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2 - MDS

# Machine Learning Lab - 4

```
PCA v/s LDA

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```

CHRIST (Deemed to be University)

In [1]:

```
#Import statements
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
```

In [2]:

```
#ML libraries import
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score, roc_auc_score
from sklearn.feature_selection import VarianceThreshold
from sklearn.preprocessing import StandardScaler
```

In [3]:

```
#Using the inbuilt breast cancer dataset from scikit learn
from sklearn.datasets import load_breast_cancer
cancer = load_breast_cancer()
fl = pd.DataFrame(cancer['data'], columns=cancer['feature_names'])
fl.head()
```

Out[3]:

| | mean radius | mean texture | mean perimeter | mean area | mean smoothness | mean compactness | mean concavity | mean concave points | mean symmetry | mean fractal dimension | ... | worst radius | worst texture | wors perimete |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | 17.99 | 10.38 | 122.80 | 1001.0 | 0.11840 | 0.27760 | 0.3001 | 0.14710 | 0.2419 | 0.07871 | ... | 25.38 | 17.33 | 184.6 |
| **1** | 20.57 | 17.77 | 132.90 | 1326.0 | 0.08474 | 0.07864 | 0.0869 | 0.07017 | 0.1812 | 0.05667 | ... | 24.99 | 23.41 | 158.8 |
| **2** | 19.69 | 21.25 | 130.00 | 1203.0 | 0.10960 | 0.15990 | 0.1974 | 0.12790 | 0.2069 | 0.05999 | ... | 23.57 | 25.53 | 152.5 |
| **3** | 11.42 | 20.38 | 77.58 | 386.1 | 0.14250 | 0.28390 | 0.2414 | 0.10520 | 0.2597 | 0.09744 | ... | 14.91 | 26.50 | 98.8 |
| **4** | 20.29 | 14.34 | 135.10 | 1297.0 | 0.10030 | 0.13280 | 0.1980 | 0.10430 | 0.1809 | 0.05883 | ... | 22.54 | 16.67 | 152.2 |

5 rows × 30 columns

# Data Pre-processing

1. Dataset shape

In [4]:

```
print("Number of rows in dataset:", fl.shape[0])
print("Number of columns in dataset:", fl.shape[1])
```

```
Number of rows in dataset: 569
Number of columns in dataset: 30
```

2. Null Values

In [5]:
```
fl.isnull().sum()
```

Out[5]:
```
mean radius                0
mean texture               0
mean perimeter             0
mean area                  0
mean smoothness            0
mean compactness           0
mean concavity             0
mean concave points        0
mean symmetry              0
mean fractal dimension     0
radius error               0
texture error              0
perimeter error            0
area error                 0
smoothness error           0
compactness error          0
concavity error            0
concave points error       0
symmetry error             0
fractal dimension error    0
worst radius               0
worst texture              0
worst perimeter            0
worst area                 0
worst smoothness           0
worst compactness          0
worst concavity            0
worst concave points       0
worst symmetry             0
worst fractal dimension    0
dtype: int64
```

*There are no null values in the dataset.*

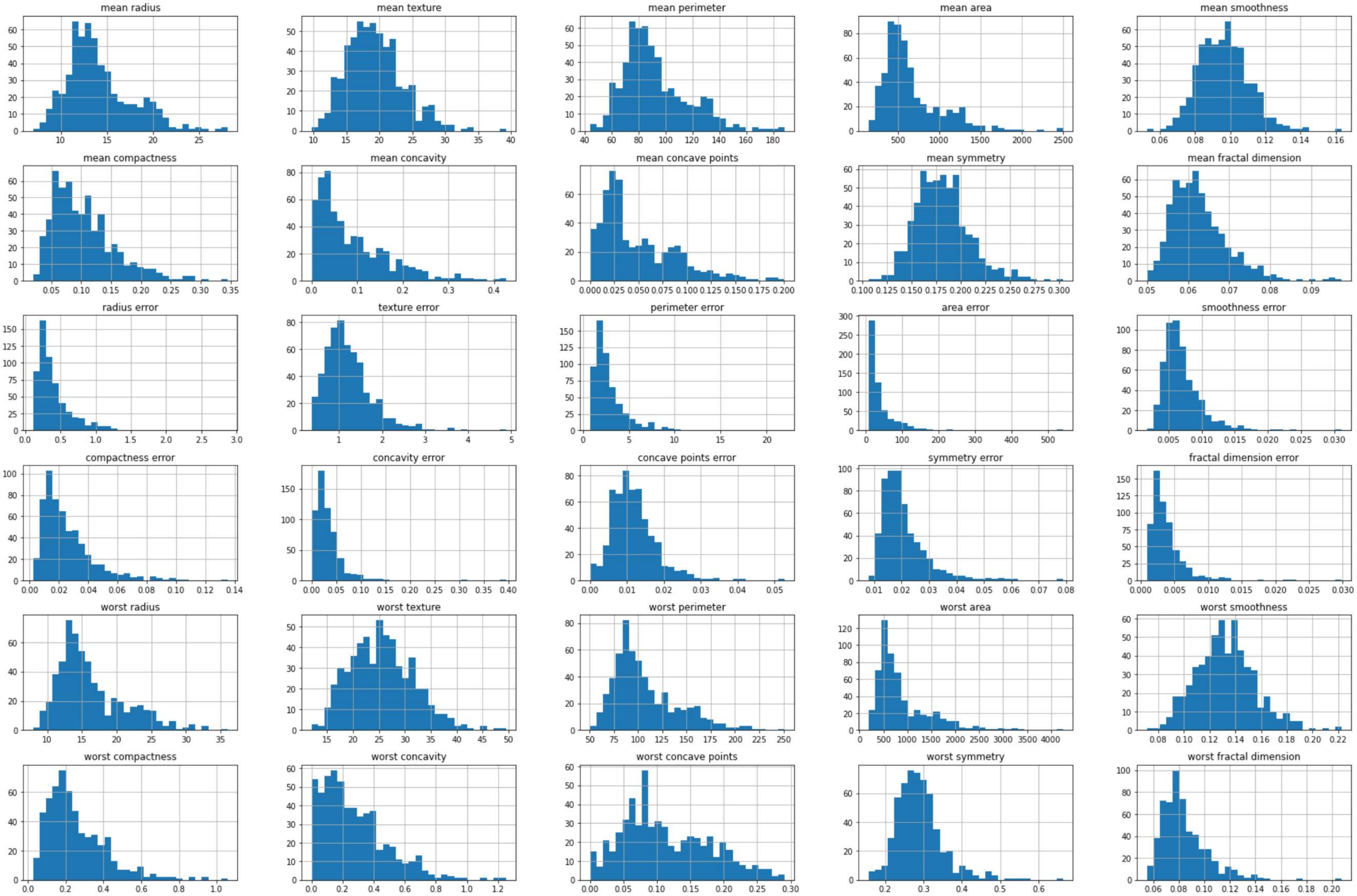
3. Data Distribution

In [6]:

```
fl.hist(bins=30, figsize=(30, 20))
```

Out[6]:

```
array([[<AxesSubplot:title={'center':'mean radius'}>,
        <AxesSubplot:title={'center':'mean texture'}>,
        <AxesSubplot:title={'center':'mean perimeter'}>,
        <AxesSubplot:title={'center':'mean area'}>,
        <AxesSubplot:title={'center':'mean smoothness'}>],
       [<AxesSubplot:title={'center':'mean compactness'}>,
        <AxesSubplot:title={'center':'mean concavity'}>,
        <AxesSubplot:title={'center':'mean concave points'}>,
        <AxesSubplot:title={'center':'mean symmetry'}>,
        <AxesSubplot:title={'center':'mean fractal dimension'}>],
       [<AxesSubplot:title={'center':'radius error'}>,
        <AxesSubplot:title={'center':'texture error'}>,
        <AxesSubplot:title={'center':'perimeter error'}>,
        <AxesSubplot:title={'center':'area error'}>,
        <AxesSubplot:title={'center':'smoothness error'}>],
       [<AxesSubplot:title={'center':'compactness error'}>,
        <AxesSubplot:title={'center':'concavity error'}>,
        <AxesSubplot:title={'center':'concave points error'}>,
        <AxesSubplot:title={'center':'symmetry error'}>,
        <AxesSubplot:title={'center':'fractal dimension error'}>],
       [<AxesSubplot:title={'center':'worst radius'}>,
        <AxesSubplot:title={'center':'worst texture'}>,
        <AxesSubplot:title={'center':'worst perimeter'}>,
        <AxesSubplot:title={'center':'worst area'}>,
        <AxesSubplot:title={'center':'worst smoothness'}>],
       [<AxesSubplot:title={'center':'worst compactness'}>,
        <AxesSubplot:title={'center':'worst concavity'}>,
        <AxesSubplot:title={'center':'worst concave points'}>,
        <AxesSubplot:title={'center':'worst symmetry'}>,
        <AxesSubplot:title={'center':'worst fractal dimension'}>]],
      dtype=object)
```



*The maximum number of columns in the dataset is not normally distributed. There is skewness in the data.*

# PCA & LDA

In [7]:

```
x = fl
y = pd.DataFrame(cancer['target'])
y.columns = ['CancerType']
```

In [8]:

```
x.shape, y.shape
```

Out[8]:

```
((569, 30), (569, 1))
```

In [9]:

```
#Splitting into training and testing set
X_train, X_test, Y_train, Y_test = train_test_split(x, y, test_size=0.3, random_state=11, stratify=y)
```

In [10]:

```
#Removing constant features using variance threshold
constant_filter = VarianceThreshold(threshold=0.10)

#Applying the filter on the training set
constant_filter.fit(X_train)

#Remove constant features from training and test sets
X_train_filter = constant_filter.transform(X_train)
X_test_filter = constant_filter.transform(X_test)
```

In [11]:

```
#Number of duplicated features in the dataset, We remove one of the feature
X_train_T = X_train_filter.T
X_test_T = X_test_filter.T
X_train_T = pd.DataFrame(X_train_T)
X_test_T =pd.DataFrame(X_test_T)
X_train_T.duplicated().sum()
```

Out[11]:

```
0
```

In [12]:

```
duplicated_features = X_train_T.duplicated()
features_to_keep = [not index for index in duplicated_features]
X_train_unique = X_train_T[features_to_keep].T
X_test_unique = X_test_T[features_to_keep].T
```

In [13]:

```
#standardize the data to get the same scale
scaler = StandardScaler().fit(X_train_unique)
X_train_unique = scaler.transform(X_train_unique)
X_test_unique = scaler.transform(X_test_unique)
X_train_unique = pd.DataFrame(X_train_unique)
X_test_unique = pd.DataFrame(X_test_unique)
X_train_unique.shape, X_test_unique.shape
```

Out[13]:

```
((398, 11), (171, 11))
```

In [14]:

```
#Correlation matrix
corrmat = X_train_unique.corr()
corrmat.head()
```

Out[14]:

| | 0 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | 1.000000 | 0.333688 | 0.997769 | 0.986198 | -0.104559 | 0.685085 | 0.728089 | 0.969942 | 0.289167 | 0.965239 | 0.941609 |
| **1** | 0.333688 | 1.000000 | 0.339211 | 0.326528 | 0.370602 | 0.279599 | 0.246912 | 0.362535 | 0.911823 | 0.365127 | 0.345418 |
| **2** | 0.997769 | 0.339211 | 1.000000 | 0.985262 | -0.094629 | 0.703385 | 0.735965 | 0.969725 | 0.295405 | 0.970500 | 0.942013 |
| **3** | 0.986198 | 0.326528 | 0.985262 | 1.000000 | -0.074554 | 0.749316 | 0.804229 | 0.961981 | 0.273572 | 0.958070 | 0.960621 |
| **4** | -0.104559 | 0.370602 | -0.094629 | -0.074554 | 1.000000 | 0.204193 | 0.078361 | -0.119353 | 0.413891 | -0.111507 | -0.093683 |

In [15]:

```
#Finding the number of correlated features
def get_correlation(data, threshold):
    corr_col = set()
    corrmat = data.corr()
    for i in range(len(corrmat.columns)):
        for j in range(i):
            if abs(corrmat.iloc[i, j]) > threshold:
                colname = corrmat.columns[i]
                corr_col.add(colname)
    return corr_col

corr_features = get_correlation(X_train_unique, 0.40)
print('correlated features: ', len(set(corr_features)) )
```

```
correlated features:  8
```

In [16]:

```
X_train_uncorr = X_train_unique.drop(labels=corr_features, axis = 1)
X_test_uncorr = X_test_unique.drop(labels = corr_features, axis = 1)
X_train_uncorr.shape, X_test_uncorr.shape
```

Out[16]:

```
((398, 3), (171, 3))
```

# Dimensionality Reduction using LDA

In [17]:

```
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis as LDA
#Transforming the data by using fit_transform()
lda = LDA(n_components=1)
X_train_lda = lda.fit_transform(X_train_uncorr, Y_train)
X_test_lda = lda.transform(X_test_uncorr)
```

```
D:\Anaconda3\lib\site-packages\sklearn\utils\validation.py:72: DataConversionWarning: A column-vector y was pa
ssed when a 1d array was expected. Please change the shape of y to (n_samples, ), for example using ravel().
  return f(**kwargs)
```

In [18]:

```
#Transformed data
X_train_lda.shape, X_test_lda.shape
```

Out[18]:

```
((398, 1), (171, 1))
```

In [19]:

```
from sklearn.ensemble import RandomForestClassifier
def run_randomForest(X_train, X_test, y_train, y_test):
    clf = RandomForestClassifier(n_estimators=100, random_state=0, n_jobs=-1)
    clf.fit(X_train, y_train)
    y_pred = clf.predict(X_test)
    print('Accuracy on test set: ')
    print(accuracy_score(y_test, y_pred))
```

In [20]:
```
%%time
run_randomForest(X_train_lda, X_test_lda, Y_train, Y_test)
```

```
<ipython-input-19-e37fb2efe457>:4: DataConversionWarning: A column-vector y was passed when a 1d array was exp
ected. Please change the shape of y to (n_samples,), for example using ravel().
  clf.fit(X_train, y_train)

Accuracy on test set:
0.8245614035087719
Wall time: 460 ms
```

In [21]:
```
%%time
run_randomForest(X_train, X_test, Y_train, Y_test)
```

```
<ipython-input-19-e37fb2efe457>:4: DataConversionWarning: A column-vector y was passed when a 1d array was exp
ected. Please change the shape of y to (n_samples,), for example using ravel().
  clf.fit(X_train, y_train)

Accuracy on test set:
0.9415204678362573
Wall time: 475 ms
```

# Dimensionality Reduction using PCA

In [22]:
```
from sklearn.decomposition import PCA
#Removing the features
pca = PCA(n_components=2, random_state=11)
pca.fit(X_train_uncorr)
PCA(copy=True, iterated_power='auto', n_components=2, random_state=11, svd_solver='auto', tol=0.0, whiten=False)
```

Out[22]:
```
PCA(n_components=2, random_state=11)
```

In [23]:
```
#Training and testing dataset by PCA transformation
X_train_pca = pca.transform(X_train_uncorr)
X_test_pca = pca.transform(X_test_uncorr)
X_train_pca.shape, X_test_pca.shape
```

Out[23]:
```
((398, 2), (171, 2))
```

In [24]:

```
%%time
run_randomForest(X_train_pca, X_test_pca, Y_train, Y_test)
```

```
<ipython-input-19-e37fb2efe457>:4: DataConversionWarning: A column-vector y was passed when a 1d array was exp
ected. Please change the shape of y to (n_samples,), for example using ravel().
  clf.fit(X_train, y_train)


Accuracy on test set:
0.847953216374269
Wall time: 600 ms
```

In [25]:

```
%%time
run_randomForest(X_train, X_test, Y_train, Y_test)
```

```
<ipython-input-19-e37fb2efe457>:4: DataConversionWarning: A column-vector y was passed when a 1d array was exp
ected. Please change the shape of y to (n_samples,), for example using ravel().
  clf.fit(X_train, y_train)

Accuracy on test set:
0.9415204678362573
Wall time: 475 ms
```

In [26]:

```
#Checking the accuracy for various selected components
for component in range(1,4):
    pca = PCA(n_components=component, random_state=11)
    pca.fit(X_train_uncorr)
    X_train_pca = pca.transform(X_train_uncorr)
    X_test_pca = pca.transform(X_test_uncorr)
    print('Selected Components: ', component)
    run_randomForest(X_train_pca, X_test_pca, Y_train, Y_test)
    print()
```

```
Selected Components:  1

<ipython-input-19-e37fb2efe457>:4: DataConversionWarning: A column-vector y was passed when a 1d array was exp
ected. Please change the shape of y to (n_samples,), for example using ravel().
  clf.fit(X_train, y_train)

Accuracy on test set:
0.6549707602339181

Selected Components:  2

<ipython-input-19-e37fb2efe457>:4: DataConversionWarning: A column-vector y was passed when a 1d array was exp
ected. Please change the shape of y to (n_samples,), for example using ravel().
  clf.fit(X_train, y_train)

Accuracy on test set:
0.847953216374269

Selected Components:  3

<ipython-input-19-e37fb2efe457>:4: DataConversionWarning: A column-vector y was passed when a 1d array was exp
ected. Please change the shape of y to (n_samples,), for example using ravel().
  clf.fit(X_train, y_train)

Accuracy on test set:
0.8771929824561403
```