breast-cancer-prediction-model

May 3, 2024

1 Machine Learning in Medical Industry - Breast Cancer Study Case

Breast cancer is cancer that develops from breast tissue. Signs of breast cancer may include a lump in the breast, a change in breast shape, dimpling of the skin, milk rejection, fluid coming from the nipple, a newly inverted nipple, or a red or scaly patch of skin. In those with distant spread of the disease, there may be bone pain, swollen lymph nodes, shortness of breath, or yellow skin. Outcomes for breast cancer vary depending on the cancer type, the extent of disease, and the person's age. Based on data from GLOBOCAN 2022, breast cancer is the number 1 cancer suffered by Indonesian women. A total of 66,271 new cases of breast cancer occurred in Indonesia in 2022. In addition, breast cancer has the highest case in Indonesia when calculated from the overall gender cancer case.

About the dataset

The dataset is taken from UCI Machine Learning Repository. There are 3 things to achieve in this code:

1. In-Depth Data Analysis
2. Predict Breast Cancer Risk based on clinical features
3. Machine Learning Model Comparison with Gradient Boosting, Random Forest, and Stacking

Attribute information:

- (1) ID number
- (2) Diagnosis (M = malignant, B = benign)
- (3-32) Ten real-valued features are computed for each cell nucleus:
  - radius (mean of distances from center to points on the perimeter)
  - texture (standard deviation of gray-scale values)
  - perimeter
  - area
  - smoothness (local variation in radius lengths)
  - compactness (perimeter^2 / area - 1.0)
  - concavity (severity of concave portions of the contour)

- concave points (number of concave portions of the contour)
- symmetry
- 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.

1.1 Import Library

[1]:
```
import pandas as pd
import numpy as np

import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.metrics import classification_report
from sklearn.model_selection import train_test_split
from sklearn.metrics import roc_auc_score
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import confusion_matrix

import warnings
warnings.filterwarnings('ignore')
```

1.2 Load Dataset

[2]:
```
url = 'https://raw.githubusercontent.com/pkmklong/
 ↪Breast-Cancer-Wisconsin-Diagnostic-DataSet/master/data.csv'
df = pd.read_csv(url)
```

1.2.1 Sneak Peak Data

[3]:
```
#Looking at the first 5 rows of the dataset
df.head()
```

[3]:
```
         id diagnosis  radius_mean  texture_mean  perimeter_mean  area_mean  \
0    842302         M        17.99         10.38          122.80     1001.0
1    842517         M        20.57         17.77          132.90     1326.0
2  84300903         M        19.69         21.25          130.00     1203.0
3  84348301         M        11.42         20.38           77.58      386.1
4  84358402         M        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

   …  texture_worst  perimeter_worst  area_worst  smoothness_worst  \
0  …          17.33           184.60      2019.0            0.1622
1  …          23.41           158.80      1956.0            0.1238
2  …          25.53           152.50      1709.0            0.1444
3  …          26.50            98.87       567.7            0.2098
4  …          16.67           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  Unnamed: 32
0                  0.11890          NaN
1                  0.08902          NaN
2                  0.08758          NaN
3                  0.17300          NaN
4                  0.07678          NaN

[5 rows x 33 columns]
```

[4]:
```python
#Looking at the last 5 rows of the dataset
df.tail()
```

[4]:
```
         id diagnosis  radius_mean  texture_mean  perimeter_mean  area_mean  \
564  926424         M        21.56         22.39          142.00     1479.0
565  926682         M        20.13         28.25          131.20     1261.0
566  926954         M        16.60         28.08          108.30      858.1
567  927241         M        20.60         29.33          140.10     1265.0
568   92751         B         7.76         24.54           47.92      181.0

     smoothness_mean  compactness_mean  concavity_mean  concave points_mean  \
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

     …  texture_worst  perimeter_worst  area_worst  smoothness_worst  \
564  …          26.40           166.10      2027.0           0.14100
565  …          38.25           155.00      1731.0           0.11660
```

```
566  …         34.12          126.70      1124.0           0.11390
567  …         39.42          184.60      1821.0           0.16500
568  …         30.37           59.16       268.6           0.08996

     compactness_worst  concavity_worst  concave points_worst  symmetry_worst  \
564            0.21130           0.4107                0.2216          0.2060
565            0.19220           0.3215                0.1628          0.2572
566            0.30940           0.3403                0.1418          0.2218
567            0.86810           0.9387                0.2650          0.4087
568            0.06444           0.0000                0.0000          0.2871

     fractal_dimension_worst  Unnamed: 32
564                  0.07115          NaN
565                  0.06637          NaN
566                  0.07820          NaN
567                  0.12400          NaN
568                  0.07039          NaN

[5 rows x 33 columns]
```

[5]:
```python
#How many rows and columns in the dataset?
df.shape
```

[5]:
```
(569, 33)
```

[6]:
```python
#Removing unused columns
df.drop('id', axis=1, inplace=True)
df.drop('Unnamed: 32', axis=1, inplace=True)
```

The data had 1 identity column (ID) and 1 ‘unknown’ column that had no use, so both columns were removed. The identity column must be removed to prevent overfitting of the model, because if there is a distinguishing identity, the model will learn to memorize the identity instead of seeing the pattern.

[7]:
```python
#General information of the dataset
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 31 columns):
 #   Column                   Non-Null Count  Dtype
---  ------                   --------------  -----
 0   diagnosis                569 non-null    object
 1   radius_mean              569 non-null    float64
 2   texture_mean             569 non-null    float64
 3   perimeter_mean           569 non-null    float64
 4   area_mean                569 non-null    float64
 5   smoothness_mean          569 non-null    float64
```

```
 6   compactness_mean         569 non-null    float64
 7   concavity_mean           569 non-null    float64
 8   concave points_mean      569 non-null    float64
 9   symmetry_mean            569 non-null    float64
 10  fractal_dimension_mean   569 non-null    float64
 11  radius_se                569 non-null    float64
 12  texture_se               569 non-null    float64
 13  perimeter_se             569 non-null    float64
 14  area_se                  569 non-null    float64
 15  smoothness_se            569 non-null    float64
 16  compactness_se           569 non-null    float64
 17  concavity_se             569 non-null    float64
 18  concave points_se        569 non-null    float64
 19  symmetry_se              569 non-null    float64
 20  fractal_dimension_se     569 non-null    float64
 21  radius_worst             569 non-null    float64
 22  texture_worst            569 non-null    float64
 23  perimeter_worst          569 non-null    float64
 24  area_worst               569 non-null    float64
 25  smoothness_worst         569 non-null    float64
 26  compactness_worst        569 non-null    float64
 27  concavity_worst          569 non-null    float64
 28  concave points_worst     569 non-null    float64
 29  symmetry_worst           569 non-null    float64
 30  fractal_dimension_worst  569 non-null    float64
dtypes: float64(30), object(1)
memory usage: 137.9+ KB
```

1.2.2 Handling Missing Values

[8]:

```
#Checking for missing values
df.isnull().sum()
```

[8]:

```
diagnosis                  0
radius_mean                0
texture_mean               0
perimeter_mean             0
area_mean                  0
smoothness_mean            0
compactness_mean           0
concavity_mean             0
concave points_mean        0
symmetry_mean              0
fractal_dimension_mean     0
radius_se                  0
texture_se                 0
perimeter_se               0
```

```
area_se                    0
smoothness_se              0
compactness_se             0
concavity_se               0
concave points_se          0
symmetry_se                0
fractal_dimension_se       0
radius_worst               0
texture_worst              0
perimeter_worst            0
area_worst                 0
smoothness_worst           0
compactness_worst          0
concavity_worst            0
concave points_worst       0
symmetry_worst             0
fractal_dimension_worst    0
dtype: int64
```

1.3 Exploratory Data Analysis

[9]:
```
#Describing the dataset
df.describe()
```

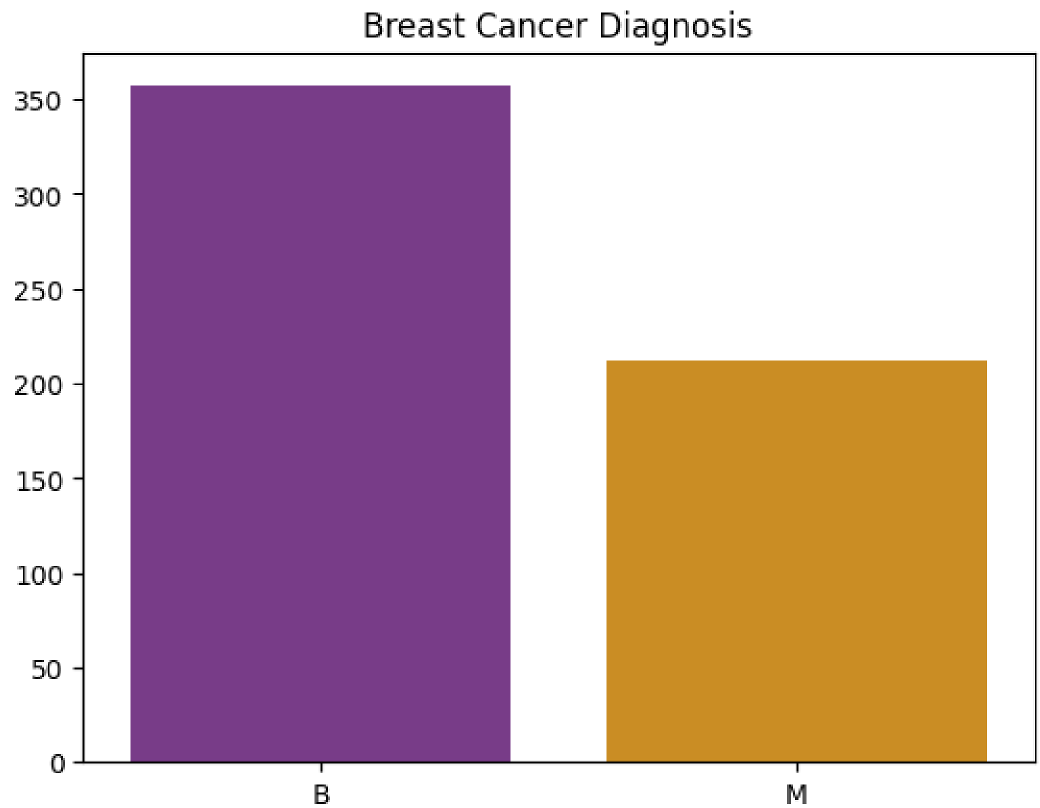
[9]:
```
       radius_mean  texture_mean  perimeter_mean    area_mean  \
count   569.000000    569.000000      569.000000   569.000000
mean     14.127292     19.289649       91.969033   654.889104
std       3.524049      4.301036       24.298981   351.914129
min       6.981000      9.710000       43.790000   143.500000
25%      11.700000     16.170000       75.170000   420.300000
50%      13.370000     18.840000       86.240000   551.100000
75%      15.780000     21.800000      104.100000   782.700000
max      28.110000     39.280000      188.500000  2501.000000

       smoothness_mean  compactness_mean  concavity_mean  concave points_mean  \
count       569.000000        569.000000      569.000000           569.000000
mean          0.096360          0.104341        0.088799             0.048919
std           0.014064          0.052813        0.079720             0.038803
min           0.052630          0.019380        0.000000             0.000000
25%           0.086370          0.064920        0.029560             0.020310
50%           0.095870          0.092630        0.061540             0.033500
75%           0.105300          0.130400        0.130700             0.074000
max           0.163400          0.345400        0.426800             0.201200

       symmetry_mean  fractal_dimension_mean  …  radius_worst  \
count     569.000000              569.000000  …    569.000000
mean        0.181162                0.062798  …     16.269190
```

```
std         0.027414                0.007060  ...     4.833242
min         0.106000                0.049960  ...     7.930000
25%         0.161900                0.057700  ...    13.010000
50%         0.179200                0.061540  ...    14.970000
75%         0.195700                0.066120  ...    18.790000
max         0.304000                0.097440  ...    36.040000

       texture_worst  perimeter_worst   area_worst  smoothness_worst  \
count     569.000000       569.000000   569.000000        569.000000
mean       25.677223       107.261213   880.583128          0.132369
std         6.146258        33.602542   569.356993          0.022832
min        12.020000        50.410000   185.200000          0.071170
25%        21.080000        84.110000   515.300000          0.116600
50%        25.410000        97.660000   686.500000          0.131300
75%        29.720000       125.400000  1084.000000          0.146000
max        49.540000       251.200000  4254.000000          0.222600

       compactness_worst  concavity_worst  concave points_worst  \
count         569.000000       569.000000            569.000000
mean            0.254265         0.272188              0.114606
std             0.157336         0.208624              0.065732
min             0.027290         0.000000              0.000000
25%             0.147200         0.114500              0.064930
50%             0.211900         0.226700              0.099930
75%             0.339100         0.382900              0.161400
max             1.058000         1.252000              0.291000

       symmetry_worst  fractal_dimension_worst
count      569.000000               569.000000
mean         0.290076                 0.083946
std          0.061867                 0.018061
min          0.156500                 0.055040
25%          0.250400                 0.071460
50%          0.282200                 0.080040
75%          0.317900                 0.092080
max          0.663800                 0.207500

[8 rows x 30 columns]
```

[10]:

```
#Univariate analysis 'diagnosis'
data_plot  = df['diagnosis'].value_counts().to_list()
label_plot = df['diagnosis'].value_counts().index.to_list()

title = 'Breast Cancer Diagnosis'

plot       = sns.barplot(x = label_plot, y = data_plot, palette = 'CMRmap')
plot_title = plt.title(title)
```

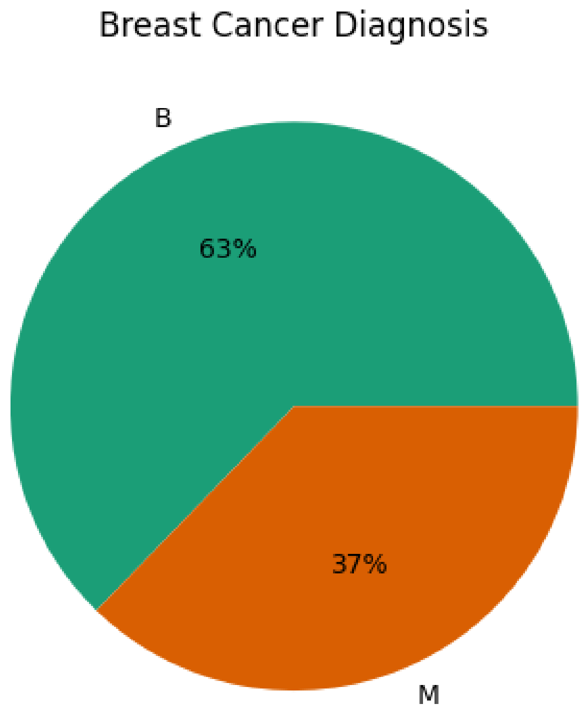
```
plt.show()
```



[11]:
```
df['diagnosis'].value_counts()
```

[11]:
```
diagnosis
B    357
M    212
Name: count, dtype: int64
```

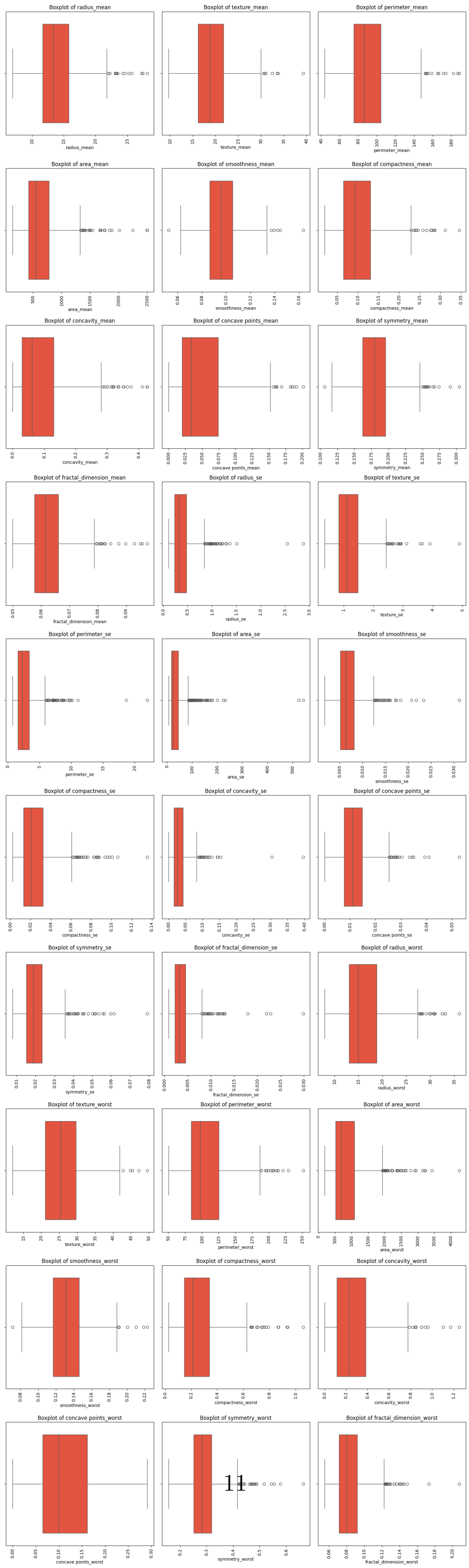
[12]:
```
color = sns.color_palette('Dark2')

plot       = plt.pie(data_plot, labels=label_plot, colors=color, autopct='%.
 ↪0f%%')
plot_title = plt.title(title)

plt.show()
```



Create a chart to see the distribution of diagnosis data.In the dataset, there are 357 patients with benign status, and 212 patients with malignant status. With this, 63% of patients in the dataset have benign status while 37% had breast cancer (malignant).

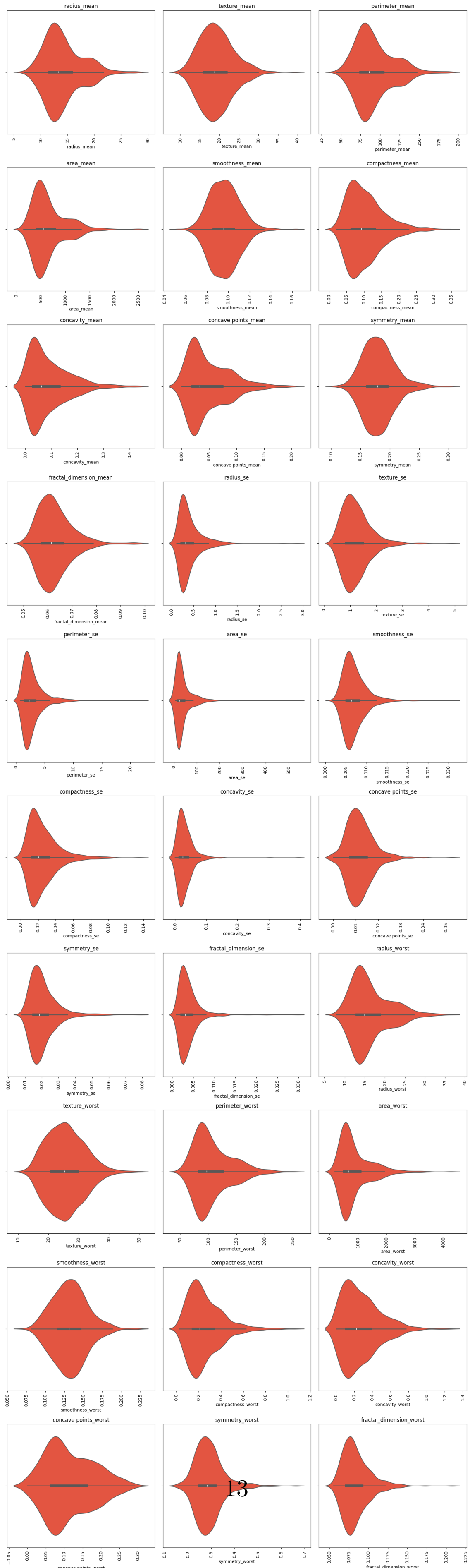
[13]:
```
#Boxplot of numeric variables
column_name_list_num = ['radius_mean', 'texture_mean', 'perimeter_mean',
       'area_mean', 'smoothness_mean', 'compactness_mean', 'concavity_mean',
       'concave points_mean', 'symmetry_mean', 'fractal_dimension_mean',
       'radius_se', 'texture_se', 'perimeter_se', 'area_se', 'smoothness_se',
       'compactness_se', 'concavity_se', 'concave points_se', 'symmetry_se',
       'fractal_dimension_se', 'radius_worst', 'texture_worst',
       'perimeter_worst', 'area_worst', 'smoothness_worst',
       'compactness_worst', 'concavity_worst', 'concave points_worst',
       'symmetry_worst', 'fractal_dimension_worst']

#Create subplots
num_cols = len(column_name_list_num)
num_rows = (num_cols + 2) // 3
fig, axs = plt.subplots(nrows=num_rows, ncols=3, figsize=(15,5*num_rows))
axs = axs.flatten()

#Boxplot for each variables
```

```
for i, var in enumerate (column_name_list_num):
  sns.boxplot(x=var, data=df, palette = 'CMRmap', ax=axs[i])
  axs[i].set_title("Boxplot of" + " " + var)
  axs[i].tick_params(axis='x', rotation=90)

#Removes extra empty subplots
if num_cols < len(axs):
  for i in range(num_cols, len(axs)):
    fig.delaxes(axs[i])

fig.tight_layout()
plt.show()
```


Boxplot of radius_mean
radius_mean
Boxplot of texture_mean
texture_mean
Boxplot of perimeter_mean
perimeter_mean
Boxplot of area_mean
area_mean
Boxplot of smoothness_mean
smoothness_mean
Boxplot of compactness_mean
compactness_mean
Boxplot of concavity_mean
concavity_mean
Boxplot of concave points_mean
concave points_mean
Boxplot of symmetry_mean
symmetry_mean
Boxplot of fractal_dimension_mean
fractal_dimension_mean
Boxplot of radius_se
radius_se
Boxplot of texture_se
texture_se
Boxplot of perimeter_se
perimeter_se
Boxplot of area_se
area_se
Boxplot of smoothness_se
smoothness_se
Boxplot of compactness_se
compactness_se
Boxplot of concavity_se
concavity_se
Boxplot of concave points_se
concave points_se
Boxplot of symmetry_se
symmetry_se
Boxplot of fractal_dimension_se
fractal_dimension_se
Boxplot of radius_worst
radius_worst
Boxplot of texture_worst
texture_worst
Boxplot of perimeter_worst
perimeter_worst
Boxplot of area_worst
area_worst
Boxplot of smoothness_worst
smoothness_worst
Boxplot of compactness_worst
compactness_worst
Boxplot of concavity_worst
concavity_worst
Boxplot of concave points_worst
concave points_worst
Boxplot of symmetry_worst
symmetry_worst
Boxplot of fractal_dimension_worst
fractal_dimension_worst

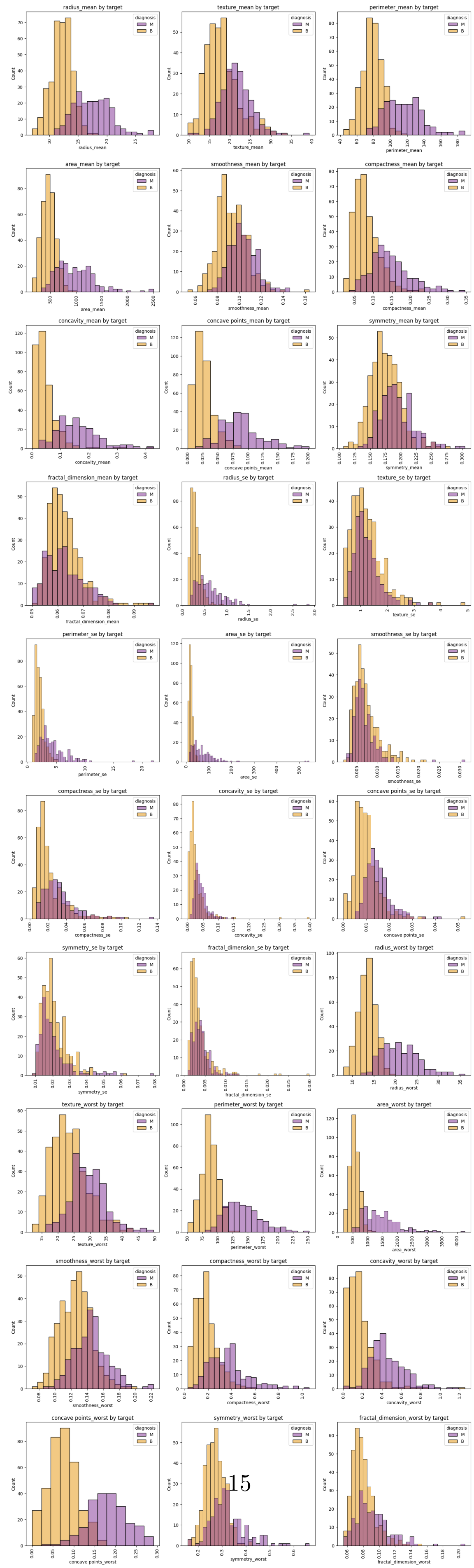
A box plot is a visualization created to illustrate the shape of the distribution and spread of data.The box plot shows the quartiles, distance between quartiles, minimum and maximum limits, and outliers in the data. A box plot is created for each numerical column.

[14]:
```
#Create subplots
num_cols = len(column_name_list_num)
num_rows = (num_cols + 2) // 3
fig, axs = plt.subplots(nrows=num_rows, ncols=3, figsize=(15,5*num_rows))
axs = axs.flatten()

#Violin plot for each variables
for i, var in enumerate (column_name_list_num):
  sns.violinplot(x=var, data=df, palette = 'CMRmap', ax=axs[i])
  axs[i].set_title(var)
  axs[i].tick_params(axis='x', rotation=90)

#Removes extra empty subplots
if num_cols < len(axs):
  for i in range(num_cols, len(axs)):
    fig.delaxes(axs[i])

fig.tight_layout()
plt.show()
```


radius_mean
texture_mean
perimeter_mean
area_mean
smoothness_mean
compactness_mean
concavity_mean
concave points_mean
symmetry_mean
fractal_dimension_mean
radius_se
texture_se
perimeter_se
area_se
smoothness_se
compactness_se
concavity_se
concave points_se
symmetry_se
fractal_dimension_se
radius_worst
texture_worst
perimeter_worst
area_worst
smoothness_worst
compactness_worst
concavity_worst
concave points_worst
symmetry_worst
fractal_dimension_worst

Violin plot is a variation of box plot plus kernel density plot. A violin plot is created for each numerical column.

[15]:
```
#Histogram overlay of 'diagnosis' with the independent variables
#Create subplots
num_cols = len(column_name_list_num)
num_rows = (num_cols + 2) // 3
fig, axs = plt.subplots(nrows=num_rows, ncols=3, figsize=(15,5*num_rows))
axs = axs.flatten()

#Histplot for each variables
for i, var in enumerate (column_name_list_num):
  sns.histplot(x=var, hue = 'diagnosis', data=df, palette = 'CMRmap', ax=axs[i])
  axs[i].set_title(var + " " + "by target")
  axs[i].tick_params(axis='x', rotation=90)

#Removes extra empty subplots
if num_cols < len(axs):
  for i in range(num_cols, len(axs)):
    fig.delaxes(axs[i])

fig.tight_layout()
plt.show()
```

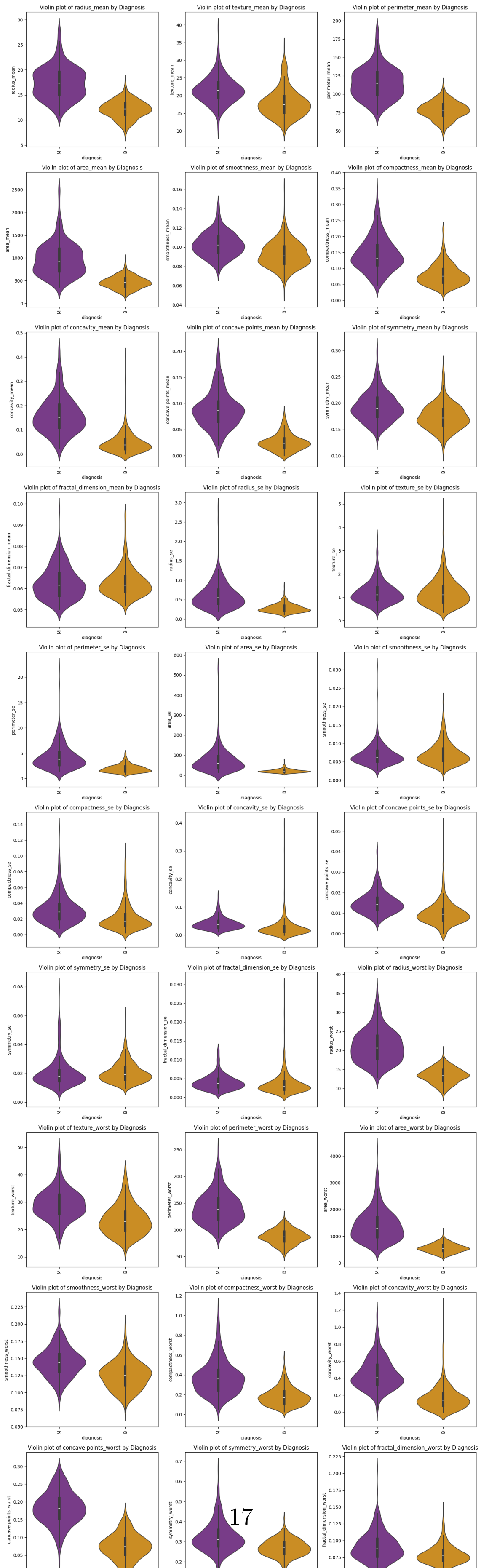

radius_mean by target
texture_mean by target
perimeter_mean by target
area_mean by target
smoothness_mean by target
compactness_mean by target
concavity_mean by target
concave points_mean by target
symmetry_mean by target
fractal_dimension_mean by target
radius_se by target
texture_se by target
perimeter_se by target
area_se by target
smoothness_se by target
compactness_se by target
concavity_se by target
concave points_se by target
symmetry_se by target
fractal_dimension_se by target
radius_worst by target
texture_worst by target
perimeter_worst by target
area_worst by target
smoothness_worst by target
compactness_worst by target
concavity_worst by target
concave points_worst by target
symmetry_worst by target
fractal_dimension_worst by target
diagnosis
M
B
Count

Histograms are graphs to view data distribution patterns.Histograms were created for each numeric column with an overlay of diagnosis status to see the difference in the distribution of numeric data for each type of diagnosis.

It can be seen that in the dataset, the majority of patients with benign status have smaller tumor measurements.

[16]:

```
#Create subplots
num_cols = len(column_name_list_num)
num_rows = (num_cols + 2) // 3
fig, axs = plt.subplots(nrows=num_rows, ncols=3, figsize=(15,5*num_rows))
axs = axs.flatten()

#Violin plot for each variables
for i, var in enumerate (column_name_list_num):
  sns.violinplot(y=var, x='diagnosis', data=df, palette = 'CMRmap', ax=axs[i])
  axs[i].set_title("Violin plot of" + " " + var + " " + "by Diagnosis")
  axs[i].tick_params(axis='x', rotation=90)

#Removes extra empty subplots
if num_cols < len(axs):
  for i in range(num_cols, len(axs)):
    fig.delaxes(axs[i])

fig.tight_layout()
plt.show()
```



Violin plot of radius_mean by Diagnosis
Violin plot of texture_mean by Diagnosis
Violin plot of perimeter_mean by Diagnosis
Violin plot of area_mean by Diagnosis
Violin plot of smoothness_mean by Diagnosis
Violin plot of compactness_mean by Diagnosis
Violin plot of concavity_mean by Diagnosis
Violin plot of concave points_mean by Diagnosis
Violin plot of symmetry_mean by Diagnosis
Violin plot of fractal_dimension_mean by Diagnosis
Violin plot of radius_se by Diagnosis
Violin plot of texture_se by Diagnosis
Violin plot of perimeter_se by Diagnosis
Violin plot of area_se by Diagnosis
Violin plot of smoothness_se by Diagnosis
Violin plot of compactness_se by Diagnosis
Violin plot of concavity_se by Diagnosis
Violin plot of concave points_se by Diagnosis
Violin plot of symmetry_se by Diagnosis
Violin plot of fractal_dimension_se by Diagnosis
Violin plot of radius_worst by Diagnosis
Violin plot of texture_worst by Diagnosis
Violin plot of perimeter_worst by Diagnosis
Violin plot of area_worst by Diagnosis
Violin plot of smoothness_worst by Diagnosis
Violin plot of compactness_worst by Diagnosis
Violin plot of concavity_worst by Diagnosis
Violin plot of concave points_worst by Diagnosis
Violin plot of symmetry_worst by Diagnosis
Violin plot of fractal_dimension_worst by Diagnosis
diagnosis

Violin plot for each numerical column with diagnosis status overlay to see the difference in numerical data distribution in each diagnosis type.

[17]:
```
#Mean of each column values in each class
df.groupby(by = 'diagnosis').mean()
```

[17]:
```
           radius_mean  texture_mean  perimeter_mean   area_mean  \
diagnosis
B            12.146524     17.914762       78.075406  462.790196
M            17.462830     21.604906      115.365377  978.376415

           smoothness_mean  compactness_mean  concavity_mean  \
diagnosis
B                 0.092478          0.080085        0.046058
M                 0.102898          0.145188        0.160775

           concave points_mean  symmetry_mean  fractal_dimension_mean  …  \
diagnosis                                                              …
B                     0.025717       0.174186                0.062867  …
M                     0.087990       0.192909                0.062680  …

           radius_worst  texture_worst  perimeter_worst   area_worst  \
diagnosis
B             13.379801      23.515070        87.005938   558.899440
M             21.134811      29.318208       141.370330  1422.286321

           smoothness_worst  compactness_worst  concavity_worst  \
diagnosis
B                  0.124959           0.182673         0.166238
M                  0.144845           0.374824         0.450606

           concave points_worst  symmetry_worst  fractal_dimension_worst
diagnosis
B                      0.074444        0.270246                 0.079442
M                      0.182237        0.323468                 0.091530

[2 rows x 30 columns]
```

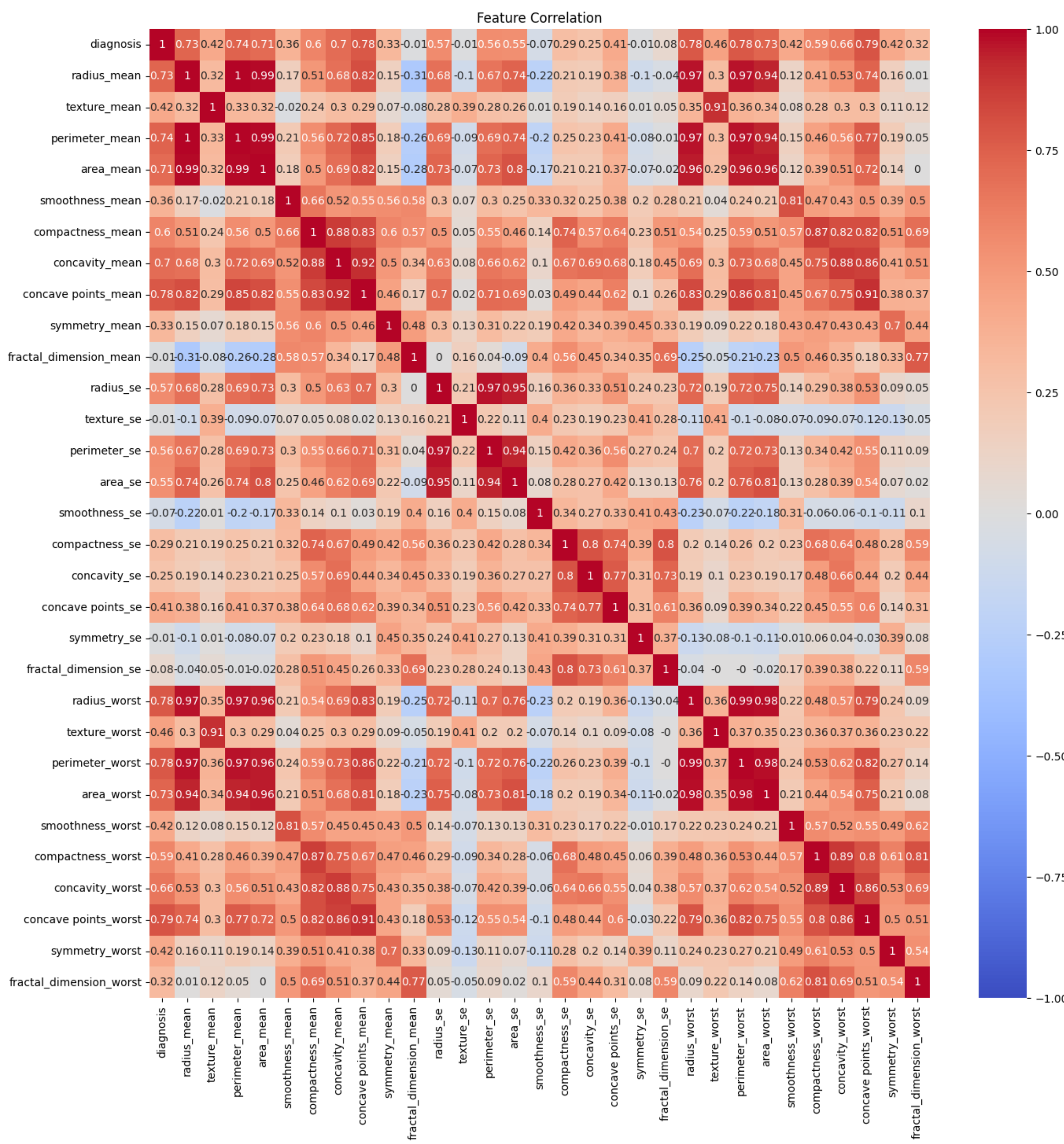
1.4 Labelling Categorical Data

[18]:
```
#Labeling categorical data
diagnosis = {
    "B": 0,
    "M": 1
}
```

```
df['diagnosis'] = df['diagnosis'].map(diagnosis)
```

Diagnosis results are categorical so they must be converted to numeric in order to use the model. Labeling the diagnosis column value with "B" = 0 and "M" = 1. Labeling is done by mapping values based on the dictionary that has been created.

[19]:
```
#Correlations between features
matrix = df.corr().round(2)
plt.figure(figsize=(16,16))
sns.heatmap(matrix, annot=True, vmax=1, vmin=-1, center=0, cmap='coolwarm')
plt.title("Feature Correlation")
plt.show()
```



The correlation between numerical features can be seen in the figure above. The correlation value is rounded to 2 numbers behind zero. The higher the value, the stronger the correlation. A positive correlation means that it is directly proportional, if the correlation is negative then the correlation is inversely proportional.

1.5 Balancing Data + Splitting the dataset into the Training set and Test set

[20]:
```
#Defining x and y
x = df.drop(columns=['diagnosis'])
y = df['diagnosis']
```

The dataset is split into train and test with a ratio of 80:20. The reason why this number is set is because 80/20 is generally considered good enough (unless the training data is very large, then the split data ratio may change). In this project dataset, the number of columns is not too large so enough training data is needed to ensure the model is well trained.

[21]:
```
from sklearn.model_selection import train_test_split
x_train, x_test, y_train, y_test = train_test_split(x, y, test_size = 0.2,␣
↪random_state = 42)
```

Data balancing is carried out with the SMOTE oversampling method because the amount of data is not balanced. Data balancing is done so that the model can achieve higher accuracy.

[22]:
```
from imblearn.over_sampling import SMOTE
#define oversampling strategy
SMOTE = SMOTE()

#fit and apply the transform
x_train, y_train = SMOTE.fit_resample(x_train, y_train)
```

[23]:
```
x_train.shape, x_test.shape
```

[23]:
```
((572, 30), (114, 30))
```

1.6 Modelling

1.6.1 Gradient Boosting

[45]:
```
from sklearn.ensemble import GradientBoostingClassifier
gb = GradientBoostingClassifier()
```

[46]:
```
#Training the model
gb.fit(x_train, y_train)
```

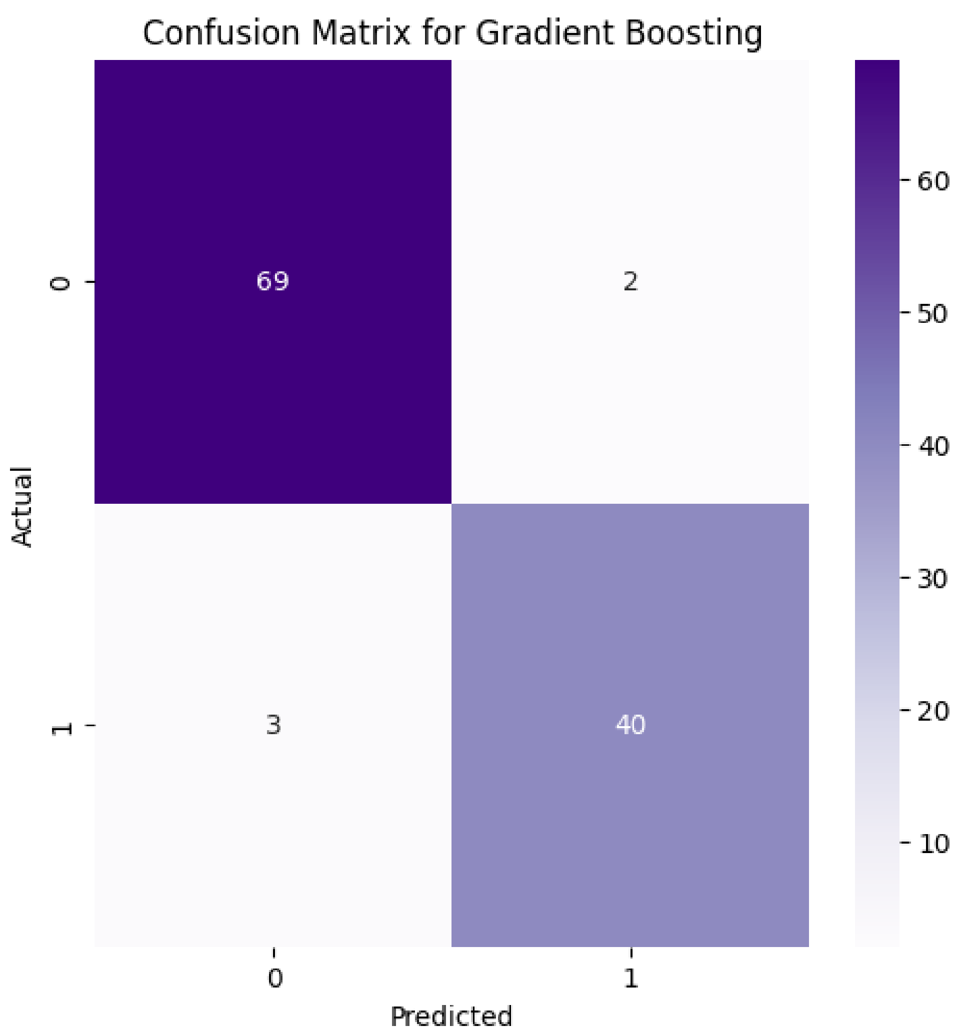
[46]:
```
GradientBoostingClassifier()
```

[47]:
```
#Predict testing set
y_pred_gb = gb.predict(x_test)
```

[48]:
```
print('Training-set accuracy score:', gb.score(x_train, y_train))
print('Test-set accuracy score:', gb.score(x_test, y_test))
```

```
Training-set accuracy score: 1.0
Test-set accuracy score: 0.956140350877193
```

[49]:
```
plt.figure(figsize=(6,6))
sns.heatmap(confusion_matrix(y_test,y_pred_gb), annot=True, fmt='d',␣
↪cmap='Purples')
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix for Gradient Boosting')
plt.show()
```



[50]:
```
#Check model performance using classification_report
print(classification_report(y_test, y_pred_gb))
```

```
              precision    recall  f1-score   support

           0       0.96      0.97      0.97        71
           1       0.95      0.93      0.94        43

    accuracy                           0.96       114
   macro avg       0.96      0.95      0.95       114
weighted avg       0.96      0.96      0.96       114
```

[51]:
```
#Specificity
cm = confusion_matrix(y_test, y_pred_gb)

specificity = cm[1,1]/(cm[1,0] + cm[1,1])
print('Specificity : ', specificity)
```

```
Specificity :  0.9302325581395349
```

[52]:
```
#Check model performance using auc score
roc_auc_score(y_test, y_pred_gb)*100
```

[52]:
```
95.10317720275138
```

1.6.2 Random Forest

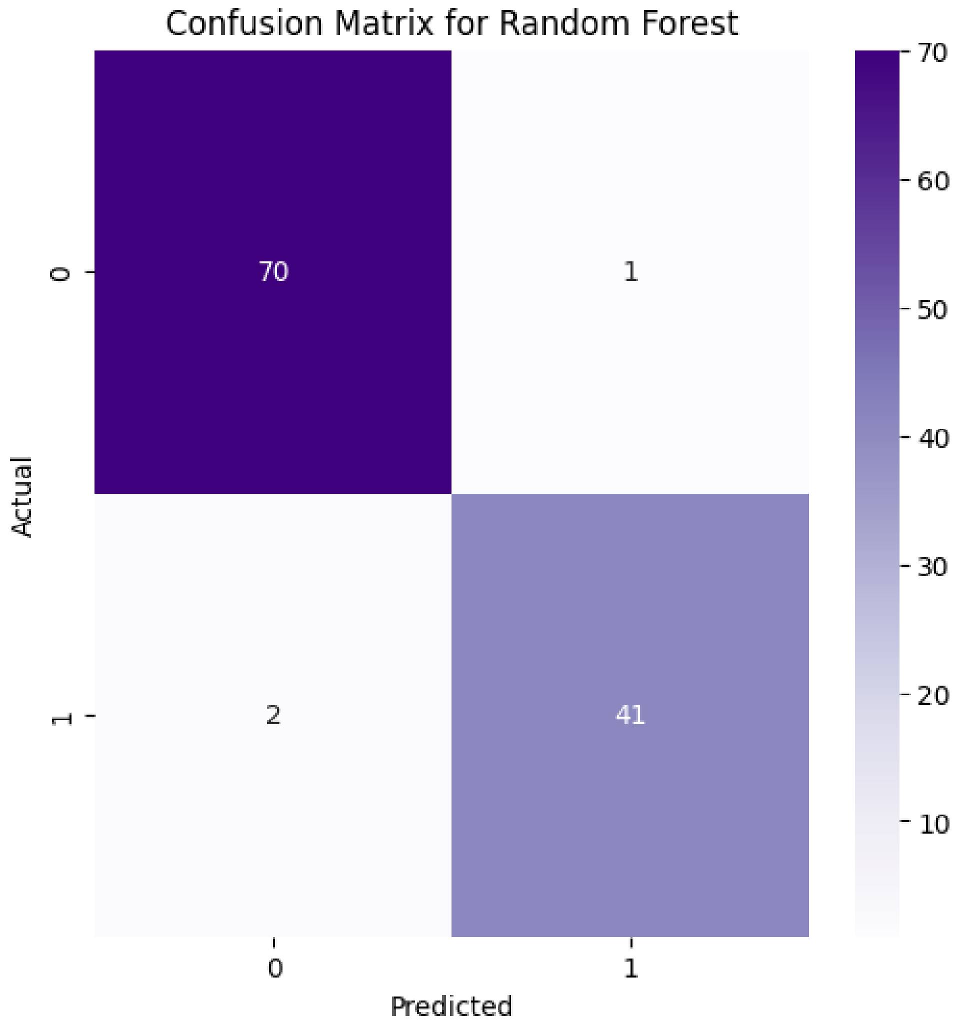
[53]:
```
from sklearn.ensemble import RandomForestClassifier

classifier_rf = RandomForestClassifier()
classifier_rf.fit(x_train, y_train)
y_pred_rf = classifier_rf.predict(x_test)
```

[54]:
```
print('Training-set accuracy score:', classifier_rf.score(x_train, y_train))
print('Test-set accuracy score:', classifier_rf.score(x_test, y_test))
```

```
Training-set accuracy score: 1.0
Test-set accuracy score: 0.9736842105263158
```

[55]:
```
plt.figure(figsize=(6,6))
sns.heatmap(confusion_matrix(y_test,y_pred_rf), annot=True, fmt='d',␣
 ↪cmap='Purples')
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix for Random Forest')
```

```
plt.show()
```



[56]:

```
#Classification report
print(classification_report(y_test, y_pred_rf))
```

```
              precision    recall  f1-score   support

           0       0.97      0.99      0.98        71
           1       0.98      0.95      0.96        43

    accuracy                           0.97       114
   macro avg       0.97      0.97      0.97       114
weighted avg       0.97      0.97      0.97       114
```

[57]:
```
#Specificity
cm = confusion_matrix(y_test, y_pred_rf)

specificity = cm[1,1]/(cm[1,0] + cm[1,1])
print('Specificity : ', specificity)
```

```
Specificity :  0.9534883720930233
```

[58]:
```
roc_auc_score(y_test, y_pred_rf)*100
```

[58]:
```
96.97019325253848
```

1.6.3 Stacking Model

[59]:
```
from sklearn.tree import DecisionTreeClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from xgboost import XGBClassifier
from sklearn.ensemble import StackingClassifier

base_models = [('Decision Tree',DecisionTreeClassifier()),('Logistic␣
↪Regression',LogisticRegression()), ('Random Forest',␣
↪RandomForestClassifier()), ('xgb', XGBClassifier())]
stacking = StackingClassifier(estimators = base_models, final_estimator =␣
↪LogisticRegression(), cv = 5)
stacking.fit(x_train , y_train)
```

[59]:
```
StackingClassifier(cv=5,
                   estimators=[('Decision Tree', DecisionTreeClassifier()),
                               ('Logistic Regression', LogisticRegression()),
                               ('Random Forest', RandomForestClassifier()),
                               ('xgb',
                                XGBClassifier(base_score=None, booster=None,
                                              callbacks=None,
                                              colsample_bylevel=None,
                                              colsample_bynode=None,
                                              colsample_bytree=None,
                                              device=None,
                                              early_stopping_rounds=None,
                                              enable_categori…
                                              interaction_constraints=None,
                                              learning_rate=None, max_bin=None,
                                              max_cat_threshold=None,
                                              max_cat_to_onehot=None,
                                              max_delta_step=None,
                                              max_depth=None, max_leaves=None,
                                              min_child_weight=None,
```

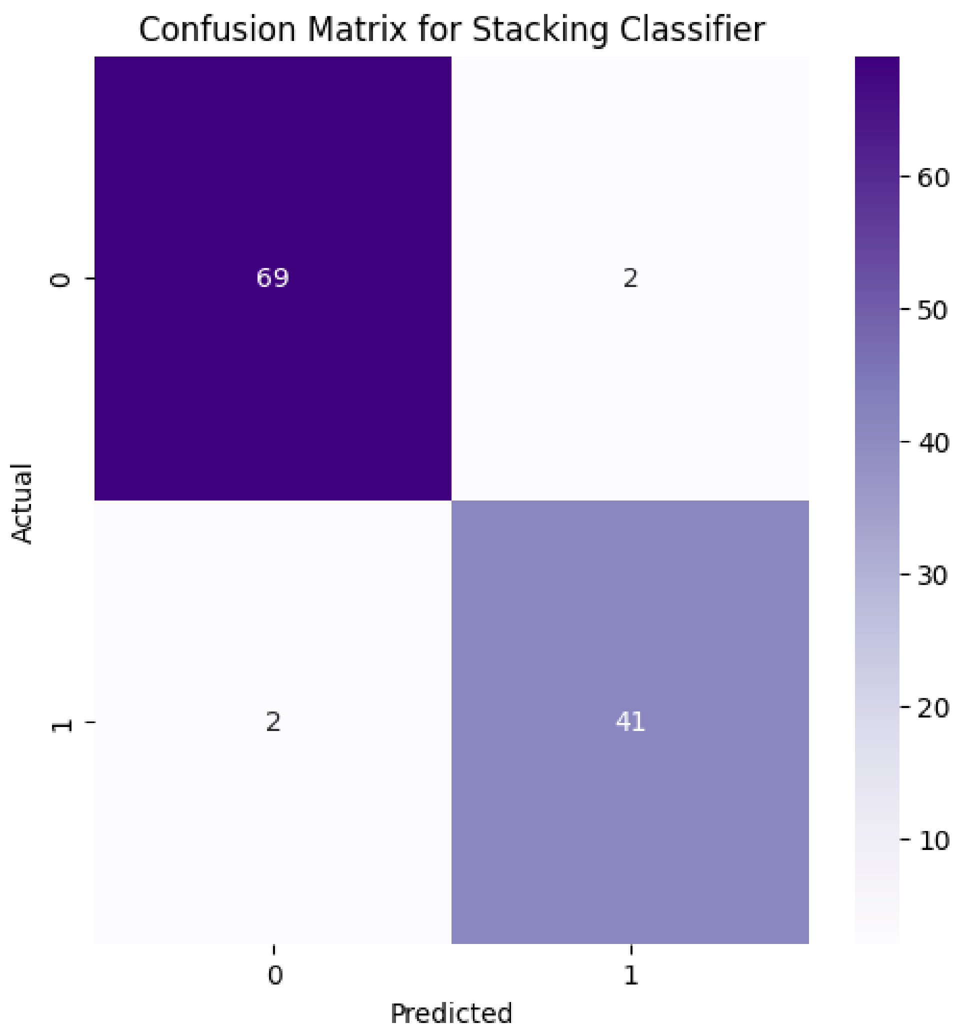
```
                                                    missing=nan,
                                                    monotone_constraints=None,
                                                    multi_strategy=None,
                                                    n_estimators=None, n_jobs=None,
                                                    num_parallel_tree=None,
                                                    random_state=None, …))],
                           final_estimator=LogisticRegression())
```

[60]:
```
y_pred_st = stacking.predict(x_test)
```

[61]:
```
print('Training-set accuracy score:', stacking.score(x_train, y_train))
print('Test-set accuracy score:', stacking.score(x_test, y_test))
```

```
Training-set accuracy score: 1.0
Test-set accuracy score: 0.9649122807017544
```

[62]:
```
plt.figure(figsize=(6,6))
sns.heatmap(confusion_matrix(y_test,y_pred_st), annot=True, fmt='d',␣
 ↪cmap='Purples')
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix for Stacking Classifier')
plt.show()
```



[63]:
```
#Classification report
print(classification_report(y_test, y_pred_st))
```

```
              precision    recall  f1-score   support

           0       0.97      0.97      0.97        71
           1       0.95      0.95      0.95        43

    accuracy                           0.96       114
   macro avg       0.96      0.96      0.96       114
weighted avg       0.96      0.96      0.96       114
```

[64]:
```
#Specificity
cm = confusion_matrix(y_test, y_pred_st)
```

```
specificity = cm[1,1]/(cm[1,0] + cm[1,1])
print('Specificity : ', specificity)
```

```
Specificity :  0.9534883720930233
```

[65]:
```
roc_auc_score(y_test, y_pred_st)*100
```

[65]:
```
96.2659679004258
```

2 Conclusion

Based on the results of the evaluation metrics, the best model is **Random Forest** with a slightly higher difference in metric results than Gradient Boosting and Stacking Classifier. In the health context, recall (sensitivity) and specificity values are taken into consideration as these affect the diagnosis of a disease. The Random Forest model has the highest value on these two metrics, it is hoped that this can help the accuracy of patient diagnosis and reduce false positive results so as not to waste hospital resources and ensure patients with cancer get fast treatment.