Pre-processing of 2-Lead ECG Data

```
close all
clear all
```

Load data

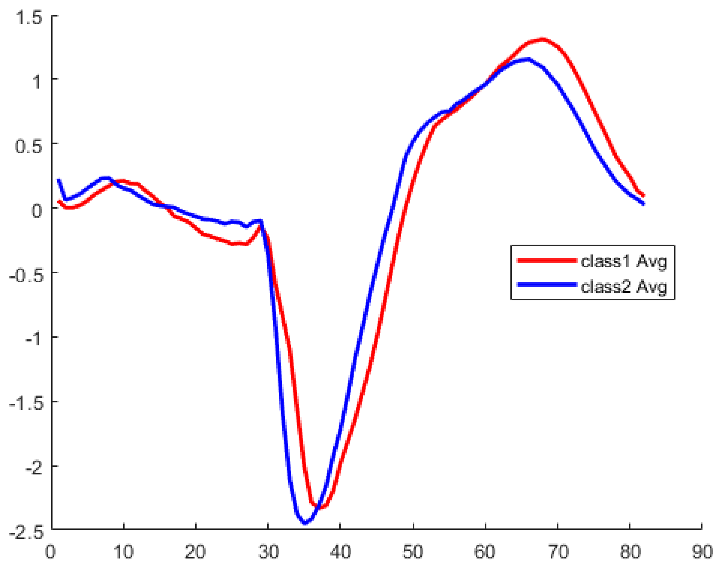
```
data_train = importdata("TwoLeadECG_TRAIN.txt");
data_train = sortrows(data_train);
data_test = importdata("TwoLeadECG_TEST.txt");
data_test = sortrows(data_test);
```

Separate labels and data

```
labels_train = data_train(:,1);
labels_train_dup = labels_train;
data_train(:,1)=[];

labels_test = data_test(:,1);
data_test(:,1)=[];
```

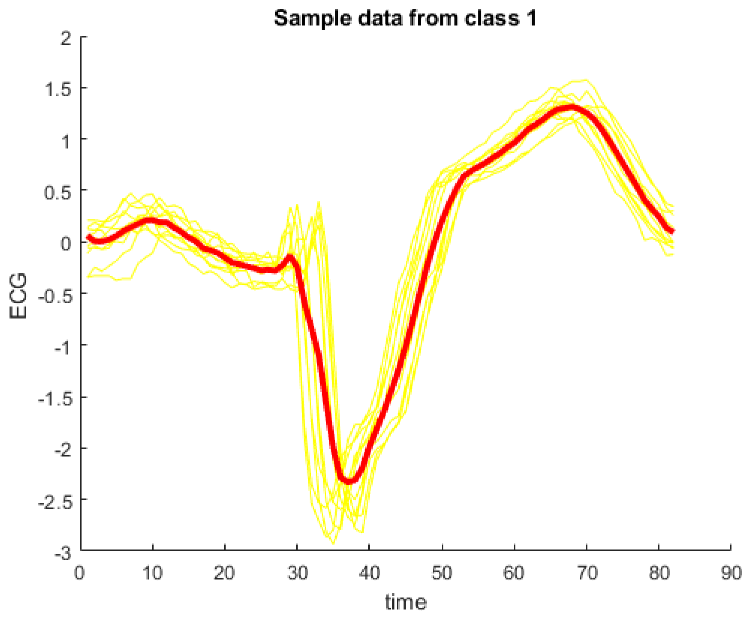
Visualise some sample ECG time series

```
timeArray=1:82;

avg_1 = mean(data_train(1:12,:),1);
avg_2 = mean(data_train(13:23,:),1);

figure
hold on
plot(timeArray,avg_1,'r-','LineWidth',2)
plot(timeArray,avg_2,'b-','LineWidth',2)
hold off
legend("class1 Avg","class2 Avg", 'Location','best')
```



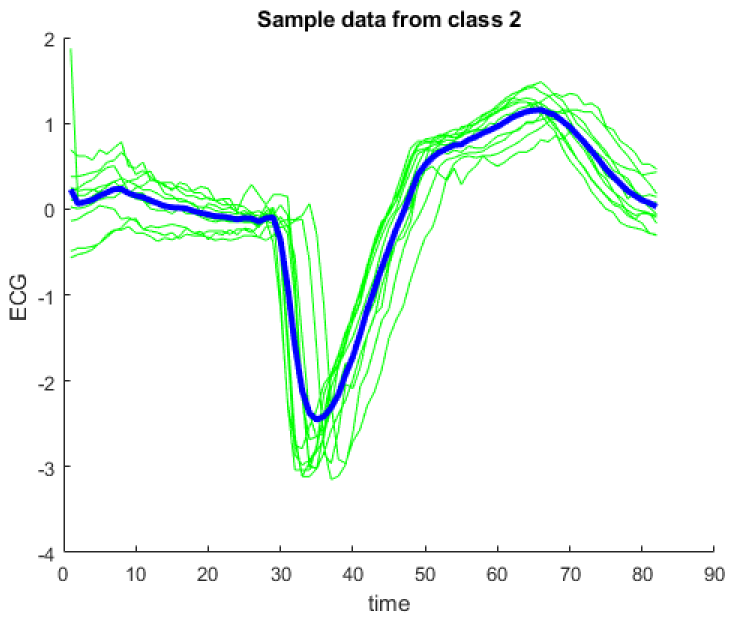
Visualise ECG Lead-1 in training dataset

```
figure
hold on
plot(timeArray,data_train((1:11),:),'y-', "LineWidth",0.1)
plot(timeArray,avg_1,'r-','LineWidth',3)
hold off
title("Sample data from class 1")
xlabel("time")
ylabel("ECG ")
```



Visualise ECG Lead-2 in training dataset

```
figure
hold on
plot(timeArray,data_train((13:23),:),'g-', "LineWidth",0.1)
plot(timeArray,avg_2,'b-','LineWidth',3)
hold off
title("Sample data from class 2")
xlabel("time")
ylabel("ECG ")
```

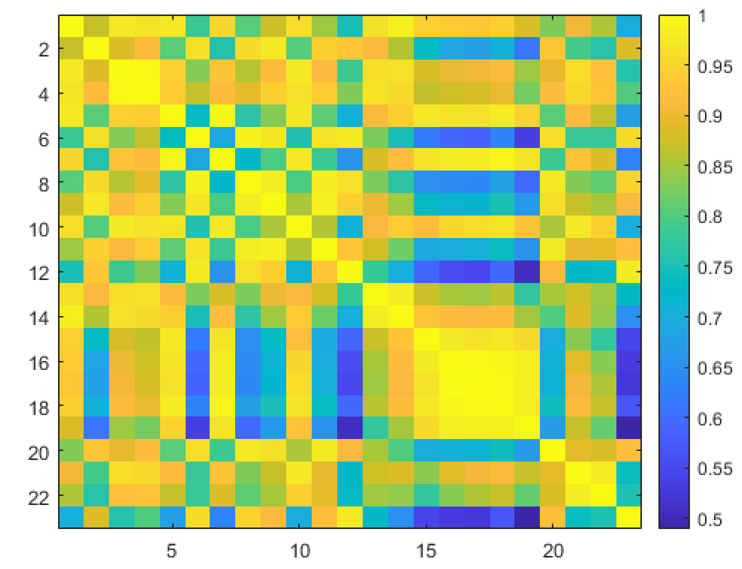


Correlation

```
corr_matrix_train = corr(data_train'); dup = corr_matrix_train;
corr_matrix_test = corr(data_test');
```

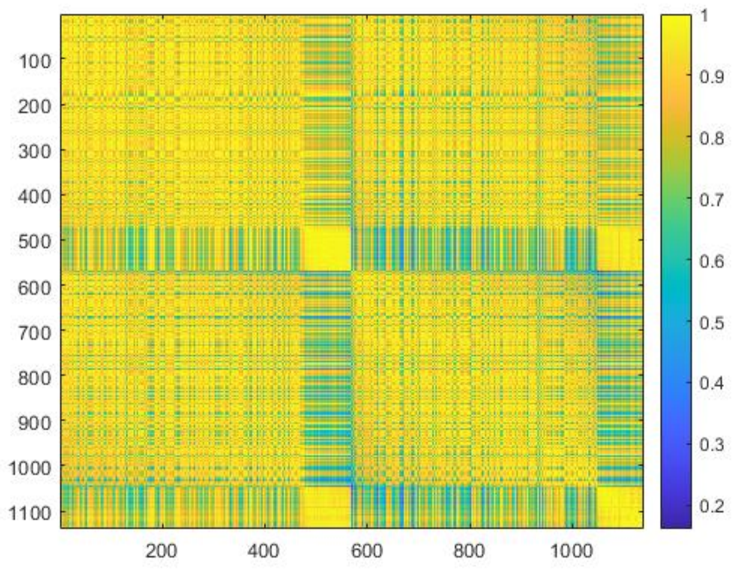
Colour map of un-thresholded test data

```
figure
imagesc(corr_matrix_train)
colorbar
```



Colour map of unthresholded training data

```
figure
imagesc(corr_matrix_test)
colorbar
```



Getting the threshold using modularity

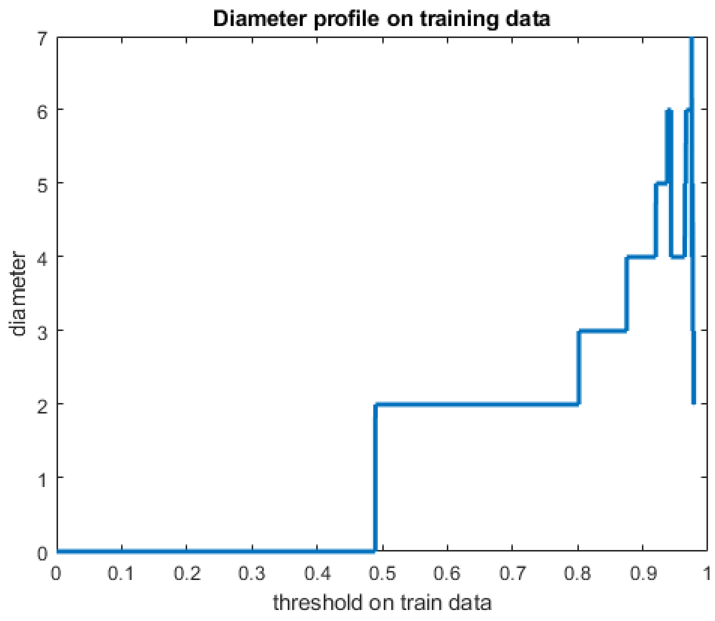
Plotting the modularity and diameter profile of the training data wrt threshold

```
th = 0:0.0001:0.98; diam =[]; Q = [];
```

```
for i = 1:length(th)
        dup = corr_matrix_train; % this is now our adj matrix
        dup = dup > th(i);
        diam = [diam, getDiameter(dup)];
        Q = [Q, getMod(dup, labels_train)];
end
```

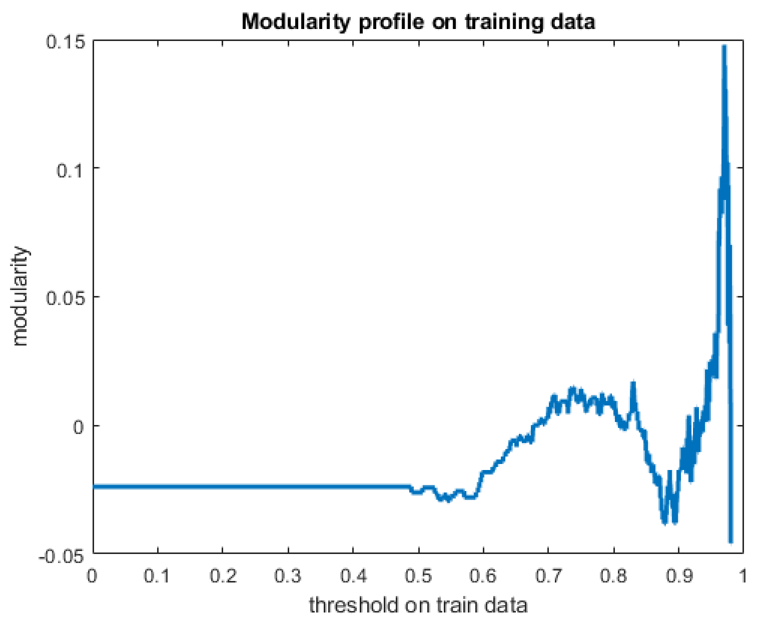
Diameter profile

```
figure
plot(th, diam, "LineWidth",2)
title('Diameter profile on training data')
xlabel('threshold on train data')
ylabel('diameter')
```



Modularity profile

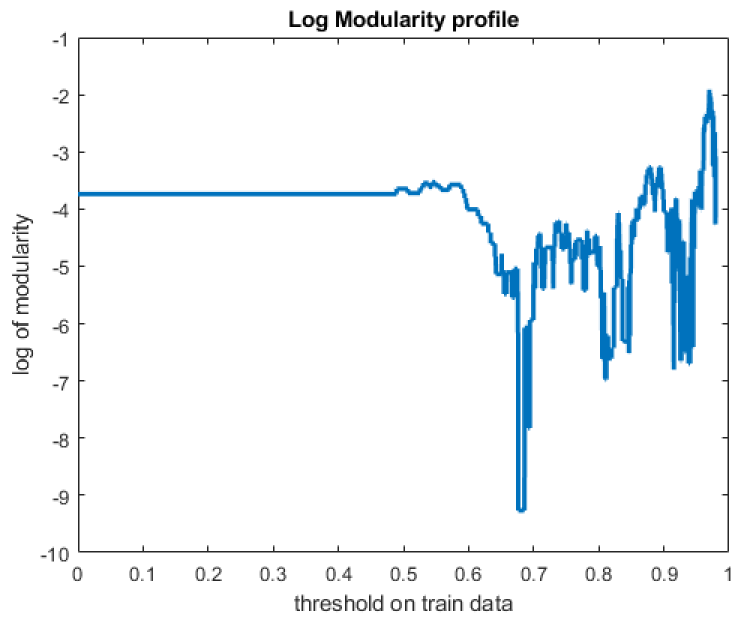
```
figure
plot(th,Q, "LineWidth",2)
title('Modularity profile on training data')
xlabel('threshold on train data')
ylabel('modularity')
```



```
figure
plot(th,log(Q), "LineWidth",2)
```

```
Warning: Imaginary parts of complex X and/or Y arguments ignored.
```

```
title('Log Modularity profile')
xlabel('threshold on train data')
ylabel('log of modularity')
```



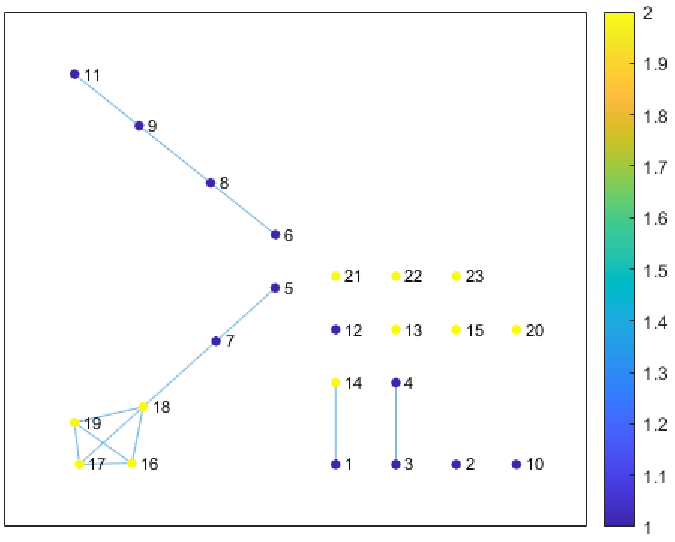
From the modularity profile as a function of the correlation threshold, we get some idea about how the modularity is changing with linear correlation coeff. **The threshold is set as the correlation coeff corresponding MAX of modularity**

```
threshold = min(th(find(Q==max(Q))))
```

```
threshold = 0.9697
```

Plot TRAIN data with the MAX modularity threshold

```
dup_train = corr_matrix_train > threshold;
G = graph(dup,'omitselfloops');

figure
plot(G,'NodeCData',labels_train)
colorbar
```



```
[~,binsize] = conncomp(G);
components = sort(binsize,"descend")
```

```
components = 1×13
      6       4       2       2       1       1       1       1       1       1       1       1
1
```

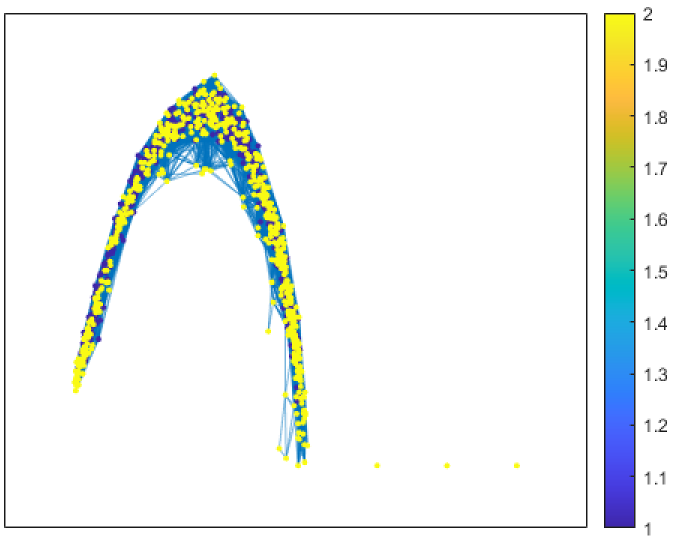
```
diam_train = getDiameter(dup_train)
```

```
diam_train = 6
```

We can see that there is very poor class separation on the training data with our modularity-based thresholding method. We are getting a lot more than two communities. It is expected that we should get two communities as this is a two-class problem.

Plot TEST data with the modularity threshold

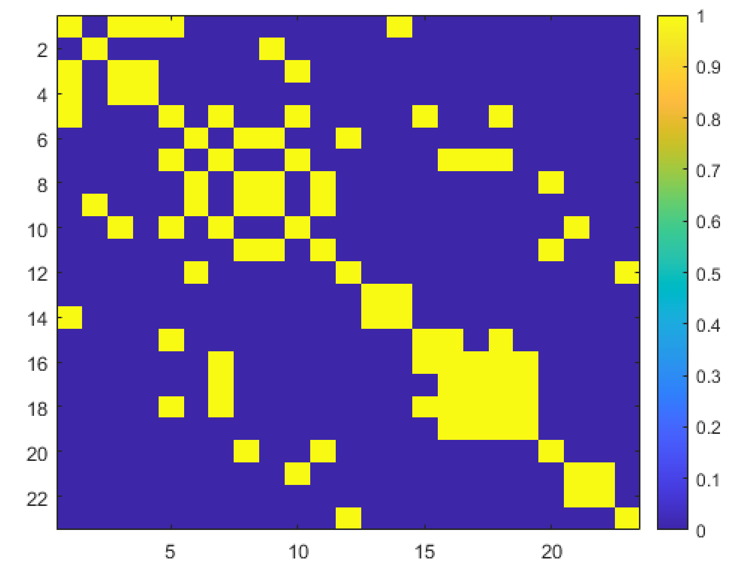
```
dup_test = corr_matrix_test > threshold;
Graph_test = graph(dup_test, 'omitselfloops');
figure
plot(Graph_test,'NodeCData',labels_test)
colorbar
```



Because of the bad thresholding from the training data, we failed to get good classification on our test data

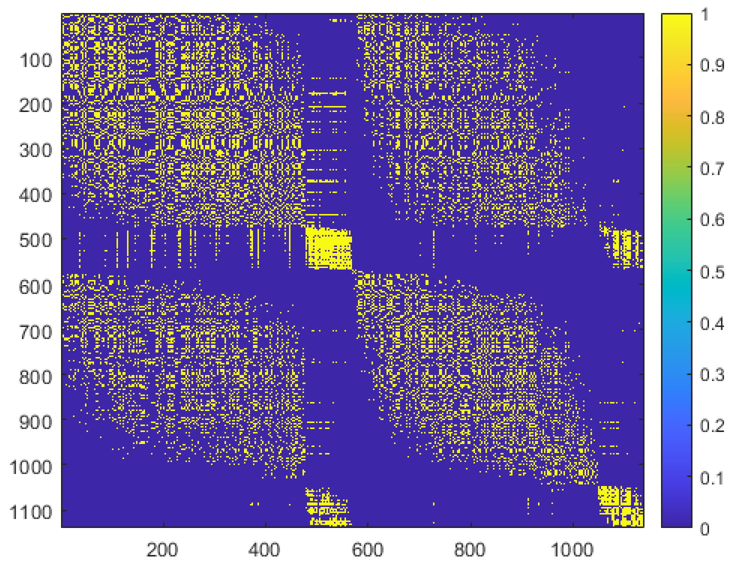
Colour map of TRAIN adj mat

```
figure
imagesc(dup_train)
colorbar
```



Colour map of TEST adj mat

```
figure
imagesc(dup_test)
colorbar
```



Another way to get a correlation threshold, is to break the loop when modularity reaches an acceptable value

The modularity value was set arbitrarily by looking at the modularity profile of training data

```
set_mod_thresh = 0.05
```

```
set_mod_thresh = 0.0500
```

We break the loop when the set modularity is achieved and take the corresponding correlation coeff as our threshold for the test corr matrix

```
for i = 1:length(th)
        dup = corr_matrix_train; % this is our adj matrix
        dup = dup > th(i);
        Q = [Q, getMod(dup, labels_test)];
        if Q(i)> set_mod_thresh
                thresh_value = th(i);
                break
        end
end
```

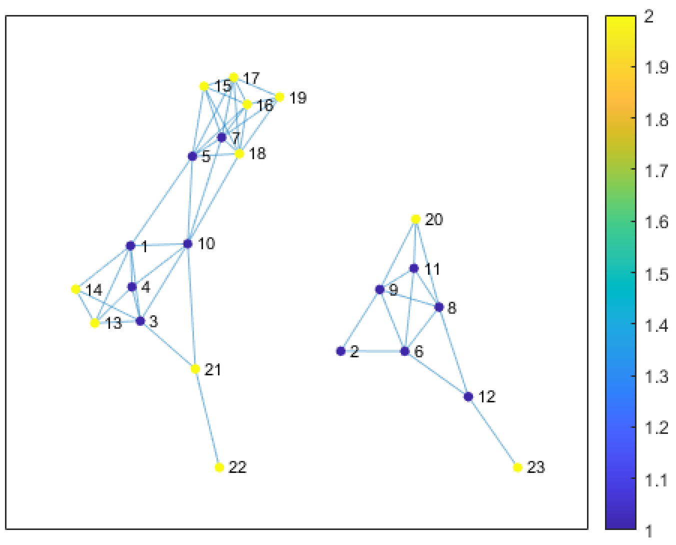
We thus obtain a threshold from our training data whuch can be used on the test data

```
threshold = thresh_value
```

```
threshold = 0.9611
```

Plot TRAIN data with the modularity threshold

```
dup_train = corr_matrix_train > threshold;
G = graph(dup,'omitselfloops');

figure
plot(G,'NodeCData',labels_train)
colorbar
```



```
[~,binsize] = conncomp(G);
components = sort(binsize,"descend")
```

```
components = 1×2
    15      8
```

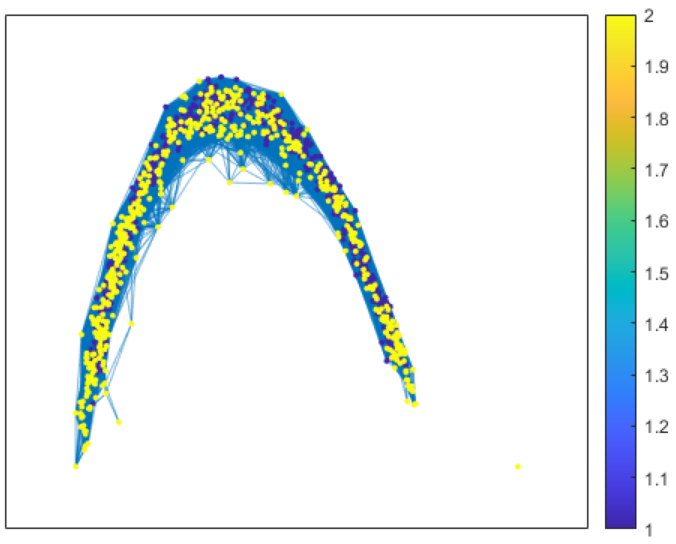
```
diam_train = getDiameter(dup_train)
```

```
diam_train = 4
```

We can see that there is very poor class separation on the training data with our modularity-based thresholding method. But we are getting two communities. It is expected that we should get two communities as this is a two-class problem. **Therefore, this method is better than the MAX modularity method.**

Plot TEST data with the modularity threshold

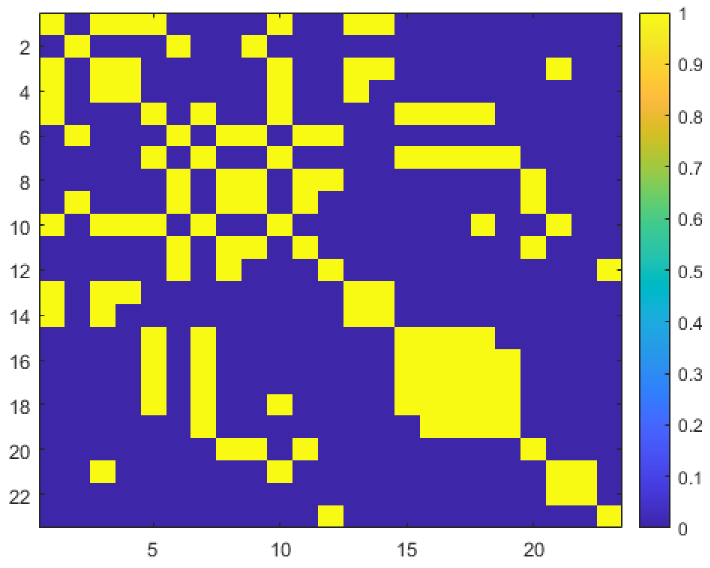
```
dup_test = corr_matrix_test > threshold;

Graph_test = graph(dup_test, 'omitselfloops');
figure
plot(Graph_test,'NodeCData',labels_test)
colorbar
```



Because of the bad thresholding from the training data, we failed to get good classification on our test data

Colour map of TRAIN adj mat

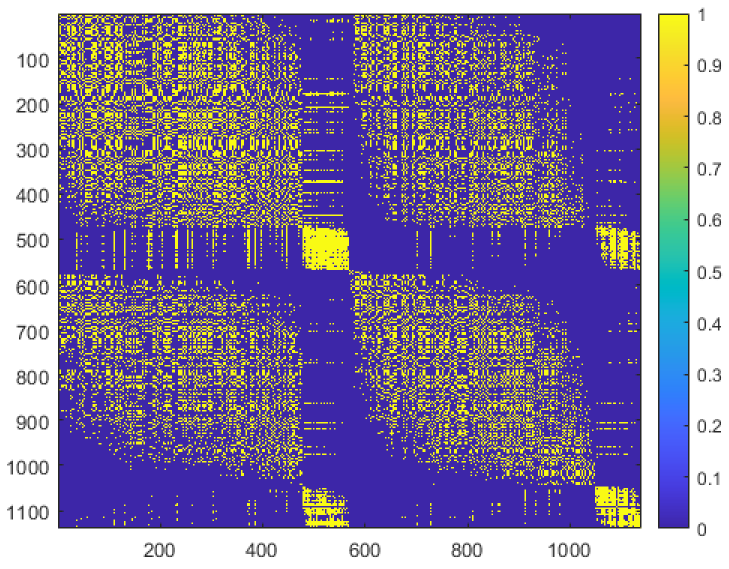
```
figure
imagesc(dup_train)
colorbar
```



Colour map of TEST adj mat

```
figure
```

```
imagesc(dup_test)
colorbar
```



Getting the threshold using connected components

```
threshold = 1;
dup = dup > threshold;
G = graph(dup,'omitselfloops');
[bin,binsize] = conncomp(G);
```

We run a loop until the number of communities is 2 i.e., two classes are separated. This is accomplished by checking the connected components.

```
while length(binsize) > 2
        dup = corr_matrix_train;
        dup = dup > threshold;
        G = graph(dup);
        [bin,binsize] = conncomp(G);
        threshold = threshold - 0.0001;
end
```

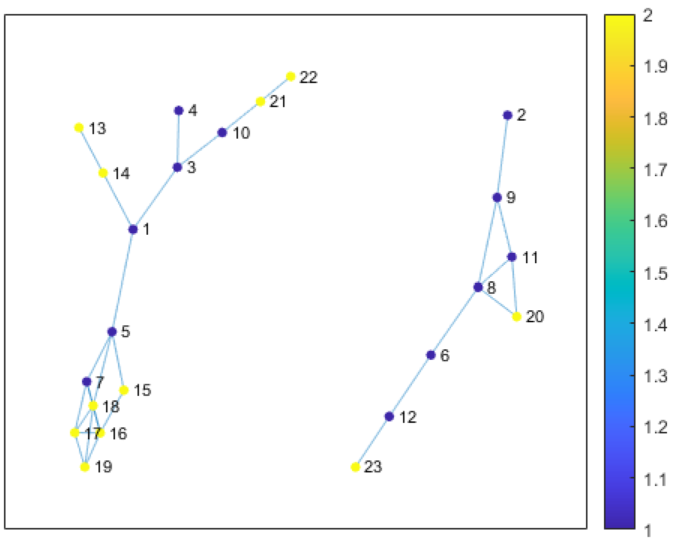
Plot TRAIN data with the threshold

```
threshold
```

```
threshold = 0.9749
```

```
dup_train = corr_matrix_train > threshold;
```

```
G = graph(dup_train,'omitselfloops');

figure
plot(G,'NodeCData',labels_train)
colorbar
```

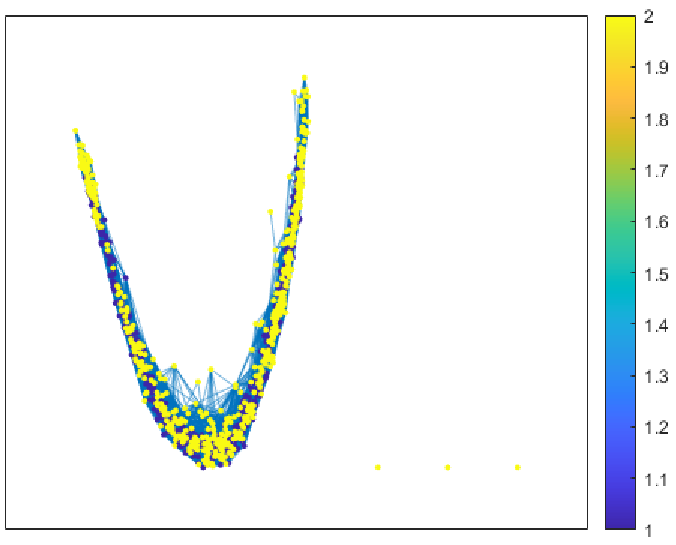


```
[bin,binsize] = conncomp(G);
components = sort(binsize,"descend")
```

```
components = 1×2
    15      8
```

Plot TEST data with same threshold

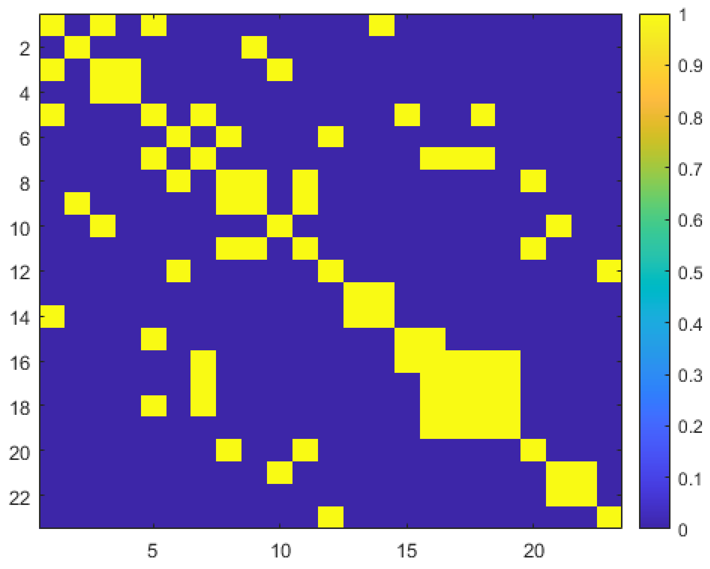
```
dup_test = corr_matrix_test > threshold;

Graph_test = graph(dup_test, 'omitselfloops');
figure
plot(Graph_test,'NodeCData',labels_test)
colorbar
```



This method yields similar results as the previous method of modularity-based thresholding with loop break. The threshold values are also comparable.

Colour map of test adj mat

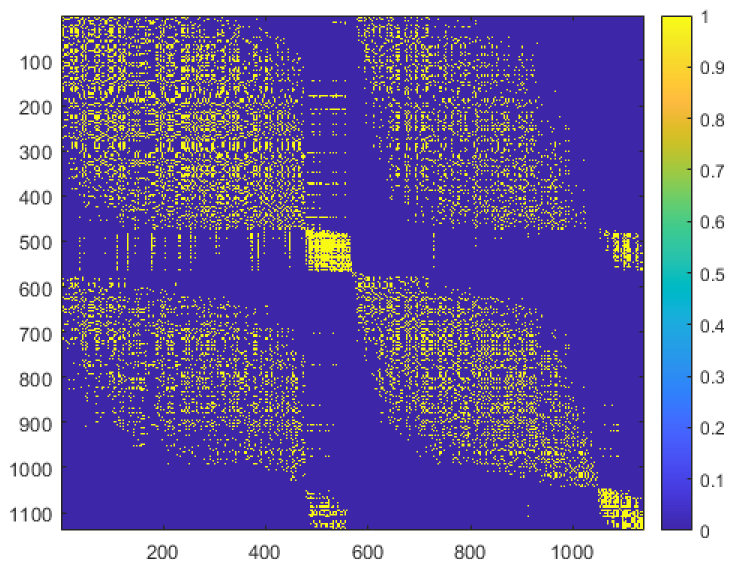
```
figure
imagesc(dup_train)
colorbar
```



Colour map of training adj mat

```
figure
```

```
imagesc(dup_test)
colorbar
```



Conclusions driven from network analysis-based classification

The network analysis could not give good classification of the data. We believe that this is the case because the using linear correlation coefficient and thresholding it might not be a good approach to determine the connectedness of the data. Using weighted correlation coefficients in which the class weights can be incorporated while finding the correlation may improve the classification efficiency.

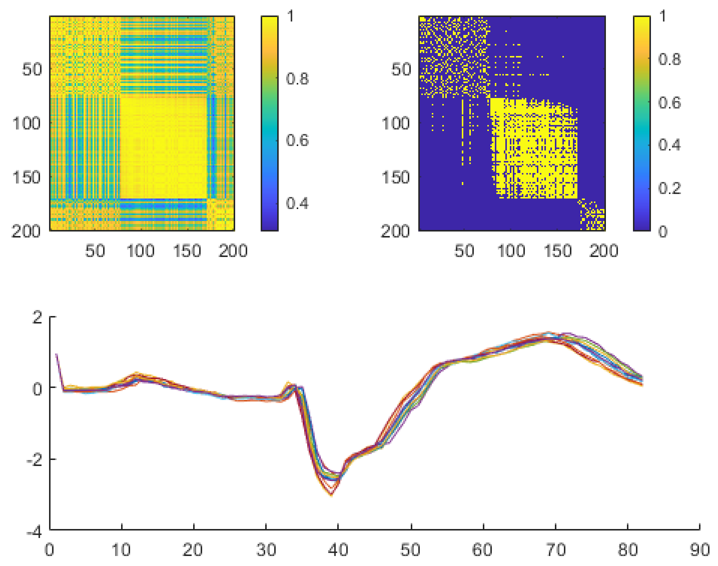
Identifying interesting features of the ECG data from clusters

```
data_test = importdata("TwoLeadECG_TEST.txt");
data = sortrows(data_test);
labels = data(:,1);
data(:,1)=[];
threshold
```

```
threshold = 0.9749
```

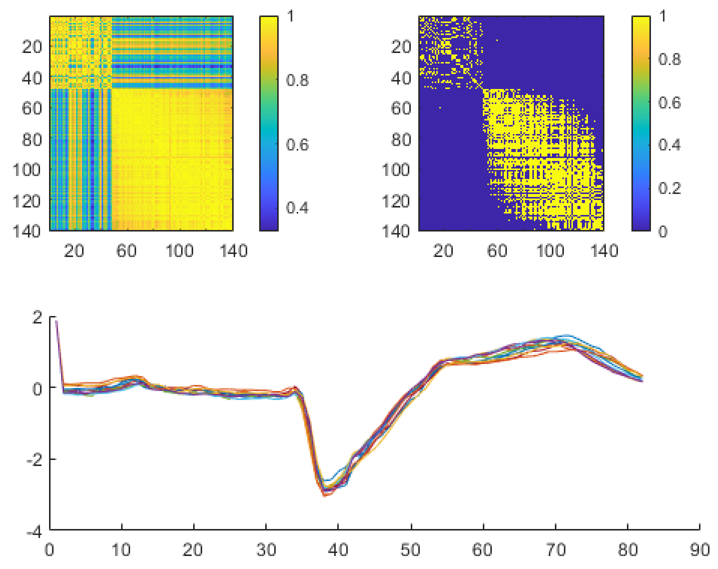
Dense Cluster around 500

```
part = data(400:600,:); corr_part = corr(part');
LowerLimit = 500; UpperLimit = 510;

figure
subplot(2,2,1);
imagesc(corr_part)
colorbar

subplot(2,2,[3,4]);
hold on
for i = LowerLimit:UpperLimit
        plot(timeArray,data(i,:))
end
hold off

subplot(2,2,2);
corr_part = corr_part > threshold;
imagesc(corr_part)
colorbar
```



Dense Cluster around 1100

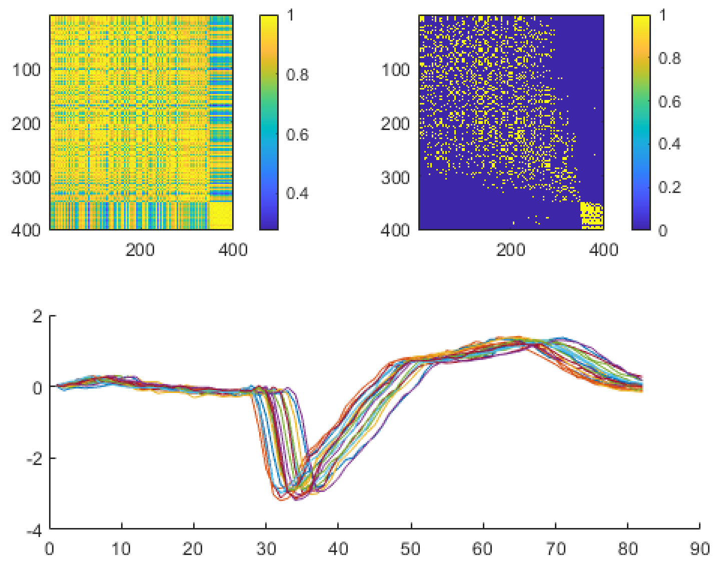
```
part = data(1000:end,:);corr_part = corr(part');
LowerLimit = 1100; UpperLimit = 1110;

figure
subplot(2,2,1);
imagesc(corr_part)
colorbar

subplot(2,2,[3,4]);
hold on
for i = LowerLimit:UpperLimit
        plot(timeArray,data(i,:))
end
hold off

subplot(2,2,2);
corr_part = corr_part > threshold;
imagesc(corr_part)
colorbar
```



For the two dense clusters shown above (region around 500 and region around 1100), the subplots on the top show the correlation matrix and the subplot on the bottom shows a sample of 10 time series data in that general region. We can see that the high correlation coefficients in the matrix corresponds to high similarity between the ECG waveforms.

Sparse Cluster around 700 - 1100

```
part = data(700:1100,:);corr_part = corr(part');
LowerLimit = 810;UpperLimit = 830;

figure
subplot(2,2,1);
imagesc(corr_part)
colorbar

subplot(2,2,[3,4]);
hold on
for i = LowerLimit:UpperLimit
        plot(timeArray,data(i,:))
end
hold off

subplot(2,2,2);
corr_part = corr_part > threshold;
imagesc(corr_part)
colorbar
```



For the figure shown above (region 700 - 1100), the subplots on the top show the correlation matrix and the subplot on the bottom shows a sample of 30 time series data in that general region. This is indeed a sparse cluster. We can see that the low correlation coefficients (indicated by blue puncta) in the matrix corresponds to low similarity between the ECG waveforms.