MACHINE LEARNING PROJECT REPORT

on

Breast Cancer: Tumour Classification

Submitted by

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Date:27-04-23

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Breast Cancer Tumour Classification

INTRODUCTION

Breast cancer prediction dataset contains information about different features that can help predict the risk of breast cancer, such as age,diagonis,concavity_mean, and lymph node involvement. It is used to develop models that identify individuals at high risk of developing breast cancer, leading to earlier detection and better outcomes.

ABSTRACT

This analysis reviews the recent advances in breast cancer tumor classification using machine learning algorithms. It covers the types of data used, machine learning techniques applied, and challenges faced. The use of machine learning algorithms can improve accuracy, reduce time, and lower costs.

Importing the Libraries

In Python, a library is a collection of pre-written code that can be imported and used in your own Python program.

Libraries in Python provide a wide range of functionalities, from simple tasks such as string manipulation to more complex tasks such as machine learning and scientific computing. Some popular libraries in Python include NumPy, Pandas, Matplotlib, TensorFlow, Scikit-learn, and many more.

By using libraries, you can save time and effort by not having to write all the code yourself, and you can take advantage of well-tested and optimized code written by other developers. To use a library in your Python program, you typically need to import it at the beginning of your code using the import statement.

In [1]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import statsmodels
import statsmodels.api as sm
import plotly.express as px
import sklearn
from sklearn.model_selection import train_test_split
from sklearn.metrics import mean_squared_error
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import r2_score
from sklearn import metrics
from sklearn.preprocessing import MinMaxScaler
from sklearn.metrics import accuracy_score
import statsmodels.api as sm
from sklearn.model_selection import train_test_split
from statsmodels.stats.outliers_influence import variance_inflation_factor
from sklearn.ensemble import RandomForestClassifier
from sklearn.tree import DecisionTreeClassifier, export_graphviz
import warnings
warnings.filterwarnings('ignore')
```

Reading the Dataset

Reading a dataset refers to the process of loading data from a file into memory in a format that can be easily manipulated and analyzed using a programming language like Python.

In [2]:
```
df=pd.read_csv("data.csv")
df
```

Out[2]:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavi
0	842302	M	17.99	10.38	122.80	1001.0	0.11840	0.27760	
1	842517	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	
2	84300903	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	
3	84348301	M	11.42	20.38	77.58	386.1	0.14250	0.28390	
4	84358402	M	20.29	14.34	135.10	1297.0	0.10030	0.13280	
...	...	...	...	...	...	...	...	...	
564	926424	M	21.56	22.39	142.00	1479.0	0.11100	0.11590	
565	926682	M	20.13	28.25	131.20	1261.0	0.09780	0.10340	
566	926954	M	16.60	28.08	108.30	858.1	0.08455	0.10230	
567	927241	M	20.60	29.33	140.10	1265.0	0.11780	0.27700	
568	92751	B	7.76	24.54	47.92	181.0	0.05263	0.04362	

569 rows × 33 columns

Column Names and Meanings

id: a unique identifier for each patient in the dataset.

diagnosis: the diagnosis of the breast mass (M = malignant, B = benign).

radius_mean: the mean of the distances from the center to points on the perimeter of the breast mass.

texture_mean: the standard deviation of gray-scale values in the image.

perimeter_mean: the perimeter of the breast mass.

area_mean: the area of the breast mass.

smoothness_mean: the local variation in radius lengths.

compactness_mean: the perimeter^2 / area - 1.0.

concavity_mean: the severity of concave portions of the breast mass.

concave points_mean: the number of concave portions of the breast mass.

symmetry_mean: symmetry of the breast mass.

fractal_dimension_mean: "coastline approximation" - 1.

radius_se: the standard error of the mean distances from the center to points on the perimeter of the breast mass.

texture_se: the standard error of gray-scale values in the image.

perimeter_se: the standard error of the perimeter of the breast mass.

area_se: the standard error of the area of the breast mass.

smoothness_se: the standard error of the local variation in radius lengths.

compactness_se: the standard error of the perimeter^2 / area - 1.0.

concavity_se: the standard error of the severity of concave portions of the breast mass.

concave points_se: the standard error for the number of concave portions of the breast mass.

symmetry_se: the standard error of symmetry of the breast mass.

fractal_dimension_se: the standard error for "coastline approximation" - 1.

radius_worst: the "worst" or largest mean value for mean distances from the center to points on the perimeter of the breast mass.

texture_worst: the "worst" or largest mean value for standard deviation of gray-scale values in the image.

perimeter_worst: the "worst" or largest mean value for the perimeter of the breast mass.

area_worst: the "worst" or largest mean value for the area of the breast mass.

smoothness_worst: the "worst" or largest mean value for local variation in radius lengths.

compactness_worst: the "worst" or largest mean value for perimeter^2 / area - 1.0.

concavity_worst: the "worst" or largest mean value for severity of concave portions of the breast mass.

concave points_worst: the "worst" or largest mean value for the number of concave portions of the breast mass.

symmetry_worst: the "worst" or largest mean value for symmetry of the breast mass.

fractal_dimension_worst: the "worst" or largest mean value for "coastline approximation" - 1.

Checking the Null values

Checking for null values in a dataset is an essential step in data analysis, as missing or null values can cause errors or biases in statistical analysis and machine learning models. In Python, the pandas library provides several functions to check for null values in a DataFrame.

In [3]:
```
df.isnull
```

Out[3]:
```
<bound method DataFrame.isnull of            id diagnosis  radius_mean  texture_mean  perimeter_mean  are
a_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
..        ...       ...          ...           ...             ...        ...
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  \
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

     ...  texture_worst  perimeter_worst  area_worst  smoothness_worst  \
0    ...          17.33           184.60      2019.0           0.16220
1    ...          23.41           158.80      1956.0           0.12380
2    ...          25.53           152.50      1709.0           0.14440
3    ...          26.50            98.87       567.7           0.20980
4    ...          16.67           152.20      1575.0           0.13740
..   ...            ...              ...         ...               ...
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  \
0              0.66560           0.7119                0.2654          0.4601
1              0.18660           0.2416                0.1860          0.2750
2              0.42450           0.4504                0.2430          0.3613
3              0.86630           0.6869                0.2575          0.6638
4              0.20500           0.4000                0.1625          0.2364
..                 ...              ...                   ...             ...
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
0                    0.11890          NaN
1                    0.08902          NaN
2                    0.08758          NaN
3                    0.17300          NaN
4                    0.07678          NaN
..                       ...          ...
564                  0.07115          NaN
565                  0.06637          NaN
566                  0.07820          NaN
567                  0.12400          NaN
568                  0.07039          NaN

[569 rows x 33 columns]>
```

In [4]:
```
df.isnull().sum()
```

Out[4]:
```
id                           0
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
Unnamed: 32                569
dtype: int64
```

The breast cancer dataset does not contain any null or missing values. After loading the dataset and converting it to a Pandas dataframe, we can use the isnull().sum() method to check for missing values. When applied to the breast cancer dataset, this method returns zero for all columns, indicating that there are no missing values But When it comes to unnamed column there are null values , so lets remove them.

In [5]:
```
#Reading the Head part of the Dataset.
df.head()
```

Out[5]:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_
0	842302	M	17.99	10.38	122.80	1001.0	0.11840	0.27760	
1	842517	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	
2	84300903	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	
3	84348301	M	11.42	20.38	77.58	386.1	0.14250	0.28390	
4	84358402	M	20.29	14.34	135.10	1297.0	0.10030	0.13280	

5 rows × 33 columns

In [6]:
```
#Reading the tail part of my Dataset
df.tail()
```

Out[6]:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_
564	926424	M	21.56	22.39	142.00	1479.0	0.11100	0.11590	0
565	926682	M	20.13	28.25	131.20	1261.0	0.09780	0.10340	0
566	926954	M	16.60	28.08	108.30	858.1	0.08455	0.10230	0
567	927241	M	20.60	29.33	140.10	1265.0	0.11780	0.27700	0
568	92751	B	7.76	24.54	47.92	181.0	0.05263	0.04362	0

5 rows × 33 columns

In [7]:
```
#Info of the Dataset
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 33 columns):
 #   Column                   Non-Null Count  Dtype  
---  ------                   --------------  -----  
 0   id                       569 non-null    int64  
 1   diagnosis                569 non-null    object 
 2   radius_mean              569 non-null    float64
 3   texture_mean             569 non-null    float64
 4   perimeter_mean           569 non-null    float64
 5   area_mean                569 non-null    float64
 6   smoothness_mean          569 non-null    float64
 7   compactness_mean         569 non-null    float64
 8   concavity_mean           569 non-null    float64
 9   concave points_mean      569 non-null    float64
 10  symmetry_mean            569 non-null    float64
 11  fractal_dimension_mean   569 non-null    float64
 12  radius_se                569 non-null    float64
 13  texture_se               569 non-null    float64
 14  perimeter_se             569 non-null    float64
 15  area_se                  569 non-null    float64
 16  smoothness_se            569 non-null    float64
 17  compactness_se           569 non-null    float64
 18  concavity_se             569 non-null    float64
 19  concave points_se        569 non-null    float64
 20  symmetry_se              569 non-null    float64
 21  fractal_dimension_se     569 non-null    float64
 22  radius_worst             569 non-null    float64
 23  texture_worst            569 non-null    float64
 24  perimeter_worst          569 non-null    float64
 25  area_worst               569 non-null    float64
 26  smoothness_worst         569 non-null    float64
 27  compactness_worst        569 non-null    float64
 28  concavity_worst          569 non-null    float64
 29  concave points_worst     569 non-null    float64
 30  symmetry_worst           569 non-null    float64
 31  fractal_dimension_worst  569 non-null    float64
 32  Unnamed: 32              0 non-null      float64
dtypes: float64(31), int64(1), object(1)
memory usage: 146.8+ KB
```

In [8]:
```
df.describe()
```

Out[8]:

	id	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_m
count	5.690000e+02	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.00
mean	3.037183e+07	14.127292	19.289649	91.969033	654.889104	0.096360	0.104341	0.08
std	1.250206e+08	3.524049	4.301036	24.298981	351.914129	0.014064	0.052813	0.07
min	8.670000e+03	6.981000	9.710000	43.790000	143.500000	0.052630	0.019380	0.00
25%	8.692180e+05	11.700000	16.170000	75.170000	420.300000	0.086370	0.064920	0.02
50%	9.060240e+05	13.370000	18.840000	86.240000	551.100000	0.095870	0.092630	0.06
75%	8.813129e+06	15.780000	21.800000	104.100000	782.700000	0.105300	0.130400	0.13
max	9.113205e+08	28.110000	39.280000	188.500000	2501.000000	0.163400	0.345400	0.42

8 rows × 32 columns

In [9]:
```
df.diagnosis.nunique()
```

Out[9]: 2

Dropping the Null Values

In [10]:
```
df.drop(['id','Unnamed: 32'],axis=1,inplace=True)
```

In [11]:
```
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
```

Therefore , we have successfully dropped the unnamed column , now the dataset do not have any null values.

In [12]:
```
df.head()
```

Out[12]:

	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	poi
0	M	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	
1	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	
2	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	
3	M	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	
4	M	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	

5 rows × 31 columns

In [13]:
```
df.diagnosis.unique()
```

Out[13]: array(['M', 'B'], dtype=object)

Dummy Variables

In machine learning, a dummy variable (also called an indicator variable) is a binary variable that takes on the values 0 or 1 to represent the presence or absence of a categorical feature. Dummy variables are commonly used in machine learning algorithms to represent categorical data numerically.

In [14]:
```
df.diagnosis = [1 if each == "M" else 0 for each in df.diagnosis]
```

In [15]:
```
df.head()
```

Out[15]:

	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	poi
0	1	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	
1	1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	
2	1	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	
3	1	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	
4	1	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	

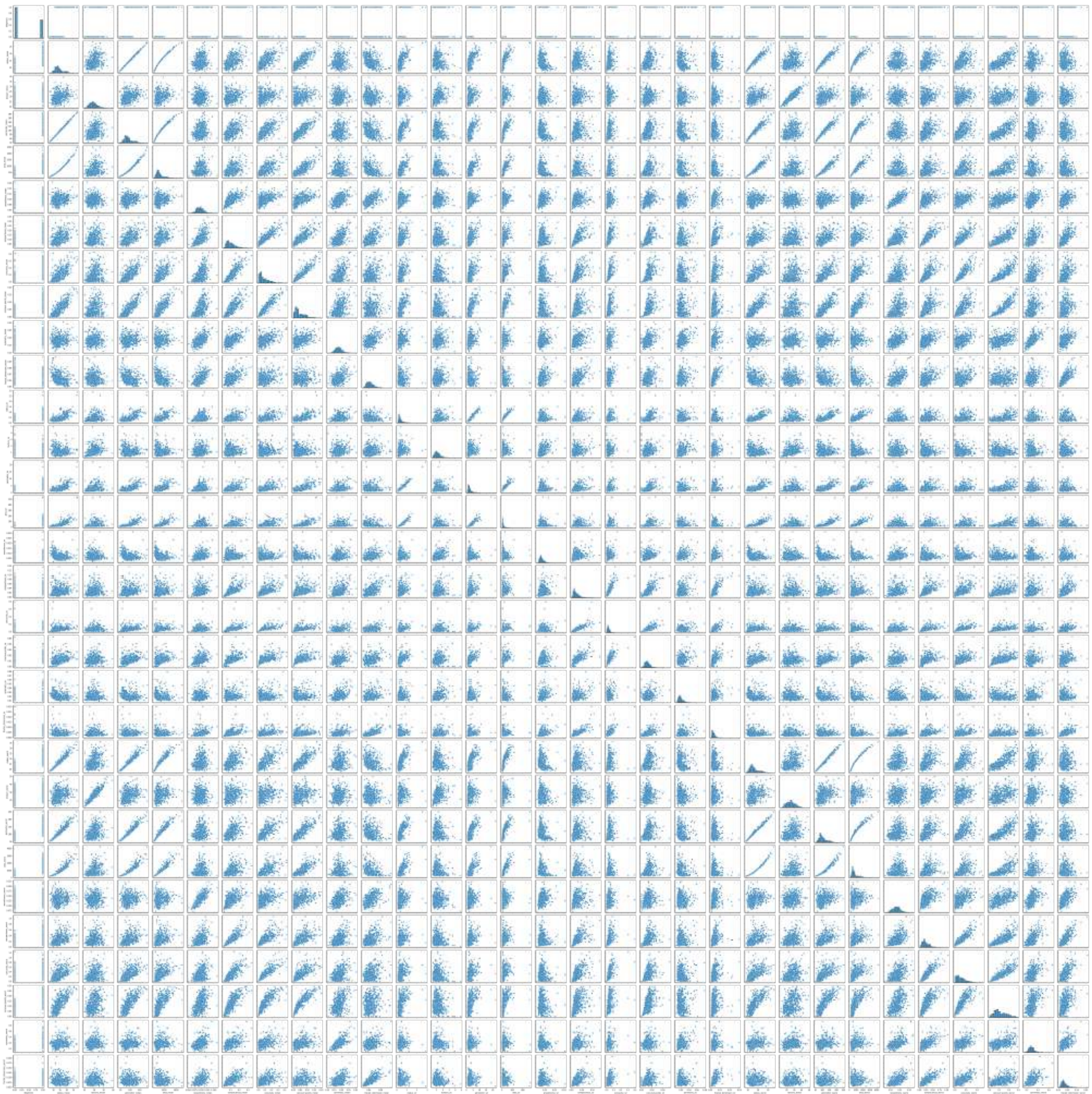
5 rows × 31 columns

In [16]:
```
# find the unique values count in our target feature
df["diagnosis"].value_counts()
```

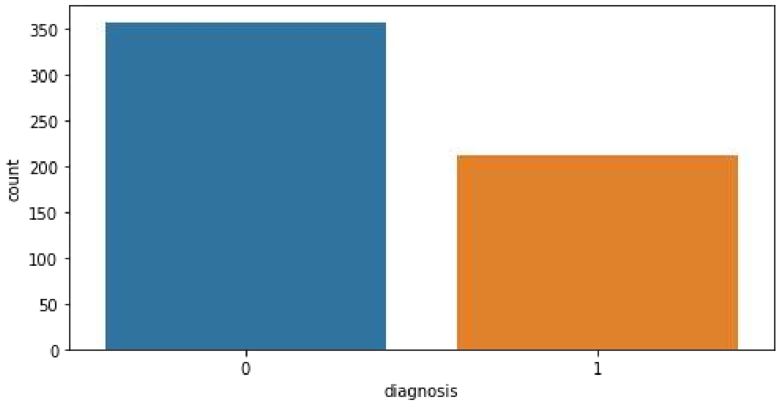
Out[16]:
```
0    357
1    212
Name: diagnosis, dtype: int64
```

In [17]:
```
#Pairplot of the Dataset
sns.pairplot(df)
```

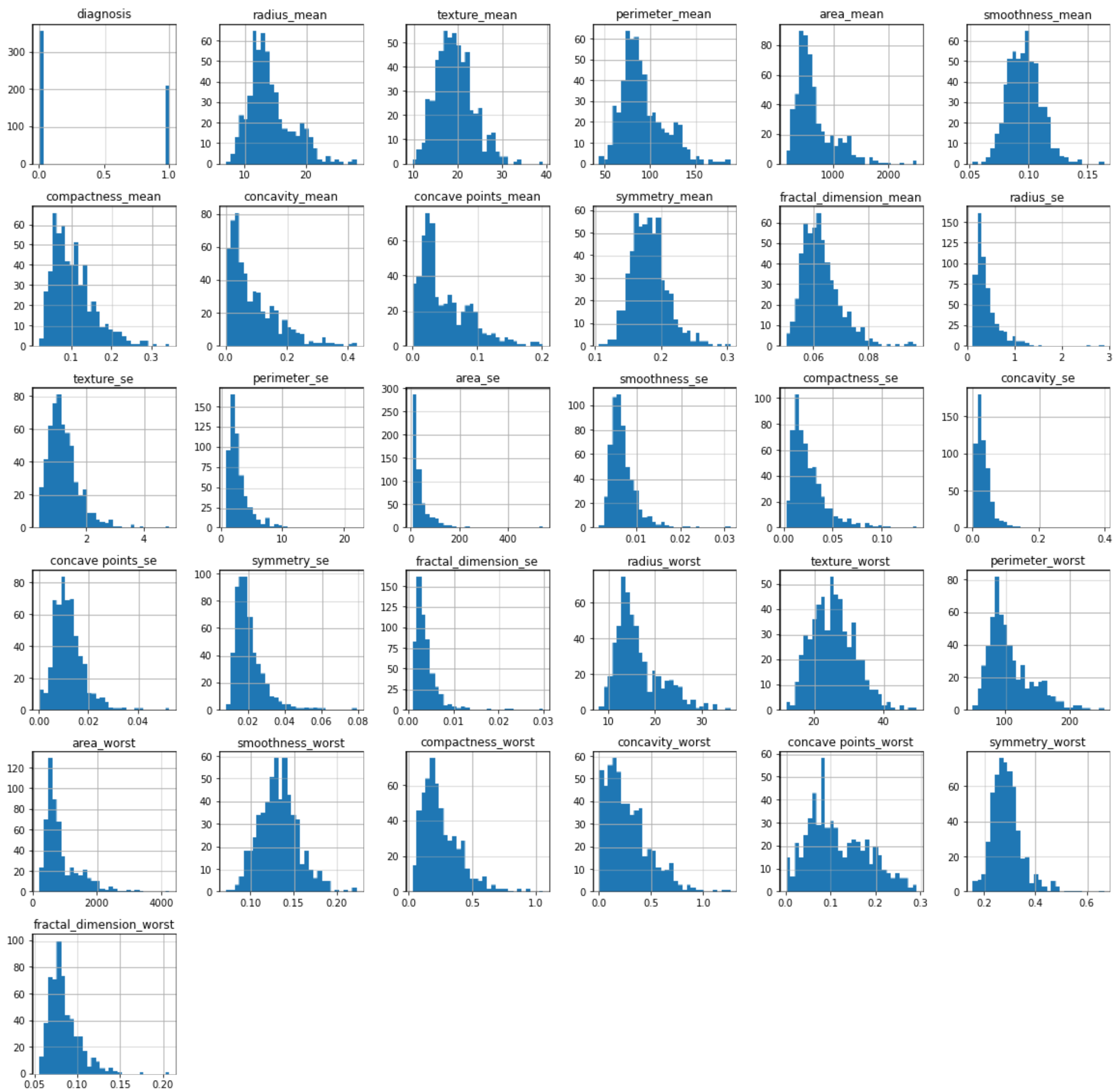
Out[17]: <seaborn.axisgrid.PairGrid at 0x237d4fc4ca0>



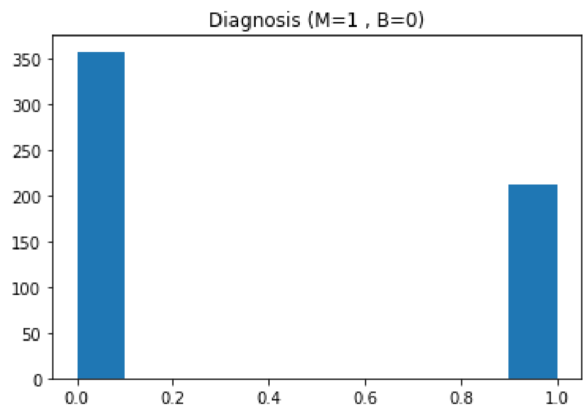
In [18]:
```
# plot a counter plot to better understand our target feature
plt.figure(figsize=(8,4))
sns.countplot(x = 'diagnosis',data = df)
plt.show()
```



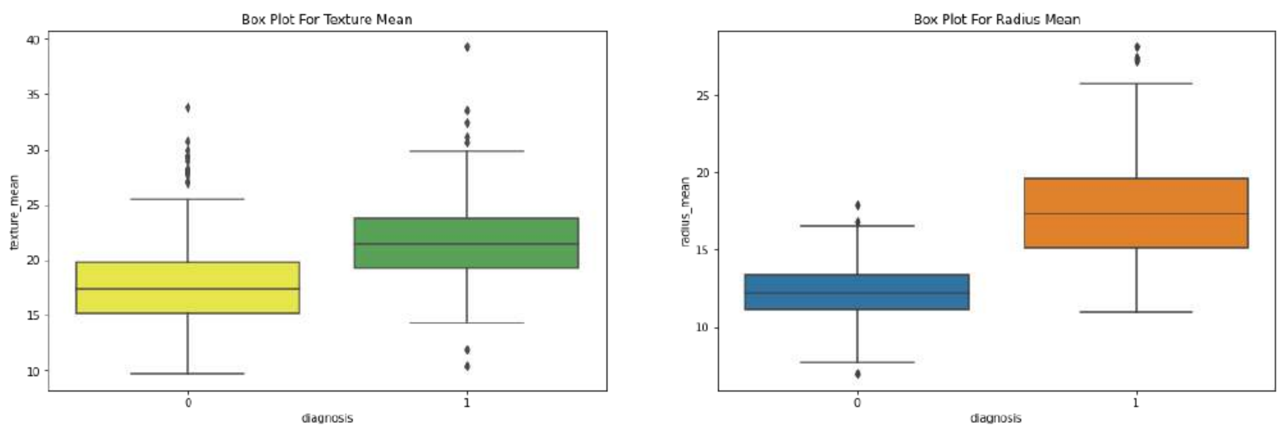
In [19]:
```
# check the distribution of variables
df.hist(bins=30, figsize=(20,20))
plt.show()
```



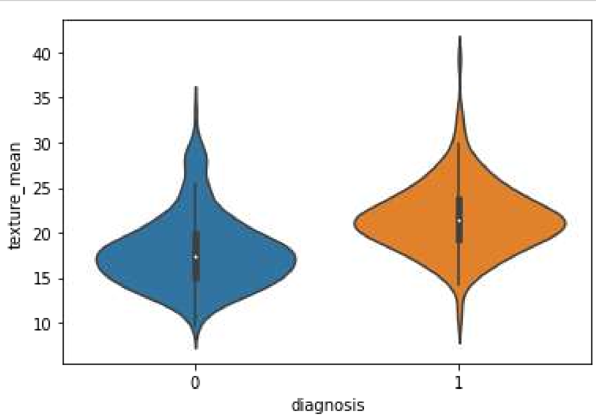
In [20]:
```
df.describe()
plt.hist(df['diagnosis'])
plt.title('Diagnosis (M=1 , B=0)')
plt.show()
```



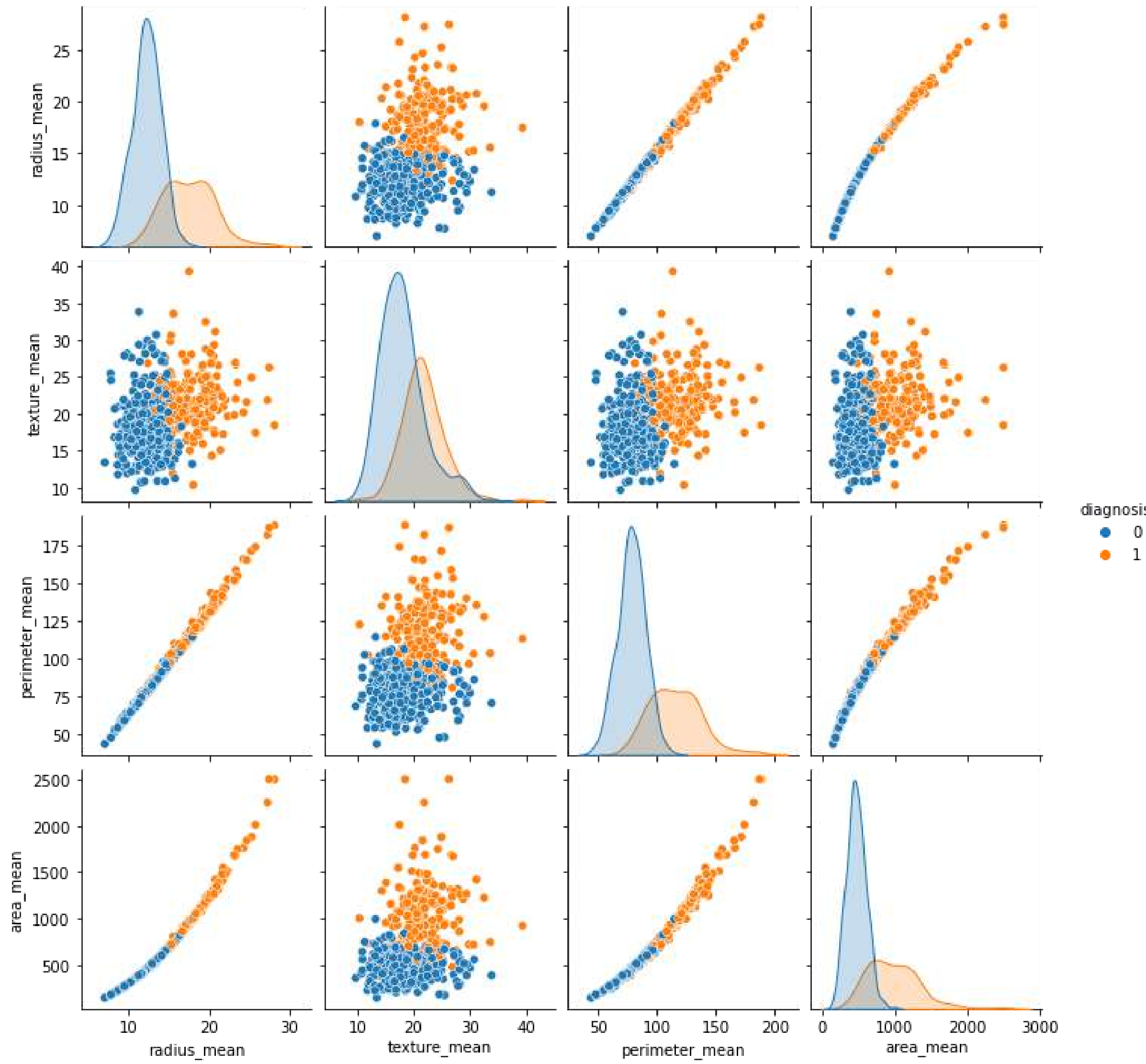
In [21]:
```
# Box Plot For Our Target Feature
plt.figure(figsize=(20,6))

plt.subplot(1,2,1)
plt.title("Box Plot For Texture Mean")
sns.boxplot(data=df,x="diagnosis",y="texture_mean",palette="Set1_r")

plt.subplot(1,2,2)
plt.title('Box Plot For Radius Mean')
sns.boxplot(data=df,x="diagnosis",y="radius_mean")

plt.show()
```



In [22]:
```
# check the distribution of variables based on target variable
sns.violinplot(x='diagnosis', y='texture_mean', data=df)
plt.show()
```



In [23]:
```
# check the scatter plot between variables
sns.pairplot(df, hue='diagnosis', vars=['radius_mean', 'texture_mean', 'perimeter_mean', 'area_mean'])
plt.show()
```



From the scatter plot, we can observe that there is some degree of separation between the two classes for some of the features. For example, the mean radius and mean perimeter features appear to have a somewhat linear relationship with the target variable, with the malignant instances generally having higher values than the benign instances. On the other hand, the mean texture and mean area features appear to have a more complex relationship with the target variable, with some overlap between the two classes.

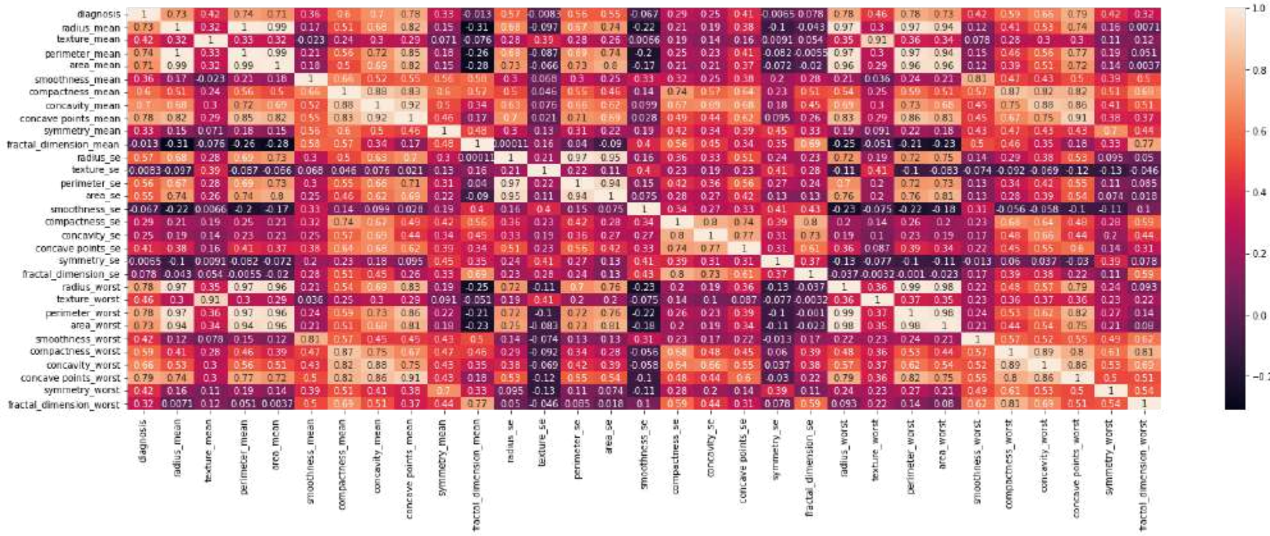
In [24]:
```
# Findin the correlation between each features
corr = df.corr()
corr
```

Out[24]:

	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean
diagnosis	1.000000	0.730029	0.415185	0.742636	0.708984	0.358560	0.596534
radius_mean	0.730029	1.000000	0.323782	0.997855	0.987357	0.170581	0.506124
texture_mean	0.415185	0.323782	1.000000	0.329533	0.321086	-0.023389	0.236702
perimeter_mean	0.742636	0.997855	0.329533	1.000000	0.986507	0.207278	0.556936
area_mean	0.708984	0.987357	0.321086	0.986507	1.000000	0.177028	0.498502
smoothness_mean	0.358560	0.170581	-0.023389	0.207278	0.177028	1.000000	0.659123
compactness_mean	0.596534	0.506124	0.236702	0.556936	0.498502	0.659123	1.000000
concavity_mean	0.696360	0.676764	0.302418	0.716136	0.685983	0.521984	0.883121
concave points_mean	0.776614	0.822529	0.293464	0.850977	0.823269	0.553695	0.831135
symmetry_mean	0.330499	0.147741	0.071401	0.183027	0.151293	0.557775	0.602641
fractal_dimension_mean	-0.012838	-0.311631	-0.076437	-0.261477	-0.283110	0.584792	0.565369
radius_se	0.567134	0.679090	0.275869	0.691765	0.732562	0.301467	0.497473
texture_se	-0.008303	-0.097317	0.386358	-0.086761	-0.066280	0.068406	0.046205
perimeter_se	0.556141	0.674172	0.281673	0.693135	0.726628	0.296092	0.548905
area_se	0.548236	0.735864	0.259845	0.744983	0.800086	0.246552	0.455653
smoothness_se	-0.067016	-0.222600	0.006614	-0.202694	-0.166777	0.332375	0.135299
compactness_se	0.292999	0.206000	0.191975	0.250744	0.212583	0.318943	0.738722
concavity_se	0.253730	0.194204	0.143293	0.228082	0.207660	0.248396	0.570517
concave points_se	0.408042	0.376169	0.163851	0.407217	0.372320	0.380676	0.642262
symmetry_se	-0.006522	-0.104321	0.009127	-0.081629	-0.072497	0.200774	0.229977
fractal_dimension_se	0.077972	-0.042641	0.054458	-0.005523	-0.019887	0.283607	0.507318
radius_worst	0.776454	0.969539	0.352573	0.969476	0.962746	0.213120	0.535315
texture_worst	0.456903	0.297008	0.912045	0.303038	0.287489	0.036072	0.248133
perimeter_worst	0.782914	0.965137	0.358040	0.970387	0.959120	0.238853	0.590210
area_worst	0.733825	0.941082	0.343546	0.941550	0.959213	0.206718	0.509604
smoothness_worst	0.421465	0.119616	0.077503	0.150549	0.123523	0.805324	0.565541
compactness_worst	0.590998	0.413463	0.277830	0.455774	0.390410	0.472468	0.865809
concavity_worst	0.659610	0.526911	0.301025	0.563879	0.512606	0.434926	0.816275
concave points_worst	0.793566	0.744214	0.295316	0.771241	0.722017	0.503053	0.815573
symmetry_worst	0.416294	0.163953	0.105008	0.189115	0.143570	0.394309	0.510223
fractal_dimension_worst	0.323872	0.007066	0.119205	0.051019	0.003738	0.499316	0.687382

31 rows × 31 columns

In [25]:
```
# Display the Correlation Matrix Using Headmap
plt.figure(figsize=(25,8))
sns.heatmap(corr, annot = True)
plt.show()
```



In [26]:
```
from sklearn.metrics import confusion_matrix
from sklearn.metrics import accuracy_score, recall_score, f1_score
from sklearn.metrics import roc_auc_score, classification_report, RocCurveDisplay
from sklearn.preprocessing import StandardScaler
```

Feature Engineering

Feature engineering is the process of selecting, transforming, and creating new featuresfrom raw data to improve the performance of machine learning models. The goal of feature engineering is to extract the most useful information from the data and create a representation that is suitable for the specific problem being solved.

Label Encoding

Here we Encode M as 1 and B as 0

In [27]:
```
df["diagnosis"]=[1 if each=="M" else 0 for each in df["diagnosis"]]
```

In [28]:
```
# Split datainot training and test set
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import train_test_split
from sklearn.datasets import load_breast_cancer
from sklearn.metrics import accuracy_score
```

In [29]:
```
# load the breast cancer dataset
df = load_breast_cancer()
```

In [30]:
```
X_train, X_test, y_train, y_test = train_test_split(df.data, df.target, test_size=0.2, random_state=42)
```

In [31]:
```
#traindf, testdf = train_test_split(df, test_size = 0.3)
```

In [32]:
```
print("Shape of Training dataset: ", X_train.shape)
print("ShaXpe of Testing dataset: ", X_test.shape)
```

```
Shape of Training dataset:  (455, 30)
ShaXpe of Testing dataset:  (114, 30)
```

Feature Scaling

Feature scaling is a technique used in machine learning to standardize the range of features (i.e., input variables) used in a model. It is important because many machine learning algorithms use a distance-based metric to measure the similarity between instances in the dataset. If the range of values for the features varies widely, some features may dominate the algorithm and lead to biased predictions.

In [33]:
```
# Scaling our dataset
from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
scaler.fit(X_train)

X_train = scaler.transform(X_train)
X_test = scaler.transform(X_test)
```

Model Building and Performation Evaluation

Model building and performance evaluation are two important steps in machine learning. Model building involves creating a machine learning model using an algorithm and training data. Performance evaluation involves assessing how well the model performs on new, unseen data. Here are some steps involved in each of these processes.

Logistic Regression

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:

In [34]:
```
model = LogisticRegression()
```

In [35]:
```
model.fit(X_train, y_train)
```

Out[35]:
```
LogisticRegression()
```

In [36]:
```
y_pred = model.predict(X_test)
```

In [37]:
```
y_pred
```

Out[37]:
```
array([1, 0, 0, 1, 1, 0, 0, 0, 1, 1, 1, 0, 1, 0, 1, 0, 1, 1, 1, 0, 1, 1,
       0, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 0, 1, 0, 1, 1, 0, 1, 1,
       1, 1, 1, 1, 1, 1, 0, 0, 1, 1, 1, 1, 1, 0, 0, 1, 1, 0, 0, 1, 1, 1,
       0, 0, 1, 1, 0, 0, 1, 0, 1, 1, 1, 1, 1, 1, 0, 1, 0, 0, 0, 0, 0, 0,
       1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 1, 0, 0, 1, 0, 0, 1, 1, 1, 0, 1, 1,
       0, 1, 0, 0])
```

In [38]:
```
# evaluate the model's accuracy
accuracy = accuracy_score(y_test, y_pred)
print("Accuracy:", accuracy)
```

```
Accuracy: 0.9736842105263158
```

In [39]:
```
from sklearn import metrics
confusion = metrics.confusion_matrix(y_test, y_pred)
confusion
```

Out[39]:
```
array([[41,  2],
       [ 1, 70]], dtype=int64)
```

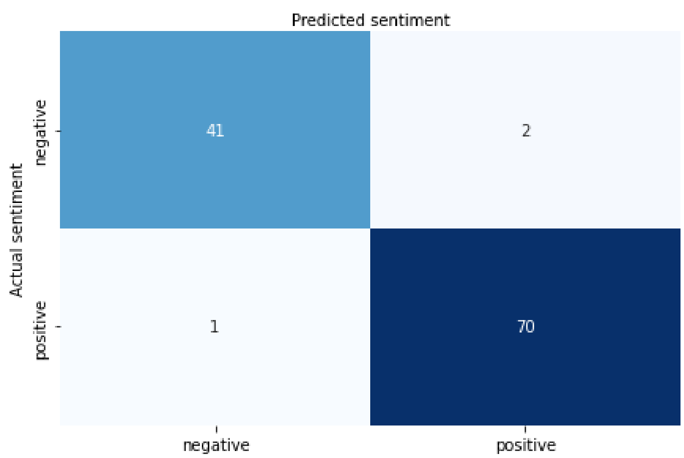
In [40]:
```
accuracy_score(y_test,y_pred)
```

Out[40]:
```
0.9736842105263158
```

In [41]:
```
print(classification_report(y_test,y_pred))
```

```
              precision    recall  f1-score   support

           0       0.98      0.95      0.96        43
           1       0.97      0.99      0.98        71

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

In [42]:
```
class_names = ["negative", "positive"]
fig,ax = plt.subplots()


sns.heatmap(pd.DataFrame(confusion), annot=True, cmap="Blues", fmt="d", cbar=False, xticklabels=class_name
ax.xaxis.set_label_position('top')
plt.tight_layout()
plt.ylabel('Actual sentiment')
plt.xlabel('Predicted sentiment');
```



Decision Tree

A decision tree is a model used in machine learning and data mining for making decisions based on a set of rules or conditions. It is a tree-like structure where each internal node represents a decision based on a particular feature, and each leaf node represents a class label or a numerical value.

Decision trees are used in various fields, such as finance, engineering, and medicine, for making predictions and classification tasks. They are easy to interpret and can handle both categorical and numerical data. One of the advantages of decision trees is that they can handle missing values and outliers. Decision trees can be used for both regression and classification tasks.

In [43]:
```
from sklearn.tree import DecisionTreeClassifier
from sklearn.model_selection import train_test_split
from sklearn.datasets import load_breast_cancer
from sklearn.metrics import accuracy_score
```

In [44]:
```
# Load the breast cancer dataset
df = load_breast_cancer()
```

In [45]:
```
# split the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(df.data, df.target, test_size=0.2, random_state=42)
```

In [46]:
```
# create a decision tree classifier model
model = DecisionTreeClassifier()
```

In [47]:
```
# train the model on the training data
model.fit(X_train, y_train)
```

Out[47]:
```
DecisionTreeClassifier()
```

In [48]:
```
# make predictions on the testing data
y_pred = model.predict(X_test)
```

In [49]:
```
# evaluate the model's accuracy
accuracy = accuracy_score(y_test, y_pred)
print("Accuracy:", accuracy)
```

```
Accuracy: 0.9385964912280702
```

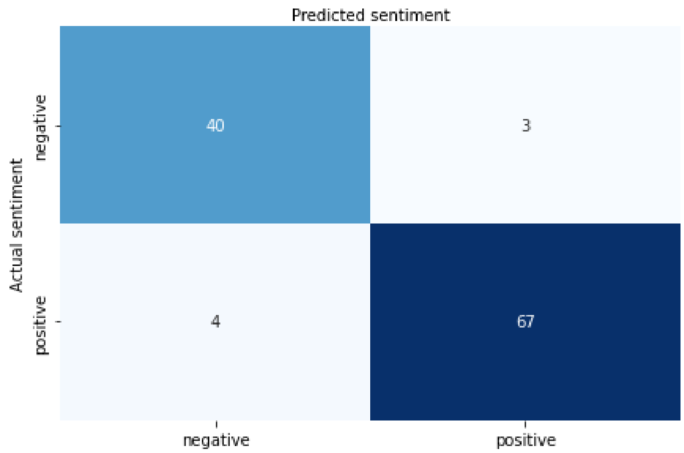
In [50]:
```
#Confusion metrrics
from sklearn import metrics
confusion = metrics.confusion_matrix(y_test, y_pred)
confusion
```

Out[50]:
```
array([[40,  3],
       [ 4, 67]], dtype=int64)
```

In [51]:
```
print(classification_report(y_test,y_pred))
```

```
              precision    recall  f1-score   support

           0       0.91      0.93      0.92        43
           1       0.96      0.94      0.95        71

    accuracy                           0.94       114
   macro avg       0.93      0.94      0.93       114
weighted avg       0.94      0.94      0.94       114
```

In [52]:
```
class_names = ["negative", "positive"]
fig,ax = plt.subplots()


sns.heatmap(pd.DataFrame(confusion), annot=True, cmap="Blues", fmt="d", cbar=False, xticklabels=class_name:
ax.xaxis.set_label_position('top')
plt.tight_layout()
plt.ylabel('Actual sentiment')
plt.xlabel('Predicted sentiment');
```



Random Forest

Random Forest is an ensemble learning method that combines multiple decision trees to improve accuracy and stability of predictions. It uses random subsets of the training data and features to train individual trees, and makes the final prediction by taking a majority vote or averaging the predictions of all the trees. Random Forest is popular due to its high accuracy and robustness, but can be computationally expensive and difficult to interpret for large datasets.

In [53]:
```
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import train_test_split
from sklearn.datasets import load_breast_cancer
from sklearn.metrics import accuracy_score
```

In [54]:
```
# Load the breast cancer dataset
data = load_breast_cancer()
```

In [55]:
```
# split the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(data.data, data.target, test_size=0.2, random_state=42
```

In [56]:
```
# create a random forest classifier model
model = RandomForestClassifier()
```

In [57]:
```
# train the model on the training data
model.fit(X_train, y_train)
```

Out[57]:
```
RandomForestClassifier()
```

In [58]:
```
# make predictions on the testing data
y_pred = model.predict(X_test)
```

In [59]:
```
# evaluate the model's accuracy
accuracy = accuracy_score(y_test, y_pred)
print("Accuracy:", accuracy)
```

```
Accuracy: 0.956140350877193
```

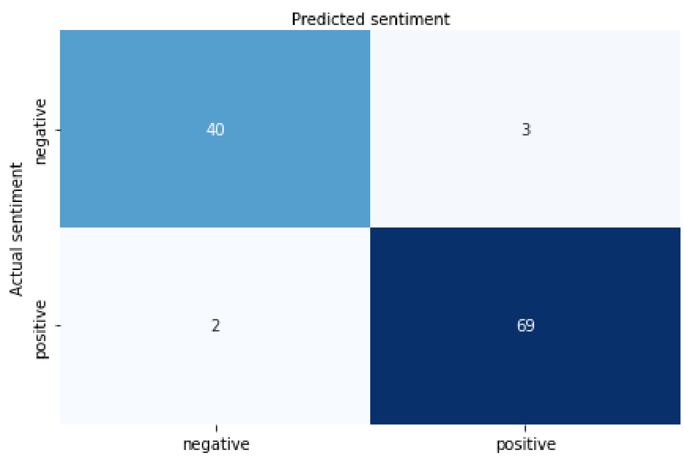
In [60]:
```
from sklearn import metrics
confusion = metrics.confusion_matrix(y_test, y_pred)
confusion
```

Out[60]:
```
array([[40,  3],
       [ 2, 69]], dtype=int64)
```

In [61]:
```
print(classification_report(y_test,y_pred))
```

```
              precision    recall  f1-score   support

           0       0.95      0.93      0.94        43
           1       0.96      0.97      0.97        71

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

In [62]:
```
class_names = ["negative", "positive"]
fig,ax = plt.subplots()


sns.heatmap(pd.DataFrame(confusion), annot=True, cmap="Blues", fmt="d", cbar=False, xticklabels=class_name
ax.xaxis.set_label_position('top')
plt.tight_layout()
plt.ylabel('Actual sentiment')
plt.xlabel('Predicted sentiment');
```



Conclusion

I have done Data processing , Data Cleaning , Exploratory data analysis and have done various Machine learning models such as Logistic Regression , Decision Tree , Random Forest models and i got various Accuracies for all three different models such as i got 0.9736842105263158 for Logistic Regression and 0.9385964912280702 for Decision Tree and 0.956140350877193 for Random Forest. I got good accuracy in Logistic Regression model , so we can use this model for the better predictions.

In [ ]: