MACHINE LEARNING PROJECT

Submitted By :

GROUP 2

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Breast Cancer Classification

PHASE 2

Problem Definition :

Breast cancer is one of the main causes of cancer death worldwide. Early diagnostics significantly increases the chances of correct treatment and survival, but this process is tedious and often leads to a disagreement between pathologists. Computer-aided diagnosis systems showed the potential for improving diagnostic accuracy. But early detection and prevention can significantly reduce the chances of death. It is important to detect breast cancer as early as possible.Breast cancer is a cancer in which the cells of breast tissue get altered and undergo uncontrolled division, resulting in a lump or mass in that region. It is generally diagnosed as one of the two types:

- Benign (Non-cancerous)
- Malignant (Cancerous)

Python packages used:

- Numpy v1.19.1
- Matplotlib v3.3.1
- Plotly v4.9.0
- Seaborn v0.10.1
- Sci-kit learn v0.23.2

Numpy is a general-purpose array-processing package. It provides a high-performance multidimensional array object, and tools for working with these arrays. It is the fundamental package for scientific computing with Python. Besides its obvious scientific uses, Numpy can also be used as an efficient multi-dimensional container of generic data.

Matplotlib is one of the most popular Python packages used for data visualization. It is a cross-platform library for making 2D plots from data in arrays.One of the greatest benefits of visualization is that it allows us visual access to huge amounts of data in easily digestible visuals. Matplotlib consists of several plots like line, bar, scatter, histogram etc.

The Plotly Python library is an interactive, open-source plotting library that supports over 40 unique chart types covering a wide range of statistical, financial, geographic, scientific, and 3-dimensional use-cases.

Seaborn is a library mostly used for statistical plotting in Python. It is built on top of Matplotlib and provides beautiful default styles and color palettes to make statistical plots more attractive.

Scikit-learn (Sklearn) is the most useful and robust library for machine learning in Python. It provides a selection of efficient tools for machine learning and statistical modeling including classification, regression, clustering and dimensionality reduction via a consistent interface in Python. This library, which is largely written in Python, is built upon NumPy, SciPy and Matplotlib.

Datasets:

1. The Wisconsin breast cancer diagnostic data set for predictive analysis
    - 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 (perimeter² / 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)
      All columns contain numerical data except the “diagnosis” attribute. This diagnosis attribute contains cancer type, i.e.- M(for malignant) or B(for benign), it is text data.

- **Data Set 1 :** Colab notebook link for the first dataset used
- **Data Set 2 :** Colab notebook link for the second dataset used
- **Data Set 3 :** Colab notebook link for the third dataset used

Prepare Data :

- Data Pre-processing:
  - Numerical data
    - Normalization
    - Standardization
    - Imputing Missing values
    - Discretization

1) **Normalization** :
   a) Removing unwanted attributes such as 'id' since id is not relevant in prediction of breast cancer.
   b) Removing attribute 'unnamed' as well since NaN value.

```
[ ] from sklearn import preprocessing
```

Removing unwanted attributes such as 'id' since id is not relevant in prediction of breast cancer. Removing attribute 'unnamed' as well since NaN value.

```
[ ] df.drop('id',axis=1,inplace=True)
    df.drop('Unnamed: 32',axis=1,inplace=True)
```

```
[ ] df.head()
```

	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	symmetry_mean	...	radius_worst	texture_worst	perimeter_worst	area_worst	smoothnes
0	M	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419	...	25.38	17.33	184.60	2019.0	
1	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812	...	24.99	23.41	158.80	1956.0	
2	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2069	...	23.57	25.53	152.50	1709.0	
3	M	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2597	...	14.91	26.50	98.87	567.7	
4	M	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1809	...	22.54	16.67	152.20	1575.0	

5 rows × 31 columns

o Text data

- Text related preprocessing (stop words removal, word stemming)
- Conversionof text data to numeric (Tf-idf),

Note:[Use python nltk package –eg: vectorization]

```
df.diagnosis.unique()
```

```
array(['M', 'B'], dtype=object)
```

```
[ ] df['diagnosis'] = df['diagnosis'].map({'M':1,'B':0})
    df.head()
```

	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	symmetry_mean	...	radius_worst	texture_worst	perimeter_worst	area_worst	smoothnes
0	1	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419	...	25.38	17.33	184.60	2019.0	
1	1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812	...	24.99	23.41	158.80	1956.0	
2	1	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2069	...	23.57	25.53	152.50	1709.0	
3	1	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2597	...	14.91	26.50	98.87	567.7	
4	1	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1809	...	22.54	16.67	152.20	1575.0	

5 rows × 31 columns

Assigned M - malignant the numeric value 1 and B - benign the value 0

2) Standardization:

```
[ ] from sklearn.model_selection import train_test_split
    X_train, X_test, y_train, y_test = train_test_split(df.drop('compactness_worst', axis=1),
                                                        df['compactness_worst'],
                                                        test_size=0.3,
                                                        random_state=0)

    X_train.shape, X_test.shape
```

```
((398, 30), (171, 30))
```

```
[ ] from sklearn.preprocessing import StandardScaler

    scaler = StandardScaler()

    # fit the scaler to the train set, it will learn the parameters
    scaler.fit(X_train)

    # transform train and test sets
    X_train_scaled = scaler.transform(X_train)
    X_test_scaled = scaler.transform(X_test)
```

```
[ ] scaler.mean_
```

```
array([3.74371859e-01, 1.41855000e+01, 1.91928392e+01, 9.23355025e+01,
       6.61859045e+02, 9.64749497e-02, 1.04080000e-01, 8.87943058e-02,
       4.94785528e-02, 1.80698241e-01, 6.26464573e-02, 4.09096231e-01,
       1.20445829e+00, 2.86661859e+00, 4.13843643e+01, 6.98354020e-03,
       2.50993719e-02, 3.12257678e-02, 1.16784749e-02, 2.04023819e-02,
       3.73508116e-03, 1.63596206e+01, 2.55345226e+01, 1.07736030e+02,
       8.94246985e+02, 1.32529045e-01, 2.68530796e-01, 1.15221410e-01,
       2.89186935e-01, 8.37181407e-02])
```

```
[ ] X_train_scaled = pd.DataFrame(X_train_scaled, columns=X_train.columns)
    X_test_scaled = pd.DataFrame(X_test_scaled, columns=X_test.columns)
```

```
[ ] X_train_scaled.head()
```

	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	symmetry_mean	...	fractal_dimension_se	radius_worst	texture_worst	perimeter_worst
0	-0.773559	-0.749980	-1.099787	-0.741586	-0.701887	0.584593	-0.427726	-0.457550	-0.760550	-0.099860	...	-0.045963	-0.798483	-0.591967	-0.746602
1	-0.773559	-1.028214	-0.139262	-1.029804	-0.894732	0.742882	-0.731843	-0.843301	-0.808805	-1.159759	...	-0.158707	-1.068703	-0.161981	-1.074343
2	-0.773559	-0.538522	-0.299349	-0.568574	-0.550561	-0.714814	-0.731647	-0.639856	-0.668125	0.581758	...	-0.474919	-0.558512	-0.051227	-0.614110
3	1.292726	1.147577	-0.146430	1.061698	1.035628	-0.762301	-0.380637	-0.091016	0.221141	-0.663712	...	-1.005230	0.998276	0.134448	0.914190
4	-0.773559	-2.004538	-1.376954	-1.962370	-1.415904	1.476766	-0.557221	-1.137578	-1.263267	0.439011	...	0.138526	-1.699888	-0.976348	-1.665615

5 rows × 30 columns

3) Discretization:

```
[ ] df['binned']=pd.cut(x=df['radius_worst'], bins=[0,25,50,100,200])
```

```
df.head
```

```
<bound method NDFrame.head of      diagnosis  radius_mean  texture_mean  perimeter_mean  area_mean  \
0            1        17.99         10.38          122.80     1001.0
1            1        20.57         17.77          132.90     1326.0
2            1        19.69         21.25          130.00     1203.0
3            1        11.42         20.38           77.58      386.1
4            1        20.29         14.34          135.10     1297.0
..         ...          ...           ...             ...        ...
564          1        21.56         22.39          142.00     1479.0
565          1        20.13         28.25          131.20     1261.0
566          1        16.60         28.08          108.30      858.1
567          1        20.60         29.33          140.10     1265.0
568          0         7.76         24.54           47.92      181.0

     smoothness_mean  compactness_mean  concavity_mean  concave points_mean  \
0            0.11840           0.27760         0.30010              0.14710
1            0.08474           0.07864         0.08690              0.07017
2            0.10960           0.15990         0.19740              0.12790
3            0.14250           0.28390         0.24140              0.10520
4            0.10030           0.13280         0.19800              0.10430
..               ...               ...             ...                  ...
564          0.11100           0.11590         0.24390              0.13890
565          0.09780           0.10340         0.14400              0.09791
566          0.08455           0.10230         0.09251              0.05302
567          0.11780           0.27700         0.35140              0.15200
568          0.05263           0.04362         0.00000              0.00000

     symmetry_mean  ...  texture_worst  perimeter_worst  area_worst  \
0           0.2419  ...          17.33           184.60      2019.0
1           0.1812  ...          23.41           158.80      1956.0
2           0.2069  ...          25.53           152.50      1709.0
3           0.2597  ...          26.50            98.87       567.7
4           0.1809  ...          16.67           152.20      1575.0
..             ...  ...            ...              ...         ...
564         0.1726  ...          26.40           166.10      2027.0
565         0.1752  ...          38.25           155.00      1731.0
566         0.1590  ...          34.12           126.70      1124.0
567         0.2397  ...          39.42           184.60      1821.0
568         0.1587  ...          30.37            59.16       268.6

     smoothness_worst  compactness_worst  concavity_worst  \
0             0.16220            0.66560           0.7119
```

```
[ ] df['height_bin']=pd.cut(x = df['radius_mean'],
                            bins = [0,25,50,100,200],
                            labels = [0, 1, 2,3])
    df
```

	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	symmetry_mean	...	perimeter_worst	area_worst	smoothness_worst	compactness_worst
0	1	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.30010	0.14710	0.2419	...	184.60	2019.0	0.16220	0.66560
1	1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.08690	0.07017	0.1812	...	158.80	1956.0	0.12380	0.18660
2	1	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.19740	0.12790	0.2069	...	152.50	1709.0	0.14440	0.42450
3	1	11.42	20.38	77.58	386.1	0.14250	0.28390	0.24140	0.10520	0.2597	...	98.87	567.7	0.20980	0.86630
4	1	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.19800	0.10430	0.1809	...	152.20	1575.0	0.13740	0.20500
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
564	1	21.56	22.39	142.00	1479.0	0.11100	0.11590	0.24390	0.13890	0.1726	...	166.10	2027.0	0.14100	0.21130
565	1	20.13	28.25	131.20	1261.0	0.09780	0.10340	0.14400	0.09791	0.1752	...	155.00	1731.0	0.11660	0.19220
566	1	16.60	28.08	108.30	858.1	0.08455	0.10230	0.09251	0.05302	0.1590	...	126.70	1124.0	0.11390	0.30940
567	1	20.60	29.33	140.10	1265.0	0.11780	0.27700	0.35140	0.15200	0.2397	...	184.60	1821.0	0.16500	0.86810
568	0	7.76	24.54	47.92	181.0	0.05263	0.04362	0.00000	0.00000	0.1587	...	59.16	268.6	0.08996	0.06444

569 rows × 33 columns

```
df['height_bin']=pd.cut(x=df['radius_mean'], bins=[0,25,50,100,200],
                        labels=[ " very small", "small","medium","huge",])
print(df.head())
```

```
   diagnosis  radius_mean  texture_mean  perimeter_mean  area_mean  \
0          1        17.99         10.38          122.80     1001.0
1          1        20.57         17.77          132.90     1326.0
2          1        19.69         21.25          130.00     1203.0
3          1        11.42         20.38           77.58      386.1
4          1        20.29         14.34          135.10     1297.0

   smoothness_mean  compactness_mean  concavity_mean  concave points_mean  \
0          0.11840           0.27760          0.3001              0.14710
1          0.08474           0.07864          0.0869              0.07017
2          0.10960           0.15990          0.1974              0.12790
3          0.14250           0.28390          0.2414              0.10520
4          0.10030           0.13280          0.1980              0.10430

   symmetry_mean  ...  perimeter_worst  area_worst  smoothness_worst  \
0         0.2419  ...           184.60      2019.0            0.1622
1         0.1812  ...           158.80      1956.0            0.1238
2         0.2069  ...           152.50      1709.0            0.1444
3         0.2597  ...            98.87       567.7            0.2098
4         0.1809  ...           152.20      1575.0            0.1374

   compactness_worst  concavity_worst  concave points_worst  symmetry_worst  \
0             0.6656           0.7119                0.2654          0.4601
1             0.1866           0.2416                0.1860          0.2750
2             0.4245           0.4504                0.2430          0.3613
3             0.8663           0.6869                0.2575          0.6638
4             0.2050           0.4000                0.1625          0.2364

   fractal_dimension_worst    binned   height_bin
0                  0.11890  (25, 50]   very small
1                  0.08902   (0, 25]   very small
2                  0.08758   (0, 25]   very small
3                  0.17300   (0, 25]   very small
4                  0.07678   (0, 25]   very small

[5 rows x 33 columns]
```

Data Summarization:

- Use statistical methods to understand the data and apply the required methods
- For instance, we can calculate various statistics on all numeric columns with just one function: describe():

```
[ ] df.describe()
```

	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	symmetry_mean	...	radius_worst	texture_worst	perimeter_worst	area_worst	smoo
count	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	...	569.000000	569.000000	569.000000	569.000000	
mean	0.372583	14.127292	19.289649	91.969033	654.889104	0.096360	0.104341	0.088799	0.048919	0.181162	...	16.269190	25.677223	107.261213	880.583128	
std	0.483918	3.524049	4.301036	24.298981	351.914129	0.014064	0.052813	0.079720	0.038803	0.027414	...	4.833242	6.146258	33.602542	569.356993	
min	0.000000	6.981000	9.710000	43.790000	143.500000	0.052630	0.019380	0.000000	0.000000	0.106000	...	7.930000	12.020000	50.410000	185.200000	
25%	0.000000	11.700000	16.170000	75.170000	420.300000	0.086370	0.064920	0.029560	0.020310	0.161900	...	13.010000	21.080000	84.110000	515.300000	
50%	0.000000	13.370000	18.840000	86.240000	551.100000	0.095870	0.092630	0.061540	0.033500	0.179200	...	14.970000	25.410000	97.660000	686.500000	
75%	1.000000	15.780000	21.800000	104.100000	782.700000	0.105300	0.130400	0.130700	0.074000	0.195700	...	18.790000	29.720000	125.400000	1084.000000	
max	1.000000	28.110000	39.280000	188.500000	2501.000000	0.163400	0.345400	0.426800	0.201200	0.304000	...	36.040000	49.540000	251.200000	4254.000000	

8 rows × 31 columns

A data summary in Python can be created for a specific part of the DataFrame. We just need to filter the relevant part before applying the functions.

We group the rows by the distinct values in a column with the groupby() function. The following code groups the rows by product group.

```
[ ] df.groupby("diagnosis")
```

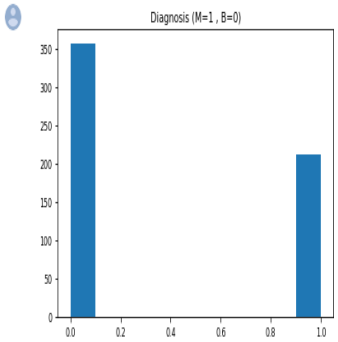
```
<pandas.core.groupby.generic.DataFrameGroupBy object at 0x7f1424804c40>
```

Once the groups are formed, we can calculate any statistic and describe or summarize the data.

```
[ ] df.groupby("diagnosis")["radius_mean"].mean()
```

```
diagnosis
0    12.146524
1    17.462830
Name: radius_mean, dtype: float64
```

```
df.describe()
plt.hist(df['diagnosis'])
plt.title('Diagnosis (M=1 , B=0)')
plt.show()
```

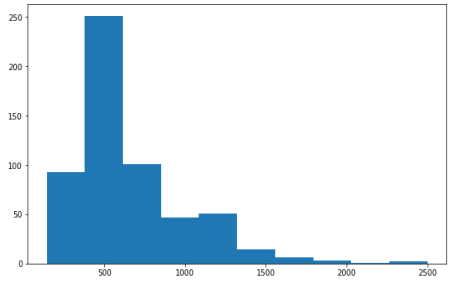


Data Visualization:

- Histogram

```
import matplotlib.pyplot as plt
plt.figure(figsize=(10,6))
plt.hist(df["area_mean"], bins=10)
```

```
(array([ 93., 251., 101.,  47.,  51.,  14.,   6.,   3.,   1.,   2.]),
 array([ 143.5 ,  379.25,  615.  ,  850.75, 1086.5 , 1322.25, 1558.  ,
        1793.75, 2029.5 , 2265.25, 2501.  ]),
 <a list of 10 Patch objects>)
```



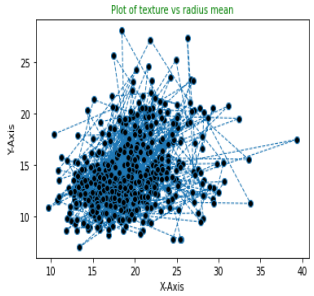

```
[ ] df.head(2)
```

	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	symmetry_mean	...	perimeter_worst	area_worst	smoothness_worst	compactness_worst	c
0	1	17.99	10.38	122.8	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419	...	184.6	2019.0	0.1622	0.6656	
1	1	20.57	17.77	132.9	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812	...	158.8	1956.0	0.1238	0.1866	

2 rows × 33 columns

- **Line plot**

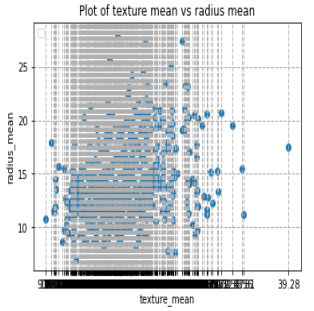
```
# plotting the data
texture = df ['texture_mean'].tolist()
meanofradius  = df ['radius_mean'].tolist()
plt.plot(texture, meanofradius,
       marker='o', markerfacecolor='k',
      linestyle='--', linewidth=1)

# Adding title to the plot
plt.title("Plot of texture vs radius mean", fontsize=10, color="green")

# Adding label on the y-axis
plt.ylabel('Y-Axis')

# Adding label on the x-axis
plt.xlabel('X-Axis')

plt.show()
```



- **Scatter plot:**

```
texture  = df ['texture_mean'].tolist()
meanofradius = df ['radius_mean'].tolist()
plt.scatter(texture, meanofradius)
plt.xlabel('texture_mean')
plt.ylabel('radius_mean')
plt.legend(loc='upper left')
plt.title('Plot of texture mean vs radius mean')
plt.xticks(texture)
plt.grid(True, linewidth= 1, linestyle="--")
plt.show()
```

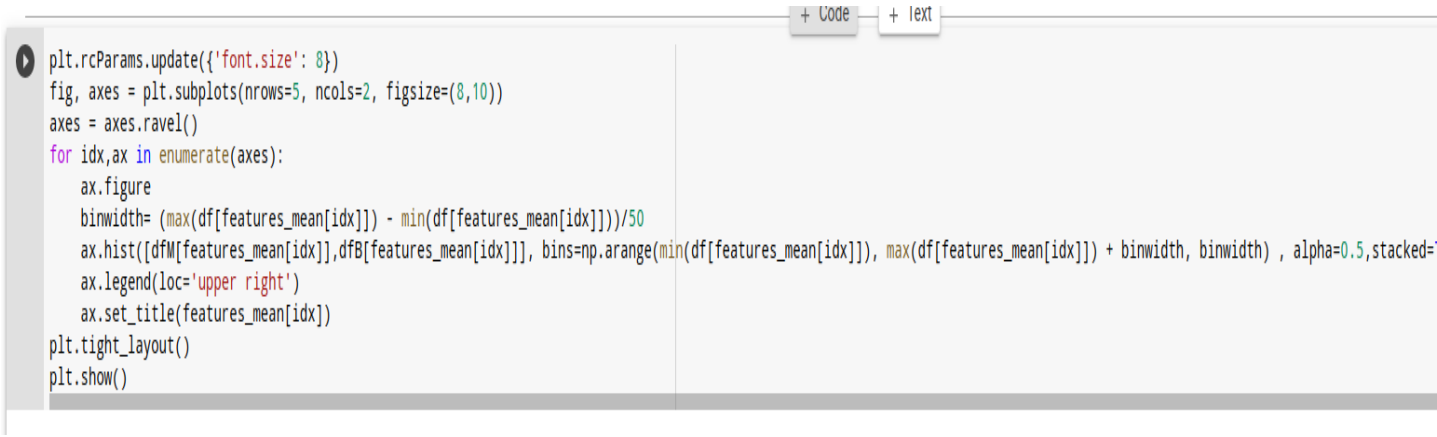
```
WARNING:matplotlib.legend:No handles with labels found to put in legend.
```

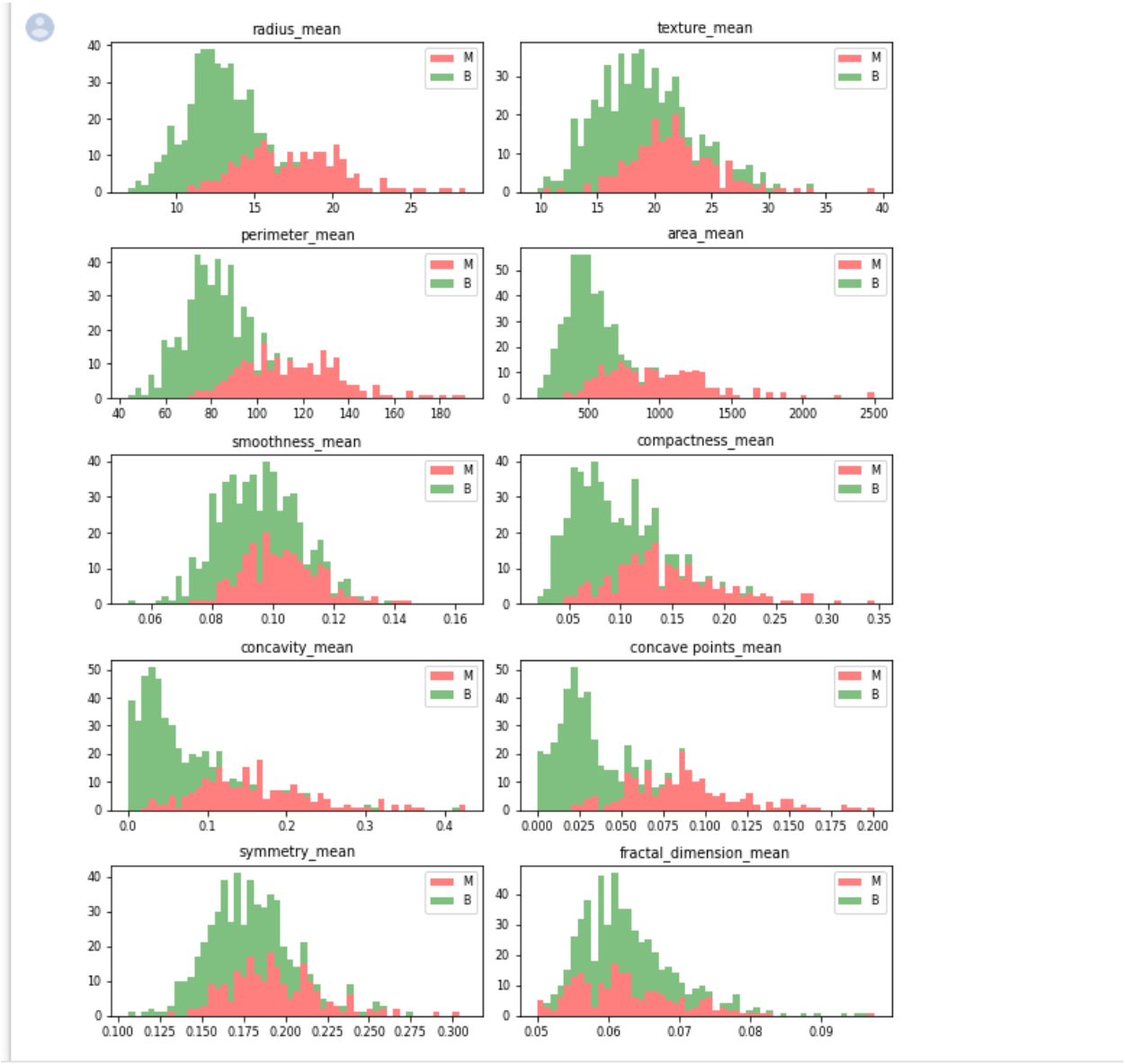


Nucleus features vs diagnosis :

```
[ ]  features_mean=list(df.columns[1:11])

     dfM=df[df['diagnosis'] ==1]
     dfB=df[df['diagnosis'] ==0]
```

Stack the data :



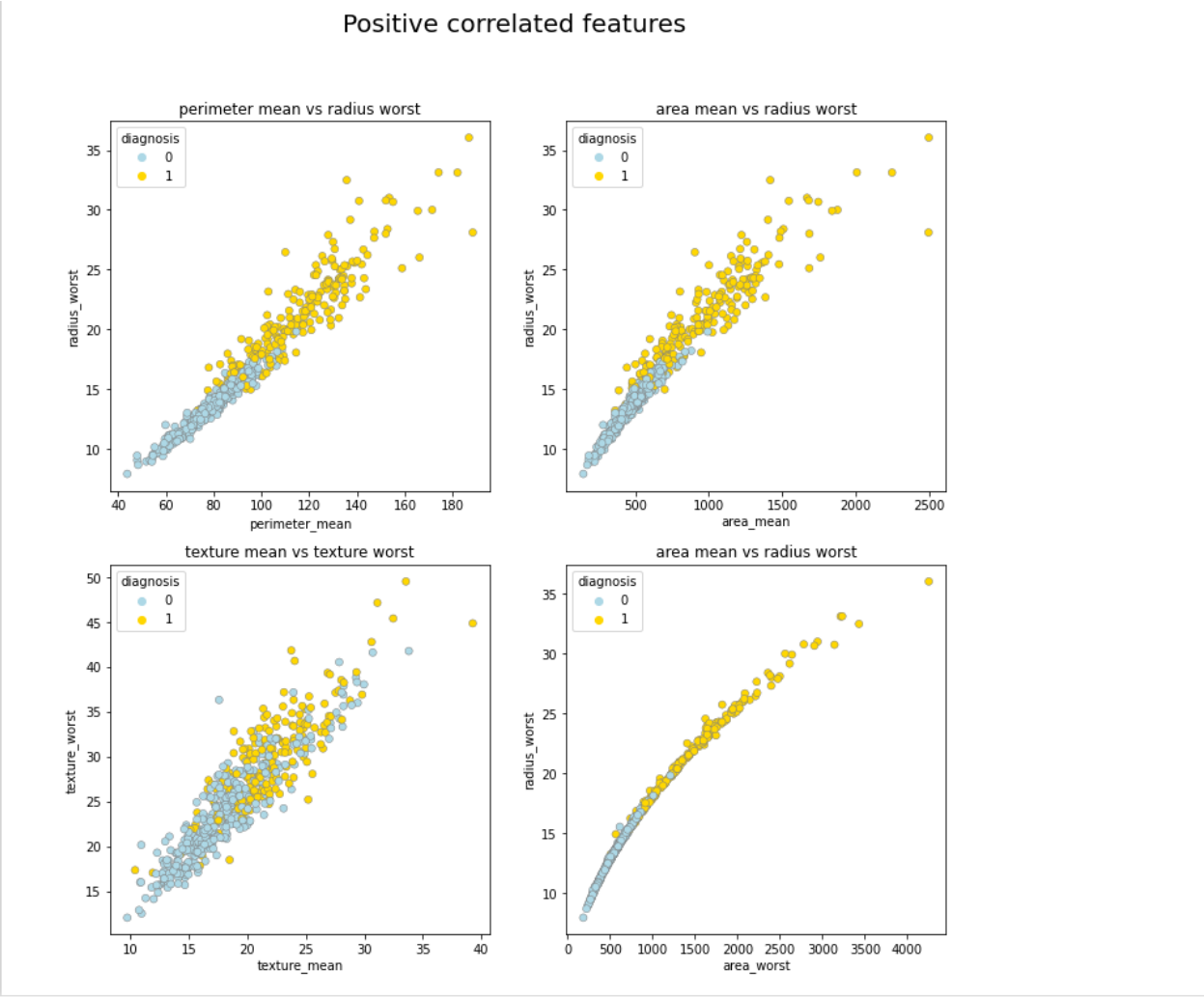


Observations:

- mean values of cell radius, perimeter, area, compactness, concavity and concave points can be used in classification of the cancer. Larger values of these parameters tend to show a correlation with malignant tumors.
- mean values of texture, smoothness, symmetry or fractal dimension does not show a particular preference of one diagnosis over the other. In any of the histograms there are no noticeable large outliers that warrants further cleanup.

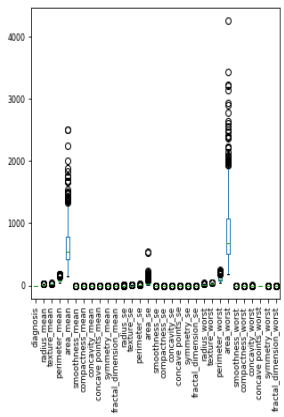
Positive correlated features :

```
#seaborn version :

palette ={0 : 'lightblue', 1 : 'gold'}
edgecolor = 'grey'

# Plot +
fig = plt.figure(figsize=(12,12))

plt.subplot(221)
ax1 = sns.scatterplot(x = df['perimeter_mean'], y = df['radius_worst'], hue = "diagnosis",
                      data = df, palette = palette, edgecolor=edgecolor)
plt.title('perimeter mean vs radius worst')
plt.subplot(222)
ax2 = sns.scatterplot(x = df['area_mean'], y = df['radius_worst'], hue = "diagnosis",
                      data = df, palette =palette, edgecolor=edgecolor)
plt.title('area mean vs radius worst')
plt.subplot(223)
ax3 = sns.scatterplot(x = df['texture_mean'], y = df['texture_worst'], hue = "diagnosis",
                      data = df, palette =palette, edgecolor=edgecolor)
plt.title('texture mean vs texture worst')
plt.subplot(224)
ax4 = sns.scatterplot(x = df['area_worst'], y = df['radius_worst'], hue = "diagnosis",
                      data = df, palette =palette, edgecolor=edgecolor)
plt.title('area mean vs radius worst')

fig.suptitle('Positive correlated features', fontsize = 20)
plt.savefig('1')
plt.show()
```



Box plot

```
boxplot = df.boxplot(figsize = (5,5), rot = 90, fontsize= '8', grid = False)
```



Data Interpretation

Record all your findings and summary about data
Creating a test set and a training set
Since this data set is not ordered, I am going to do a simple 70:30 split to create a training data set and a test data set.

```
[ ]  traindf, testdf = train_test_split(df, test_size = 0.3)
```

Model Classification

```
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import KFold
from sklearn.ensemble import RandomForestClassifier
from sklearn.tree import DecisionTreeClassifier, export_graphviz
from sklearn import metrics
```

```
[ ] #Generic function for making a classification model and accessing the performance.
    from sklearn.model_selection import cross_validate
    def classification_model(model, data, predictors, outcome):
      #Fit the model:
      model.fit(data[predictors],data[outcome])

      #Make predictions on training set:
      predictions = model.predict(data[predictors])

      #Print accuracy
      accuracy = metrics.accuracy_score(predictions,data[outcome])
      print("Accuracy : %s" % "{0:.3%}".format(accuracy))
```

```
[ ]  #Perform k-fold cross-validation with 5 folds
      kf = KFold(data.shape[0], n_splits=5)
      error = []
      for train, test in kf:
        # Filter training data
        train_predictors = (data[predictors].iloc[train,:])

        # The target we're using to train the algorithm.
        train_target = data[outcome].iloc[train]

        # Training the algorithm using the predictors and target.
        model.fit(train_predictors, train_target)

        #Record error from each cross-validation run
        error.append(model.score(data[predictors].iloc[test,:], data[outcome].iloc[test]))

        print("Cross-Validation Score : %s" % "{0:.3%}".format(np.mean(error)))

      #Fit the model again so that it can be refered outside the function:
      model.fit(data[predictors],data[outcome])
```

Logistic Regression model

Logistic regression is widely used for classification of discrete data. In this case we will use it for binary (1,0) classification.

Based on the observations in the histogram plots, we can reasonably hypothesize that the cancer diagnosis depends on the mean cell radius, mean perimeter, mean area, mean compactness, mean concavity and mean concave points. We can then perform a logistic regression analysis using those features as follows:

```
predictor_var = ['radius_mean','perimeter_mean','area_mean','compactness_mean','concave points_mean']
outcome_var='diagnosis'
model=LogisticRegression()
classification_model(model,traindf,predictor_var,outcome_var)
```

```
Accuracy : 87.940%
```

The prediction accuracy is reasonable. What happens if we use just one predictor? Use the mean_radius:

```
[ ] predictor_var = ['radius_mean']
    model=LogisticRegression()
    classification_model(model,traindf,predictor_var,outcome_var)
```

```
Accuracy : 87.186%
```

The accuracy of the predictions are good but not great.

Decision Tree Model

```
[ ] predictor_var = ['radius_mean','perimeter_mean','area_mean','compactness_mean','concave points_mean']
    model = DecisionTreeClassifier()
    classification_model(model,traindf,predictor_var,outcome_var)
```

```
Accuracy : 100.000%
```

Here we are over-fitting the model probably due to the large number of predictors. Let use a single predictor, the obvious one is the radius of the cell.

```
[ ] predictor_var = ['radius_mean']
    model = DecisionTreeClassifier()
    classification_model(model,traindf,predictor_var,outcome_var)
```

```
Accuracy : 96.985%
```

The accuracy of the prediction is much much better here. But does it depend on the predictor?

Using a single predictor gives a 97% prediction accuracy for this model but the cross-validation score is not that great.

Random Forest

```
[ ] # Use all the features of the nucleus
    predictor_var = features_mean
    model = RandomForestClassifier(n_estimators=100,min_samples_split=25, max_depth=7, max_features=2)
    classification_model(model, traindf,predictor_var,outcome_var)
```

```
Accuracy : 94.472%
```

Using all the features improves the prediction accuracy and the cross-validation score is great.

An advantage with Random Forest is that it returns a feature importance matrix which can be used to select features. So lets select the top 5 features and use them as predictors.

```
[ ] #Create a series with feature importances:
    featimp = pd.Series(model.feature_importances_, index=predictor_var).sort_values(ascending=False)
    print(featimp)
```

```
concave points_mean       0.275236
concavity_mean            0.173132
area_mean                 0.170957
perimeter_mean            0.117815
radius_mean               0.115605
texture_mean              0.049910
compactness_mean          0.044423
smoothness_mean           0.029888
fractal_dimension_mean    0.012835
symmetry_mean             0.010200
dtype: float64
```

```
[ ] # Using top 5 features
    predictor_var = ['concave points_mean','area_mean','radius_mean','perimeter_mean','concavity_mean',]
    model = RandomForestClassifier(n_estimators=100, min_samples_split=25, max_depth=7, max_features=2)
    classification_model(model,traindf,predictor_var,outcome_var)
```

```
Accuracy : 93.970%
```

Using the top 5 features only changes the prediction accuracy a bit but I think we get a better result if we use all the predictors.

What happens if we use a single predictor as before? Just check.

```
[ ] predictor_var =  ['radius_mean']
    model = RandomForestClassifier(n_estimators=100)
    classification_model(model, traindf,predictor_var,outcome_var)
```

This gives a better prediction accuracy too but the cross-validation is not great.

Using on the test data set

```
[ ] # Use all the features of the nucleus
    predictor_var = features_mean
    model = RandomForestClassifier(n_estimators=100,min_samples_split=25, max_depth=7, max_features=2)
    classification_model(model, testdf,predictor_var,outcome_var)
```

```
Accuracy : 97.076%
```

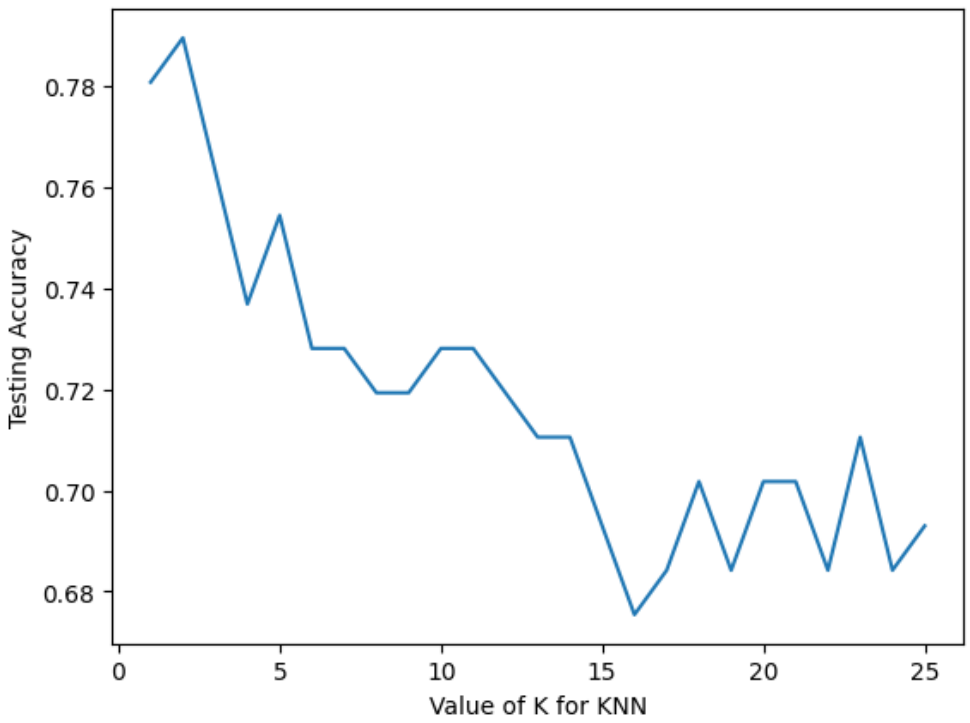
The prediction accuracy for the test data set using the above Random Forest model is 97%

KNN :

```
[ ]  from sklearn.neighbors import KNeighborsClassifier

     k_range=range(1,26)

     scores={}
     h_score = 0       # to find the best score
     best_k=0          # to find the best k
     scores_list=[]

     for k in k_range:

         knn=KNeighborsClassifier(n_neighbors=k)
         knn.fit(X_train,y_train)
         prediction_knn=knn.predict(X_test)
         scores[k]=accuracy_score(y_test,prediction_knn)

         if scores[k]>h_score:
             h_score = scores[k]
             best_k = k

         scores_list.append(accuracy_score(y_test,prediction_knn))

     print('The best value of k is {} with score : {}'.format(best_k,h_score))
```

```
The best value of k is 2 with score : 0.7894736842105263
```

```
[ ]  #Plotting accuracy for different values of k

     plt.plot(k_range,scores_list)
     plt.xlabel('Value of K for KNN')
     plt.ylabel('Testing Accuracy')
     plt.show()
```




```
[ ] knn=KNeighborsClassifier(n_neighbors=best_k)
    knn.fit(X_train,y_train)


    prediction_knn=knn.predict(X_test)
    accuracy_knn=accuracy_score(y_test,prediction_knn)*100
    print('accuracy_score :',accuracy_score(y_test,prediction_knn)*100,'%')
    print('mean_squared_error :',mean_squared_error(y_test,prediction_knn)*100,'%')
```

```
accuracy_score : 78.94736842105263 %
mean_squared_error : 21.052631578947366 %
```

```
[ ] scores_dict['KNeighborsClassifier'] = accuracy_knn
    print("Accuracy with KKN: " +str(accuracy_knn))
```

```
Accuracy with KKN: 78.94736842105263
```

```
[ ] print("Accuracy on training set: {:.3f}".format(knn.score(X_train, y_train)))
    print("Accuracy on test set: {:.3f}".format(knn.score(X_test, y_test)))
```

```
Accuracy on training set: 0.890
Accuracy on test set: 0.789
```

Support Vector Classifier:

```
[ ] from sklearn.svm import SVC

    model = SVC(C=2.0,kernel='rbf',gamma='auto').fit(X_train,y_train)
    Y_predict = model.predict(X_test)
    print('Accuracy score : {}%'.format(accuracy_score(y_test,Y_predict)*100))
    scores_dict['SVC'] = accuracy_score(y_test,Y_predict)*100
```

```
Accuracy score : 62.28070175438597%
```

Performing K Fold Cross Validation:

```
from sklearn.model_selection import cross_val_score
from sklearn.model_selection import KFold


acc_scores={}
cv = KFold(n_splits=3,shuffle=True)
cv_score_lr = cross_val_score(DecisionTreeClassifier(), X, y, cv=cv)
print(cv_score_lr)

mean_accuracy_lr = sum(cv_score_lr)/len(cv_score_lr)
mean_accuracy_lr = mean_accuracy_lr*100
mean_accuracy_lr = round(mean_accuracy_lr, 2)
print("Mean Accuracy In Desicion Tree Classifier: "+str(mean_accuracy_lr)+"%")
acc_scores['Desicion Tree Classifer']=mean_accuracy_lr
```

```
[0.92105263 0.91578947 0.8994709 ]
Mean Accuracy In Desicion Tree Classifier: 91.21%
```

```
[ ] from sklearn.model_selection import cross_val_score
    cv = KFold(n_splits=3, shuffle=True)
    cv_score_lr = cross_val_score(KNeighborsClassifier(), X, y, cv=cv)
    print(cv_score_lr)

    mean_accuracy_lr = sum(cv_score_lr)/len(cv_score_lr)
    mean_accuracy_lr = mean_accuracy_lr*100
    mean_accuracy_lr = round(mean_accuracy_lr, 2)
    print("Mean Accuracy In KNN: "+str(mean_accuracy_lr)+"%")
    acc_scores['K Neighbors Classifier']=mean_accuracy_lr
```

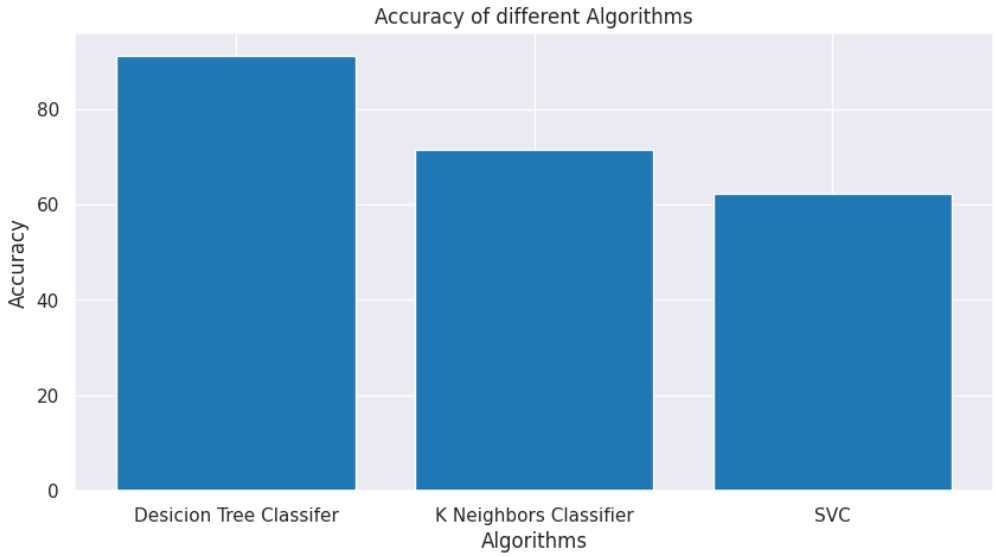
```
[0.78421053 0.67894737 0.68253968]
Mean Accuracy In KNN: 71.52%
```

```
[ ]  from sklearn.model_selection import cross_val_score
     cv = KFold(n_splits=3,  shuffle=True)
     cv_score_lr = cross_val_score(SVC(), X, y, cv=cv)
     print(cv_score_lr)
     mean_accuracy_lr = sum(cv_score_lr)/len(cv_score_lr)
     mean_accuracy_lr = mean_accuracy_lr*100
     mean_accuracy_lr = round(mean_accuracy_lr, 2)
     print("Mean Accuracy In SVC: "+str(mean_accuracy_lr)+"%")
     acc_scores['SVC']=mean_accuracy_lr
```

```
[0.62105263 0.62631579 0.61904762]
Mean Accuracy In SVC: 62.21%
```

Comparing the 3 Models

```
[ ]  # comparing the accuracy of the 3 models

     plt.figure(figsize=(10,5))
     plt.bar(acc_scores.keys(),acc_scores.values())
     plt.title('Accuracy of different Algorithms')
     plt.xlabel('Algorithms')
     plt.ylabel('Accuracy')
     plt.show()
```



Conclusion

- By comparing the 3 models (decision tree, KNN, SVC) we get to know that Decision tree has the highest accuracy
- Mean Accuracy In Decision Tree Classifier: 91.21%
- We will see if we can improve this more by tweaking the model further and trying out other models in a later version of this analysis.

Resources :

- Geeks for Geeks
- Kaggle

****