Pre-Processing the data

Introduction

Data preprocessing (http://www.cs.ccsu.edu/~markov/ccsu_courses/datamining-3.html) is a crucial step for any data analysis problem. It is often a very good idea to prepare your data in such way to best expose the structure of the problem to the machine learning algorithms that you intend to use.This involves a number of activities such as:

- Assigning numerical values to categorical data;
- Handling missing values; and
- Normalizing the features (so that features on small scales do not dominate when fitting a model to the data).

In [1]:

```
%matplotlib inline
import matplotlib.pyplot as plt

#Load libraries for data processing
import pandas as pd #data processing, CSV file I/O (e.g. pd.read_csv)
import numpy as np
from scipy.stats import norm

# visualization
import seaborn as sns
plt.style.use('fivethirtyeight')
sns.set_style("white")


plt.rcParams['figure.figsize'] = (8,4)
#plt.rcParams['axes.titlesize'] = 'large'

data = pd.read_csv('C:\data\clean-data.csv', index_col=False)
data.drop('Unnamed: 0',axis=1, inplace=True)
#data.head()
```

Label encoding

Here, I assign the 30 features to a NumPy array X, and transform the class labels from their original string representation (M and B) into integers

In [2]:

```
#Assign predictors to a variable of ndarray (matrix) type
array = data.values
X = array[:,1:31]
y = array[:,0]
```

In [3]:

```
#transform the class labels from their original string representation (M and B) into intege
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()
y = le.fit_transform(y)

#Call the transform method of LabelEncorder on two dummy variables
#le.transform (['M', 'B'])
```

> *After encoding the class labels(diagnosis) in an array y, the malignant tumors are now represented as class 1(i.e presence of cancer cells) and the benign tumors are represented as class 0 (i.e no cancer cells detection), respectively*, illustrated by calling the transform method of LabelEncorder on two dummy variables.**

Assesing Model Accuracy: Split data into training and test sets

The simplest method to evaluate the performance of a machine learning algorithm is to use different training and testing datasets. Here I will

- Split the available data into a training set and a testing set. (75% training, 25% test)
- Train the algorithm on the first part,
- make predictions on the second part and
- evaluate the predictions against the expected results.

In [7]:

```
from sklearn.model_selection import train_test_split

##Split data set in train 75% and test 25%
X_train, X_test, y_train, y_test = train_test_split( X, y, test_size=0.25, random_state=7)
```

Feature Standardization

- Standardization is a useful technique to transform attributes with a Gaussian distribution and differing means and standard deviations to a standard Gaussian distribution with a mean of 0 and a standard deviation of 1.
- As seen in NB2_Exploratory data analysis (https://github.com/ShiroJean/Breast-cancer-risk-prediction/blob/master/NB2_ExploratoryDataAnalysis.ipynb) the raw data has differing distributions which may have an impact on the most ML algorithms. Most machine learning and optimization algorithms behave much better if features are on the same scale.

Let's evaluate the same algorithms with a standardized copy of the dataset. Here, I use sklearn to scale and transform the data such that each attribute has a mean value of zero and a standard deviation of one

In [8]:

```
from sklearn.preprocessing import StandardScaler

# Normalize the  data (center around 0 and scale to remove the variance).
scaler =StandardScaler()
Xs = scaler.fit_transform(X)
```

```
F:\anaconda\lib\site-packages\sklearn\utils\validation.py:475: DataConversio
nWarning: Data with input dtype object was converted to float64 by StandardS
caler.
  warnings.warn(msg, DataConversionWarning)
F:\anaconda\lib\site-packages\sklearn\utils\validation.py:475: DataConversio
nWarning: Data with input dtype object was converted to float64 by StandardS
caler.
  warnings.warn(msg, DataConversionWarning)
```

Feature decomposition using Principal Component Analysis(PCA)

From the pair plot in NB2, lot of feature pairs divide nicely the data to a similar extent, therefore, it makes sense to use one of the dimensionality reduction methods to try to use as many features as possible and maintian as much information as possible when working with only 2 dimensions. I will use PCA

In [9]:

```
from sklearn.decomposition import PCA
# feature extraction
pca = PCA(n_components=10)
fit = pca.fit(Xs)
```

In [7]:

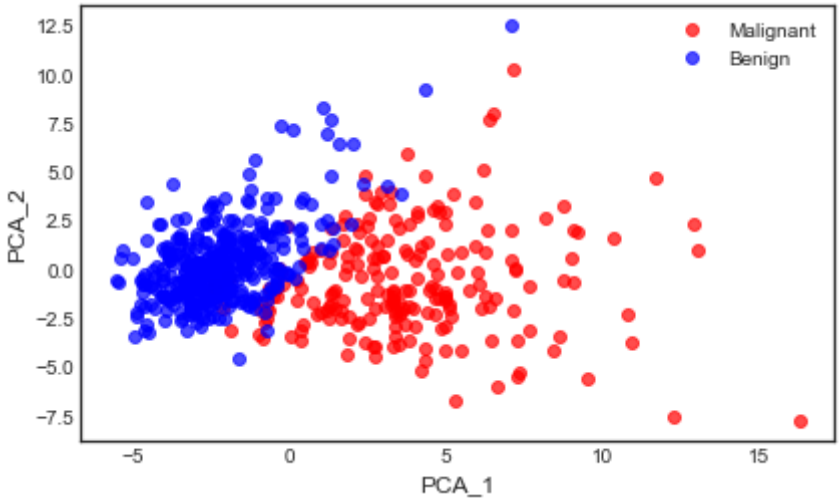
```
X_pca = pca.transform(Xs)

PCA_df = pd.DataFrame()

PCA_df['PCA_1'] = X_pca[:,0]
PCA_df['PCA_2'] = X_pca[:,1]

plt.plot(PCA_df['PCA_1'][data.diagnosis == 'M'],PCA_df['PCA_2'][data.diagnosis == 'M'],'o',
plt.plot(PCA_df['PCA_1'][data.diagnosis == 'B'],PCA_df['PCA_2'][data.diagnosis == 'B'],'o',

plt.xlabel('PCA_1')
plt.ylabel('PCA_2')
plt.legend(['Malignant','Benign'])
plt.show()
```



Now, what we got after applying the linear PCA transformation is a lower dimensional subspace (from 3D to 2D in this case), where the samples are “most spread” along the new feature axes.

In [10]:

```
#The amount of variance that each PC explains
var= pca.explained_variance_ratio_
```

Deciding How Many Principal Components to Retain

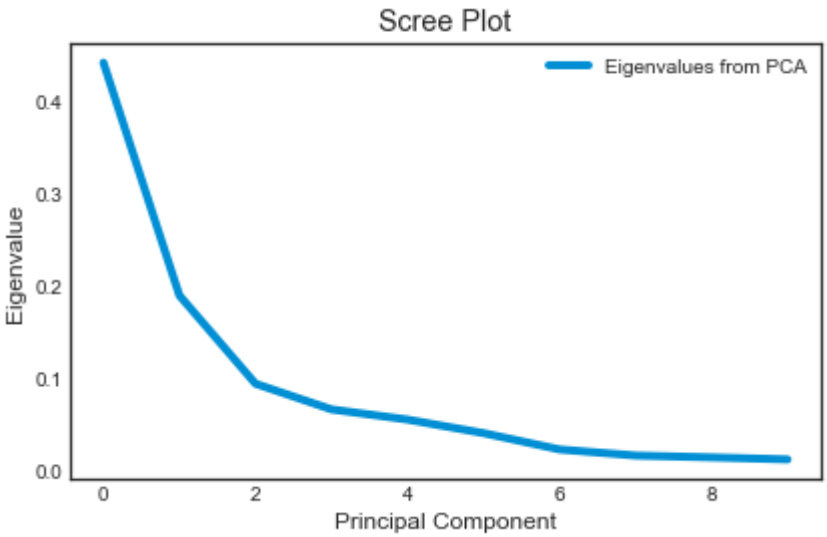
In order to decide how many principal components should be retained, it is common to summarise the results of a principal components analysis by making a scree plot.

In [11]:

```
#The amount of variance that each PC explains
var= pca.explained_variance_ratio_

plt.plot(var)
plt.title('Scree Plot')
plt.xlabel('Principal Component')
plt.ylabel('Eigenvalue')

leg = plt.legend(['Eigenvalues from PCA'], loc='best', borderpad=0.3,shadow=False,markersca
leg.get_frame().set_alpha(0.4)
leg.draggable(state=True)
plt.show()
```



Observation

The most obvious change in slope in the scree plot occurs at component 2, which is the “elbow” of the scree plot. Therefore, it cound be argued based on the basis of the scree plot that the first three components should be retained.