```
In [ ]:
```

```
import numpy as np # linear algebra
import matplotlib.pyplot as plt
import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import RobustScaler #for robust feature scaling
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay, classification_repo
rt, accuracy_score, roc_curve, auc
from scipy import stats # Hypthesis testing
import seaborn as sns
```

Note1

In []:

```
data df = pd.read csv("/kaggle/input/breast-cancer-wisconsin/data.csv")
data_df.head().T
#data df.info()
data_df.diagnosis = data_df.diagnosis.apply(lambda x: 1 if x == 'M' else 0)
#data df.info()
data df.shape
data df.columns
print(data df.isnull().sum().sum())
data df = data df.dropna(axis = 1)
B, M = data df.diagnosis.value counts()
xtickmarks = ['B', 'M']
print(f'Number of Malignant tumours: {M}')
print(f'Number of Benign tumours : {B}')
def createCountplot():
   fig = plt.figure(figsize = (8, 6))
   ax = fig.add subplot()
    sns.set_theme(style = 'whitegrid')
    sns.countplot(data = data df,
             x = data df.diagnosis,
              label = 'Count',
             lw = 4,
              ec = 'black').set(title = 'A count of benign and malignant tumours',
                                  xlabel = 'Diagnosis',
                                  ylabel = 'Count')
    ax.set xticklabels(xtickmarks)
   plt.show()
createCountplot()
variables_to_omit = ['id', 'diagnosis']
input data = data df.drop(variables to omit, axis = 1)
r, c = input data.shape
print(f'Sample size
                                       : {r}')
print(f'Number of independent variables: {c}')
```

Histograms

```
In [ ]:
```

```
Malignant = data df[data df['diagnosis'] == 1]
Benign = data df[data df['diagnosis'] == 0]
worst mean se = ['area worst', 'fractal dimension mean', 'radius se']
def makeHistogram(features):
    for feature in features:
       if not type(feature) is str:
            raise TypeError('Only strings are permitted')
    fig = plt.figure(figsize = (10, 8))
    for i, feature in enumerate(features):
        ax = fig.add_subplot(1, 3, i + 1)
        sns.histplot(Malignant[feature],
                   bins = bins,
                   color = 'red',
                   label = 'Malignant',
                   kde = True)
        sns.histplot(Benign[feature],
                   bins = bins,
                   color = 'green',
                   label = 'Benign',
                   kde = True)
        plt.title(str(' Distribution of ') + str(feature.replace('_', ' ').capitalize()
) )
        plt.xlabel(str(feature.replace(' ', ' ').capitalize()))
        plt.ylabel('Density function')
        plt.legend(loc = 'upper right')
        ax.grid(False)
    plt.tight_layout()
    plt.show()
bins = 'fd' #Freedman and Diaconis
makeHistogram(worst mean se)
```

Heatmaps provide an informative way to depict two-dimensional data of the kind we have before us. A *heatmap* is an image in which the colour of each pixel is determined by the corresponding value in the array of data.

```
In [ ]:
```

```
def createHeatmap():
   sns.set theme(style ='white')
   #Generate a mask for the upper triangular matrix
   mask = np.triu(input_data.corr(), k = 0)
   fig = plt.figure(figsize = (18, 18))
   ax = fig.add_subplot()
    # Generate a custom diverging palette of colours
   cmap = sns.diverging palette(230, 20, as cmap = True)
   sns.heatmap(data = input data.corr(),
                annot = True,
                linewidths = 0.5,
                fmt = '.1f',
                ax = ax,
                mask = mask,
                cmap = cmap)
   plt.title('A correlation heatmap of the features', fontsize = 20)
   plt.show()
createHeatmap()
```

More plots

```
In [ ]:
```

Create box and whiskers plot for texture mean by diagnosis of tumour

```
Diagnosis = 'diagnosis'
def makeBoxplot(features):
    fig = plt.figure(figsize = (8, 12))
    for i, feature in enumerate(features):
        ax = fig.add subplot(2, 2, i + 1)
        sns.boxplot(x = Diagnosis,
                   y = feature,
                   data = data df,
                   showfliers = True)
        plt.title(str(feature.replace('_', ' ').capitalize()))
        ax.set xticklabels(xtickmarks)
        ax.set xlabel(Diagnosis.capitalize())
        ax.set_ylabel(str(feature.replace('_', ' ').capitalize()))
        ax.grid(False)
    fig.tight_layout()
    plt.show()
makeBoxplot(worst mean se)
```

Logistic regression plots

Some more box and whiskers plots

```
In [ ]:
def logistic regression plot(features):
    fig = plt.figure(figsize = (11, 5))
    for i, feature in enumerate(features):
        ax = fig.add subplot(1, 3, i + 1)
         sns.regplot(data = data df,
                      x = feature,
                      y = Diagnosis,
                      logistic = True,
                      color = 'black',
                      line_kws = {'lw' : 1, 'color' : 'red'},
        label = str(feature.replace('_', '').capitalize()))
ax.set_xlabel(str(feature.replace('_', '').capitalize()))
        plt.ylabel('Probability')
        plt.title('Logistic regression')
        plt.legend()
        plt.tight layout()
        plt.show
    return None
logistic regression plot(worst mean se)
```

Hypothesis testing using Student's t-test.

In []:

```
In []:

# Make a new dataframe with only the desired feature for t test
hypothesis_test_data = pd.DataFrame(data = data_df[['area_worst', 'diagnosis']])
hypothesis_test_data = hypothesis_test_data.set_index(Diagnosis)
t, p = stats.ttest_ind(hypothesis_test_data.loc[0], hypothesis_test_data.loc[1])
print(f'The t-value: {t}')
print(f'The p-value: {p}')
```

```
class Hypothesis_T_Test(object):
    def __init__(self, feature, ind_variable = Diagnosis):
        self.feature = feature
        self.ind_variable = ind_variable

def computeTandPValues(self):
```

```
hypothesis_test_data = pd.DataFrame(data = data_df[[self.feature, self.ind_varia
ble]])
    hypothesis_test_data = hypothesis_test_data.set_index(self.ind_variable)
    self.variable_name = lambda : data_df[self.feature].name.replace('_', '').capit
alize()
    self.t_value, self.p_value = stats.ttest_ind(hypothesis_test_data.loc[0], hypoth
esis_test_data.loc[1])
    print(f'Variable name: {self.variable_name()}: t-value: {self.t_value}, p-value:
{self.p_value}')
    return self.t_value, self.p_value

for feature in worst_mean_se:
    HTT = Hypothesis_T_Test(feature)
    HTT.computeTandPValues()
```

Some correlation

In []:

```
# Create a correlation matrix
corr_matrix = input_data.corr().abs()
# Select upper triangle of correlation matrix
upper_triangular = corr_matrix.where(np.triu(np.ones(corr_matrix.shape), k = 1).astype(b
ool))
# Find index of feature columns with correlation greater than 0.95
correlation_threshold = 0.95
features_to_omit = [column for column in upper_triangular.columns if any(upper_triangula
r[column] > correlation_threshold)]
# Remove features to omit
correlation_data = input_data.drop(input_data[features_to_omit], axis = 1)
correlation_data.columns
```

Machine learning

```
In [ ]:
```

```
X = input data
Y = data_df.diagnosis
X train, X test, y train, y test = train test split(X,
                                                     test size = 0.20,
                                                     stratify = Y,
                                                    random state = 1234)
#Robust feature scaling
rs_object = RobustScaler()
X train = rs object.fit transform(X train)
X test = rs object.transform(X test)
# Define a function which trains a logistic model
def createModel(X train, y train):
    LogitModel = LogisticRegression(solver = 'lbfgs',
                             max iter = 100,
                             random state = 1234)
    LogitModel.fit(X train, y train)
    #Display model accuracy on the training data.
    print(f'Accuracy for the training sample: {LogitModel.score(X train, y train):.2f}')
    return LogitModel
#Obtain the training results
model = createModel(X_train, y_train)
```

Confusion matrix

```
In [ ]:
cm = confusion matrix(y test, model.predict(X test))
TN = cm[0][0]
TP = cm[1][1]
FN = cm[1][0]
FP = cm[0][1]
print(cm)
print(f'Accuracy on the test data: {(TP + TN) / (TP + TN + FN + FP): .2f}')
print() # Print a new line
def displayConfusionMatrix():
   disp = ConfusionMatrixDisplay(confusion_matrix = cm,
                                  display labels = model.classes )
    disp.plot()
    plt.grid(visible = False)
    plt.title('Confusion matrix')
    plt.show()
displayConfusionMatrix()
```

Classification report is used in machine learning to compute accuracy of a classification model from the values of the confusion matrix. In the classification report, precision is a measure of positive predictions.

```
In [ ]:
```

```
print(f'Logistic regression model ')
#Check precision, recall, f1-score
print(f'Classification report')
print(classification_report(y_test, model.predict(X_test)))
#Another way to get the models accuracy on the test data
print(f'Accuracy score {accuracy_score(y_test, model.predict(X_test)):.4f}')
print() #Print a new line
```

ROC Curve

```
In [ ]:
```

```
# Compute predicted probabilities and keep results only for positive outcome
y pred prob = model.predict proba(X test)[:,1]
# Generate ROC curve values and capture only fpr, and tpr, but not thresholds
fpr, tpr, _ = roc_curve(y_test, y_pred_prob)
print(f'The AUC score for the logistic regression model is: {auc(fpr, tpr):.4f}')
def createROC():
   fig = plt.figure()
   ax = fig.add subplot()
   plt.plot([0, 1], [0, 1], 'k-.', label = 'Random prediction')
   plt.plot(fpr, tpr, label = 'Logistic regression model: AUC = %0.4f' % auc(fpr, tpr))
   plt.xlabel('False Positive Rate')
   plt.ylabel('True Positive Rate')
   plt.title('ROC Curve for Logistic Regression')
   ax.grid(False)
   plt.legend()
   plt.show()
createROC()
```