Cohort Analysis

May 6, 2018

```
In [1]: import numpy as np
        import pandas as pd
        import seaborn as sns
        from sklearn.cluster import KMeans
        from sklearn.decomposition import PCA
        from scipy.spatial.distance import cdist
        from sklearn import metrics
        from sklearn.cluster import DBSCAN
        from sklearn.cluster import hierarchical
        from scipy.cluster import hierarchy
        from sklearn.cluster import AgglomerativeClustering
        import matplotlib.pyplot as plt
        from matplotlib.path import Path
        from matplotlib.spines import Spine
        from matplotlib.projections.polar import PolarAxes
        from matplotlib.projections import register_projection
        import csv
        import math
        from random import randint
        from scipy import stats
        from statsmodels.stats.weightstats import ztest
        from statsmodels.stats.weightstats import ttest_ind
        from scipy.stats import chisquare
        import matplotlib.cm as cm
        from sklearn.metrics import silhouette_samples, silhouette_score
        from sklearn.metrics import calinski_harabaz_score
        from math import pi
```

1 1. cohort clustering: k means

elbow method, usually the elbow is the best k : numbers of clusters

```
In [11]: def elbow_method(X):
             '''
             Using elbow method to find the best k of the kmeans.
             X is feature matrix.
             '''
```

```
    distorsion = []
    K = range(2,15)
    for k in K:
        kmeanModel = KMeans(n_clusters=k).fit(X)
        distorsion.append(kmeanModel.inertia_)

    fig = plt.figure(figsize=(15, 5))
    plt.grid(True)
    plt.plot(range(2, 15), distorsion)
    plt.xlabel('k')
    plt.ylabel('Distortion')
    plt.title('The Elbow Method showing the optimal k')
    plt.savefig('The Elbow Method showing the optimal k')
    plt.show()
```

sihouette score analysis, the smaller, the better

```
In [ ]: def silhouette_score_analysis(X):
            '''
            Do silhouette analysis and make plots
            X : feature matrix

            '''
            avr_ss = []
            range_n_clusters = range(2,10)
            for n_clusters in range_n_clusters:
            # Create a subplot with 1 row and 2 columns
                fig, (ax1, ax2) = plt.subplots(1, 2)
                fig.set_size_inches(18, 7)

            # The 1st subplot is the silhouette plot
            # The silhouette coefficient can range from -1, 1 but in this example all
            # lie within [-0.1, 1]
                ax1.set_xlim([-0.1, 1])
            # The (n_clusters+1)*10 is for inserting blank space between silhouette
            # plots of individual clusters, to demarcate them clearly.
                ax1.set_ylim([0, len(X) + (n_clusters + 1) * 10])

            # Initialize the clusterer with n_clusters value and a random generator
            # seed of 10 for reproducibility.
                clusterer = KMeans(n_clusters=n_clusters)
                cluster_labels = clusterer.fit_predict(X)


            # The silhouette_score gives the average value for all the samples.
            # This gives a perspective into the density and separation of the formed
            # clusters
                silhouette_avg = silhouette_score(X, cluster_labels)
```

```
        avr_ss.append(silhouette_avg)
#         print("For n_clusters = "+str(n_clusters) +" The average silhouette_score is :

    # Compute the silhouette scores for each sample
        sample_silhouette_values = silhouette_samples(X, cluster_labels)

        y_lower = 10
        for i in range(n_clusters):
        # Aggregate the silhouette scores for samples belonging to
        # cluster i, and sort them
            ith_cluster_silhouette_values = sample_silhouette_values[cluster_labels == i

            ith_cluster_silhouette_values.sort()

            size_cluster_i = ith_cluster_silhouette_values.shape[0]
            y_upper = y_lower + size_cluster_i

            color = plt.cm.Spectral(float(i) / n_clusters)
            ax1.fill_betweenx(np.arange(y_lower, y_upper),0, ith_cluster_silhouette_valu
                              facecolor=color, edgecolor=color, alpha=0.7)

        # Label the silhouette plots with their cluster numbers at the middle
            ax1.text(-0.05, y_lower + 0.5 * size_cluster_i, str(i))

        # Compute the new y_lower for next plot
            y_lower = y_upper + 10  # 10 for the 0 samples

        ax1.set_title("The silhouette plot for the various clusters.")
        ax1.set_xlabel("The silhouette coefficient values")
        ax1.set_ylabel("Cluster label")

        # The vertical line for average silhouette score of all the values
        ax1.axvline(x=silhouette_avg, color="red", linestyle="--")

        ax1.set_yticks([])  # Clear the yaxis labels / ticks
        ax1.set_xticks([-0.1, 0, 0.2, 0.4, 0.6, 0.8, 1])

        # 2nd Plot showing the actual clusters formed
        colors = plt.cm.Spectral(cluster_labels.astype(float) / n_clusters)
        X = PCA(n_components=2).fit_transform(X)
        ax2.scatter(X[:, 0], X[:, 1], marker='.', s=30, lw=4, alpha=0.7,
                    c=colors, edgecolor='k')

        # Labeling the clusters
        centers = clusterer.cluster_centers_
        # Draw white circles at cluster centers
        ax2.scatter(centers[:, 0], centers[:, 1], marker='o',c="white", alpha=1, s=200,
```

```
    for i, c in enumerate(centers):
        ax2.scatter(c[0], c[1], marker='$%d$' % i, alpha=1,
                    s=50, edgecolor='k')

    ax2.set_title("The visualization of the clustered data.")
    ax2.set_xlabel("Feature space for the 1st feature")
    ax2.set_ylabel("Feature space for the 2nd feature")

    plt.suptitle(("Silhouette analysis for KMeans clustering on sample data "
                  "with n_clusters = %d" % n_clusters),
                 fontsize=14, fontweight='bold')



K = range_n_clusters


plt.figure(figsize=(9, 7))
plt.plot(K, avr_ss, 'bx-')
plt.title('The Silhouette score with different k')
plt.xlabel('Number of Clusters',fontsize = 15)
plt.ylabel('Average Silhouette Score',fontsize =15)
plt.grid(True)
plt.show()
```

2 2. Attributes Analysis

Draw radar chart to analyze the important attributes

```
In [ ]: def cal_avg(data):
            '''
            radar chart helper function
            @parameters:
            data: 3d-list
            @return:
            result: the data of attributes of every patient in each cohort
            '''
            result = []
            for da in data:
                oneline = [0 for i in range(len(da[0]))]
                max_ele = [0 for i in range(len(da[0]))]
                for i in range(len(da)):
                    for j in range(len(da[i])):
                        oneline[j] = oneline[j] + int(da[i][j])
                        if int(da[i][j]) > max_ele[j]:
                            max_ele[j] = int(da[i][j])
                for i in range(len(oneline)):
```

```
                if oneline[i]!=0:
                    oneline[i] = oneline[i]/float(max_ele[i])/float(len(da))
            result.append(oneline)
        return result
```

```
In [18]: def radar(cat, data):
             '''
             category: attributes' names
             data: shape: 3d-list
             @return:
             a radar chart
             the attribute distribution
             '''
         #     index that weight is non zero
             diff = [4,5,6,7,8,9,10,15,17,21,23]
             number = [55,13,49,6]
             colors = ['#5a9c4b', '#d58edc', '#5dc2c4', '#ec615c', 'm']
             colors = colors[:len(data)]
             each_group = cal_avg(data)

             new_cat = []
             new_each_group = [[] for i in range(len(each_group))]

             for i in range(len(cat)):
                 if i in diff:
                     new_cat.append(cat[i])

             for i in range(len(each_group)):
                 for j in range(len(each_group[i])):
                     if j in diff:
                         new_each_group[i].append(each_group[i][j])

             each_group = new_each_group
             cat = new_cat
             N = len(cat)
             for values, color, ii in zip(each_group, colors, range(len(data))):
                 plt.figure(ii+2, figsize=(9,7))

                 x_as = [n / float(N) * 2 * pi for n in range(N)]

                 # Because our chart will be circular we need to append a copy of the first
                 # value of each list at the end of each list with data
                 values += values[:1]
                 x_as += x_as[:1]

                 # Set color of axes
                 plt.rc('axes', linewidth=0.5, edgecolor="#888888")
```

```
        # Create polar plot
        ax = plt.subplot(111, polar=True)
#          ax.set_size_inches(9, 7)
        # Set clockwise rotation. That is:
        ax.set_theta_offset(pi / 2)
        ax.set_theta_direction(-1)

        # Set color and linestyle of grid
        ax.xaxis.grid(True, color="#888888", linestyle='solid', linewidth=0.5)
        ax.yaxis.grid(True, color="#888888", linestyle='solid', linewidth=0.5)




        # Set number of radial axes and remove labels
        plt.xticks(x_as[:-1], [])

        # Set yticks
        plt.yticks([0.2, 0.4, 0.6, 0.8, 1], ["0.2", "0.4", "0.6", "0.8", "1"])

        # Plot data
        ax.plot(x_as, values, color, linewidth=1.5, linestyle='solid', zorder=3)

        # Fill area
        ax.fill(x_as, values, color, alpha=0.45)

        # Set axes limits
        plt.ylim(0, 1)

        # Draw ytick labels to make sure they fit properly
        for i in range(N):
            angle_rad = i / float(N) * 2 * pi

            if angle_rad == 0:
                ha, distance_ax = "center", 1
            elif 0 < angle_rad < pi:
                ha, distance_ax = "left", 1
            elif angle_rad == pi:
                ha, distance_ax = "center", 1
            else:
                ha, distance_ax = "right", 1

            ax.text(angle_rad,  0.08  + distance_ax, cat[i], size=15, horizontalalignme

        font = {'family': 'serif',
            'color':  colors[ii],
            'weight': 'normal',
            'size': 25}
```

```
            plt.text(0.25, 1.25, 'Cohort '+ str(ii)+' (' +str(number[ii]) +')', fontdict =
            plt.show()
```

3 3. Visualize analysis

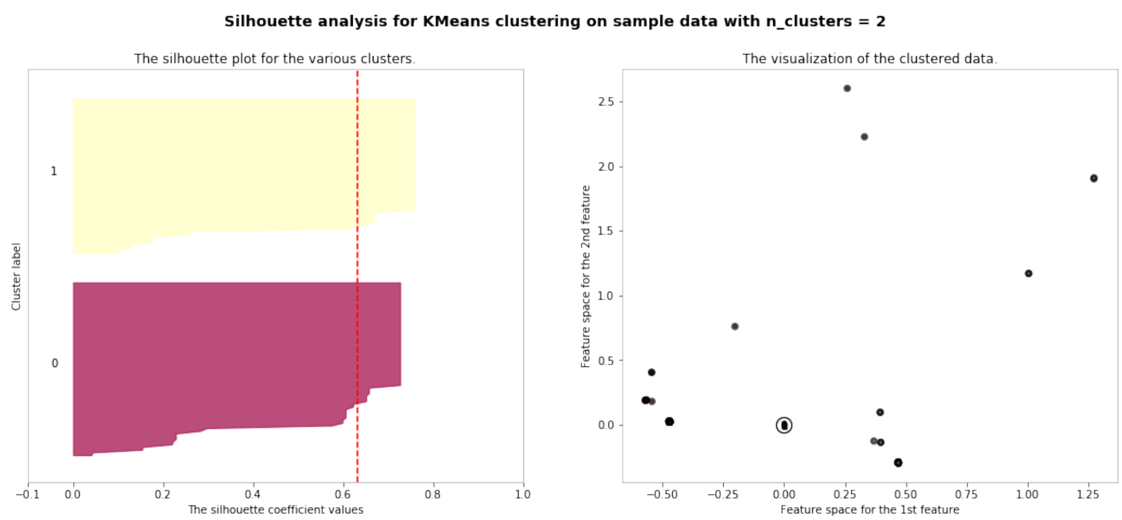
The weights we used are from the Greedy Search Algorithm

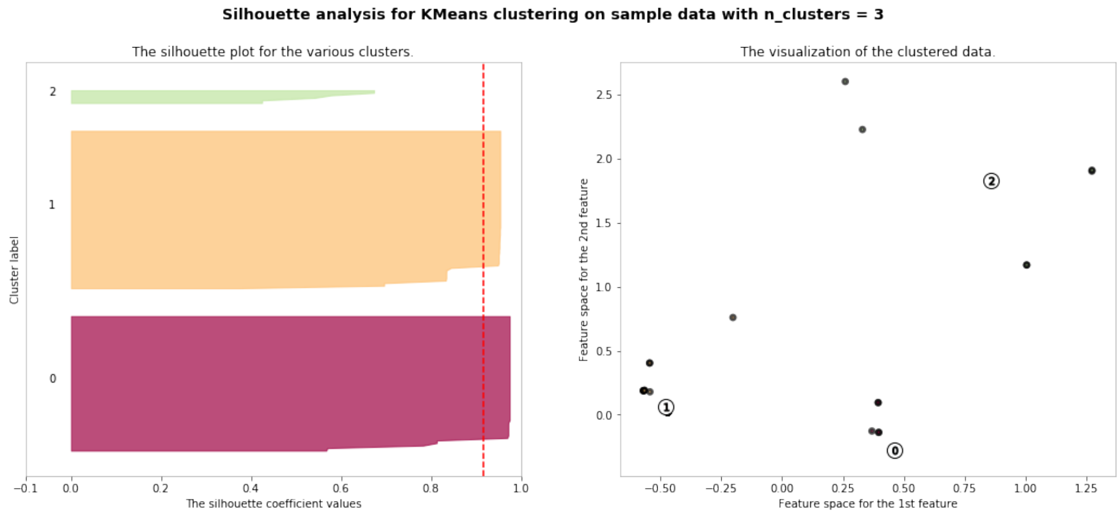
```
In [19]: def main(filename):
             '''
             first: explore optimal number of clusters
             second: visualize kmeans and hierarchical clustering
             @Parameter
             filename: the name of a csv file
             w: learnt weights for feature
             k: number of clusters for k means
             '''

             w = [0.0, 0.0, 0.0, 0.0, 0.1428571428571428, 1.0, 1.3095238095238089, 0.80952380952
             0.25, 0.0, 0.0]
             k =4
             data = pd.read_csv(filename)
             feature = np.array(data.drop('id',axis =1,inplace=False))
             weighted_feature = (w * feature)
             X = weighted_feature
             silhouette_score_analysis(X)
             elbow_method(X)

             range_n_clusters = [ 3,4 ]

             for n_clusters in range_n_clusters:
                 print("Now number of clusters:" + str(n_clusters))
             # Create a subplot with 1 row and 2 columns
                 fig, (ax1, ax2) = plt.subplots(1, 2)
                 fig.set_size_inches(18, 7)
                 y_lower = 10

                 clusterer_1 = KMeans(n_clusters=n_clusters)
                 cluster_labels_1 = clusterer_1.fit_predict(feature)
                 X_1 = PCA(n_components=2).fit_transform(feature)
                 colors = ['#5a9c4b', '#d58edc',  '#ec615c','#5dc2c4']
                 markers =['X','o','^','d'];
                 for i in range(len(X_1)):
                     ax1.scatter(X_1[i, 0], X_1[i, 1], marker=markers[cluster_labels_1[i]], s=10
                             c= colors[cluster_labels_1[i]], edgecolor='k')
                 ax1.set_xlabel("Feature projection to x feature space",fontsize=15,labelpad= 10
                 ax1.set_ylabel("Feature projection to y feature space",fontsize=15,labelpad= 10
```

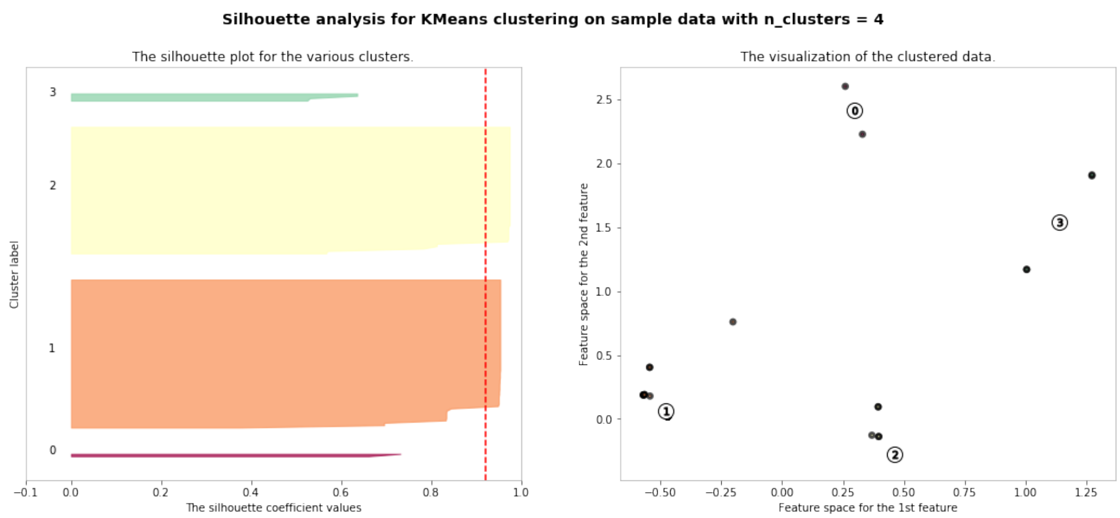
```
        clusterer = KMeans(n_clusters=n_clusters)
        cluster_labels = clusterer.fit_predict(X)
        X = PCA(n_components=2).fit_transform(weighted_feature)

        colors = plt.cm.Spectral(cluster_labels.astype(float) / n_clusters)
        colors = ['#5a9c4b', '#d58edc', '#5dc2c4', '#ec615c']
        markers =['X','o','d','^'];
        for i in range(len(X)):
            ax2.scatter(X[i, 0], X[i, 1], marker=markers[cluster_labels[i]], s=100, lw=
                c= colors[cluster_labels[i]], edgecolor='k')

    # Labeling the clusters
        centers = clusterer.cluster_centers_

        ax2.set_xlabel("Feature projection to x feature space",fontsize=15,labelpad= 10
        ax2.set_ylabel("Feature projection to y feature space",fontsize=15,labelpad= 10


        plt.show()
        plt.savefig("kmeans_k_" +str(n_clusters) )
        print("-----------------------------------------------------------------------


    # draw hierachical clustering dendrogrm
    print ('Hierachical dendrogram')
    link ='ward'
    ac = AgglomerativeClustering(linkage=link, n_clusters=4)
    ac.fit(weighted_feature)
    Z = hierarchy.linkage(weighted_feature, 'ward')
    plt.figure(figsize=(9, 7))
    plt.xlabel('Index',fontsize = 15)
    plt.ylabel('Distance',fontsize = 15)
    print('n = ', 4)
    hierarchy.dendrogram(Z,leaf_rotation=90.,  # rotates the x axis
                         leaf_font_size=8.,  # font size for the x axis labels
                         color_threshold =4,no_labels =True
    )
    plt.show()


#    draw radar chart
    kmeans = KMeans(n_clusters= 4)
    kmeans.fit(weighted_feature)
    kl = kmeans.labels_
#     exchange labels to make color consistent with Hierachical Dendrogram
    for idx in range(len(kl)):
        if kl[idx] == 0:
```

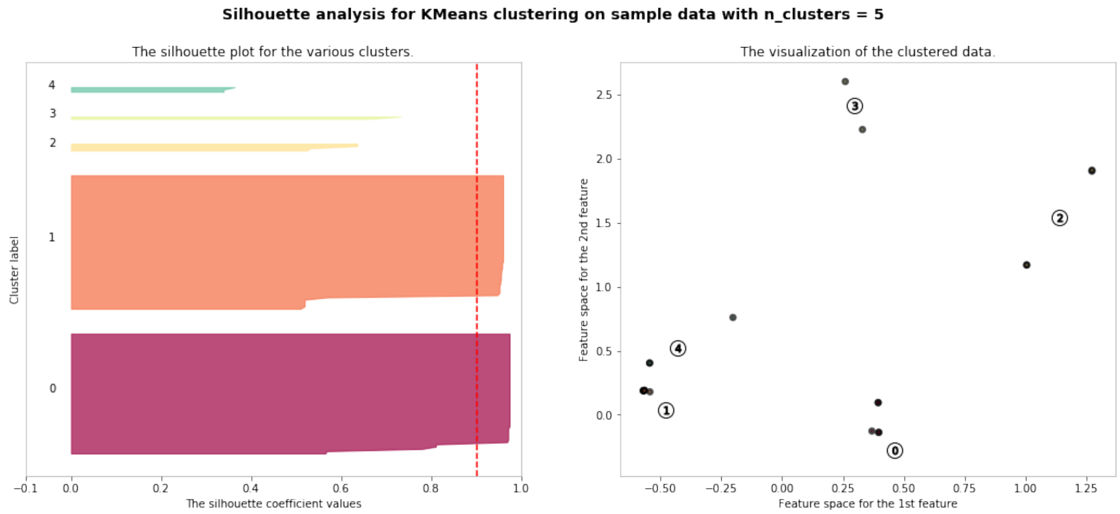
```
                kl[idx] == 2
            elif kl[idx] == 1:
                kl[idx] == 0
            elif kl[idx] == 3:
                kl[idx] == 1

        group_member =[]
        attr_no_ids =[]
        for k in range(0,4):
            id_list =[]
            attr=[]
            for i in range(len(data)):
                if(kl[i] == k):
                    id_list.append(int(data.iloc[i]['id']))
                    attr.append(feature[i])
            group_member.append(id_list)
            attr_no_ids.append(attr)

        attr_names =data.columns[1:]
        radar(attr_names,attr_no_ids)
```

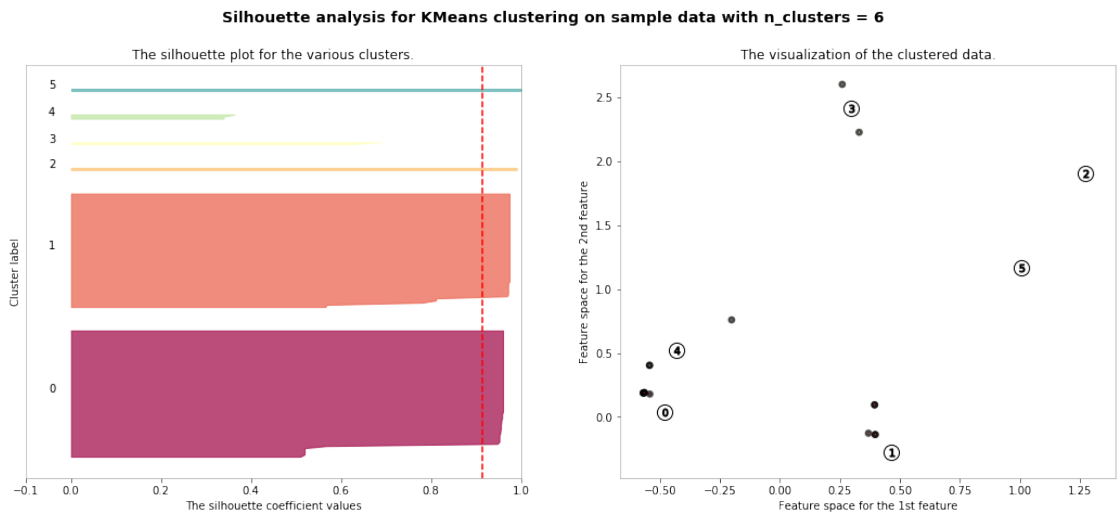
```
In [20]: if __name__ =='__main__':
             filename = "Normalized_attributes.csv"

             main(filename)
```

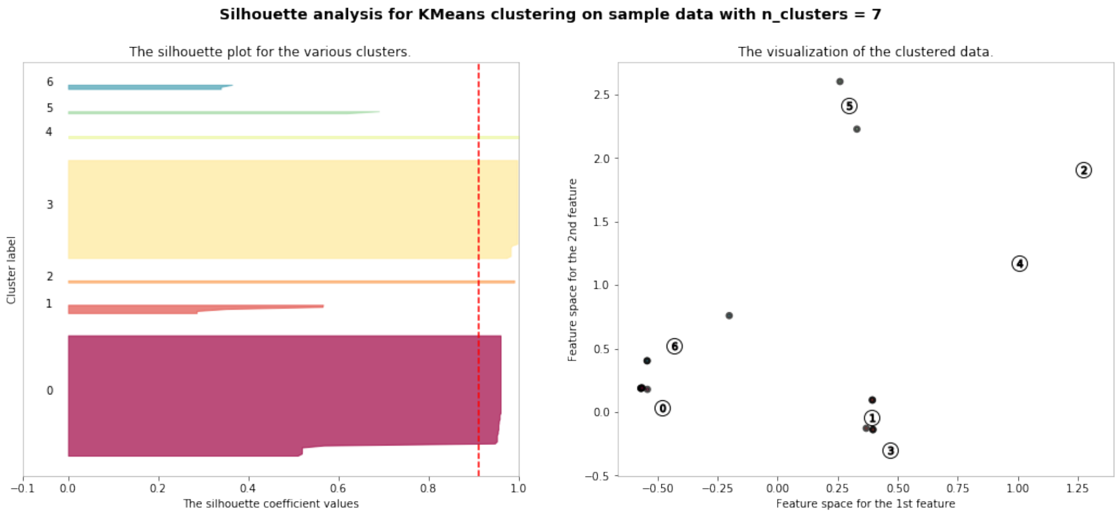


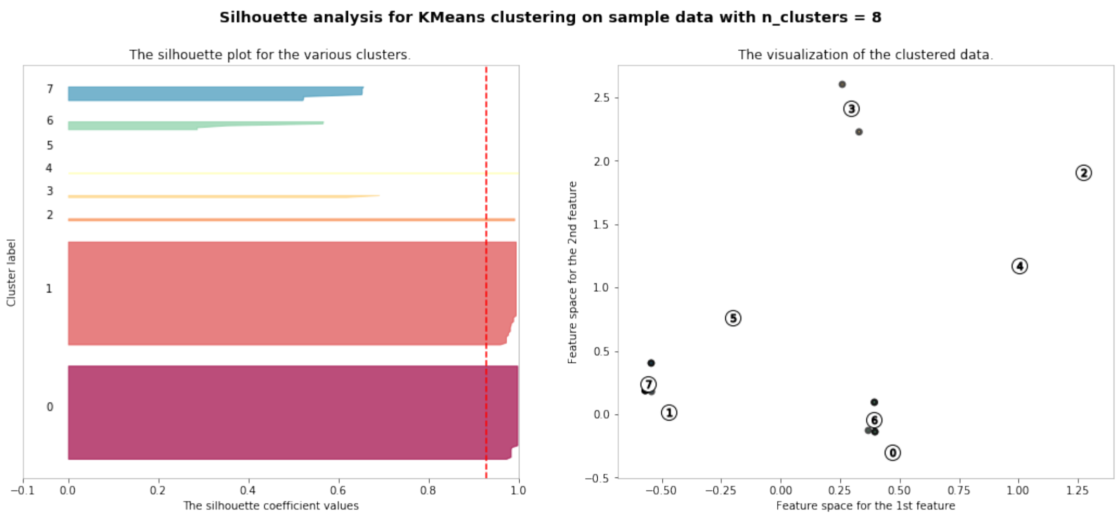

Silhouette analysis for KMeans clustering on sample data with n_clusters = 3
The silhouette plot for the various clusters.
Cluster label
The silhouette coefficient values
The visualization of the clustered data.
Feature space for the 2nd feature
Feature space for the 1st feature

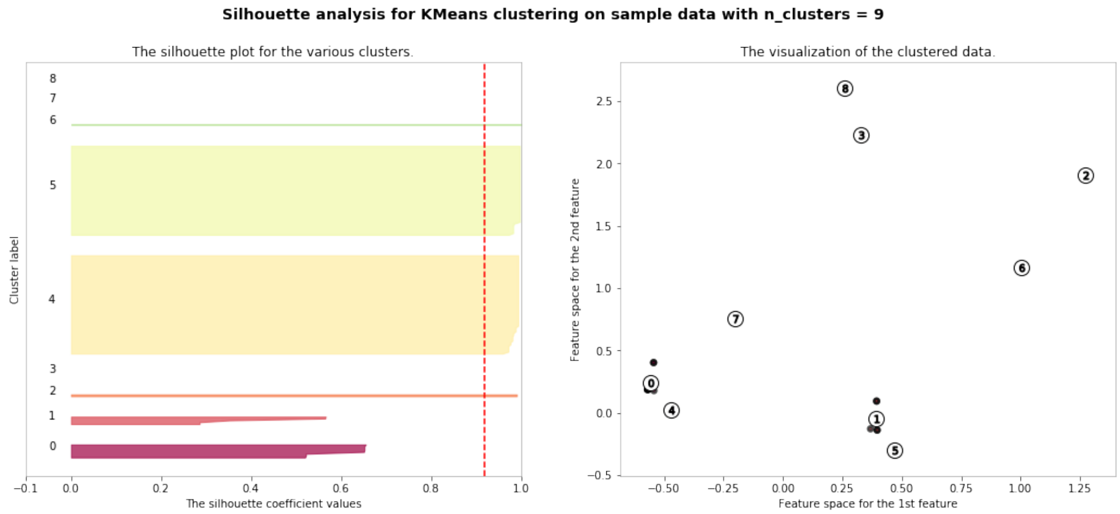

Silhouette analysis for KMeans clustering on sample data with n_clusters = 4
The silhouette plot for the various clusters.
Cluster label
The silhouette coefficient values
The visualization of the clustered data.
Feature space for the 2nd feature
Feature space for the 1st feature

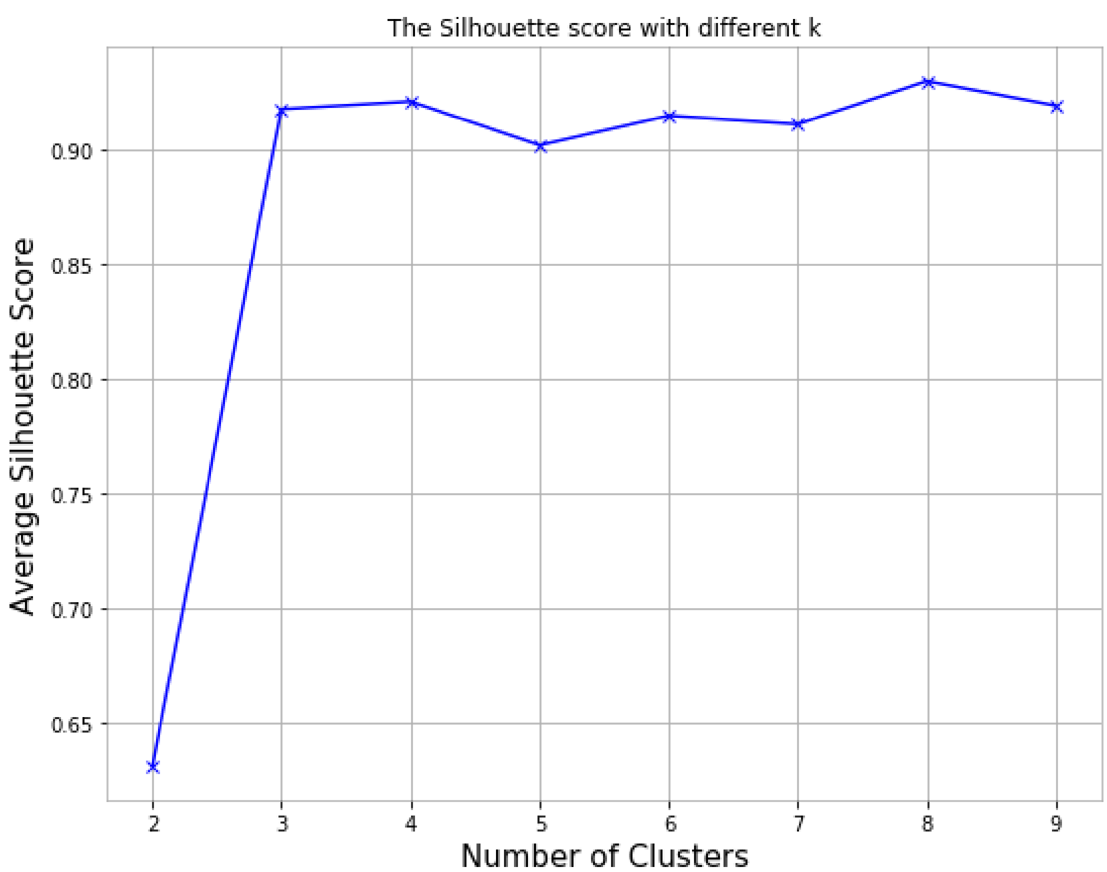

Silhouette analysis for KMeans clustering on sample data with n_clusters = 5
The silhouette plot for the various clusters.
The visualization of the clustered data.
Cluster label
The silhouette coefficient values
Feature space for the 2nd feature
Feature space for the 1st feature

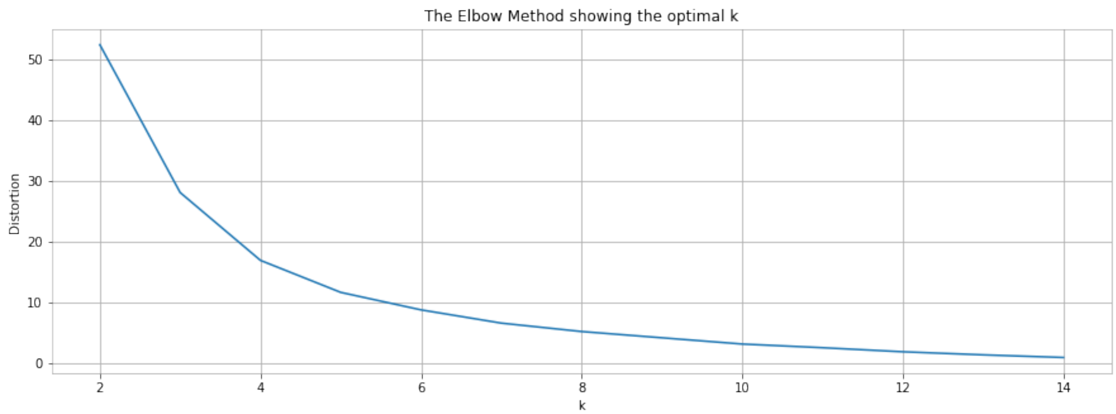

Silhouette analysis for KMeans clustering on sample data with n_clusters = 6
The silhouette plot for the various clusters.
The visualization of the clustered data.
Cluster label
The silhouette coefficient values
Feature space for the 2nd feature
Feature space for the 1st feature


Silhouette analysis for KMeans clustering on sample data with n_clusters = 7
The silhouette plot for the various clusters.
The visualization of the clustered data.
Cluster label
The silhouette coefficient values
Feature space for the 2nd feature
Feature space for the 1st feature

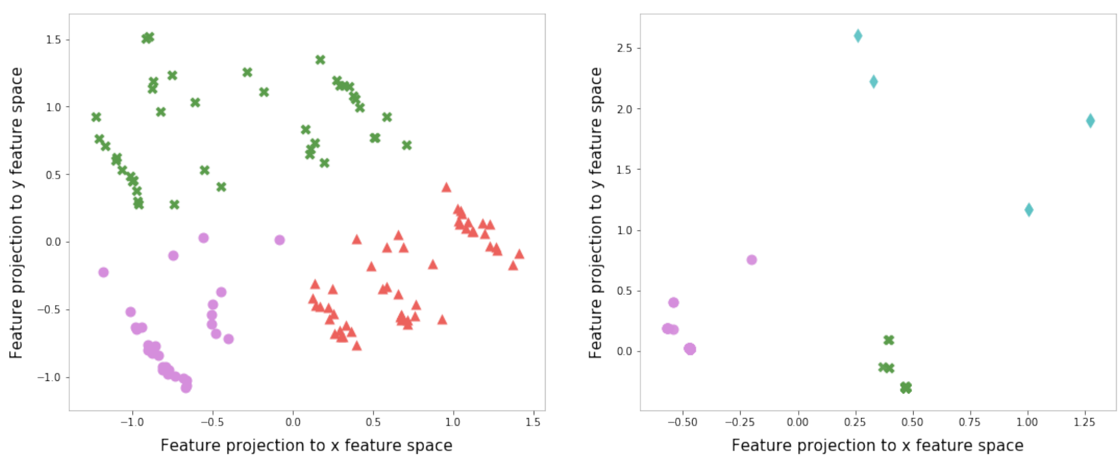

Silhouette analysis for KMeans clustering on sample data with n_clusters = 8
The silhouette plot for the various clusters.
The visualization of the clustered data.
Cluster label
The silhouette coefficient values
Feature space for the 2nd feature
Feature space for the 1st feature


Silhouette analysis for KMeans clustering on sample data with n_clusters = 9
The silhouette plot for the various clusters.
Cluster label
The silhouette coefficient values
The visualization of the clustered data.
Feature space for the 2nd feature
Feature space for the 1st feature


The Silhouette score with different k
Average Silhouette Score
Number of Clusters

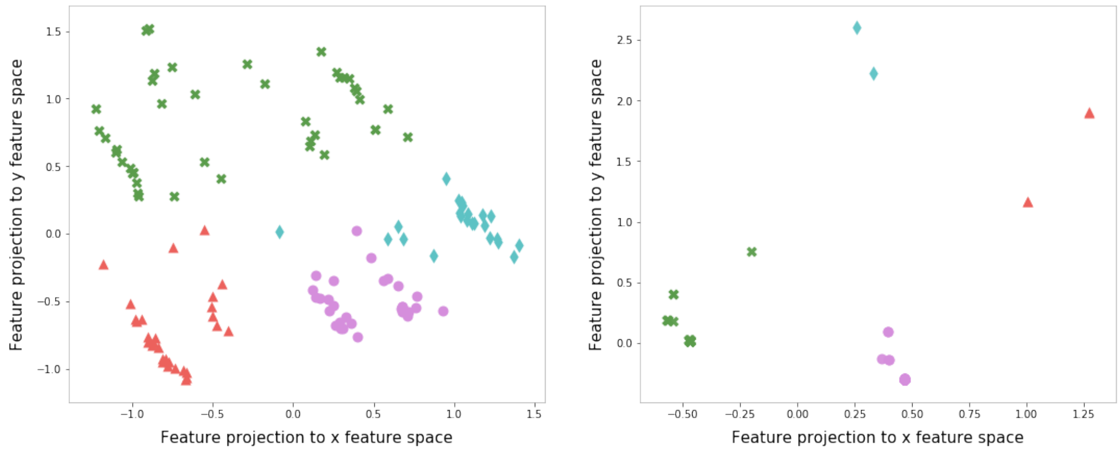


Now number of clusters:3

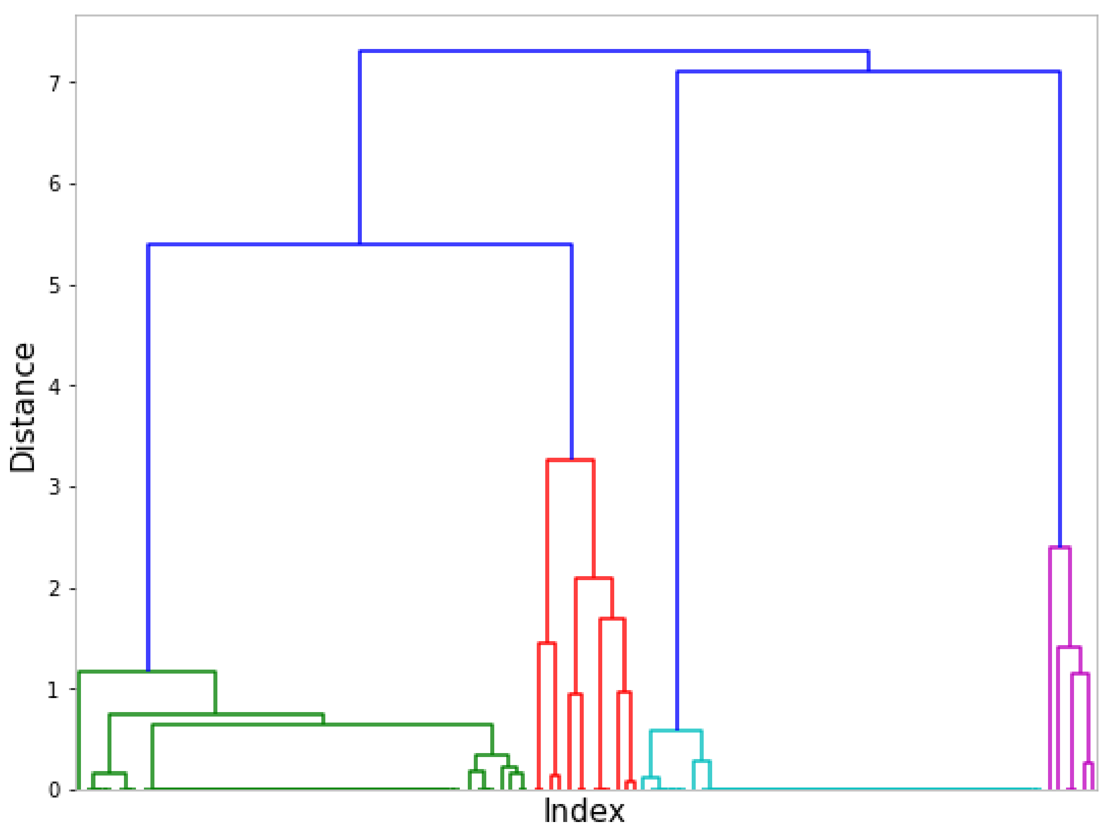


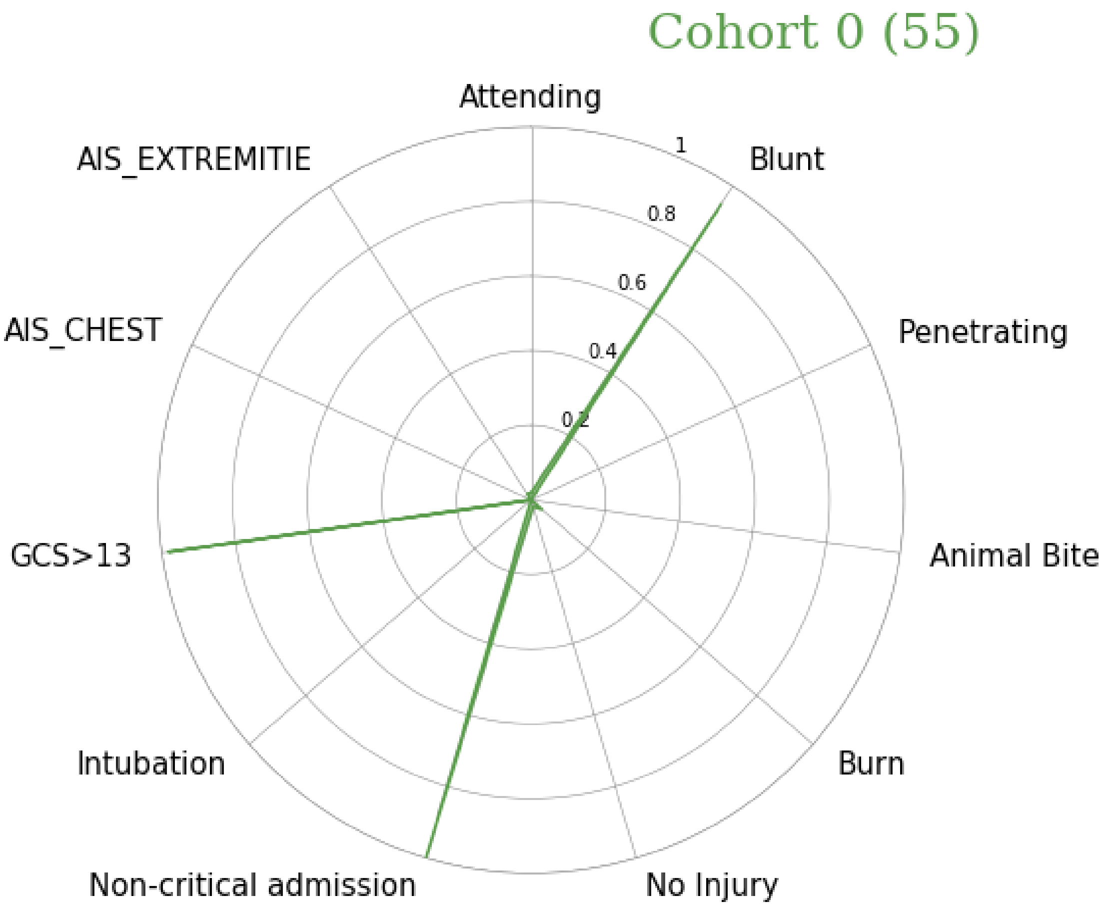
Now number of clusters:4

<Figure size 432x288 with 0 Axes>

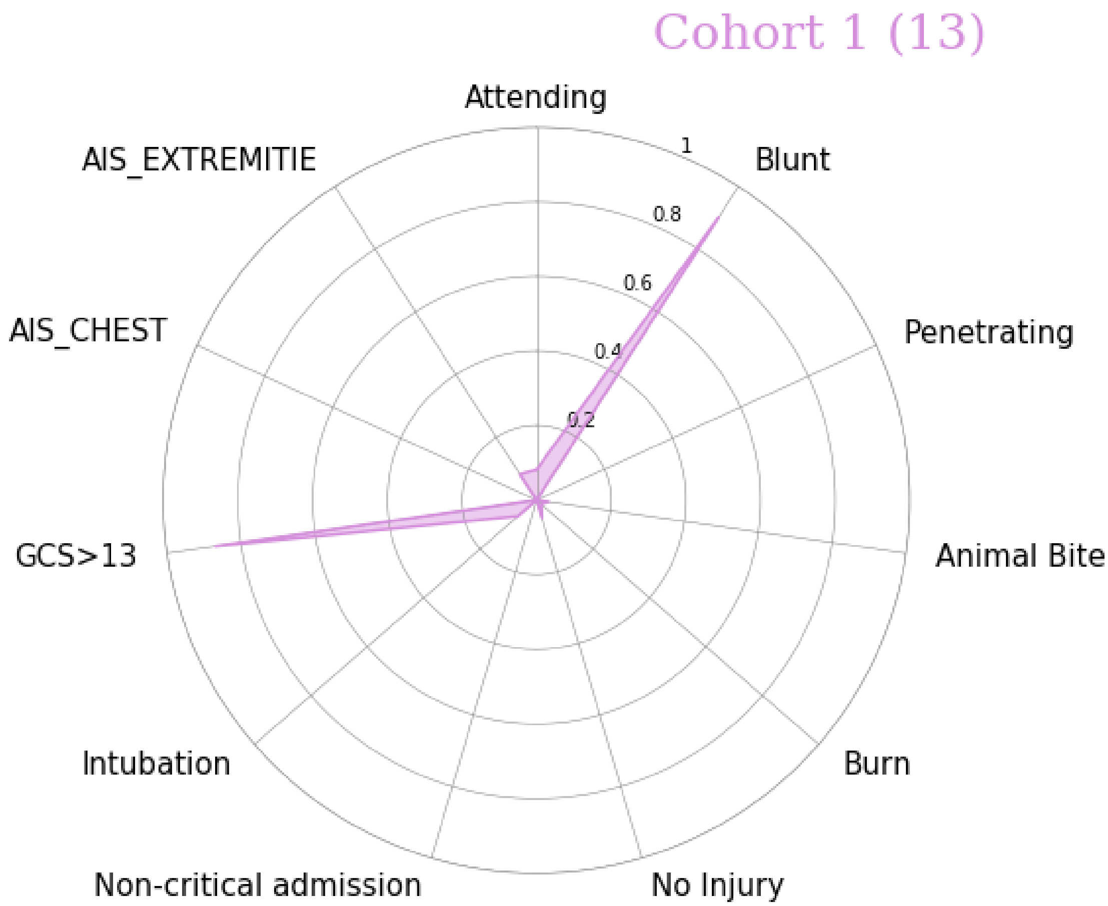



```
--------------------------------------------------------------------------------
Hierachical dendrogram
n =  4


<Figure size 432x288 with 0 Axes>
```

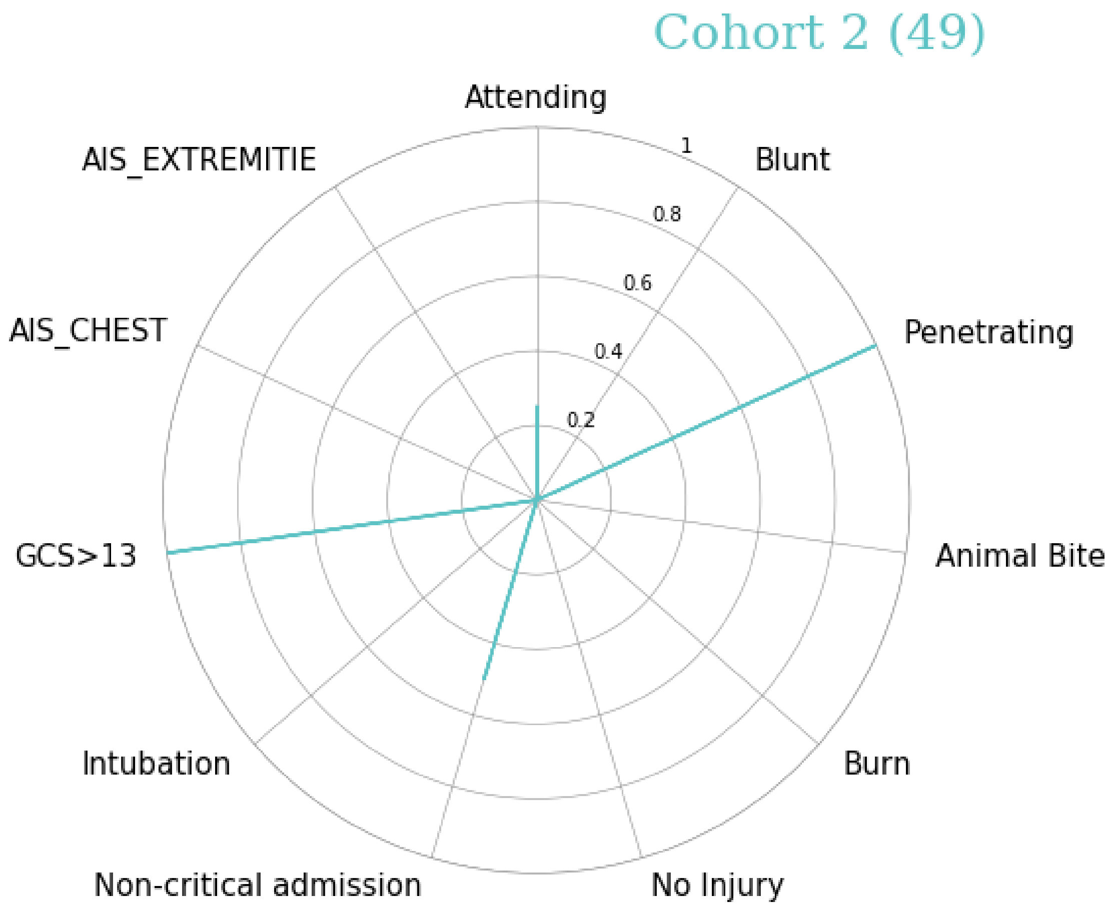




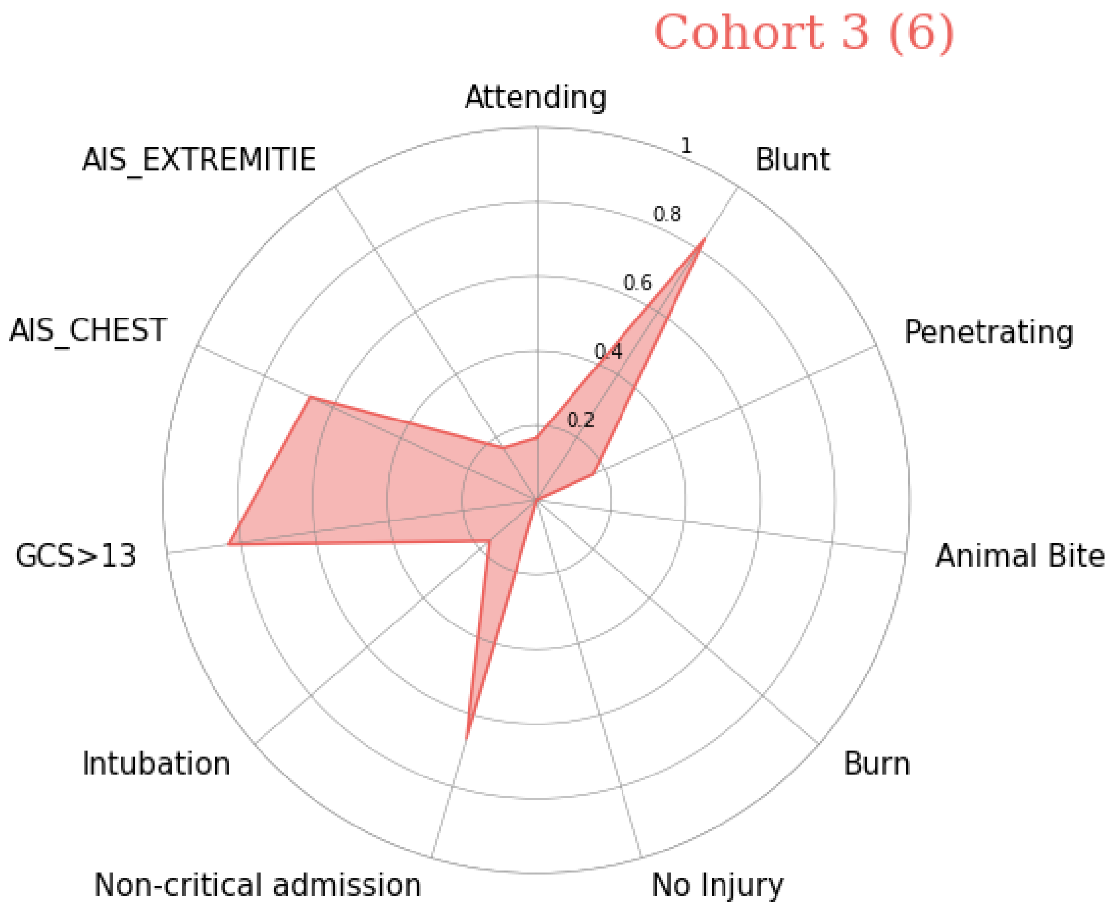
Cohort 0 (55)
Attending
Blunt
Penetrating
Animal Bite
Burn
No Injury
Non-critical admission
Intubation
GCS>13
AIS_CHEST
AIS_EXTREMITIE
1
0.8
0.6
0.4
0.2



Cohort 1 (13)
Attending
Blunt
Penetrating
Animal Bite
Burn
No Injury
Non-critical admission
Intubation
GCS>13
AIS_CHEST
AIS_EXTREMITIE
1
0.8
0.6
0.4
0.2



Cohort 2 (49)
Attending
Blunt
Penetrating
Animal Bite
Burn
No Injury
Non-critical admission
Intubation
GCS>13
AIS_CHEST
AIS_EXTREMITIE
1
0.8
0.6
0.4
0.2



Cohort 3 (6)
Attending
Blunt
Penetrating
Animal Bite
Burn
No Injury
Non-critical admission
Intubation
GCS>13
AIS_CHEST
AIS_EXTREMITIE
1
0.8
0.6
0.4
0.2