Predicting Breast Cancer - Logistic Regression

0. import dependencies

```
# import dependencies
# data cleaning and manipulation
import pandas as pd
import numpy as np

# data visualization
import matplotlib.pyplot as plt
import seaborn as sns

# machine learning
from sklearn.preprocessing import StandardScaler

import sklearn.linear_model as skl_lm
from sklearn import preprocessing
from sklearn import neighbors
from sklearn.metrics import confusion_matrix, classification_report, precision_score
from sklearn.model_selection import train_test_split


import statsmodels.api as sm
import statsmodels.formula.api as smf


# initialize some package settings
sns.set(style="whitegrid", color_codes=True, font_scale=1.3)

%matplotlib inline


# read in the data and check the first 5 rows
df = pd.read_csv('/content/data.csv', index_col=0)
df.head()
```

id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_me
842302	M	17.99	10.38	122.80	1001.0	0.118
842517	M	20.57	17.77	132.90	1326.0	0.084
84300903	M	19.69	21.25	130.00	1203.0	0.109
84348301	M	11.42	20.38	77.58	386.1	0.142
84358402	M	20.29	14.34	135.10	1297.0	0.100

5 rows × 32 columns

The last column, **Unnamed:32**, seems like it has a whole bunch of missing values. Let's quickly check for any missing values for other columns as well.

```
# general summary of the dataframe
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 569 entries, 842302 to 92751
Data columns (total 32 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
 31  Unnamed: 32              0 non-null      float64
dtypes: float64(31), object(1)
memory usage: 146.7+ KB
```

It looks like our data does not contain any missing values, except for our suspect column **Unnamed: 32**, which is full of missing values. Let's go ahead and remove this column entirely. After that, let's check for the data type of each column.

```
# remove the 'Unnamed: 32' column
df = df.drop('Unnamed: 32', axis=1)


# check the data type of each column
df.dtypes
```

```
diagnosis                 object
radius_mean              float64
texture_mean             float64
perimeter_mean           float64
area_mean                float64
smoothness_mean          float64
compactness_mean         float64
concavity_mean           float64
concave points_mean      float64
symmetry_mean            float64
fractal_dimension_mean   float64
radius_se                float64
texture_se               float64
perimeter_se             float64
area_se                  float64
smoothness_se            float64
compactness_se           float64
concavity_se             float64
concave points_se        float64
symmetry_se              float64
fractal_dimension_se     float64
radius_worst             float64
texture_worst            float64
perimeter_worst          float64
area_worst               float64
smoothness_worst         float64
compactness_worst        float64
concavity_worst          float64
concave points_worst     float64
symmetry_worst           float64
fractal_dimension_worst  float64
dtype: object
```

Our response variable, **diagnosis**, is categorical and has two classes, 'B' (Benign) and 'M' (Malignant). All explanatory variables are numerical, so we can skip data type conversion.

Let's now take a closer look at our response variable, since it is the main focus of our analysis. We begin by checking out the distribution of its classes.

Out of the 569 observations, 357 (or 62.7%) have been labeled malignant, while the rest 212 (or 37.3%) have been labeled benign. Later when we develop a predictive model and test it on unseen data, we should expect to see a similar proportion of labels.

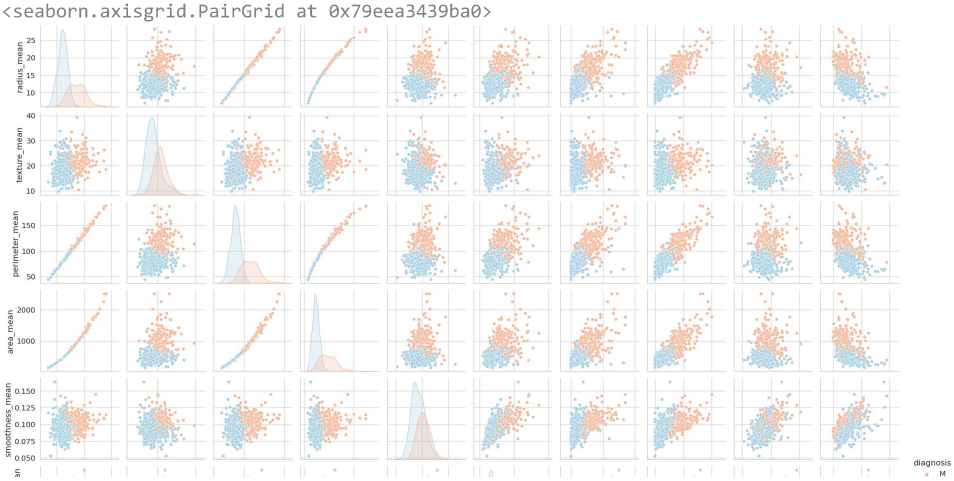
Although our dataset has 30 columns excluding the **id** and the **diagnosis** columns, they are all in fact very closely related since they all contain information on the same 10 key attributes but only differ in terms of their perspectives (i.e., the mean, standard errors, and the mean of the three largest values denoted as "worst").

In this sense, we could attempt to dig out some quick insights by analyzing the data in only one of the three perspectives. For instance, we could choose to check out the relationship between the 10 key attributes and the **diagnosis** variable by only choosing the "mean" columns.

Let's quickly scan for any interesting patterns between our 10 "mean" columns and the response variable by generating a scatter plot matrix as shown below:

```
# generate a scatter plot matrix with the "mean" columns
cols = ['diagnosis',
        'radius_mean',
        'texture_mean',
        'perimeter_mean',
        'area_mean',
        'smoothness_mean',
        'compactness_mean',
        'concavity_mean',
        'concave points_mean',
        'symmetry_mean',
        'fractal_dimension_mean']

sns.pairplot(data=df[cols], hue='diagnosis', palette='RdBu')
```

```
<seaborn.axisgrid.PairGrid at 0x79eea3439ba0>
```



There are some interesting patterns visible. For instance, the almost perfectly linear patterns between the **radius**, **perimeter** and **area** attributes are hinting at the presence of multicollinearity between these variables. Another set of variables that possibly imply multicollinearity are the **concavity**, **concave_points** and **compactness**.

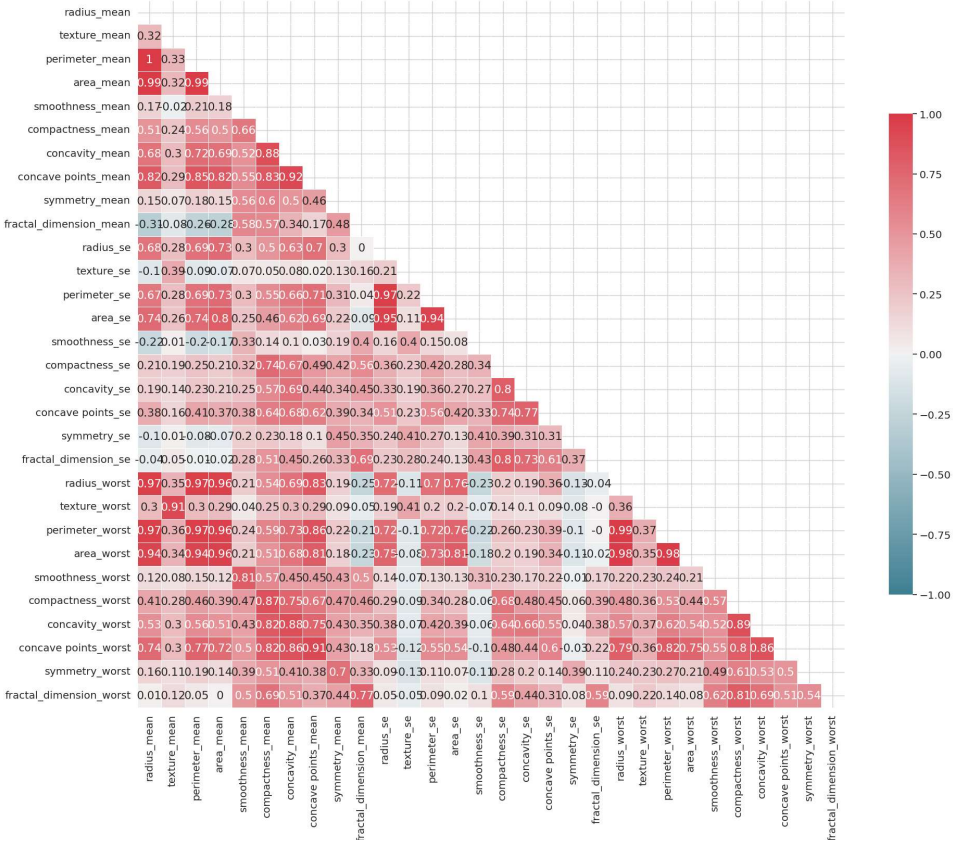
In the coming up section, we will generate a matrix similar to the one above, but this time displaying the correlations between the variables instead of a scatter plot. Let's find out if our hypothesis about the multicollinearity has any statistical support.

2. The Variables

As said earlier, let's take a look at the correlations between our variables. This time however, we will create a correlation matrix with all variables (i.e., the "mean" columns, the "standard errors" columns, as well as the "worst" columns).


```
# Generate and visualize the correlation matrix
corr = df.corr().round(2)

# Mask for the upper triangle
mask = np.zeros_like(corr, dtype=np.bool)
mask[np.triu_indices_from(mask)] = True

# Set figure size
f, ax = plt.subplots(figsize=(20, 20))

# Define custom colormap
cmap = sns.diverging_palette(220, 10, as_cmap=True)

# Draw the heatmap
sns.heatmap(corr, mask=mask, cmap=cmap, vmin=-1, vmax=1, center=0,
            square=True, linewidths=.5, cbar_kws={"shrink": .5}, annot=True)

plt.tight_layout()
```

```
<ipython-input-9-b568bacb2ac8>:2: FutureWarning: The default value of numeric_only in Da
  corr = df.corr().round(2)
<ipython-input-9-b568bacb2ac8>:5: DeprecationWarning: `np.bool` is a deprecated alias fo
Deprecated in NumPy 1.20; for more details and guidance: https://numpy.org/devdocs/relea
  mask = np.zeros_like(corr, dtype=np.bool)
```



Looking at the matrix, we can immediately verify the presence of multicollinearity between some of our variables. For instance, the **radius_mean** column has a correlation of 1 and 0.99 with **perimeter_mean** and **area_mean** columns, respectively. This is probably because the three columns essentially contain the same information, which is the physical size of the observation (the cell). Therefore we should only pick one of the three columns when we go into further analysis.

Another place where multicollienartiy is apparent is between the "mean" columns and the "worst" column. For instance, the **radius_mean** column has a correlation of 0.97 with the **radius_worst** column. In fact, each of the 10 key attributes display very high (from 0.7 up to 0.97) correlations between its "mean" and "worst" columns. This is somewhat inevitable, because the "worst" columns are essentially just a subset of the "mean" columns; the "worst" columns are also the "mean" of some values (the three largest values among all observations). Therefore, I think we should discard the "worst" columns from our analysis and only focus on the "mean" columns.

In short, we will drop all "worst" columns from our dataset, then pick only one of the three attributes that describe the size of cells. But which one should be pick?

Let's quickly go back to 6th grade and review some geometry. If we think of a cell as roughly taking a form of a circle, then the formula for its radius is, well, its radius, *r*. The formulae for its perimeter and area are then $2\pi r$ ** and *πr^2 *, respectively. As we can see, a cell's **radius** is the basic building block of its size. Therefore, I think it is reasonable to choose **radius** as our attribute to represent the size of a cell.

Similarly, it seems like there is multicollinearity between the attributes **compactness**, **concavity**, and **concave points**. Just like what we did with the size attributes, we should pick only one of these three attributes that contain information on the shape of the cell. I think **compactness** is an attribute name that is straightforward, so I will remove the other two attributes.

We will now go head and drop all unnecessary columns.

```
# first, drop all "worst" columns
cols = ['radius_worst',
        'texture_worst',
        'perimeter_worst',
        'area_worst',
        'smoothness_worst',
        'compactness_worst',
        'concavity_worst',
```

```
        'concave points_worst',
        'symmetry_worst',
        'fractal_dimension_worst']
df = df.drop(cols, axis=1)

# then, drop all columns related to the "perimeter" and "area" attributes
cols = ['perimeter_mean',
        'perimeter_se',
        'area_mean',
        'area_se']
df = df.drop(cols, axis=1)

# lastly, drop all columns related to the "concavity" and "concave points" attributes
cols = ['concavity_mean',
        'concavity_se',
        'concave points_mean',
        'concave points_se']
df = df.drop(cols, axis=1)

# verify remaining columns
df.columns
```

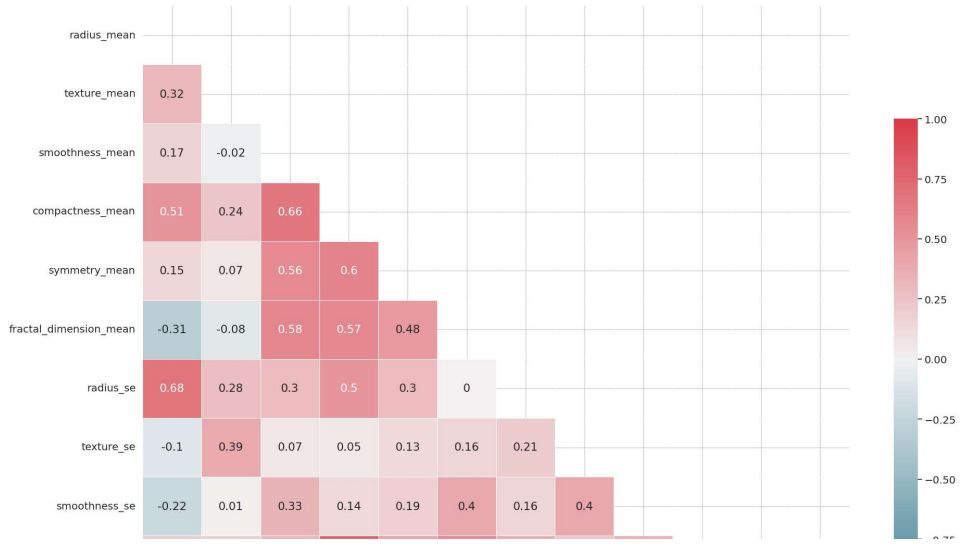
```
Index(['diagnosis', 'radius_mean', 'texture_mean', 'smoothness_mean',
       'compactness_mean', 'symmetry_mean', 'fractal_dimension_mean',
       'radius_se', 'texture_se', 'smoothness_se', 'compactness_se',
       'symmetry_se', 'fractal_dimension_se'],
      dtype='object')
```

Are we all set now?

Let's take a look at the correlation matrix once again, this time created with our trimmed-down set of variables.

```
# Draw the heatmap again, with the new correlation matrix
corr = df.corr().round(2)
mask = np.zeros_like(corr, dtype=np.bool)
mask[np.triu_indices_from(mask)] = True

f, ax = plt.subplots(figsize=(20, 20))
sns.heatmap(corr, mask=mask, cmap=cmap, vmin=-1, vmax=1, center=0,
            square=True, linewidths=.5, cbar_kws={"shrink": .5}, annot=True)
plt.tight_layout()
```

```
<ipython-input-11-d6ac4485b1df>:2: FutureWarning: The default value of numeric_only in D
  corr = df.corr().round(2)
<ipython-input-11-d6ac4485b1df>:3: DeprecationWarning: `np.bool` is a deprecated alias f
Deprecated in NumPy 1.20; for more details and guidance: https://numpy.org/devdocs/relea
  mask = np.zeros_like(corr, dtype=np.bool)
```



Looks great! Now let's move on to our model.

3. The Model

It's finally time to develop our model! We will start by first splitting our dataset into two parts; one as a training set for the model, and the other as a test set to validate the predictions that the model will make. If we omit this step, the model will be trained and tested on the same dataset, and it will underestimate the true error rate, a phenomenon known as **overfitting**. It is like writing an exam after taking a look at the questions and answers beforehand. We want to make sure that our model truly has predictive power and is able to accurately label unseen data. We will set the test size to 0.3; i.e., 70% of the data will be assigned to the training set, and the remaining 30% will be used as a test set. In order to obtain consistent results, we will set the random state parameter to a value of 40.

```
# Split the data into training and testing sets
X = df
y = df['diagnosis']

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=40)
```

Now that we have split our data into appropriate sets, let's write down the formula to be used for the `logistic regression`.

```
# Create a string for the formula
cols = df.columns.drop('diagnosis')
formula = 'diagnosis ~ ' + ' + '.join(cols)
print(formula, '\n')
```

```
diagnosis ~ radius_mean + texture_mean + smoothness_mean + compactness_mean + symmetry_mean + fractal_dimension_mean + radius_s
```

The formula includes all of the variables that were finally selected at the end of the previous section. We will now run the `logistic regression` with this formula and take a look at the results.

```
# Run the model and report the results
model = smf.glm(formula=formula, data=X_train, family=sm.families.Binomial())
logistic_fit = model.fit()

print(logistic_fit.summary())
```

```
                    Generalized Linear Model Regression Results
==============================================================================================
Dep. Variable:     ['diagnosis[B]', 'diagnosis[M]']   No. Observations:                  398
Model:                                         GLM   Df Residuals:                      385
Model Family:                             Binomial   Df Model:                           12
Link Function:                               Logit   Scale:                          1.0000
Method:                                       IRLS   Log-Likelihood:                -55.340
Date:                             Tue, 07 Nov 2023   Deviance:                       110.68
Time:                                     08:51:41   Pearson chi2:                     125.
No. Iterations:                                  9   Pseudo R-squ. (CS):             0.6539
Covariance Type:                         nonrobust
===========================================================================================
                              coef    std err          z      P>|z|      [0.025      0.975]
-------------------------------------------------------------------------------------------
Intercept                  44.5427     11.787      3.779      0.000      21.441      67.644
radius_mean                -1.1610      0.301     -3.862      0.000      -1.750      -0.572
texture_mean               -0.4237      0.087     -4.866      0.000      -0.594      -0.253
smoothness_mean           -85.3981     40.976     -2.084      0.037    -165.709      -5.088
compactness_mean          -16.7104     22.510     -0.742      0.458     -60.829      27.408
symmetry_mean             -46.2721     17.767     -2.604      0.009     -81.095     -11.449
fractal_dimension_mean    -49.1536    121.888     -0.403      0.687    -288.050     189.742
radius_se                  -7.1916      2.806     -2.563      0.010     -12.691      -1.692
texture_se                  0.1849      0.784      0.236      0.814      -1.353       1.722
smoothness_se             163.6068    159.702      1.024      0.306    -149.403     476.616
compactness_se            -31.1808     42.772     -0.729      0.466    -115.012      52.650
symmetry_se                74.7366     51.458      1.452      0.146     -26.119     175.592
fractal_dimension_se      824.1245    412.040      2.000      0.045      16.541    1631.708
===========================================================================================
```

Great! In the next section, we will feed in the test data to this model to yield predictions of labels. Then, we will evaluate how accurately the model have predicted the data.

4. The Prediction

In the previous section, we have successfully developed a logistic regression model. This model can take some unlabeled data and effectively assign each observation a probability ranging from 0 to 1. This is the key feature of a logistic regression model. However, for us to evaluate whether the predictions are accurate, the predictions must be encoded so that each instance can be compared directly with the labels in the test data. In other words, instead of numbers between 0 or 1, the predictions should show "M" or "B", denoting malignant and benign respectively. In our model, a probability of 1 corresponds to the "Benign" class, whereas a probability of 0 corresponds to the "Malignant" class. Therefore, we can apply a threshhold value of 0.5 to our predictions, assigning all values closer to 0 a label of "M" and assigniing all values closer to 1 a label of "B".

If this is confusiing, let's go through this step-by-step.

```
# predict the test data and show the first 5 predictions
predictions = logistic_fit.predict(X_test)
predictions[1:6]
```

```
id
848406      0.324251
907915      0.996906
911201      0.964710
84799002    0.000544
8911164     0.838719
dtype: float64
```

```
# Note how the values are numerical.
# Convert these probabilities into nominal values and check the first 5 predictions again.
predictions_nominal = [ "M" if x < 0.5 else "B" for x in predictions]
predictions_nominal[1:6]
```

```
['M', 'B', 'B', 'M', 'B']
```

We can confirm that probabilities closer to 0 have been labeled as "M", while the ones closer to 1 have been labeled as "B". Now we are able to evaluate the accuracy of our predictions by checking out the classification report and the confusion matrix.

```
print(classification_report(y_test, predictions_nominal, digits=3))

cfm = confusion_matrix(y_test, predictions_nominal)

true_negative = cfm[0][0]
false_positive = cfm[0][1]
false_negative = cfm[1][0]
true_positive = cfm[1][1]

print('Confusion Matrix: \n', cfm, '\n')

print('True Negative:', true_negative)
print('False Positive:', false_positive)
print('False Negative:', false_negative)
print('True Positive:', true_positive)
print('Correct Predictions',
      round((true_negative + true_positive) / len(predictions_nominal) * 100, 1), '%')
```

```
                  precision    recall  f1-score   support

               B      0.982     0.965     0.974       115
               M      0.931     0.964     0.947        56

        accuracy                          0.965       171
       macro avg      0.957     0.965     0.961       171
    weighted avg      0.966     0.965     0.965       171

    Confusion Matrix:
     [[111   4]
     [  2  54]]

    True Negative: 111
    False Positive: 4
    False Negative: 2
    True Positive: 54
    Correct Predictions 96.5 %
```

Our model have accurately labeled 96.5% of the test data. This is just the beginning however. We could try to increase the accuracy even higher by using a different algorithm other than the `logistic regression`, or try our model with different set of variables. There are defintely many more things that could be done to modify our model, but I will conclude this report here for now.

Thank you so much for reading through this report. As I mentioned in the beginning, this is my first ever Kernel on Kaggle. I hope you enjoyed it, and please leave comments below for feedbacks and suggestions!