 'linewidth', 3);
47 % plot final line
48 for i = 1:numel(u)
49     plot(d(l==u(i),1), d(l==u(i), 2), '.', 'markersize', ...
50         30, 'color', c(i,:));
51 end

1 close all
2 clear all
3 clc
4 % create dataset
5 Z = randn(100,2);
6 % label according to random linear function
7 l = Z(:,1) > 0;
8
9 % Get the weights
10 w = perceptron(Z,l,0.1);
11 w = perceptron(Z,l,0.8);

```

Output

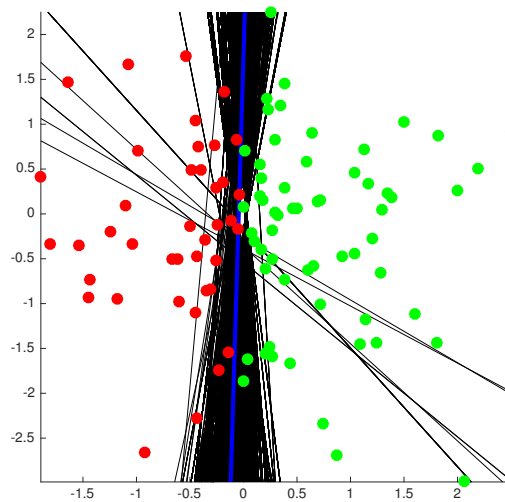


Figure 8: Perceptron Learning Rate 0.1

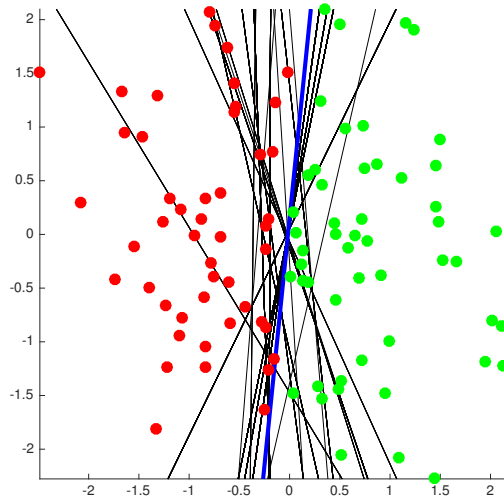


Figure 9: Perceptron Learning Rate 0.8

With a lower learning rate, the weights are updated in smaller increments. In the above case this has meant for much more iterations before converging, the higher learning rate required fewer iterations. However a higher learning rate means a larger movement in the boundary so. This large movement could ‘overshoot’ the required boundary and lead to more iterations.

As a further test both learning rates were tested 100 times and the epochs counted giving the following means as a result.

```

1 lowLR =
2   3.1100
3 highLR =
4   4.9000

```

While far from exhaustive, this test implies that a higher learning rate is less efficient than a smaller learning rate from this data.

Question 5

```

1 close all
2 clear all
3 clc
4
5 % lazy copy and paste from pdf
6 d = [0.84 0.55 0.08 -0.64;
7      0.49 0.61 0.70 0.51;
8      0.67 0.25 0.59 1.06;
9      0.92 0.50 0.18 0.51;
10     0.94 0.66 0.30 -0.35;
11     0.22 0.85 0.70 -1.49;
12     0.21 0.78 0.84 1.53;
13     0.81 0.92 0.44 -0.50;
14     0.10 0.44 0.07 0.58;
15     0.21 0.70 0.41 1.89;]';
16
17 % assign more meaningful variables to work with
18 c = d(1:2,:)';
19 s = d(3,:)';
20 w = d(4,:)';
21 b = 0.28;
22 N = 1000;
23 [x, y] = meshgrid(linspace(0,1,N));
24 % get all points as x y columns

```

```

25 ps = [x(:) y(:)];
26 n = zeros(size(ps,1),1);
27 for p = 1: size(ps,1)
28     % apply the rbf formula
29     % repeat the current point to a matrix the size of c
30     % minus c from the new point matrix
31     % elementwise square the result
32     % sum each square length along the second dimension
33     % devide each length by its counterpart in the 2 * squared sigma matrix
34     % get the exponent
35     node = exp(-sum(( repmat(ps(p,:), size(c,1), 1) - c).^2,2) ./ (2*s.^2));
36     % add all of the results together and add the bias. (bias should
37     % strictly be 1* b)
38     n(p) = sum(node .* w) + b;
39 end
40 % ij reverses the y axis so the image is plotted in image space
41 % rather than standard x and y space
42 figure, hold on, axis ij square off, colormap jet
43 imagesc(reshape(n, N, N));
44 % figure
45 % colormap jet
46 % surf(reshape(n, N, N), 'EdgeColor','none','LineStyle','none','FaceLighting','phong')
47 % rotate3d

```

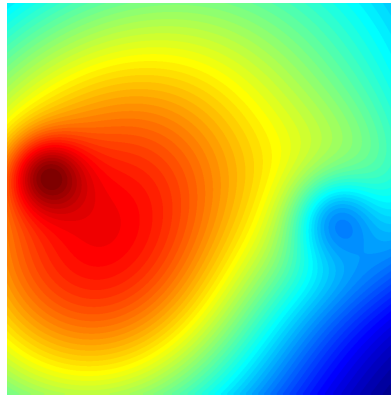


Figure 10: Visualised RBF Function

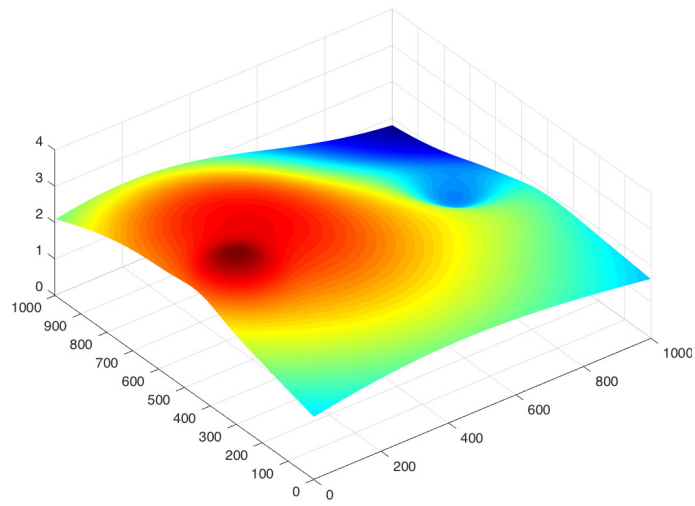


Figure 11: Visualised RBF Function Surface plot

Used a surface plot to further visualise the output of the function.