

# What is the Project?

- This project is an attempt to create a machine learning model that can accurately classify whether a tumor is malignant or benign using PCA and then applying those results to other models.

## Dataset Citation - MLA

- Learning, UCI Machine. "Breast Cancer Wisconsin (Diagnostic) Data Set." Kaggle, 25 Sept. 2016, [www.kaggle.com/datasets/uciml/breast-cancer-wisconsin-data](http://www.kaggle.com/datasets/uciml/breast-cancer-wisconsin-data).

## About the Dataset

This dataset is from the UCI machine learning repository and uploaded to kaggle where I downloaded it. The dataset is already clean; however, the data does include two unnecessary columns and it may need to be transformed or rebalanced to be used for PCA analysis.

- The dataset has 33 features with diagnosis being the only categorical feature.
- There are 569 records in this dataset.
- At this point I do not have any background information or prior knowledge on the data.

```
In [1]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import math
import seaborn as sns
import statsmodels.formula.api as smf
import statsmodels.api as sm
from sklearn.decomposition import PCA
```

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

data.shape
```

```
Out[2]: (569, 33)
```

```
In [3]: print(data.info())
print(data.head())
print(data.nunique())
print(data.isnull())
```

```
<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

None

	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]

```

id              569
diagnosis        2
radius_mean     456

```

texture_mean	479
perimeter_mean	522
area_mean	539
smoothness_mean	474
compactness_mean	537
concavity_mean	537
concave points_mean	542
symmetry_mean	432
fractal_dimension_mean	499
radius_se	540
texture_se	519
perimeter_se	533
area_se	528
smoothness_se	547
compactness_se	541
concavity_se	533
concave points_se	507
symmetry_se	498
fractal_dimension_se	545
radius_worst	457
texture_worst	511
perimeter_worst	514
area_worst	544
smoothness_worst	411
compactness_worst	529
concavity_worst	539
concave points_worst	492
symmetry_worst	500
fractal_dimension_worst	535
Unnamed: 32	0

dtype: int64

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	\
0	False	False	False	False	False	False	
1	False	False	False	False	False	False	
2	False	False	False	False	False	False	
3	False	False	False	False	False	False	
4	False	False	False	False	False	False	
..	...	...	...	...	...	...	
564	False	False	False	False	False	False	
565	False	False	False	False	False	False	
566	False	False	False	False	False	False	
567	False	False	False	False	False	False	
568	False	False	False	False	False	False	

	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	\
0	False	False	False	False	
1	False	False	False	False	
2	False	False	False	False	
3	False	False	False	False	
4	False	False	False	False	
..	...	...	...	...	
564	False	False	False	False	
565	False	False	False	False	
566	False	False	False	False	
567	False	False	False	False	
568	False	False	False	False	

	... texture_worst	perimeter_worst	area_worst	smoothness_worst	\
0	...	False	False	False	
1	...	False	False	False	
2	...	False	False	False	
3	...	False	False	False	
4	...	False	False	False	
..	...	...	...	...	
564	...	False	False	False	
565	...	False	False	False	

```

566 ... False False False False
567 ... False False False False
568 ... False False False False

compactness_worst concavity_worst concave points_worst symmetry_worst \
0 False False False False
1 False False False False
2 False False False False
3 False False False False
4 False False False False
.. ...
564 False False False False
565 False False False False
566 False False False False
567 False False False False
568 False False False False

fractal_dimension_worst Unnamed: 32
0 False True
1 False True
2 False True
3 False True
4 False True
.. ...
564 False True
565 False True
566 False True
567 False True
568 False True

[569 rows x 33 columns]

```

## Data Usefulness

- In the current state, this data is not very useful. It has 32 features. Before starting any analysis ID will be removed and also the blank column at the end.

```
In [4]: data = data.drop(['id', 'Unnamed: 32'], axis = 1)
```

We will use PCA to try to reduce the dimensions significantly. This will hopefully result in a large reduction of dimensions and possibly produce a good model as well.

```
In [5]: data.shape
```

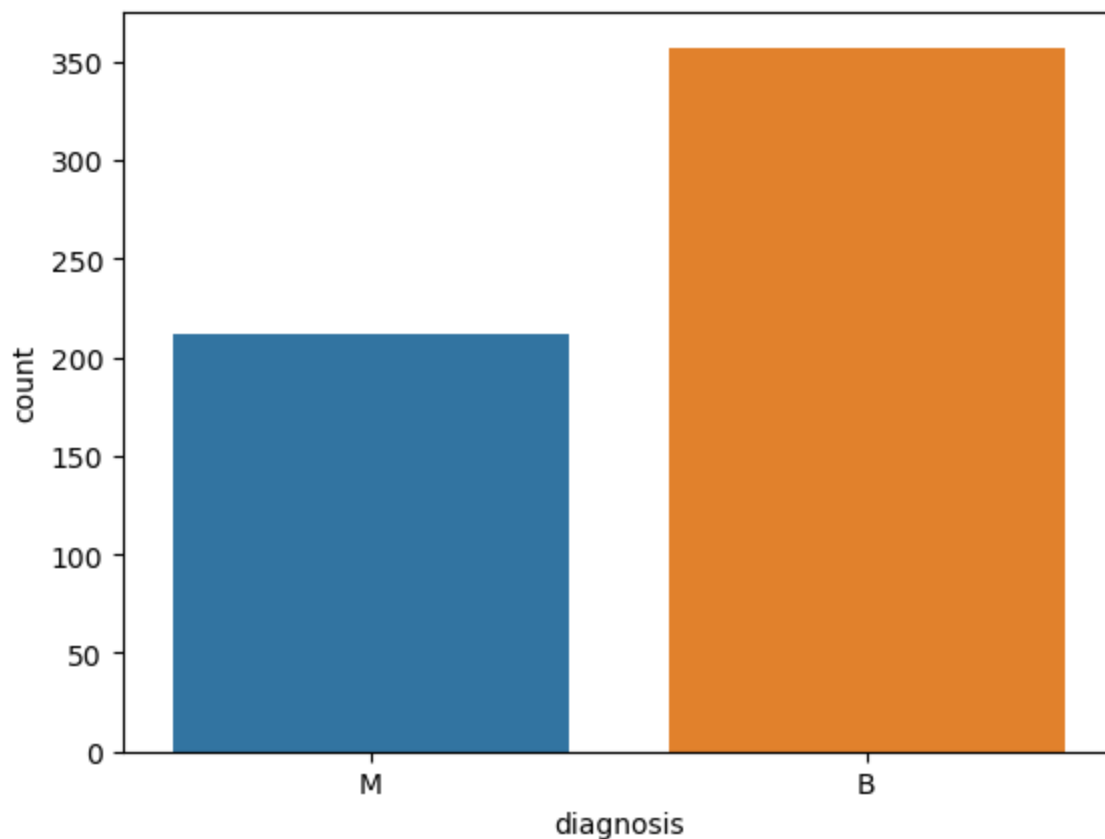
```
Out[5]: (569, 31)
```

```
In [6]: X = data.drop(['diagnosis'], axis = 1)
        y = data[['diagnosis']]
```

Looking at the plot below we can see that the data is unbalanced to a degree. We will need to solve this before making any analysis.

```
In [7]: sns.countplot(data = y, x = 'diagnosis')
```

```
Out[7]: <AxesSubplot:xlabel='diagnosis', ylabel='count'>
```



The below code is just scaling for using PCA.

```
In [8]: from scipy.stats import zscore  
X1 = X.apply(zscore)
```

```
In [9]: cov_mat = np.cov(X1, rowvar = False)
```

If we want to account for 95% of the variance we use the below code.

```
In [10]: pca = PCA(n_components=0.95)
```

```
In [11]: pca.fit(X1)
```

```
Out[11]: PCA(n_components=0.95)
```

```
In [12]: print(pca.explained_variance_ratio_)
```

```
[0.44272026 0.18971182 0.09393163 0.06602135 0.05495768 0.04024522  
0.02250734 0.01588724 0.01389649 0.01168978]
```

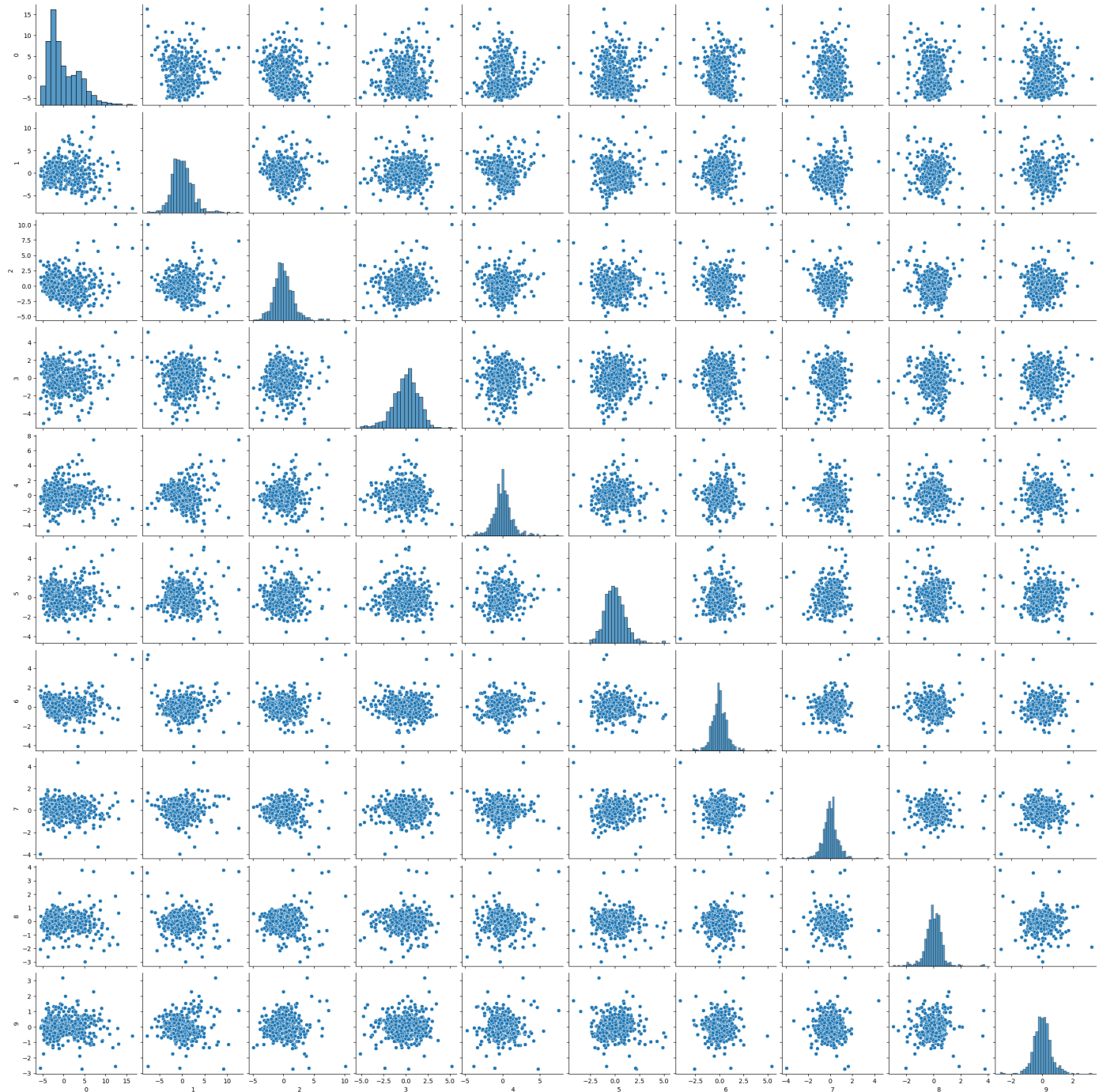
```
In [13]: print(sum(pca.explained_variance_ratio_))
```

```
0.9515688143366667
```

```
In [14]: pcafin = pca.transform(X1)
```

```
In [15]: sns.pairplot(pd.DataFrame(pcafin))
```

```
Out[15]: <seaborn.axisgrid.PairGrid at 0x2996541e790>
```



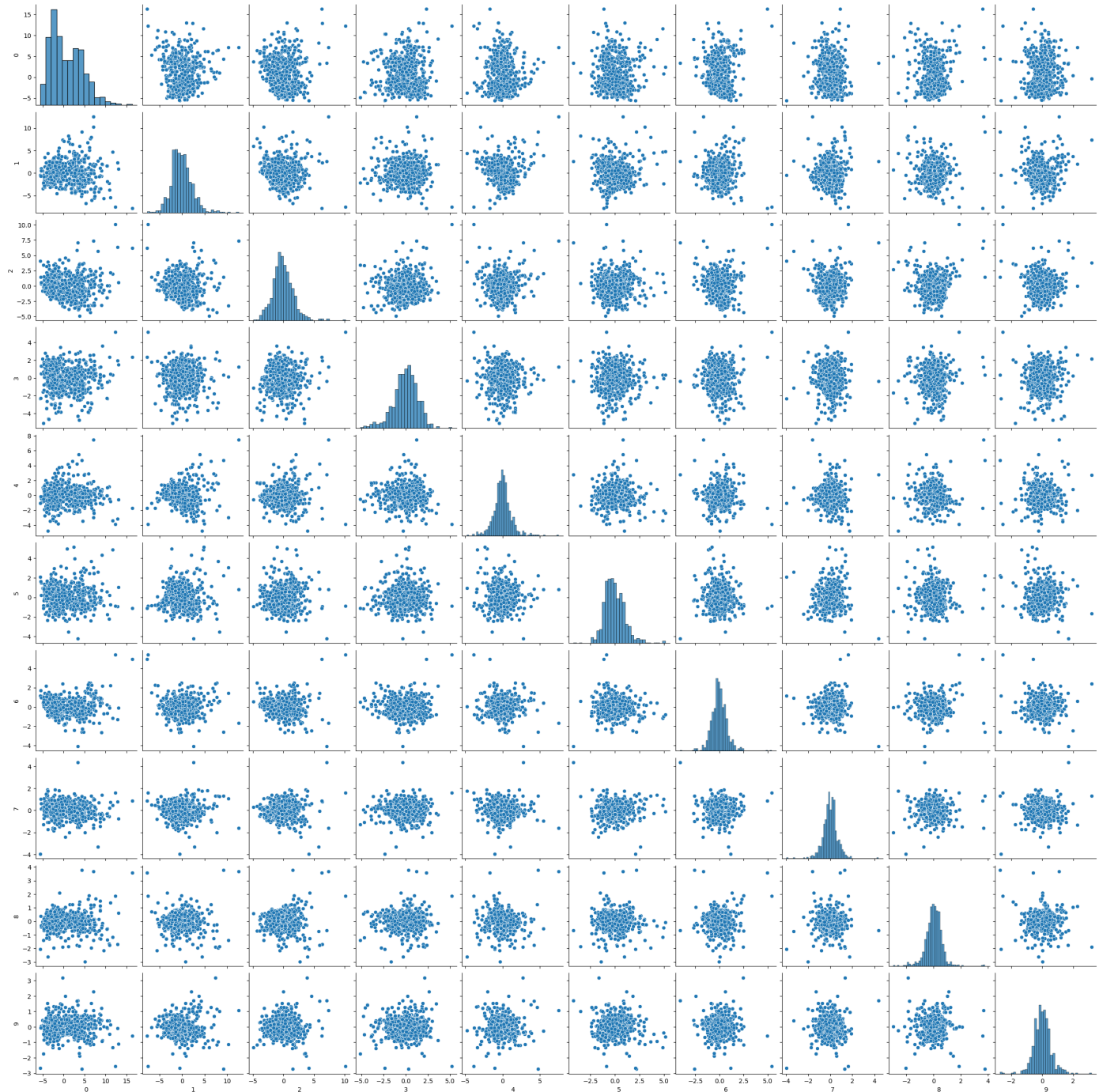
This distribution looks fairly unbalanced, so in order to use PCA most effectively we will have to balance it to some degree.

```
In [16]: from imblearn.over_sampling import SMOTE

s = SMOTE()
X_bal, y_bal = s.fit_resample(pcafin, y)
```

```
In [17]: sns.pairplot(pd.DataFrame(X_bal))
```

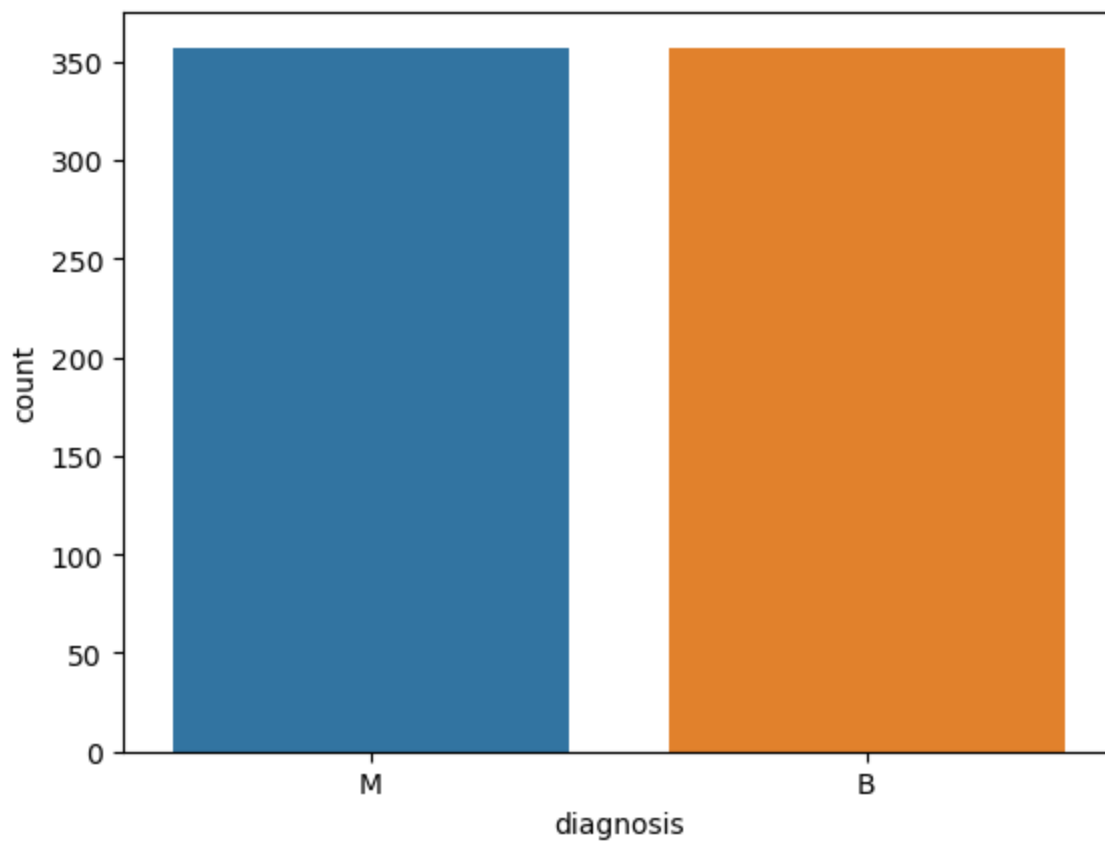
```
Out[17]: <seaborn.axisgrid.PairGrid at 0x2996f85a2e0>
```



We balance the data using SMOTE which is an oversampling technique that is designed to avoid potential overfitting caused by random oversampling. This should be very helpful in using PCA.

```
In [18]: sns.countplot(data = y_bal, x = 'diagnosis')
```

```
Out[18]: <AxesSubplot:xlabel='diagnosis', ylabel='count'>
```



```
In [19]: from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(X_bal, y_bal, test_size = 0.25, random_state=42)
```

```
Out[19]:
```

	diagnosis
416	B
346	B
517	M
553	B
21	B
...	...
218	M
223	M
271	B
474	B
355	B

535 rows × 1 columns

## Data Modeling

- As a side note, PCA is the unsupervised learning method used here. The rest of these models will be to compare how useful the PCA is for this dataset



- At this point we've balanced the dataset and used PCA to get new features, we should see how accurate models are. To do this we'll use a random forest and logistic regression model. We'll then go back and see what the results would have been without using PCA.

```
In [20]: from sklearn.ensemble import RandomForestRegressor
from sklearn.linear_model import LogisticRegression

rf = RandomForestRegressor(max_depth = 10, random_state = 5)

# This is to convert y_train to numeric values. Categorical values will not work.
y_trainrf = y_train['diagnosis'].apply(lambda val: 1 if val == 'M' else 0)
y_testrf = y_test['diagnosis'].apply(lambda val: 1 if val == 'M' else 0)
```

```
In [21]: rf_fit = rf.fit(X_train, y_trainrf)
```

```
In [22]: print(rf_fit.score(X_test, y_testrf))

0.884937776303943
```

```
In [23]: pca_mod = LogisticRegression()
pca_mod.fit(X_train, y_train)
y_pred = pca_mod.predict(X_test)
train_score = pca_mod.score(X_train, y_train)
test_score = pca_mod.score(X_test, y_test)
```

C:\Users\joeyc\anaconda3\lib\site-packages\sklearn\utils\validation.py:993: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n\_samples, ), for example using ravel().  
y = column\_or\_1d(y, warn=True)

```
In [24]: print(train_score)

0.9757009345794393
```

```
In [25]: print(test_score)

0.9832402234636871
```

This test score is very good at 0.98 after using PCA and logistic regression.

## Models w/o PCA

- Since the models above use PCA we need base models without PCA to compare to. We will create those below.

```
In [26]: X_ball, y_ball = s.fit_resample(X, y)
```

```
In [27]: X_train1, X_test1, y_train1, y_test1 = train_test_split(X_ball, y_ball, test_size = 0.25)
```

```
In [28]: y_trainrf1 = y_train1['diagnosis'].apply(lambda val: 1 if val == 'M' else 0)
y_testrf1 = y_test1['diagnosis'].apply(lambda val: 1 if val == 'M' else 0)
```

```
In [29]: rf_fit1 = rf.fit(X_train1, y_trainrf1)
```

```
In [30]: print(rf_fit1.score(X_test1, y_testrf1))

0.9283977647352647
```

So we can see that a random forest model really does not benefit from the use of PCA. This could be somewhat expected since random forest models are not necessarily suited to this type of problem.

Realistically it is a binary problem, M or B, so the real interesting model would be the logistic regression one we'll do next.

```
In [31]: mod1 = LogisticRegression(max_iter=10000)
mod1.fit(X_train1, y_train1)
y_pred1 = mod1.predict(X_test1)
train_score1 = mod1.score(X_train1, y_train1)
test_score1 = mod1.score(X_test1, y_test1)
```

```
C:\Users\joeyc\anaconda3\lib\site-packages\sklearn\utils\validation.py:993: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ), for example using ravel().
  y = column_or_1d(y, warn=True)
```

```
In [32]: print(train_score1)

0.9570093457943926
```

```
In [33]: print(test_score1)

0.9608938547486033
```

## Final Results

- Final Test Scores for each model type
  - Logistic Regression
    - PCA = 0.98
    - Non-PCA = 0.96
  - Random Forest
    - PCA = 0.88
    - Non-PCA = 0.93
      - These results do vary slightly if the code is re-ran, but the general premise remains the same.

## Conclusion

- PCA provided a significant boost to test score when it came to logistic regression and no boost to the random forest model.
- Overall this project showed significant value to using PCA when it comes to feature reduction. The model started with 31 real columns, not including ID or the blank column, and PCA brought it down to 10 features. This allowed us to make a significantly more accurate logistic regression model.
- I think the biggest improvement to this project would be more data. The dataset is small with only 569 entries, so it would be interesting to see if the model performed as well on a larger dataset.