

BREAST CANCER **Classification** USING Machine Learning



Breast Cancer Classification

Importing Libraries

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.preprocessing import LabelEncoder
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score
```

Data Understanding

```
cancer_data = pd.read_csv(r"C:\Users\user\Desktop\breast cancer.csv")
```

```
cancer_data
```

	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					
..
...					
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
0	0.66560	0.7119	0.2654
1	0.18660	0.2416	0.1860
2	0.42450	0.4504	0.2430
3	0.86630	0.6869	0.2575
4	0.20500	0.4000	0.1625
...
564	0.21130	0.4107	0.2216
565	0.19220	0.3215	0.1628
566	0.30940	0.3403	0.1418
567	0.86810	0.9387	0.2650
568	0.06444	0.0000	0.0000

	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]

getting the first 5 rows values
cancer_data.head()

	id	diagnosis	radius_mean	texture_mean	perimeter_mean
0	842302	M	17.99	10.38	122.80
1	842517	M	20.57	17.77	132.90
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]
```

```
# getting the last 5 rows values
```

```
cancer_data.tail()
```

	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]
```

```

# getting the information about the whole datasets
cancer_data.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

to check the null values in each columns

cancer_data.isnull().sum()

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


```
# getting the informarion about the shape of the dataset
```

```
cancer_data.shape
```

```
(569, 33)
```

```
# remove the last column
```

```
cancer_data = cancer_data.dropna(axis=1)
```

```
cancer_data.shape
```

```
(569, 32)
```

```
# describe the dataset
```

```
cancer_data.describe()
```

	id	radius_mean	texture_mean	perimeter_mean
area_mean \				
count	5.690000e+02	569.000000	569.000000	569.000000
569.000000				
mean	3.037183e+07	14.127292	19.289649	91.969033
654.889104				
std	1.250206e+08	3.524049	4.301036	24.298981
351.914129				
min	8.670000e+03	6.981000	9.710000	43.790000
143.500000				
25%	8.692180e+05	11.700000	16.170000	75.170000
420.300000				
50%	9.060240e+05	13.370000	18.840000	86.240000
551.100000				
75%	8.813129e+06	15.780000	21.800000	104.100000
782.700000				
max	9.113205e+08	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	...	radius_worst	texture_worst
perimeter_worst \				
count	569.000000	...	569.000000	569.000000
569.000000				
mean	0.181162	...	16.269190	25.677223
107.261213				
std	0.027414	...	4.833242	6.146258
33.602542				
min	0.106000	...	7.930000	12.020000
50.410000				
25%	0.161900	...	13.010000	21.080000
84.110000				
50%	0.179200	...	14.970000	25.410000
97.660000				
75%	0.195700	...	18.790000	29.720000
125.400000				
max	0.304000	...	36.040000	49.540000
251.200000				

	area_worst	smoothness_worst	compactness_worst
concavity_worst \			
count	569.000000	569.000000	569.000000
569.000000			
mean	880.583128	0.132369	0.254265
0.272188			
std	569.356993	0.022832	0.157336
0.208624			
min	185.200000	0.071170	0.027290
0.000000			
25%	515.300000	0.116600	0.147200
0.114500			
50%	686.500000	0.131300	0.211900
0.226700			
75%	1084.000000	0.146000	0.339100
0.382900			
max	4254.000000	0.222600	1.058000
1.252000			

	concave points_worst	symmetry_worst	fractal_dimension_worst
count	569.000000	569.000000	569.000000
mean	0.114606	0.290076	0.083946
std	0.065732	0.061867	0.018061
min	0.000000	0.156500	0.055040
25%	0.064930	0.250400	0.071460
50%	0.099930	0.282200	0.080040
75%	0.161400	0.317900	0.092080
max	0.291000	0.663800	0.207500

```
[8 rows x 31 columns]
```

Data Preparation

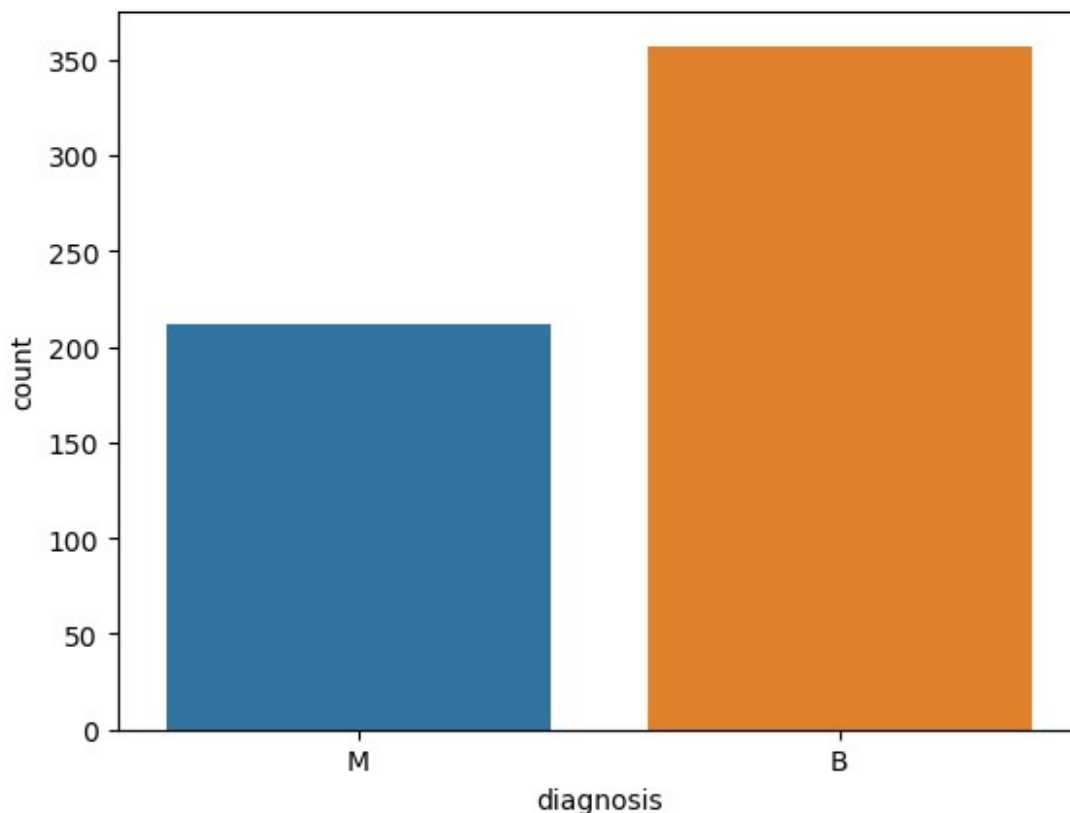
```
# checking the count of Malignant(M) and Benign(B)
cancer_data['diagnosis'].value_counts()
```

```
B    357
M    212
Name: diagnosis, dtype: int64
```

```
# Plot the bar graph
sns.countplot(cancer_data['diagnosis'], label="counts")
```

```
C:\Users\user\anaconda3\lib\site-packages\seaborn\_decorators.py:36:
FutureWarning: Pass the following variable as a keyword arg: x. From
version 0.12, the only valid positional argument will be `data`, and
passing other arguments without an explicit keyword will result in an
error or misinterpretation.
  warnings.warn(
```

```
<AxesSubplot:xlabel='diagnosis', ylabel='count'>
```



```
# converting the M and B values into 1 and 0 by the LabelEncoder
```

```
labelencoder = LabelEncoder()
```

```
cancer_data.iloc[:,1] =
```

```
labelencoder.fit_transform(cancer_data.iloc[:,1])
```

C:\Users\user\AppData\Local\Temp\ipykernel_3060\3778596548.py:3:

SettingWithCopyWarning:

A value is trying to be set on a copy of a slice from a DataFrame.

Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation:

[https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#](https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy)

returning-a-view-versus-a-copy

```
cancer_data.iloc[:,1] =
```

```
labelencoder.fit_transform(cancer_data.iloc[:,1])
```

```
cancer_data.head()
```

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

	...	radius_worst	texture_worst	perimeter_worst	area_worst \
0	...	25.38	17.33	184.60	2019.0
1	...	24.99	23.41	158.80	1956.0
2	...	23.57	25.53	152.50	1709.0
3	...	14.91	26.50	98.87	567.7
4	...	22.54	16.67	152.20	1575.0

	smoothness_worst	compactness_worst	concavity_worst	concave
points_worst \				
0	0.1622	0.6656	0.7119	
0.2654				
1	0.1238	0.1866	0.2416	
0.1860				
2	0.1444	0.4245	0.4504	
0.2430				
3	0.2098	0.8663	0.6869	
0.2575				
4	0.1374	0.2050	0.4000	
0.1625				

	symmetry_worst	fractal_dimension_worst
0	0.4601	0.11890
1	0.2750	0.08902
2	0.3613	0.08758
3	0.6638	0.17300
4	0.2364	0.07678

[5 rows x 32 columns]

cancer_data.tail()

	id	diagnosis	radius_mean	texture_mean	perimeter_mean
area_mean \					
564	926424	1	21.56	22.39	142.00
1479.0					
565	926682	1	20.13	28.25	131.20
1261.0					
566	926954	1	16.60	28.08	108.30
858.1					
567	927241	1	20.60	29.33	140.10
1265.0					
568	92751	0	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				

	...	radius_worst	texture_worst	perimeter_worst	area_worst	\
564	...	25.450	26.40	166.10	2027.0	
565	...	23.690	38.25	155.00	1731.0	
566	...	18.980	34.12	126.70	1124.0	
567	...	25.740	39.42	184.60	1821.0	
568	...	9.456	30.37	59.16	268.6	

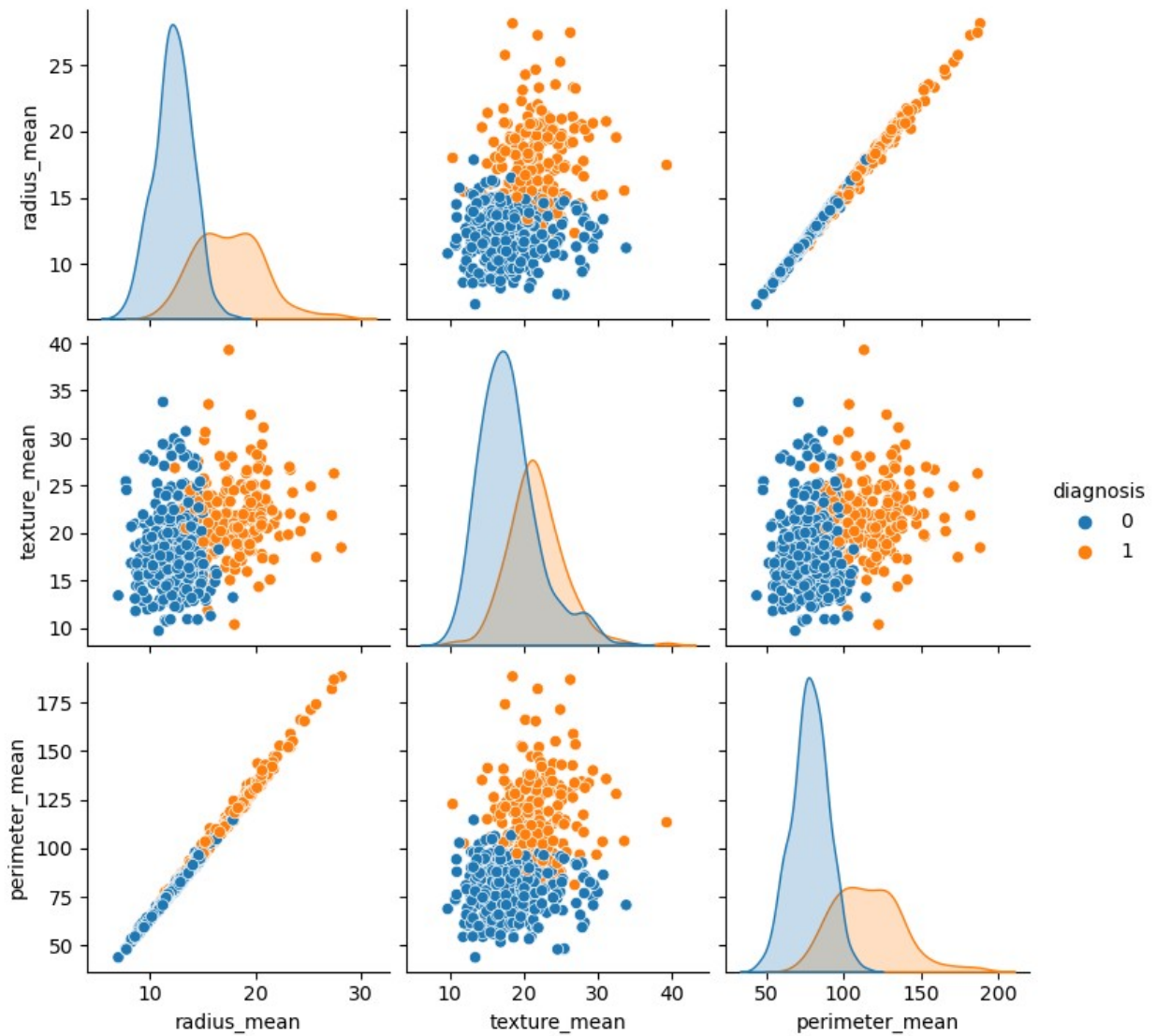
	smoothness_worst	compactness_worst	concavity_worst	\
564	0.14100	0.21130	0.4107	
565	0.11660	0.19220	0.3215	
566	0.11390	0.30940	0.3403	
567	0.16500	0.86810	0.9387	
568	0.08996	0.06444	0.0000	

	concave points_worst	symmetry_worst	fractal_dimension_worst
564	0.2216	0.2060	0.07115
565	0.1628	0.2572	0.06637
566	0.1418	0.2218	0.07820
567	0.2650	0.4087	0.12400
568	0.0000	0.2871	0.07039

[5 rows x 32 columns]

```
sns.pairplot(cancer_data.iloc[:,1:5], hue='diagnosis')
```

```
<seaborn.axisgrid.PairGrid at 0x21baf0670a0>
```

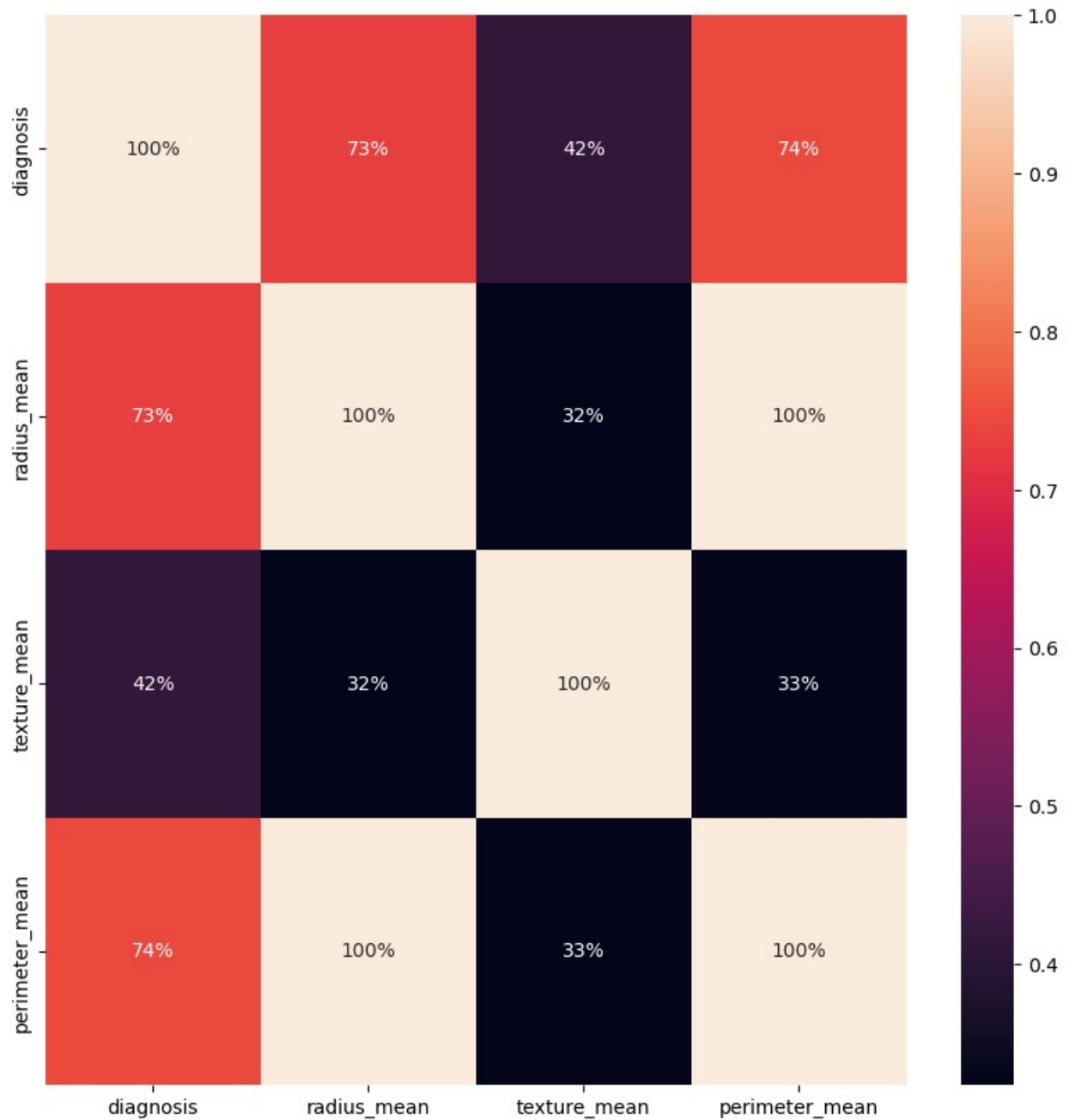


```
# Correlation
```

```
plt.figure(figsize = (10, 10))
```

```
sns.heatmap(cancer_data.iloc[:,1:5].corr(), annot = True, fmt = ".0%")
```

```
<AxesSubplot:>
```



Now splitting the dataset into Features and Targets

```
X = cancer_data.drop(columns = 'diagnosis', axis = 1)
Y = cancer_data['diagnosis']
print(X)
```


	id	radius_mean	texture_mean	perimeter_mean	area_mean	\
0	842302	17.99	10.38	122.80	1001.0	
1	842517	20.57	17.77	132.90	1326.0	
2	84300903	19.69	21.25	130.00	1203.0	
3	84348301	11.42	20.38	77.58	386.1	
4	84358402	20.29	14.34	135.10	1297.0	
...	
564	926424	21.56	22.39	142.00	1479.0	
565	926682	20.13	28.25	131.20	1261.0	
566	926954	16.60	28.08	108.30	858.1	
567	927241	20.60	29.33	140.10	1265.0	
568	92751	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	...	radius_worst	texture_worst	perimeter_worst	\
0	0.2419	...	25.380	17.33	184.60	
1	0.1812	...	24.990	23.41	158.80	
2	0.2069	...	23.570	25.53	152.50	
3	0.2597	...	14.910	26.50	98.87	
4	0.1809	...	22.540	16.67	152.20	

..
564	0.1726	...	25.450	26.40	166.10
565	0.1752	...	23.690	38.25	155.00
566	0.1590	...	18.980	34.12	126.70
567	0.2397	...	25.740	39.42	184.60
568	0.1587	...	9.456	30.37	59.16
	area_worst	smoothness_worst	compactness_worst	concavity_worst	
\					
0	2019.0	0.16220	0.66560	0.7119	
1	1956.0	0.12380	0.18660	0.2416	
2	1709.0	0.14440	0.42450	0.4504	
3	567.7	0.20980	0.86630	0.6869	
4	1575.0	0.13740	0.20500	0.4000	
..
564	2027.0	0.14100	0.21130	0.4107	
565	1731.0	0.11660	0.19220	0.3215	
566	1124.0	0.11390	0.30940	0.3403	
567	1821.0	0.16500	0.86810	0.9387	
568	268.6	0.08996	0.06444	0.0000	
	concave points_worst	symmetry_worst	fractal_dimension_worst		
0	0.2654	0.4601	0.11890		
1	0.1860	0.2750	0.08902		
2	0.2430	0.3613	0.08758		
3	0.2575	0.6638	0.17300		
4	0.1625	0.2364	0.07678		
..		
564	0.2216	0.2060	0.07115		
565	0.1628	0.2572	0.06637		
566	0.1418	0.2218	0.07820		
567	0.2650	0.4087	0.12400		
568	0.0000	0.2871	0.07039		

```
[569 rows x 31 columns]
print(Y)
0      1
1      1
2      1
3      1
4      1
..
564    1
565    1
566    1
567    1
568    0
Name: diagnosis, Length: 569, dtype: int32
```

Now splitting the dataset into training and testing dataset

```
X_train, X_test, Y_train, Y_test = train_test_split(X, Y,
test_size=0.2, random_state=0, stratify=Y)

# feature Scaling
X_train = StandardScaler().fit_transform(X_train)
X_test = StandardScaler().fit_transform(X_test)
```

Model Training

```
model = LogisticRegression()

# training the logistic regression model using training data
model.fit(X_train, Y_train)

LogisticRegression()
```

Model Evaluation

Accuracy Score

```
# Accuracy on training data
```

```
X_train_prediction = model.predict(X_train)  
training_data_accuracy = accuracy_score(Y_train, X_train_prediction)
```

```
print("Accuracy Score in Training data :", training_data_accuracy)
```

```
Accuracy Score in Training data : 0.9934065934065934
```

```
# Accuracy on test data
```

```
X_test_prediction= model.predict(X_test)  
test_data_accuracy = accuracy_score(Y_test, X_test_prediction)
```

```
print("Accuracy Score in test data :", test_data_accuracy)
```

```
Accuracy Score in test data : 0.9649122807017544
```