In [ ]:
```python
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.cluster import KMeans
from sklearn.preprocessing import MinMaxScaler, RobustScaler
from sklearn.metrics import silhouette_score
from sklearn.metrics import silhouette_samples
import matplotlib.cm as cm
import numpy as np
```

In [ ]:
```python
#reading in the dataset
df = pd.read_csv("../../../data/healthcare-dataset-stroke-data.csv")
```

Two-dimensional clustering

In [ ]:
```python
df = df.fillna(df.median())
```

In [ ]:
```python
df.head(3)
```

Out[ ]:

	id	gender	age	hypertension	heart_disease	ever_married	work_type	Residence_type	avg_glucose_level	bmi	smoking_status	stroke
0	9046	Male	67.0	0	1	Yes	Private	Urban	228.69	36.6	formerly smoked	1
1	51676	Female	61.0	0	0	Yes	Self-employed	Rural	202.21	28.1	never smoked	1
2	31112	Male	80.0	0	1	Yes	Private	Rural	105.92	32.5	never smoked	1

BMI outlier handling

In [ ]:
```python
gluc_bmi = df[["avg_glucose_level","bmi"]]
gluc_bmi.describe().round(2)
```

Out[ ]:

	avg_glucose_level	bmi
count	5110.00	5110.00
mean	106.15	28.86
std	45.28	7.70
min	55.12	10.30
25%	77.24	23.80
50%	91.88	28.10
75%	114.09	32.80
max	271.74	97.60

In [ ]:
```python
#Outlier handling
Q1 = df["bmi"].quantile(0.25)
Q3 = df["bmi"].quantile(0.75)
IQR = Q3 - Q1
gluc_bmi = gluc_bmi.loc[(gluc_bmi['bmi'] > (Q1-(1.5*IQR))) & (gluc_bmi['bmi'] < (Q3+(1.5*IQR)))]
```

In [ ]:
```python
gluc_bmi.describe().round(2)
```

Out[ ]:

	avg_glucose_level	bmi
count	4984.00	4984.00
mean	105.73	28.25
std	44.83	6.63
min	55.12	11.30
25%	77.20	23.60
50%	91.84	28.10
75%	113.76	32.30
max	271.74	46.20

In [ ]:
```python
#BMI tredshold
BMI_min = gluc_bmi["bmi"].describe()['min']
BMI_max = gluc_bmi["bmi"].describe()['max']
BMI_scaled = (25 - BMI_min)/(BMI_max-BMI_min)


#Avg_gluc_level tredshold
gluc_min = gluc_bmi["avg_glucose_level"].describe()['min']
gluc_max = gluc_bmi["avg_glucose_level"].describe()['max']
gluc_scaled = (150 - gluc_min)/(gluc_max-gluc_min)
```

Clusters by average glucose level and bmi

In [ ]:
```python
#robust scaling
#gluc_bmi = RobustScaler().fit_transform(gluc_bmi)
#gluc_bmi = pd.DataFrame(gluc_bmi,columns=["avg_glucose_level","bmi"])
#gluc_bmi.describe().round(2)
```

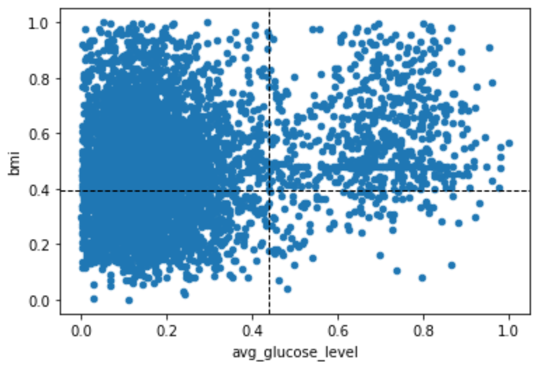
In [ ]:
```
#min-max scaling
#https://stats.stackexchange.com/questions/89809/is-it-important-to-scale-data-before-clustering
gluc_bmi = MinMaxScaler().fit_transform(gluc_bmi)
gluc_bmi = pd.DataFrame(gluc_bmi,columns=["avg_glucose_level","bmi"])
gluc_bmi.describe().round(2)
```

Out[ ]:

	avg_glucose_level	bmi
count	4984.00	4984.00
mean	0.23	0.49
std	0.21	0.19
min	0.00	0.00
25%	0.10	0.35
50%	0.17	0.48
75%	0.27	0.60
max	1.00	1.00

In [ ]:
```
gluc_bmi.plot.scatter("avg_glucose_level","bmi")
plt.axvline(gluc_scaled, color='k', linestyle='dashed', linewidth=1)
plt.axhline(BMI_scaled, color='k', linestyle='dashed', linewidth=1)
```

Out[ ]:
```
<matplotlib.lines.Line2D at 0x23e86b1b0a0>
```



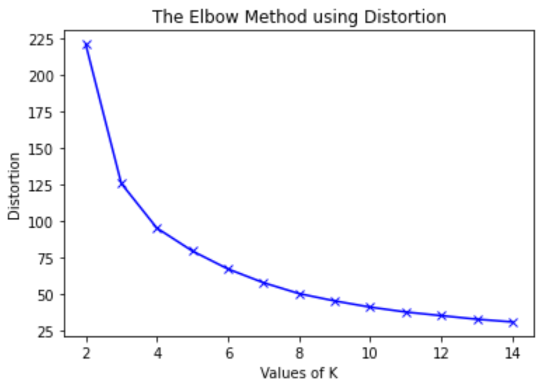
Finding the right k in k-means

In order to find the best fitting number of clusters, we evaluate different k's by the elbow and silhuette method

The elbow method

Distortion: Calculated as the avg of the squared distances from the cluster centers. Typically, the Euclidean distance metric is used.

In [ ]:
```
distortions = []

K = range(2,15,1)

for k in K:
    kmeanModel = KMeans(n_clusters=k).fit(gluc_bmi)
    kmeanModel.fit(gluc_bmi)
    distortions.append(kmeanModel.inertia_)

plt.plot(K, distortions, 'bx-')
plt.xlabel('Values of K')
plt.ylabel('Distortion')
plt.title('The Elbow Method using Distortion')
plt.savefig("two_dim_elbow.png")
plt.show()
```

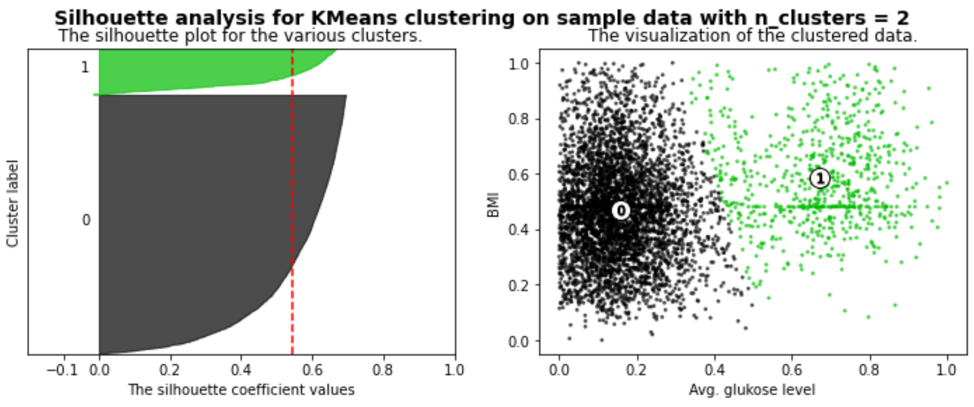


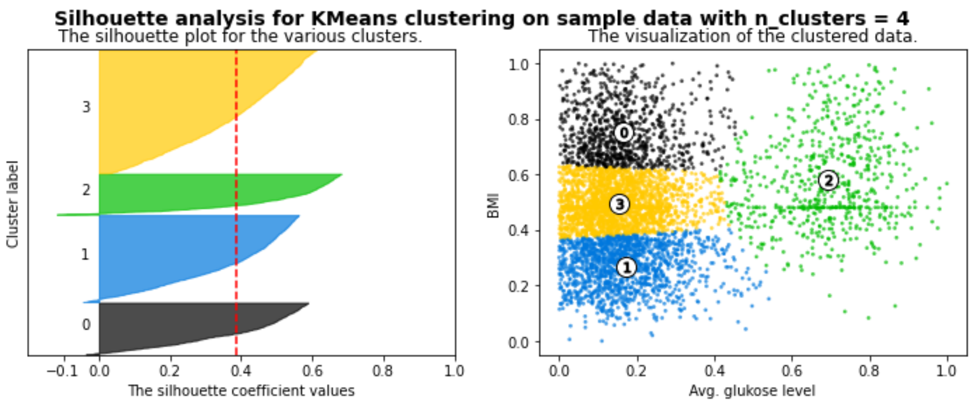
The silhouette method

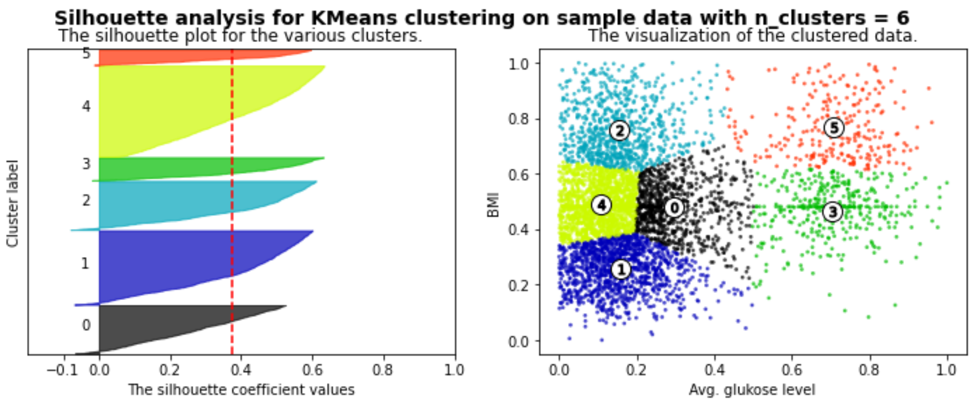
In [ ]:
```
#https://scikit-learn.org/stable/auto_examples/cluster/plot_kmeans_silhouette_analysis.html

X = gluc_bmi

range_n_clusters = range(2,10,2)

for n_clusters in range_n_clusters:
    # Create a subplot with 1 row and 2 columns
```

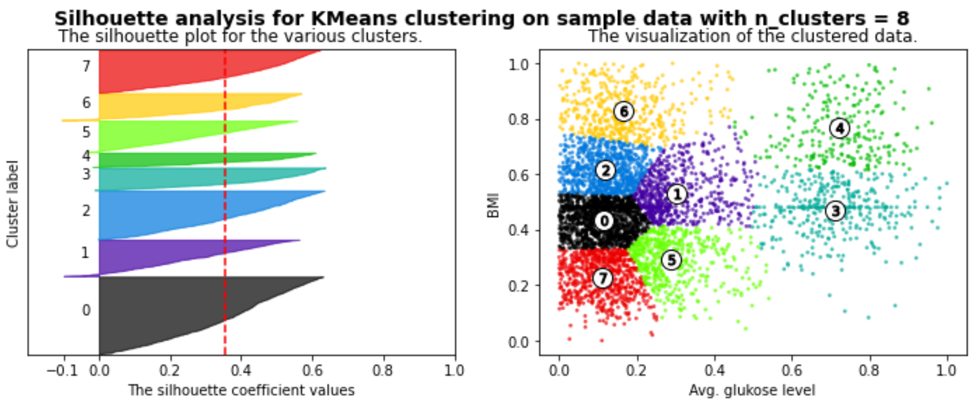
```python
    fig, (ax1, ax2) = plt.subplots(1, 2)
    fig.set_size_inches(12, 4)

    # 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([-0.2, 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, random_state=10)
    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)
    #print("For n_clusters =", n_clusters, "The average silhouette_score is :", silhouette_avg,)

    # 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 = cm.nipy_spectral(float(i) / n_clusters)
        ax1.fill_betweenx(
            np.arange(y_lower, y_upper),
            0,
            ith_cluster_silhouette_values,
            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 = cm.nipy_spectral(cluster_labels.astype(float) / n_clusters)
    ax2.scatter(
        X["avg_glucose_level"], X["bmi"], marker=".", s=30, lw=0, 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,
        edgecolor="k",
    )

    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("Avg. glukose level")
    ax2.set_ylabel("BMI")

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

```
plt.savefig("two_dim_silhouette.png")
plt.show()
```









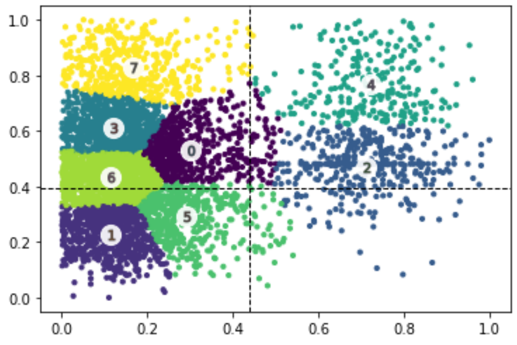
Viewing the final k-means clusters

In [ ]:

```
kmeans = KMeans(n_clusters=8)
kmeans.fit(gluc_bmi)
y_kmeans = kmeans.predict(gluc_bmi)

plt.scatter(gluc_bmi["avg_glucose_level"], gluc_bmi["bmi"], c=y_kmeans, s=10, cmap='viridis')
centers = kmeans.cluster_centers_
plt.scatter(centers[:, 0], centers[:, 1], c='white', s=200, alpha=0.9)

for i, c in enumerate(centers):
    plt.scatter(c[0], c[1], marker="$%d$" % i, alpha=0.6, s=50, edgecolor="k")

plt.axvline(gluc_scaled, color='k', linestyle='dashed', linewidth=1)
plt.axhline(BMI_scaled, color='k', linestyle='dashed', linewidth=1)
```

Out[ ]:

```
<matplotlib.lines.Line2D at 0x23e86ecf0a0>
```



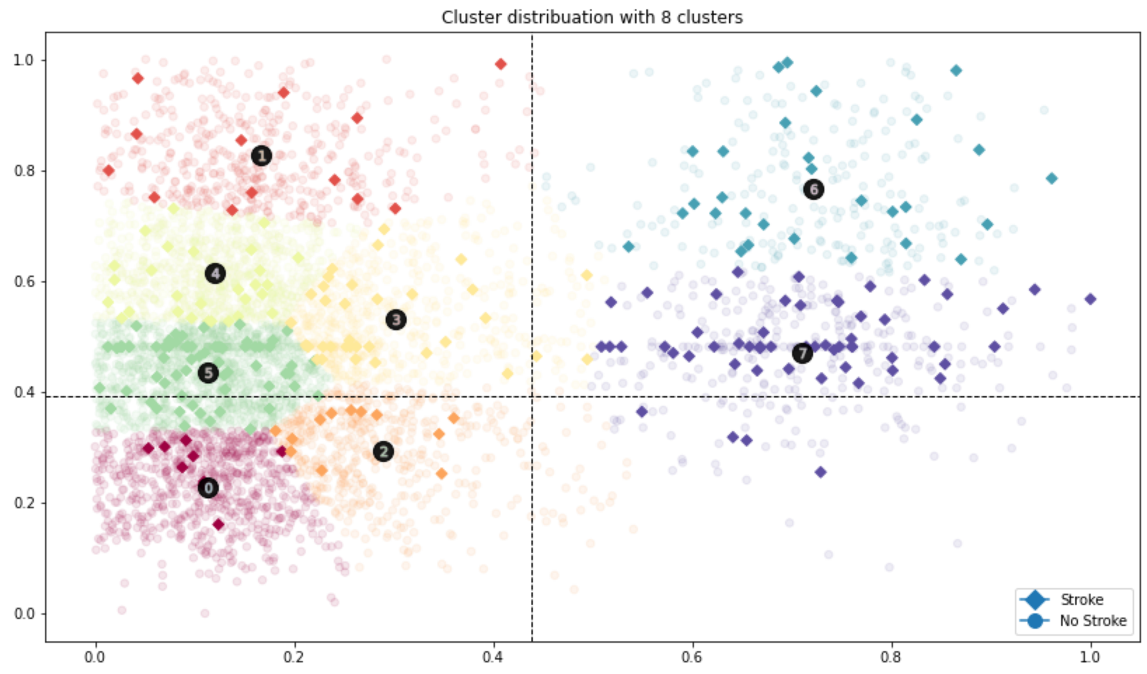
Cluster analysis

In [ ]:
```
gluc_bmi_stroke = df[["avg_glucose_level","bmi", "stroke"]]
```

In [ ]:
```
#Outlier handling
Q1 = df["bmi"].quantile(0.25)
Q3 = df["bmi"].quantile(0.75)
IQR = Q3 - Q1
gluc_bmi_stroke = gluc_bmi_stroke.loc[(gluc_bmi_stroke['bmi'] > (Q1-(1.5*IQR))) & (gluc_bmi_stroke['bmi'] < (Q3+(1.5*IQR)))]
```

In [ ]:
```
gluc_bmi_stroke = MinMaxScaler().fit_transform(gluc_bmi_stroke)
gluc_bmi_stroke = pd.DataFrame(gluc_bmi_stroke,columns=["avg_glucose_level","bmi", "stroke"])
```

In [ ]:
```
from matplotlib.lines import Line2D

kmeans = KMeans(n_clusters=8)
kmeans.fit(gluc_bmi_stroke[["avg_glucose_level","bmi"]])
y_kmeans = kmeans.predict(gluc_bmi_stroke[["avg_glucose_level","bmi"]])

fig, ax = plt.subplots(figsize=(14,8))

# add clusters to df
gluc_bmi_stroke["cluster"] = y_kmeans
# split df into strokes and non-strokes
non_strokes = gluc_bmi_stroke[gluc_bmi_stroke["stroke"] == 0]
strokes = gluc_bmi_stroke[gluc_bmi_stroke["stroke"] == 1]

# plot non-strokes
ax.scatter(non_strokes["avg_glucose_level"], non_strokes["bmi"], c=non_strokes["cluster"], s=30, marker='o', alpha=0.1, cmap='Spectral')

# plot strokes
scatter = ax.scatter(strokes["avg_glucose_level"], strokes["bmi"], c=strokes["cluster"], s=30, marker='D', cmap='Spectral')
centers = kmeans.cluster_centers_
ax.scatter(centers[:, 0], centers[:, 1], c='black', s=200, alpha=0.9)

# legend for cluster numbers
for i, c in enumerate(centers):
    plt.scatter(c[0], c[1], marker="$%d$" % i, alpha=0.6, s=50, edgecolor="white")

# legend for stroke/no stroke
legend_elements = [Line2D([0], [0], marker='D', label='Stroke', markersize=10),
                   Line2D([0], [0], marker='o', label='No Stroke', markersize=10)]

legend2 = ax.legend(handles=legend_elements, loc='lower right', prop={'size':10})


plt.axvline(gluc_scaled, color='k', linestyle='dashed', linewidth=1)
plt.axhline(BMI_scaled, color='k', linestyle='dashed', linewidth=1)

plt.title(f"Cluster distribuation with 8 clusters")
plt.savefig("two_dim_k8.png")
plt.show()
```



In [ ]:
```
# Calculate percentage of stroke cases for each cluster
total_strokes = strokes.shape[0]

for cluster in np.unique(y_kmeans):

    #share of data points
    shares = pd.DataFrame(gluc_bmi_stroke["cluster"].value_counts()/gluc_bmi_stroke.shape[0])
    shares = shares.sort_index()
    share = shares["cluster"][cluster]

    stroke_cases_cluster = strokes[strokes["cluster"] == cluster].shape[0]
    non_stroke_cases_cluster = non_strokes[non_strokes["cluster"] == cluster].shape[0]
    cluster_ratio = stroke_cases_cluster/(stroke_cases_cluster+non_stroke_cases_cluster)
    overall_stroke_percent = stroke_cases_cluster/total_strokes

    print(f"cluster {cluster}: {cluster_ratio:.2%} in cluster strokes, {overall_stroke_percent:.2%} of all strokes, {share:.2%} of all data po
```

```
cluster 0: 1.28% in cluster strokes, 3.66% of all strokes, 14.11% of all data points
cluster 1: 2.90% in cluster strokes, 5.28% of all strokes, 9.01% of all data points
cluster 2: 2.30% in cluster strokes, 4.88% of all strokes, 10.45% of all data points
cluster 3: 5.79% in cluster strokes, 14.23% of all strokes, 12.14% of all data points
cluster 4: 3.46% in cluster strokes, 11.38% of all strokes, 16.23% of all data points
cluster 5: 5.05% in cluster strokes, 26.42% of all strokes, 25.82% of all data points
cluster 6: 12.18% in cluster strokes, 11.79% of all strokes, 4.78% of all data points
cluster 7: 14.78% in cluster strokes, 22.36% of all strokes, 7.46% of all data points
```

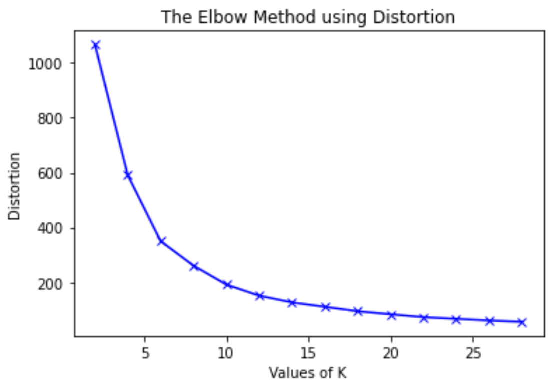
Multidimensional clustering

In [ ]:
```
data = df[["age","avg_glucose_level", "heart_disease", "hypertension", "stroke"]]
scaler = MinMaxScaler()
data = scaler.fit_transform(data)
data = pd.DataFrame(data,columns=["age","avg_glucose_level", "heart_disease", "hypertension", "stroke"])
data.head(3)
```

Out[ ]:

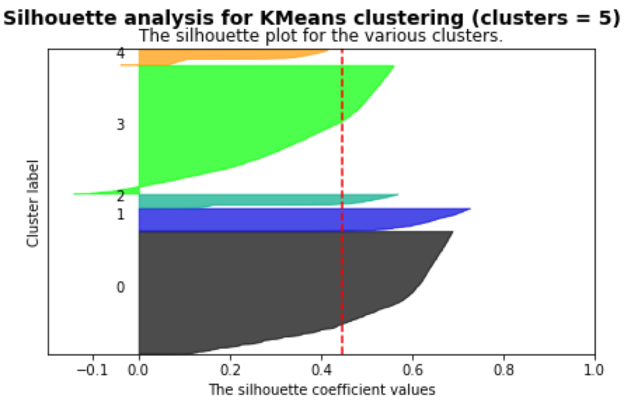
	age	avg_glucose_level	heart_disease	hypertension	stroke
0	0.816895	0.801265	1.0	0.0	1.0
1	0.743652	0.679023	0.0	0.0	1.0
2	0.975586	0.234512	1.0	0.0	1.0

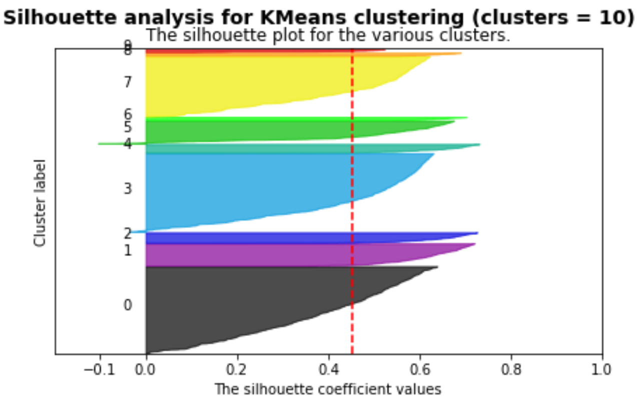
In [ ]:
```
distortions = []

K = range(2,30,2)

for k in K:
    kmeanModel = KMeans(n_clusters=k).fit(data)
    kmeanModel.fit(data)
    distortions.append(kmeanModel.inertia_)

plt.plot(K, distortions, 'bx-')
plt.xlabel('Values of K')
plt.ylabel('Distortion')
plt.title('The Elbow Method using Distortion')
plt.savefig("mul_dim_elbow.png")
plt.show()
```

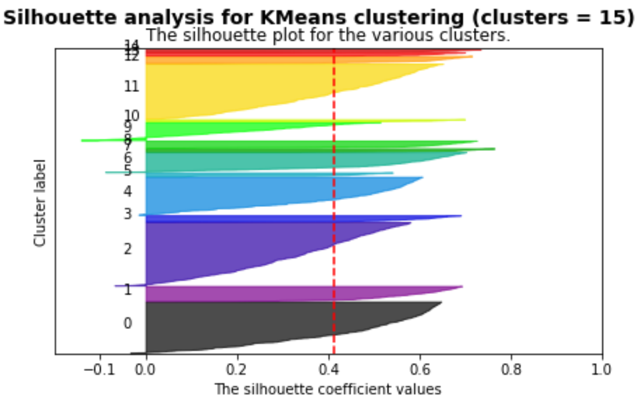


In [ ]:

```
#https://scikit-learn.org/stable/auto_examples/cluster/plot_kmeans_silhouette_analysis.html

X = data

range_n_clusters = [5,10,15]

for n_clusters in range_n_clusters:
    fig, ax = plt.subplots()
    fig.set_size_inches(7, 4)
    ax.set_xlim([-0.2, 1])
    ax.set_ylim([0, len(X) + (n_clusters + 1) * 10])

    clusterer = KMeans(n_clusters=n_clusters, random_state=10)
    cluster_labels = clusterer.fit_predict(X)

    silhouette_avg = silhouette_score(X, cluster_labels)
    sample_silhouette_values = silhouette_samples(X, cluster_labels)

    y_lower = 10
    for i in range(n_clusters):

        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 = cm.nipy_spectral(float(i) / n_clusters)
        ax.fill_betweenx(
            np.arange(y_lower, y_upper),
            0,
            ith_cluster_silhouette_values,
            facecolor=color,
            edgecolor=color,
            alpha=0.7,
        )

        # Label the silhouette plots with their cluster numbers at the middle
        ax.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

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

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

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

    plt.suptitle(
        "Silhouette analysis for KMeans clustering (clusters = %d)"
        % n_clusters,
        fontsize=14,
        fontweight="bold",
    )

    plt.savefig("mul_dim_silhouette.png")

    plt.show()
```







In [ ]:
```
kmeans = KMeans(n_clusters=15)
kmeans.fit(data[["age", "avg_glucose_level", "heart_disease", "hypertension"]])
y_kmeans = kmeans.predict(data[["age", "avg_glucose_level", "heart_disease", "hypertension"]])
data["cluster"] = y_kmeans

# split into stroke and non stroke cases
non_strokes = data[data["stroke"] == 0]
strokes = data[data["stroke"] == 1]
```

In [ ]:
```
def rev_min_max_func(scaled_val,target):
    max_val = max(df[target])
    min_val = min(df[target])
    val = (scaled_val*(max_val - min_val)) + min_val
    return val
```

In [ ]:
```
data.head()
```

Out[ ]:

	age	avg_glucose_level	heart_disease	hypertension	stroke	cluster
0	0.816895	0.801265	1.0	0.0	1.0	5
1	0.743652	0.679023	0.0	0.0	1.0	3
2	0.975586	0.234512	1.0	0.0	1.0	11
3	0.597168	0.536008	0.0	0.0	1.0	12
4	0.963379	0.549349	0.0	1.0	1.0	7

In [ ]:
```
for cluster in range(data["cluster"].max()+1):
    temp = data[data["cluster"]==cluster]
    print("cluster: " + str(cluster))
    print("age_mean: " + str(round(rev_min_max_func(temp["age"].mean(),"age"),2)))
    print("gluc_mean: " + str(round(rev_min_max_func(temp["avg_glucose_level"].mean(),"avg_glucose_level"),2)))
    print("heart_dis: " + str(temp["heart_disease"].sum()))
    print("hypertension: " + str(temp["hypertension"].sum()))
    print("size: " + str(temp.shape[0]) + ", strokes: " + str(temp["stroke"].sum()))
    print("in cluster share: " + str(round(((temp["stroke"].sum()/temp.shape[0])*100),2)) + "%")
    print("share of all strokes: " + str(round(((temp["stroke"].sum()/data["stroke"].sum())*100),2)) + "%")
    print("\n")
```

```
cluster: 0
```

```
age_mean: 56.07
gluc_mean: 80.11
heart_dis: 0.0
hypertension: 0.0
size: 707, strokes: 24.0
in cluster share: 3.39%
share of all strokes: 9.64%


cluster: 1
age_mean: 23.28
gluc_mean: 80.3
heart_dis: 0.0
hypertension: 0.0
size: 664, strokes: 1.0
in cluster share: 0.15%
share of all strokes: 0.4%


cluster: 2
age_mean: 70.89
gluc_mean: 88.73
heart_dis: 0.0
hypertension: 156.0
size: 156, strokes: 24.0
in cluster share: 15.38%
share of all strokes: 9.64%


cluster: 3
age_mean: 65.78
gluc_mean: 213.81
heart_dis: 0.0
hypertension: 0.0
size: 277, strokes: 37.0
in cluster share: 13.36%
share of all strokes: 14.86%


cluster: 4
age_mean: 70.58
gluc_mean: 151.21
heart_dis: 64.0
hypertension: 64.0
size: 64, strokes: 13.0
in cluster share: 20.31%
share of all strokes: 5.22%


cluster: 5
age_mean: 68.74
gluc_mean: 211.75
heart_dis: 72.0
hypertension: 0.0
size: 72, strokes: 18.0
in cluster share: 25.0%
share of all strokes: 7.23%


cluster: 6
age_mean: 17.91
gluc_mean: 126.73
heart_dis: 0.0
hypertension: 0.0
size: 332, strokes: 0.0
in cluster share: 0.0%
share of all strokes: 0.0%


cluster: 7
age_mean: 64.85
gluc_mean: 204.89
heart_dis: 0.0
hypertension: 142.0
size: 142, strokes: 22.0
in cluster share: 15.49%
share of all strokes: 8.84%


cluster: 8
age_mean: 50.19
gluc_mean: 122.26
heart_dis: 0.0
hypertension: 0.0
size: 401, strokes: 14.0
in cluster share: 3.49%
share of all strokes: 5.62%


cluster: 9
age_mean: 6.43
gluc_mean: 85.83
heart_dis: 0.0
hypertension: 0.0
size: 581, strokes: 1.0
in cluster share: 0.17%
share of all strokes: 0.4%


cluster: 10
age_mean: 74.11
gluc_mean: 88.76
heart_dis: 0.0
hypertension: 0.0
size: 483, strokes: 60.0
in cluster share: 12.42%
```

```
share of all strokes: 24.1%


cluster: 11
age_mean: 66.81
gluc_mean: 91.71
heart_dis: 140.0
hypertension: 0.0
size: 140, strokes: 16.0
in cluster share: 11.43%
share of all strokes: 6.43%


cluster: 12
age_mean: 36.62
gluc_mean: 198.48
heart_dis: 0.0
hypertension: 0.0
size: 138, strokes: 2.0
in cluster share: 1.45%
share of all strokes: 0.8%


cluster: 13
age_mean: 45.69
gluc_mean: 89.86
heart_dis: 0.0
hypertension: 136.0
size: 136, strokes: 7.0
in cluster share: 5.15%
share of all strokes: 2.81%


cluster: 14
age_mean: 38.7
gluc_mean: 84.56
heart_dis: 0.0
hypertension: 0.0
size: 817, strokes: 10.0
in cluster share: 1.22%
share of all strokes: 4.02%
```

Visuals

In [ ]:
```
#pip install plotly
```

In [ ]:
```
import plotly
import plotly.graph_objs as go
plotly.offline.init_notebook_mode()
```

In [ ]:
```
from sklearn.decomposition import PCA

# Create a PCA model to reduce our data to 2 dimensions for visualisation
pca = PCA(n_components=3)
pca.fit(data[["age", "avg_glucose_level", "heart_disease", "hypertension"]])

# Transform the scaled data to the new PCA space
X_reduced = pca.transform(data[["age", "avg_glucose_level", "heart_disease", "hypertension"]])

# Convert to df
reduced_df = pd.DataFrame(X_reduced, index=X.index, columns=['PC1','PC2', 'PC3'])

# # Add clusters and strokes
reduced_df["cluster"] = y_kmeans
reduced_df["stroke"] = data["stroke"]
reduced_df["heart_disease"] = data["heart_disease"]
reduced_df["hypertension"] = data["hypertension"]
```

In [ ]:
```
reduced_df.head(3)
```

Out[ ]:

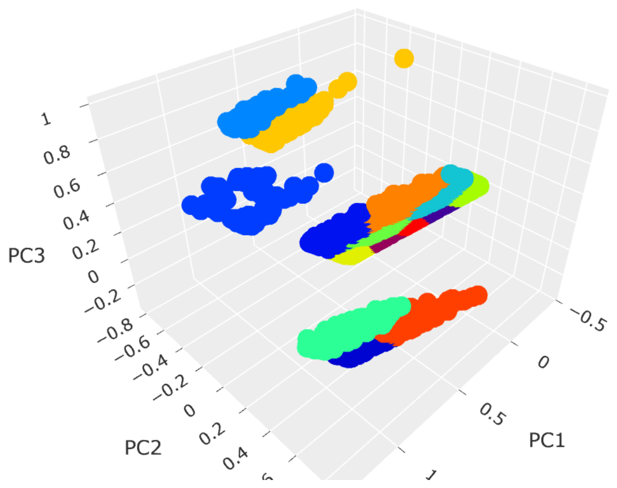
	PC1	PC2	PC3	cluster	stroke	heart_disease	hypertension
0	0.508949	-0.710741	0.708314	5	1.0	1.0	0.0
1	0.163670	-0.236083	-0.088964	3	1.0	0.0	0.0
2	0.462517	-0.709081	0.517663	11	1.0	1.0	0.0

In [ ]:
```
for x in range(0,max(reduced_df["cluster"])+1):
    temp = reduced_df[reduced_df["cluster"]==x]
    print("Cluster: " + str(x) + ", strokes: " + str(sum(temp["stroke"])) + ", out of " + str(temp.stroke.count()))
```

```
Cluster: 0, strokes: 24.0, out of 707
Cluster: 1, strokes: 1.0, out of 664
Cluster: 2, strokes: 24.0, out of 156
Cluster: 3, strokes: 37.0, out of 277
Cluster: 4, strokes: 13.0, out of 64
Cluster: 5, strokes: 18.0, out of 72
Cluster: 6, strokes: 0.0, out of 332
Cluster: 7, strokes: 22.0, out of 142
Cluster: 8, strokes: 14.0, out of 401
Cluster: 9, strokes: 1.0, out of 581
Cluster: 10, strokes: 60.0, out of 483
Cluster: 11, strokes: 16.0, out of 140
Cluster: 12, strokes: 2.0, out of 138
Cluster: 13, strokes: 7.0, out of 136
Cluster: 14, strokes: 10.0, out of 817
```

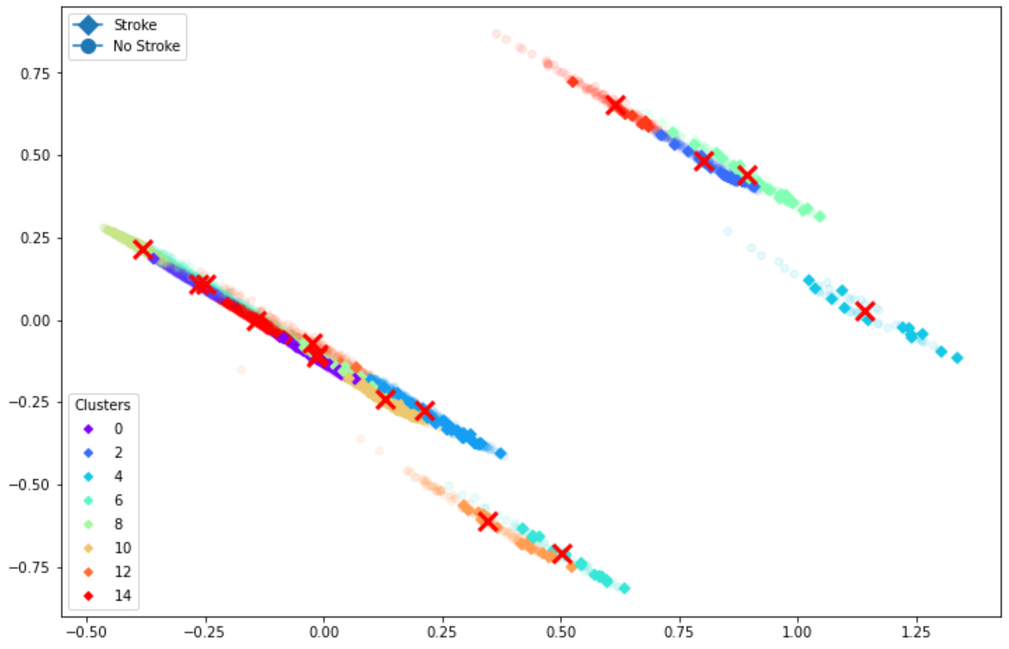
In [ ]:
```
# would also be nice to show the cluster centres,
#but we need to apply the same PCA transformation that we gave to the actual data points,
#so that they can appear in the new 2 dimensional PCA space
centres_reduced = pca.transform(kmeans.cluster_centers_)
```

In [ ]:
```
import plotly.express as px
px.defaults.color_continuous_scale = px.colors.sequential.Rainbow
px.defaults.template = "ggplot2"

df = reduced_df
fig = px.scatter_3d(df, x='PC1', y='PC2', z='PC3', color='cluster')
fig.show()
```



2-d visual

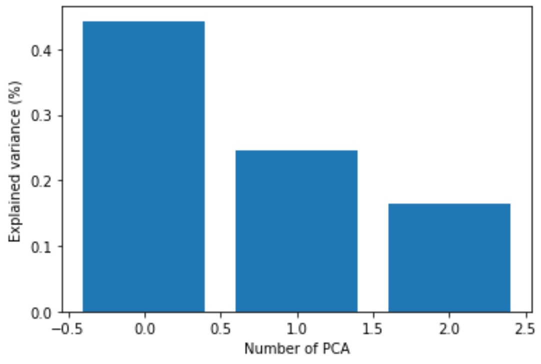
In [ ]:
```
# Plot the results (Only works for 2 dimensions)
fig, ax = plt.subplots(figsize=(12,8))

non_strokes = reduced_df[reduced_df["stroke"] == 0]
strokes = reduced_df[reduced_df["stroke"] == 1]

# plot non-strokes
ax.scatter(non_strokes["PC1"], non_strokes["PC2"], c=non_strokes["cluster"], s=30, marker='o', alpha=0.1, cmap='rainbow')
# and strokes
scatter = ax.scatter(strokes["PC1"], strokes["PC2"], c=strokes["cluster"], s=30, marker='D', cmap='rainbow')
# plot cluster centers
ax.scatter(centres_reduced[:, 0], centres_reduced[:, 1],
            marker='x', s=169, linewidths=3,
            color='r', zorder=10)
# legend for cluster numbers
legend1 = ax.legend(*scatter.legend_elements(),
                    loc="lower left", title="Clusters", prop={'size': 10})
ax.add_artist(legend1)
# legend for stroke/no stroke
legend_elements = [Line2D([0], [0], marker='D', label='Stroke', markersize=10),
                   Line2D([0], [0], marker='o', label='No Stroke', markersize=10),
                  ]
legend2 = ax.legend(handles=legend_elements, loc='upper left', prop={'size': 10})
plt.savefig("mul_dim_visu.png")
plt.show()
```



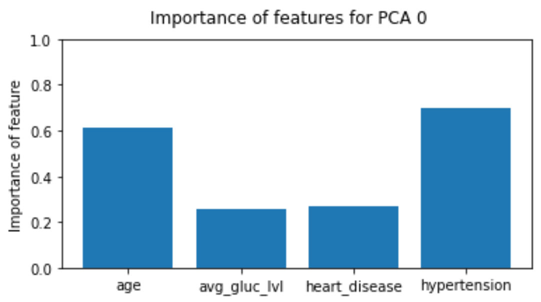
PCA visuals

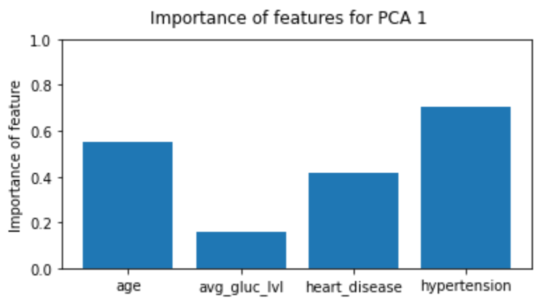
```
In [ ]: variance = pca.explained_variance_ratio_
        fig, ax = plt.subplots()
        ax.bar([0,1,2], variance)
        ax.set_ylabel("Explained variance (%)")
        ax.set_xlabel("Number of PCA")

        print("explanied variance summed: " + str(sum(variance).round(2)))
```

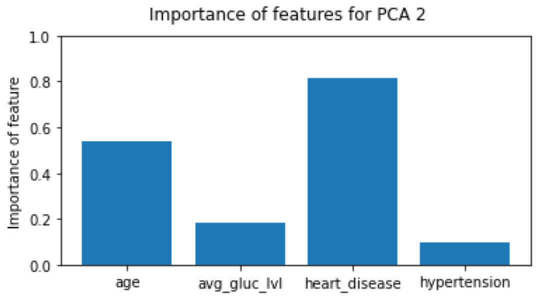
```
explanied variance summed: 0.85
```



```
In [ ]: for c in range(3):
            abs(pca.components_)
            first_component = abs(pca.components_[c])
            x = ["age", "avg_gluc_lvl", "heart_disease", "hypertension"]
            fig, ax = plt.subplots(figsize=(6, 3))
            ax.set_ylim(0, 1)
            ax.bar(x, first_component)
            ax.set_ylabel("Importance of feature")
            fig.suptitle("Importance of features for PCA " + str(c))
```






Importance of features for PCA 2
Importance of feature
1.0
0.8
0.6
0.4
0.2
0.0
age
avg_gluc_lvl
heart_disease
hypertension

```
In [ ]:
```