Assignment: Simplifying Cancer Treatment

The comments/sections provided are your cues to perform the assignment. You don't need to limit yourself to the number of rows/cells provided. You can add additional rows in each section to add more lines of code.

If at any point in time you need help on solving this assignment, view our demo video to understand the different steps of the code.

Happy coding!

Simplifying Cancer Treatment

DESCRIPTION

John Cancer Hospital (JCH) is a leading cancer hospital in USA. It specializes in treating breast cancer. Over the last few years, JCH has collected breast cancer data from patients who came for screening/treatment. However, this data has almost 30 attributes, and it is difficult to run and interpret the results. You, as an ML expert, have to reduce the number of attributes (Dimensionality Reduction) so that the results are meaningful and accurate.

Objective: Reduce the number of attributes/features in data to make the analysis of the results comprehensible to doctors.

Actions to Perform:

```
Use pandas to read data as a dataframe.
Check the data. There should be no missing values.
Convert the diagnosis column to 1/0 and store in a new column target.
Store the encoded column in dataframe and drop the diagnosis column for
simplicity.
Scale the data so that each feature has a single unit variance.
Transform this data to its first 2 principal components.
Plot the two dimensions.
Print the explained variance.
Try the same with 3 principal components.
Check the accuracy for 2nd and 3rd components.
```

Table of Contents

Import Libraries

In [1]:
```
import matplotlib.pyplot as plt
import pandas as pd
import numpy as np
import seaborn as sns
%matplotlib inline
```

Use pandas to read data as a dataframe.

In [2]:
```
df = pd.read_csv('breast-cancer-data.csv')
df.head()
```

Out[2]:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactn
0	842302	M	17.99	10.38	122.80	1001.0	0.11840	
1	842517	M	20.57	17.77	132.90	1326.0	0.08474	
2	84300903	M	19.69	21.25	130.00	1203.0	0.10960	
3	84348301	M	11.42	20.38	77.58	386.1	0.14250	
4	84358402	M	20.29	14.34	135.10	1297.0	0.10030	

5 rows × 32 columns

Data Set: Cancer Data Set

Features are computed from a digitized image of a Fine-Needle Aspirate (FNA) of a breast mass. They describe characteristics of the cell nuclei present in the image. n the 3-dimensional space is that described in: [K. P. Bennett and O. L. Mangasarian: "Robust Linear Programming Discrimination of Two Linearly Inseparable Sets", Optimization Methods and Software 1, 1992, 23-34].

This database is also available through the UW CS ftp server: ftp ftp.cs.wisc.edu cd math-prog/cpo-dataset/machine-learn/WDBC/

Also can be found on UCI Machine Learning Repository: https://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+(Diagnostic)

Attribute Information:

```
1) ID number
2) Diagnosis (M = malignant, B = benign)
```

Ten real-valued features are computed for each cell nucleus:

```
a) radius (mean of distances from center to points on the perimeter)
b) texture (standard deviation of gray-scale values)
c) perimeter
d) area
e) smoothness (local variation in radius lengths)
f) compactness (perimeter^2 / area - 1.0)
g) concavity (severity of concave portions of the contour)
h) concave points (number of concave portions of the contour)
i) symmetry
j) fractal dimension ("coastline approximation" - 1)
```

The mean, standard error and "worst" or largest (mean of the three largest values) of these features were computed for each image, resulting in 30 features. For instance, field 3 is Mean Radius, field 13 is Radius SE, field 23 is Worst Radius.

All feature values are recoded with four significant digits.

Missing attribute values: none

Class distribution: 357 benign, 212 malignant

Check the data, there should be no missing values

In [3]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 32 columns):
 #   Column                   Non-Null Count  Dtype  
---  ------                   --------------  -----  
 0   id                       569 non-null    int64  
 1   diagnosis                569 non-null    object 
 2   radius_mean              569 non-null    float64
 3   texture_mean             569 non-null    float64
 4   perimeter_mean           569 non-null    float64
 5   area_mean                569 non-null    float64
 6   smoothness_mean          569 non-null    float64
 7   compactness_mean         569 non-null    float64
 8   concavity_mean           569 non-null    float64
 9   concave points_mean      569 non-null    float64
 10  symmetry_mean            569 non-null    float64
 11  fractal_dimension_mean   569 non-null    float64
 12  radius_se                569 non-null    float64
 13  texture_se               569 non-null    float64
 14  perimeter_se             569 non-null    float64
 15  area_se                  569 non-null    float64
 16  smoothness_se            569 non-null    float64
 17  compactness_se           569 non-null    float64
 18  concavity_se             569 non-null    float64
 19  concave points_se        569 non-null    float64
 20  symmetry_se              569 non-null    float64
 21  fractal_dimension_se     569 non-null    float64
 22  radius_worst             569 non-null    float64
 23  texture_worst            569 non-null    float64
 24  perimeter_worst          569 non-null    float64
 25  area_worst               569 non-null    float64
 26  smoothness_worst         569 non-null    float64
 27  compactness_worst        569 non-null    float64
 28  concavity_worst          569 non-null    float64
 29  concave points_worst     569 non-null    float64
 30  symmetry_worst           569 non-null    float64
 31  fractal_dimension_worst  569 non-null    float64
dtypes: float64(30), int64(1), object(1)
memory usage: 140.1+ KB
```

In [4]:
```
feature_names = np.array(['mean radius' 'mean texture' 'mean perimeter' 'mean area'
 'mean smoothness' 'mean compactness' 'mean concavity'
 'mean concave points' 'mean symmetry' 'mean fractal dimension'
 'radius error' 'texture error' 'perimeter error' 'area error'
 'smoothness error' 'compactness error' 'concavity error'
 'concave points error' 'symmetry error' 'fractal dimension error'
 'worst radius' 'worst texture' 'worst perimeter' 'worst area'
 'worst smoothness' 'worst compactness' 'worst concavity'
 'worst concave points' 'worst symmetry' 'worst fractal dimension'])
```

Convert diagnosis column to 1/0 and store in new column target

In [5]:
```
from sklearn.preprocessing import LabelEncoder

# # Encode label diagnosis
# # M -> 1
# # B -> 0

# Get All rows, but only last column
target_data=df["diagnosis"]

encoder = LabelEncoder()
target_data = encoder.fit_transform(target_data)
```

Store the encoded column in dataframe and drop the diagnosis column for simpilcity

In [6]:
```
df.drop(["diagnosis"],axis = 1, inplace = True)
```

Scale data so that each feature has a single unit variance.

Principal Component Analysis: PCA

Let's use PCA to find the first two principal components, and visualize the data in this new, two-dimensional space, with a single scatter-plot

In [7]:
```
from sklearn.preprocessing import StandardScaler
```

In [8]:
```
scaler = StandardScaler()
scaler.fit(df)
```

Out[8]: `StandardScaler()`

In [9]:
```
scaled_data = scaler.transform(df)
```

Now, you can transform this data to its first 2 principal components.

In [10]:
```
from sklearn.decomposition import PCA
```

In [11]:
```
pca = PCA(n_components=2)
```

In [12]:
```
pca.fit(scaled_data)
```

Out[12]: `PCA(n_components=2)`

Transform this data to its first 2 principal components

In [13]:
```
x_pca = pca.transform(scaled_data)
```

In [14]:
```
scaled_data.shape
```

Out[14]: `(569, 31)`

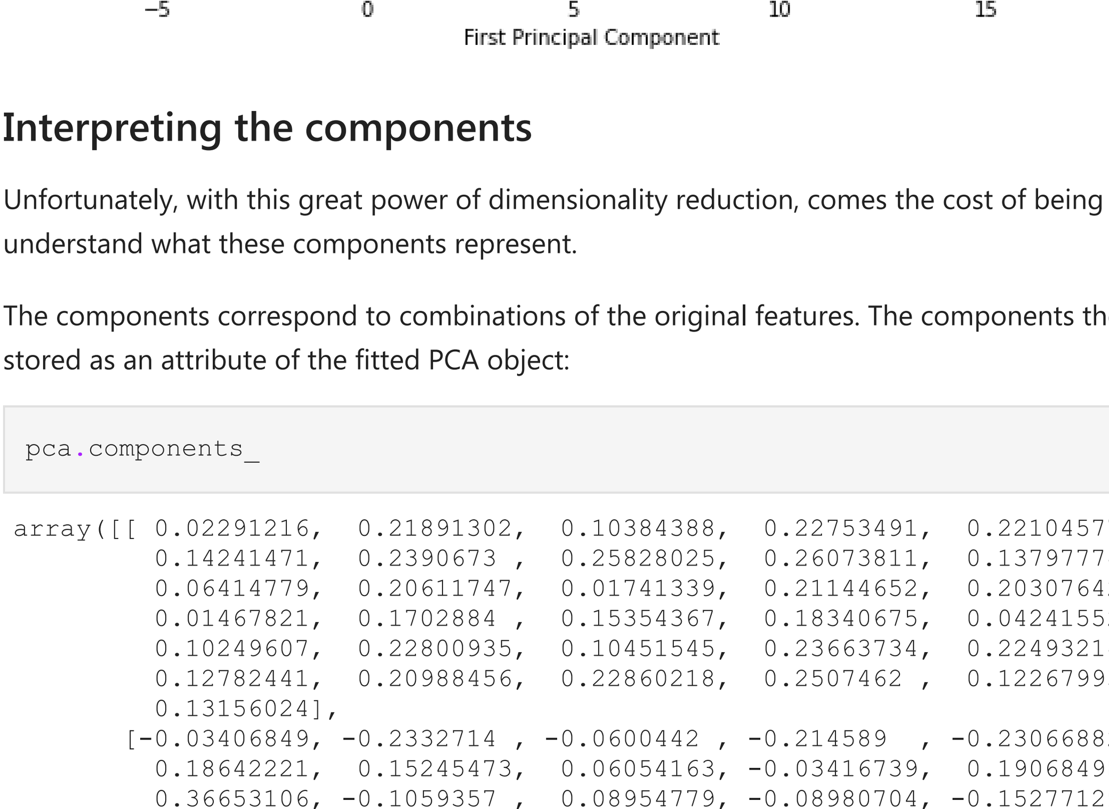
In [15]:
```
x_pca.shape
```

Out[15]: `(569, 2)`

plot the two dimensions

In [16]:
```
plt.figure(figsize=(9,6))
plt.scatter(x_pca[:,0],x_pca[:,1],c=target_data,cmap='viridis')
plt.xlabel('First Principal Component')
plt.ylabel('Second Principal Component')
```

Out[16]: `Text(0, 0.5, 'Second Principal Component')`



Interpreting the components

Unfortunately, with this great power of dimensionality reduction, comes the cost of being able to easily understand what these components represent.

The components correspond to combinations of the original features. The components themselves are stored as an attribute of the fitted PCA object:

In [17]:
```
pca.components_
```

Out[17]:
```
array([[ 0.02291216,  0.21891302,  0.10384388,  0.22753491,  0.22104577,
         0.14241471,  0.2390673 ,  0.25828025,  0.26073811,  0.13797774,
         0.06414779,  0.20611747,  0.01741339,  0.21144652,  0.20307642,
         0.01467821,  0.1702884 ,  0.15354367,  0.18340675,  0.04241552,
         0.10249607,  0.22800935,  0.10451545,  0.23663734,  0.22493214,
         0.12782441,  0.20988456,  0.22860218,  0.2507462 ,  0.12267993,
         0.13156024],
       [-0.03406849, -0.2332714 , -0.0600442 , -0.214589  , -0.23066882,
         0.18642221,  0.15245473,  0.06054163, -0.03416739,  0.19068498,
         0.36653106, -0.1059357 ,  0.08954779, -0.08980704, -0.15277129,
         0.20318988,  0.23250336,  0.19684608,  0.12996518,  0.18355863,
         0.27958414, -0.21929604, -0.04550122, -0.19929599, -0.21898546,
         0.17256296,  0.14425364,  0.09852652, -0.00753437,  0.14261944,
         0.27570208]])
```

Print the Explained Variance

The explained variance tells you how much information (variance) can be attributed to each of the principal components. This is important as you can convert n dimensional space to 2 dimensional space, you lose some of the variance (information).

In [18]:
```
print(pca.explained_variance_ratio_)
```

```
[0.42864701 0.18376792]
```

Try with 3 Principal Components

In [19]:
```
pca_3 = PCA(n_components=3)
pca_3.fit(scaled_data)
x_pca_3 = pca_3.transform(scaled_data)
```

In this numpy matrix array, each row represents a principal component, and each column relates back to the original features. You can visualize this relationship with a heatmap:

In [20]:
```
x_pca_3.shape
```

Out[20]: `(569, 3)`

In [21]:
```
pca_3.explained_variance_ratio_
```

Out[21]: `array([0.42864701, 0.18376792, 0.09146436])`

check the accuracy for 2nd and 3rd components

In [22]:
```
from sklearn.model_selection import train_test_split
```

In [23]:
```
train_data, test_data, train_output, test_output = train_test_split( df, target_data,
```

In [24]:
```
train_data = scaler.transform(train_data)
test_data = scaler.transform(test_data)
```

In [25]:
```
train_data = pca.transform(train_data)
test_data = pca.transform(test_data)
```

Score for 2nd components

In [26]:
```
from sklearn.linear_model import LogisticRegression
logisticRegr = LogisticRegression(solver = 'lbfgs')
logisticRegr.fit(train_data, train_output)
```

Out[26]: `LogisticRegression()`

In [27]:
```
logisticRegr.score(test_data, test_output)
```

Out[27]: `0.9473684210526315`

Score for 3rd components

In [28]:
```
train_data, test_data, train_output, test_output = train_test_split( df, target_data,
train_data = scaler.transform(train_data)
test_data = scaler.transform(test_data)

train_data = pca_3.transform(train_data)
test_data = pca_3.transform(test_data)
logisticRegr = LogisticRegression(solver = 'lbfgs')

logisticRegr.fit(train_data, train_output)
logisticRegr.score(test_data, test_output)
```

Out[28]: `0.9415204678362573`