

- Research Question** Brain cancer is the most common cancer diagnosis in women and the second common cause of death among women in the world. What are the most significant and impactful information can be retrieved in the diagnosis features. How can predict Breast Cancer from the available data points. According to the UC Irving Machine Learning Repository, Features are computed from a digitized image of a fine needle aspirate (FNA) of a breast mass. They describe characteristics of the cell nuclei present in the image.
- Justification** This subject is relevant to me because I want to become a Data Scientist in a Healthcare Setting. I work a lot with medical claim data and research clinical-related datasets. This is the kind of project I would like work on because the impact my work could do in the oncology department. Machine Learning can help identify patients who are most likely to develop breast cancer based on their symptoms and lab results. Therefore, we can create specific care plans to improve those patients' overall health.
- Data Sources** The Breast Cancer Dataset is available in UC Irving Machine Learning Repository in the link below:  
<https://archive.ics.uci.edu/dataset/17/breast+cancer+wisconsin+diagnostic> More information will be revealed during the Project regrading Features information and descriptions.
- Libraries** Pandas Library: Used for data analysis and loaded the dataset Numpy: Used for numerical data analysis and potentially setting seed for different machine learning algorithm. Sklearn Library: Efficient library used for machine leaning and statistical modeling including classification. Matplotlib and Seaborn: Python Libraries used for visualization for machine learning and statistical modeling including classification, regression, clustering and dimensionality reduction.
- EDA and Summary Statistics** The Data Loaded directly via UC Irving Machine Learning Repository

```
# Install UC Irving Repo
pip install ucimlrepo
```

```
Collecting ucimlrepo
  Downloading ucimlrepo-0.0.6-py3-none-any.whl (8.0 kB)
Installing collected packages: ucimlrepo
Successfully installed ucimlrepo-0.0.6
```

Start coding or [generate](#) with AI.

```
from ucimlrepo import fetch_ucirepo

# fetch dataset
breast_cancer_wisconsin_diagnostic = fetch_ucirepo(id=17)

# data (as pandas dataframes)
X = breast_cancer_wisconsin_diagnostic.data.features
y = breast_cancer_wisconsin_diagnostic.data.targets

# metadata
print(breast_cancer_wisconsin_diagnostic.metadata)

# variable information
print(breast_cancer_wisconsin_diagnostic.variables)
```

```
{'uci_id': 17, 'name': 'Breast Cancer Wisconsin (Diagnostic)', 'repository_url':
  name      role      type demographic description units \
0          ID      ID  Categorical      None      None      None
1    Diagnosis  Target  Categorical      None      None      None
2      radius1  Feature  Continuous      None      None      None
3    texture1   Feature  Continuous      None      None      None
4  perimeter1  Feature  Continuous      None      None      None
5        area1  Feature  Continuous      None      None      None
6  smoothness1  Feature  Continuous      None      None      None
7  compactness1  Feature  Continuous      None      None      None
```

TypeError   TypeError   TypeError   Type ...



You

Please explain the error:

TypeError: 'NoneType' object is not subscriptable



Colab AI

The code is attempting to access the `columns` attribute of the `data` attribute of the `breast_cancer_wisconsin_diagnostic` object. However, the `data` attribute is `None`, so the code is trying to access the `columns` attribute of a `NoneType` object, which is not possible.

To fix the code, you need to check if the `data` attribute is not `None` before accessing its `columns` attribute. You can do this by using the following code:

```
if breast_cancer_wisconsin_diagnostic.data is not
    column_names = breast_cancer_wisconsin_diagnostic.data.columns
else:
    column_names = None # or handle the case where data is None
```

[Use code with caution](#)

This code will check if the `data` attribute is not `None` before accessing its `columns` attribute. If the `data` attribute is `None`, it will set the `column_names` variable to `None` (or handle the case where the data is `None` in another way).

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8	concavity1	Feature	Continuous	None	None	None
9	concave_points1	Feature	Continuous	None	None	None
10	symmetry1	Feature	Continuous	None	None	None
11	fractal_dimension1	Feature	Continuous	None	None	None
12	radius2	Feature	Continuous	None	None	None
13	texture2	Feature	Continuous	None	None	None
14	perimeter2	Feature	Continuous	None	None	None
15	area2	Feature	Continuous	None	None	None
16	smoothness2	Feature	Continuous	None	None	None
17	compactness2	Feature	Continuous	None	None	None
18	concavity2	Feature	Continuous	None	None	None
19	concave_points2	Feature	Continuous	None	None	None
20	symmetry2	Feature	Continuous	None	None	None
21	fractal_dimension2	Feature	Continuous	None	None	None
22	radius3	Feature	Continuous	None	None	None
23	texture3	Feature	Continuous	None	None	None
24	perimeter3	Feature	Continuous	None	None	None
25	area3	Feature	Continuous	None	None	None
26	smoothness3	Feature	Continuous	None	None	None
27	compactness3	Feature	Continuous	None	None	None
28	concavity3	Feature	Continuous	None	None	None
29	concave_points3	Feature	Continuous	None	None	None
30	symmetry3	Feature	Continuous	None	None	None
31	fractal_dimension3	Feature	Continuous	None	None	None

```
missing_values
0      no
1      no
2      no
3      no
4      no
5      no
6      no
7      no
8      no
9      no
10     no
11     no
12     no
13     no
14     no
15     no
16     no
17     no
18     no
19     no
20     no
```

During our analysis, we notice that the dataset has no missing values and there is only two categorical values. The dataset has 569 observations and 30 features.

```
# Breast cancer Data
# Retrieve the ids from the data sources for all the patients
id = breast_cancer_wisconsin_diagnostic.data.ids
# creating the full data set
breast_cancer = pd.concat([id, y,X], axis=1)
```

```
print(breast_cancer.head())
print("The shape of the dataset is :",breast_cancer.shape)
```

	Diagnosis	radius1	texture1	perimeter1	area1	smoothness1	compactness1	\
0	M	17.99	10.38	122.80	1001.0	0.11840	0.27760	
1	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	
2	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	
3	M	11.42	20.38	77.58	386.1	0.14250	0.28390	
4	M	20.29	14.34	135.10	1297.0	0.10030	0.13280	

	concavity1	concave_points1	symmetry1	...	radius3	texture3	perimeter3	\
0	0.3001	0.14710	0.2419	...	25.38	17.33	184.60	
1	0.0869	0.07017	0.1812	...	24.99	23.41	158.80	
2	0.1974	0.12790	0.2069	...	23.57	25.53	152.50	
3	0.2414	0.10520	0.2597	...	14.91	26.50	98.87	
4	0.1980	0.10430	0.1809	...	22.54	16.67	152.20	

	area3	smoothness3	compactness3	concavity3	concave_points3	symmetry3	\
0	2019.0	0.1622	0.6656	0.7119	0.2654	0.4601	
1	1956.0	0.1238	0.1866	0.2416	0.1860	0.2750	
2	1709.0	0.1444	0.4245	0.4504	0.2430	0.3613	
3	567.7	0.2098	0.8663	0.6869	0.2575	0.6638	

```
4 1575.0      0.1374      0.2050      0.4000      0.1625      0.2364
```

```
fractal_dimension3
0      0.11890
1      0.08902
2      0.08758
3      0.17300
4      0.07678
```

```
[5 rows x 31 columns]
(569, 31)
```

```
breast_cancer.describe()
```

	radius1	texture1	perimeter1	area
<b>count</b>	569.000000	569.000000	569.000000	569.000000
<b>mean</b>	14.127292	19.289649	91.969033	654.88910
<b>std</b>	3.524049	4.301036	24.298981	351.91412
<b>min</b>	6.981000	9.710000	43.790000	143.50000
<b>25%</b>	11.700000	16.170000	75.170000	420.30000
<b>50%</b>	13.370000	18.840000	86.240000	551.10000
<b>75%</b>	15.780000	21.800000	104.100000	782.70000
<b>max</b>	28.110000	39.280000	188.500000	2501.00000

```
8 rows x 30 columns
```

There are about 357 malignant Diagnosis (M) and benign Diagnosis (B)

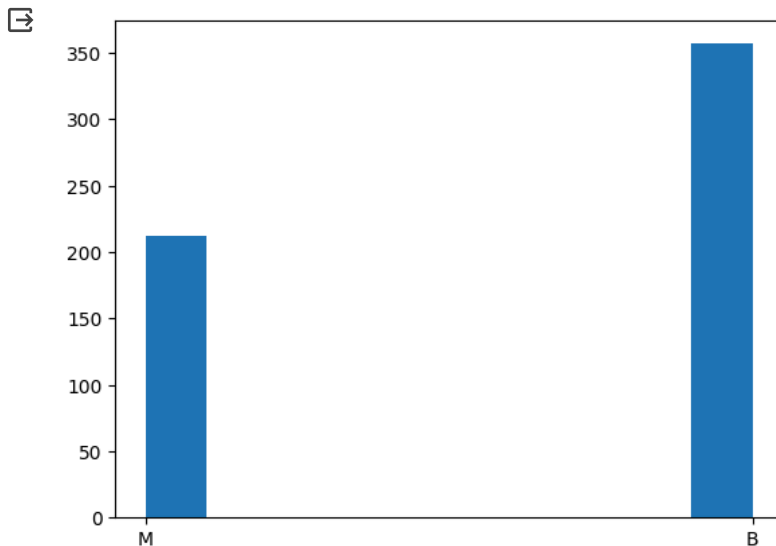
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
breast_cancer.Diagnosis.value_counts()

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

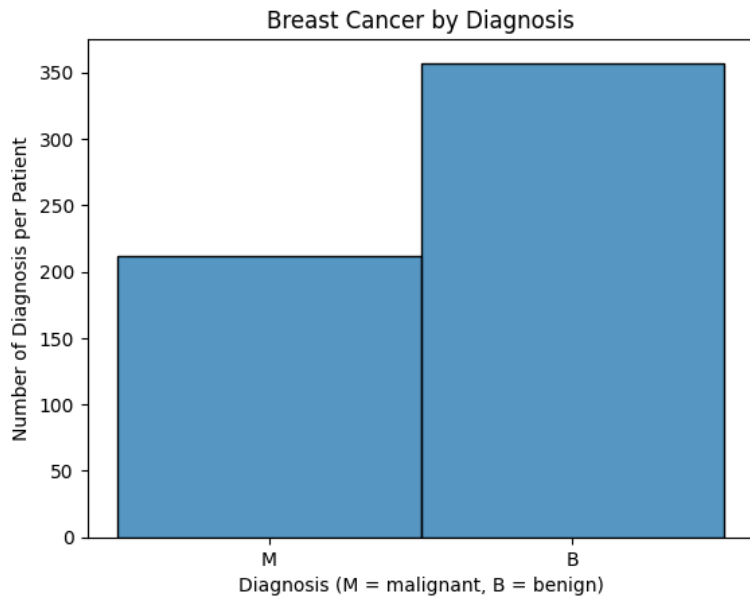
Double-click (or enter) to edit

```
# plt.figure(figsize=(7,12))
plt.hist(breast_cancer.Diagnosis)

plt.show()
```



```
sns.histplot(breast_cancer.Diagnosis, bins=10) # Adjust the number of bins as needed
plt.title('Breast Cancer by Diagnosis')
plt.xlabel('Diagnosis (M = malignant, B = benign)')
plt.ylabel('Number of Diagnosis per Patient')
plt.show()
```



For our summary, It is ideal that use graph that help use see how diagnosis is distributed among our variables. Some of Features are well correlated with each other. During our analysis, a correlation graph will be implemented. Our next step will be to implemented the machine learning and evaluation techniques to get high accuracy model.

```
breast_cancer.corr() > 0.85
```

```
<ipython-input-124-65f0e27b2c3e>:1: FutureWarning: The default value of numeric
breast_cancer.corr() > 0.85
```

	radius1	texture1	perimeter1	area1	smoothness1	compactness1
radius1	True	False	True	True	False	False
texture1	False	True	False	False	False	False
perimeter1	True	False	True	True	False	False
area1	True	False	True	True	False	False
smoothness1	False	False	False	False	True	False
compactness1	False	False	False	False	False	True
concavity1	False	False	False	False	False	True
concave_points1	False	False	True	False	False	False
symmetry1	False	False	False	False	False	False
fractal_dimension1	False	False	False	False	False	False
radius2	False	False	False	False	False	False
texture2	False	False	False	False	False	False
perimeter2	False	False	False	False	False	False
area2	False	False	False	False	False	False
smoothness2	False	False	False	False	False	False
compactness2	False	False	False	False	False	False
concavity2	False	False	False	False	False	False
concave_points2	False	False	False	False	False	False
symmetry2	False	False	False	False	False	False
fractal_dimension2	False	False	False	False	False	False
radius3	True	False	True	True	False	False
texture3	False	True	False	False	False	False
perimeter3	True	False	True	True	False	False
area3	True	False	True	True	False	False
smoothness3	False	False	False	False	False	False
compactness3	False	False	False	False	False	True
concavity3	False	False	False	False	False	False
concave_points3	False	False	False	False	False	False
symmetry3	False	False	False	False	False	False

```
# Assuming breast_cancer is your DataFrame
correlation_matrix = breast_cancer.corr()
```

```
# Filter the correlation matrix to only show correlations greater than 0.85
high_correlations = correlation_matrix[correlation_matrix > 0.85]
```

```
# Print or display the filtered correlations
print(high_correlations)
```

	radius1	texture1	perimeter1	area1	smoothness1	\
radius1	1.000000	NaN	0.997855	0.987357	NaN	
texture1	NaN	1.000000	NaN	NaN	NaN	
perimeter1	0.997855	NaN	1.000000	0.986507	NaN	
area1	0.987357	NaN	0.986507	1.000000	NaN	
smoothness1	NaN	NaN	NaN	NaN	1.0	
compactness1	NaN	NaN	NaN	NaN	NaN	
concavity1	NaN	NaN	NaN	NaN	NaN	
concave_points1	NaN	NaN	0.850977	NaN	NaN	
symmetry1	NaN	NaN	NaN	NaN	NaN	
fractal_dimension1	NaN	NaN	NaN	NaN	NaN	

radius2	NaN	NaN	NaN	NaN	NaN
texture2	NaN	NaN	NaN	NaN	NaN
perimeter2	NaN	NaN	NaN	NaN	NaN
area2	NaN	NaN	NaN	NaN	NaN
smoothness2	NaN	NaN	NaN	NaN	NaN
compactness2	NaN	NaN	NaN	NaN	NaN
concavity2	NaN	NaN	NaN	NaN	NaN
concave_points2	NaN	NaN	NaN	NaN	NaN
symmetry2	NaN	NaN	NaN	NaN	NaN
fractal_dimension2	NaN	NaN	NaN	NaN	NaN
radius3	0.969539	NaN	0.969476	0.962746	NaN
texture3	NaN	0.912045	NaN	NaN	NaN
perimeter3	0.965137	NaN	0.970387	0.959120	NaN
area3	0.941082	NaN	0.941550	0.959213	NaN
smoothness3	NaN	NaN	NaN	NaN	NaN
compactness3	NaN	NaN	NaN	NaN	NaN
concavity3	NaN	NaN	NaN	NaN	NaN
concave_points3	NaN	NaN	NaN	NaN	NaN
symmetry3	NaN	NaN	NaN	NaN	NaN
fractal_dimension3	NaN	NaN	NaN	NaN	NaN

	compactness1	concavity1	concave_points1	symmetry1	\
radius1	NaN	NaN	NaN	NaN	
texture1	NaN	NaN	NaN	NaN	
perimeter1	NaN	NaN	0.850977	NaN	
area1	NaN	NaN	NaN	NaN	
smoothness1	NaN	NaN	NaN	NaN	
compactness1	1.000000	0.883121	NaN	NaN	
concavity1	0.883121	1.000000	0.921391	NaN	
concave_points1	NaN	0.921391	1.000000	NaN	
symmetry1	NaN	NaN	NaN	1.0	
fractal_dimension1	NaN	NaN	NaN	NaN	
radius2	NaN	NaN	NaN	NaN	
texture2	NaN	NaN	NaN	NaN	
perimeter2	NaN	NaN	NaN	NaN	

Enter a prompt here

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