HW: Applying Unsupervised Learning to the Cleveland Heart Dataset

Pre-process the data

1. Import the spreadsheet as a table
2. Remove rows with missing values
3. Normalize each column to have zero mean and unit variance
4. Display table properties

```
% 1. Import spreadsheet as table
heart_data = readtable('cleveland.data_dec2019 - Copy.xlsx');
```

```
Warning: Column headers from the file were modified to make them valid MATLAB identifiers before creating
 variable names for the table. The original column headers are saved in the VariableDescriptions property.
Set 'PreserveVariableNames' to true to use the original column headers as table variable names.
```

```
% 2. Remove rows with missing values
heart_data = rmmissing(heart_data);

% 3. Normalize columns
norm_data = normalize(table2array(heart_data));

% 4. Display table properties
heart_data.Properties
```

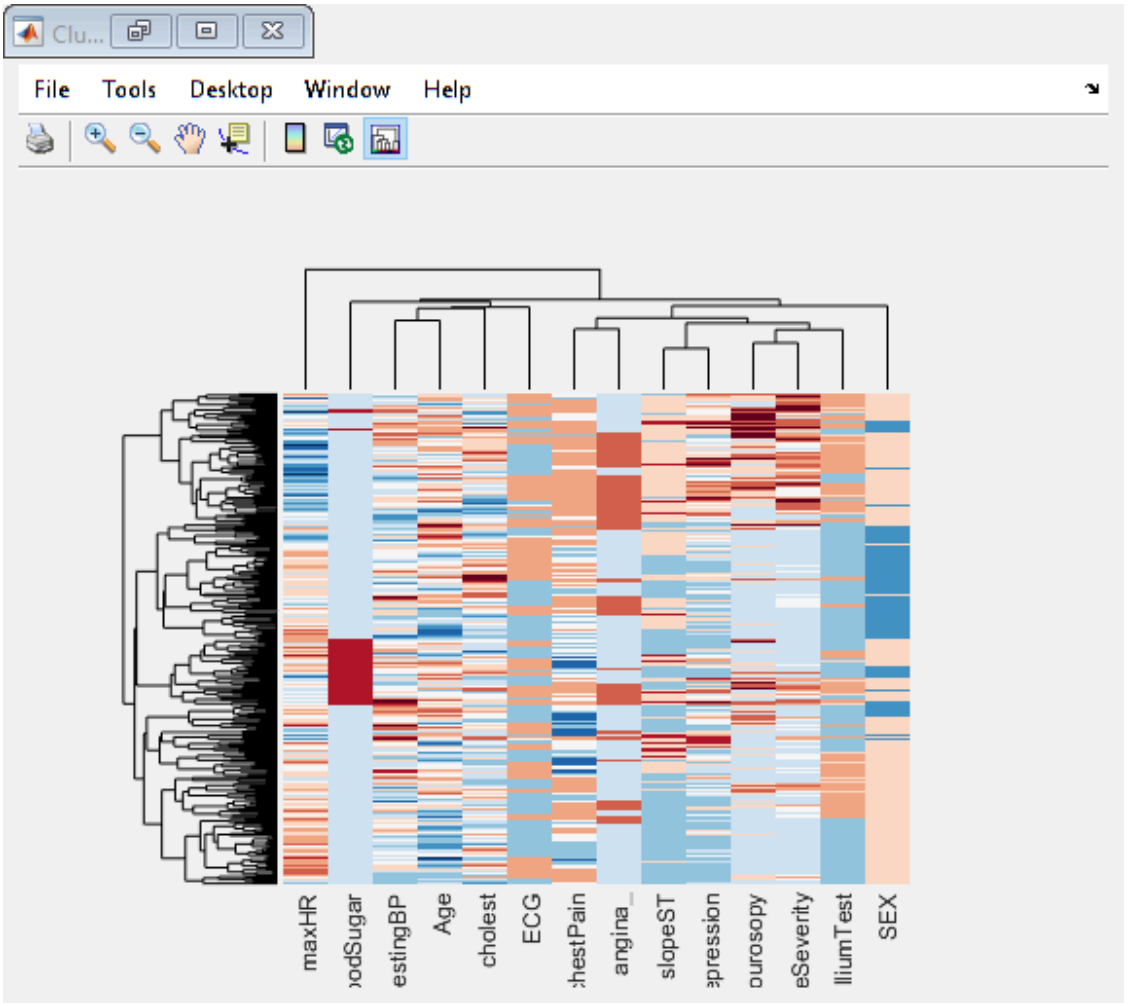
```
ans =
  TableProperties with properties:
            Description: ''
               UserData: []
         DimensionNames: {'Row'  'Variables'}
          VariableNames: {1×14 cell}
    VariableDescriptions: {1×14 cell}
          VariableUnits: {}
      VariableContinuity: []
                RowNames: {}
      CustomProperties: No custom properties are set.
      Use addprop and rmprop to modify CustomProperties.
```

Unsupervised analysis

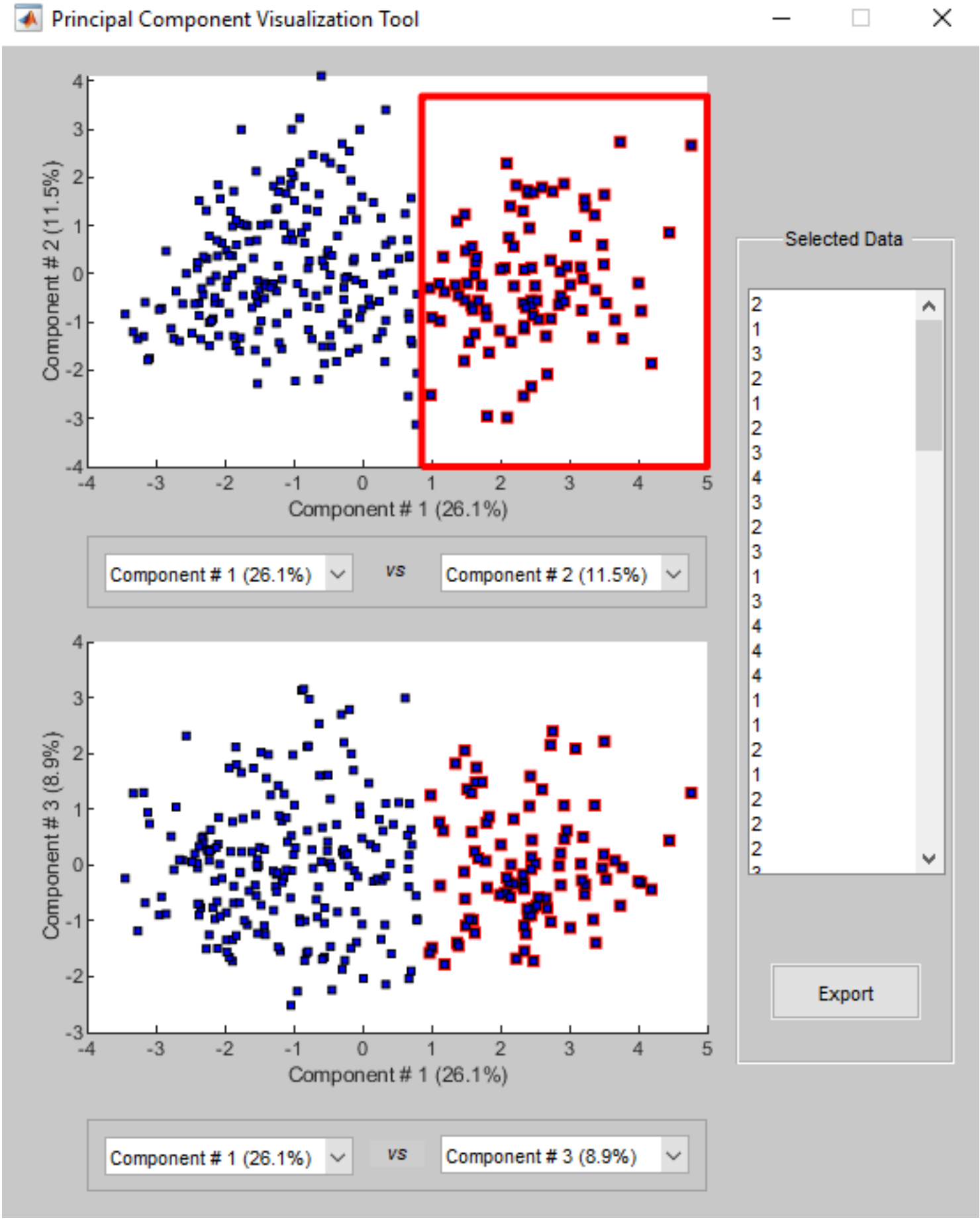
1. Create a clustergram of the entire data (distance = correlation)
2. Create a PCA plot based on patients and another based on features
3. Find optimal number of patient groups with k-means clustering + silhouette analysis
4. Determine whether k-means can be used for diagnosis

```
% 1. Create clustergram (distance = correlation)
heart_cg = clustergram(norm_data,...
    'RowLabels',heart_data.diseaseSeverity,...
    'ColumnLabels',heart_data.Properties.VariableNames,...
    'Standardize','column',...
    'RowPDist','correlation','ColumnPDist','correlation',...
```

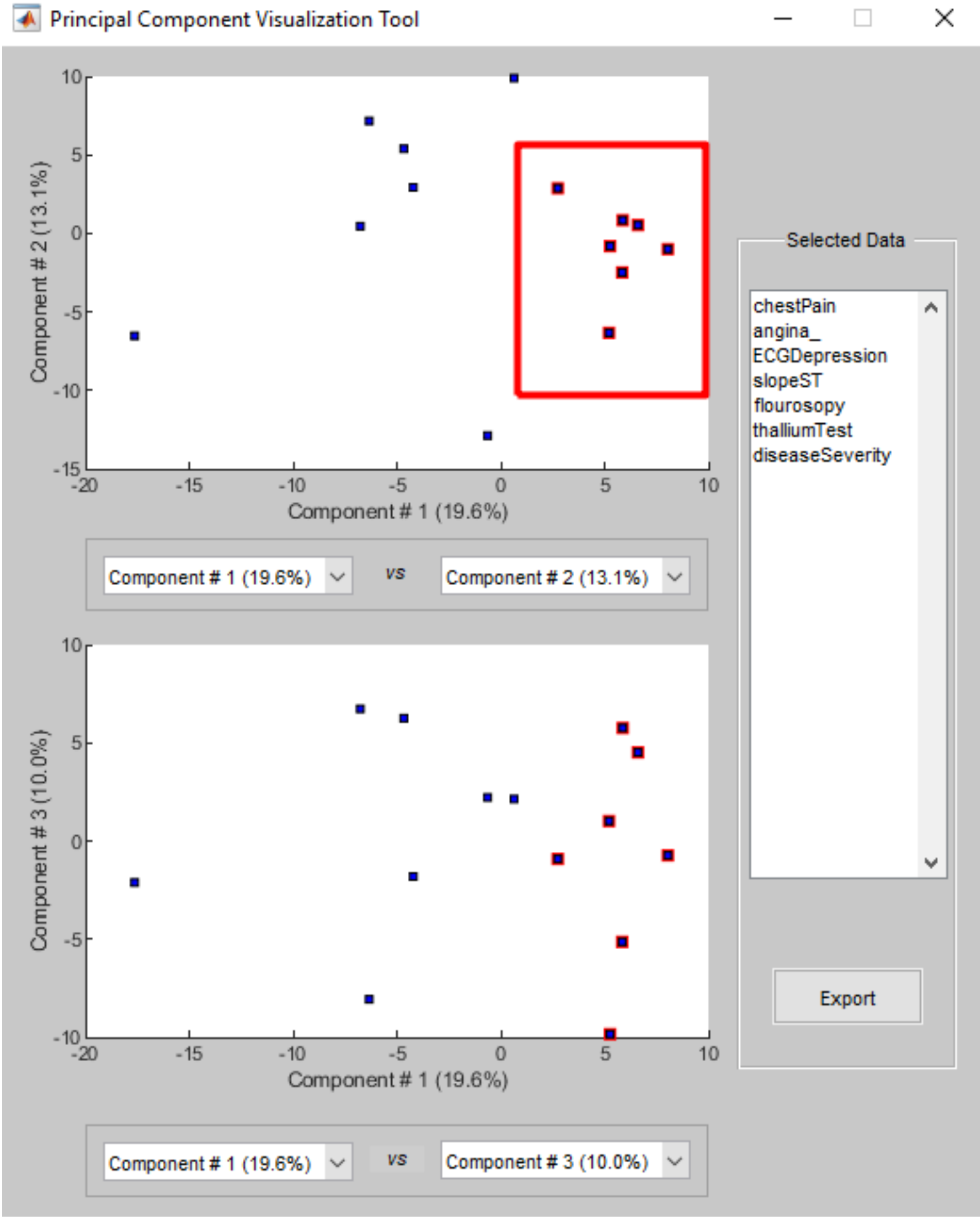
```
    'Colormap',redbluecmap);
```




```
% 2a. PCA for patients
mapcaplot(norm_data, heart_data.diseaseSeverity)
```


Principal Component Visualization Tool
Component # 2 (11.5%)
Component # 1 (26.1%)
Component # 1 (26.1%)
vs
Component # 2 (11.5%)
Component # 3 (8.9%)
Component # 1 (26.1%)
vs
Component # 3 (8.9%)
Selected Data
Export

```
% 2b. PCA for features
mapcaplot(norm_data',heart_data.Properties.VariableNames)
```


Principal Component Visualization Tool
Component # 2 (13.1%)
Component # 1 (19.6%)
Component # 1 (19.6%)
vs
Component # 2 (13.1%)
Component # 3 (10.0%)
Component # 1 (19.6%)
vs
Component # 3 (10.0%)
Selected Data
chestPain
angina_
ECGDepression
slopeST
flourosopy
thalliumTest
diseaseSeverity
Export

Q&A

Question: Based on clustergram and PCA, how many distinct patient groups are there?

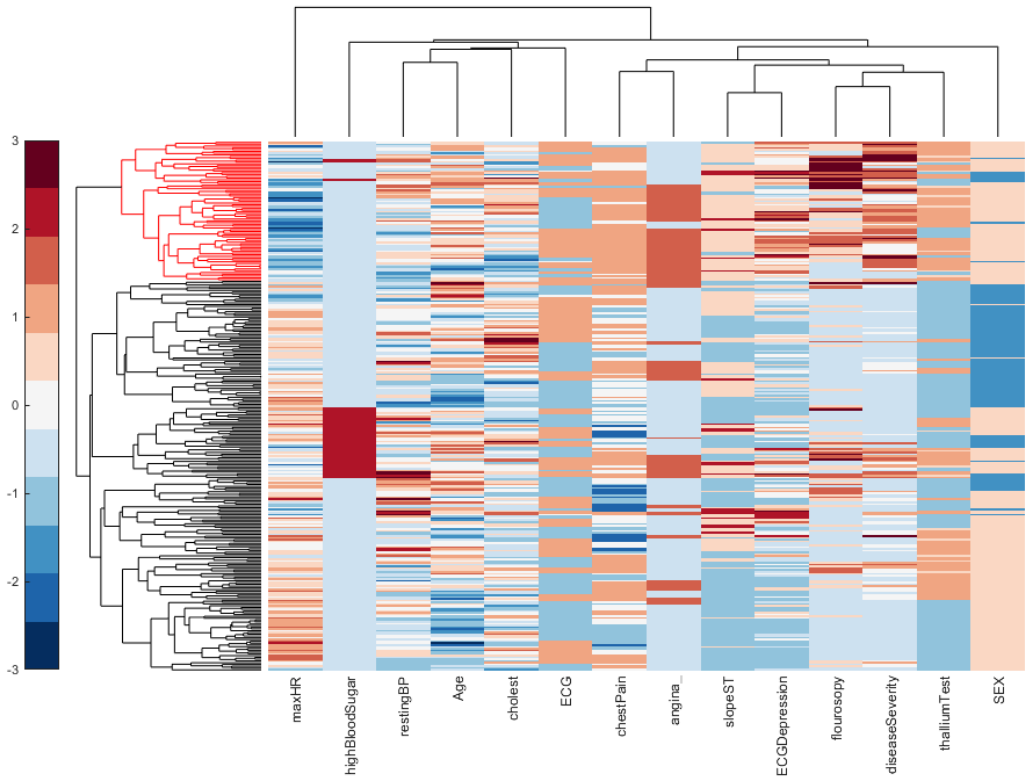
Answer: Clustergram: 4-5, PCA: 2

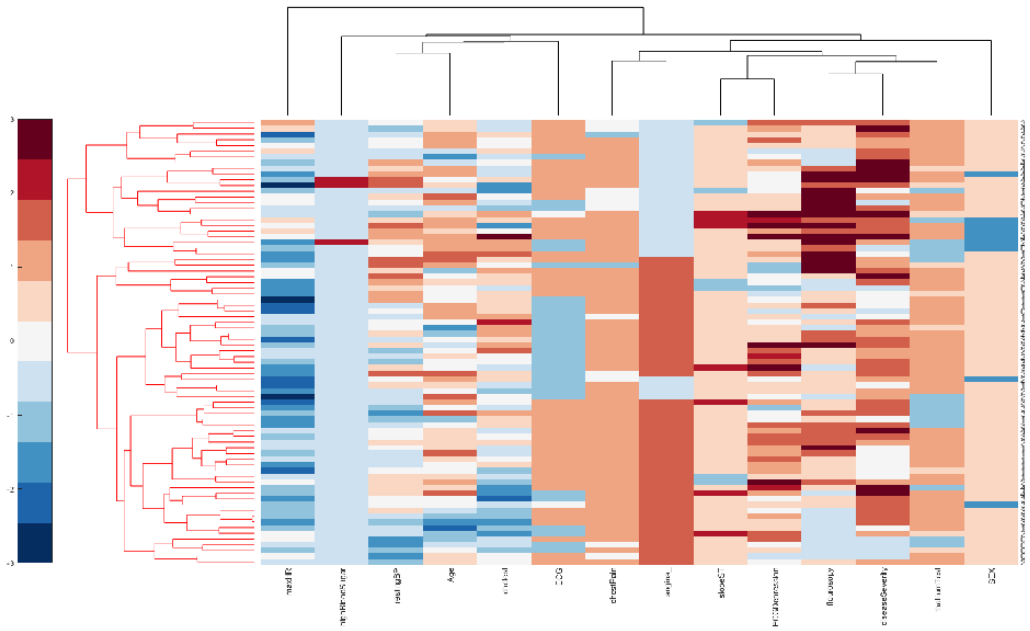
Question: Can the features (columns) be grouped into smaller set of PCs? If so, what are they?

Answer: Yes, these are: chestPain, angina_, ECGDepression, slopeST, flourosopy, thalliumTest, and diseaseSeverity

Question: Can patients with heart disease be further classified into smaller groups?

Answer: Yes, see images below:





```
% 3. k-means for determining optimal number of patient groups
k_values = 2:10;
X = table2array(heart_data(:,1:end-1));

% For-loop to calculate the silhouette statistic for different k values
n = length(k_values);       % number of k values
s_statistic = zeros(n,1);   % variable to store silhouette statistic values
for i = 1:n
    % Use the kmeans function to cluster patients into k clusters
    [idx,~] = kmeans(X,k_values(i));
    % Use the silhouette function to calculate silhouette values
    s = silhouette(X,idx);
    % Calculate a weight value proportional to positive silhouette values
    weight = sum(s > 0)/length(s);
    % Calculate the silhouette statistic by multiplying the weight with the
    % mean of silhouette values and store this to s_statistic
    s_statistic(i) = weight*mean(s);
end
max(s_statistic)
```

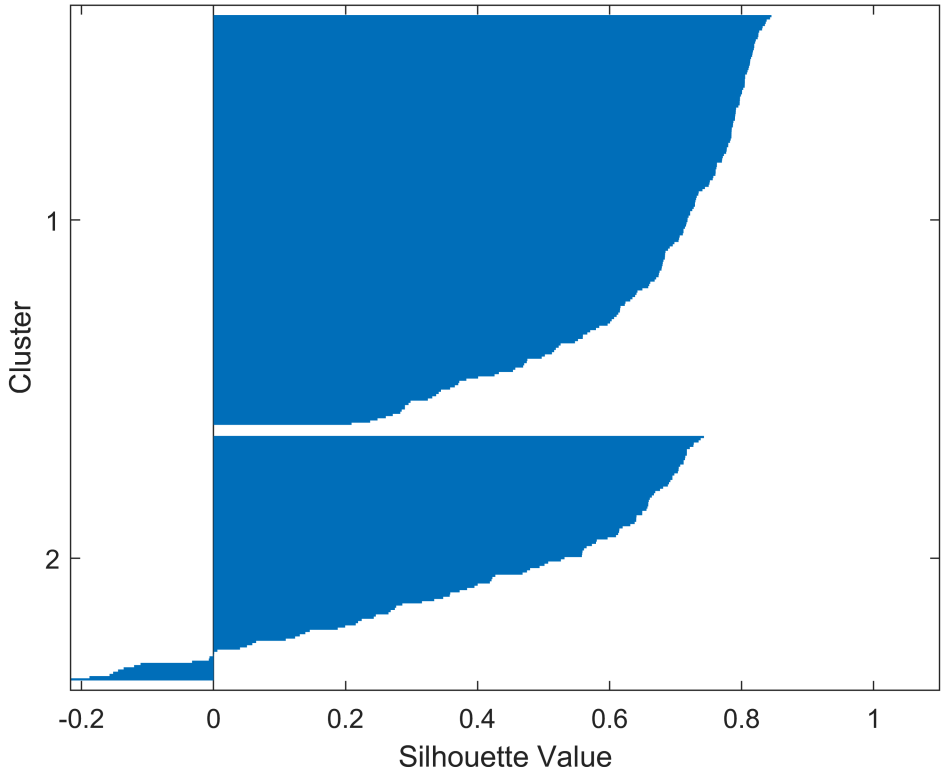
```
ans = 0.5541
```

```
k = find(s_statistic==max(s_statistic))+1
```

```
k = 2
```

Answer: Optimal k for grouping patients is k = 2.

```
% 4. k-means for diagnosis?
[idx,~] = kmeans(X,k);
silhouette(X,idx)
```




```
% Vector for normal (0) vs. diseased (1)
heart_disease = zeros(size(heart_data,2),1);
heart_disease(heart_data.diseaseSeverity > 0) = 1;

% Cluster 1 (40.86% diseased)
c1 = heart_disease(idx == 1); sum(c1)/length(c1)
```

```
ans = 0.4086
```

```
% Cluster 2 (54.95% diseased)
c2 = heart_disease(idx == 2); sum(c2)/length(c2)
```

```
ans = 0.5495
```

Answer: K-means is not a great tool to use for diagnosis.