Breast Cancer Prediction (Classicification)

We have a dataset consisting of the information of 569 patients tested for breast cancer, we have 30 predictor variables based on the lumps caused by the tumor, and the response variable is the diagnosis: Benign or Malignant

In [1]:

```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
sns.set()


df = pd.read_csv("breast-cancer.csv")

df.info()
df.head()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 32 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
dtypes: float64(30), int64(1), object(1)
memory usage: 142.4+ KB
```

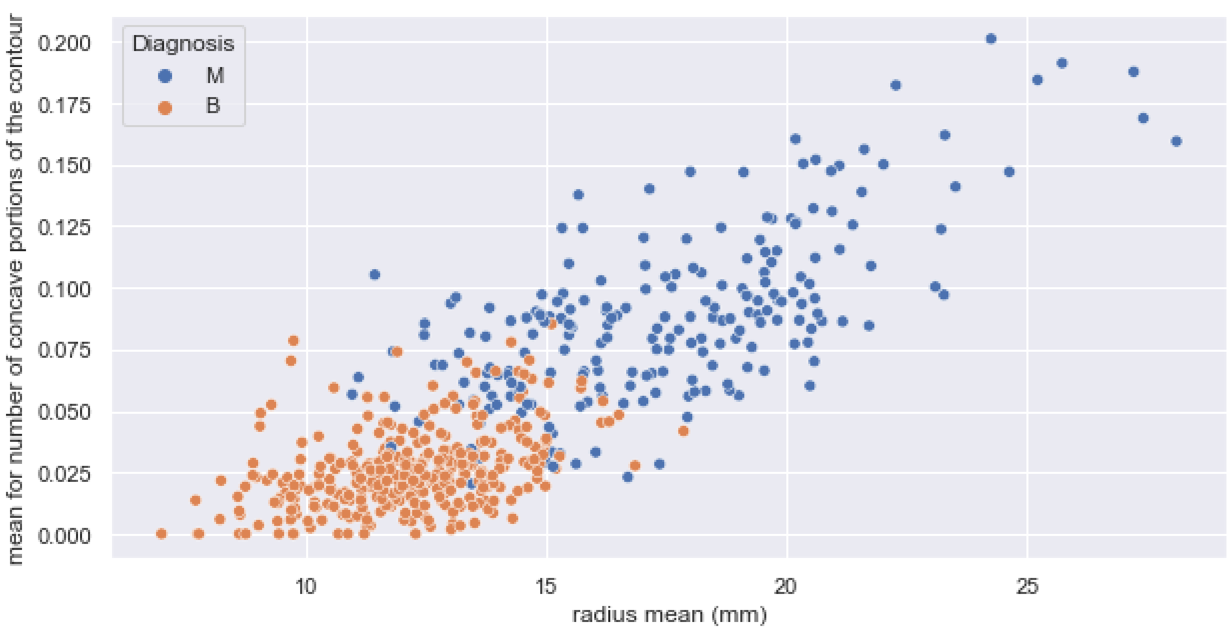
Out[1]:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	...	radius_worst	texture_worst
0	842302	M	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	...	25.38	17.33
1	842517	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	...	24.99	23.41
2	84300903	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	...	23.57	25.53
3	84348301	M	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	...	14.91	26.50
4	84358402	M	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	...	22.54	16.67

5 rows × 32 columns

In [2]:

```
fig = plt.figure(figsize=[10, 5])
sns.scatterplot(x="radius_mean", y="concave points_mean", hue="diagnosis", data=df)
plt.ylabel("mean for number of concave portions of the contour")
plt.xlabel("radius mean (mm)")
plt.legend(title="Diagnosis")
plt.show()
```



In [3]:

```
def Bool(string):
    re = 0
    if string == "M":
        re = 1
    elif string != "B": #this shouldn't occur. We want to know if it happens, so we return nan
        re = np.nan #nan throws an error in regression models, so it will let us know if this happened
    return re
```

In [8]:

```
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.ensemble import GradientBoostingClassifier
from sklearn.linear_model import LogisticRegression #random forest performed better than GBoost & logistic Regression
from sklearn.metrics import r2_score
from sklearn.metrics import accuracy_score
from sklearn.metrics import confusion_matrix

df_new = df.drop(columns = ['diagnosis'])
df_new['diagnosis'] = [Bool(i) for i in df['diagnosis']]

y = df_new["diagnosis"]
X = df_new.drop(columns = ['diagnosis', "id"]) #remove patient id

rf = RandomForestClassifier(random_state=42)

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.25, random_state=42)

rf.fit(X_train, y_train)
pred_tr = rf.predict(X_train)
pred_te = rf.predict(X_test)

r2_tr = r2_score(y_train, pred_tr)
r2_te = r2_score(y_test, pred_te)

print("r2 score for training set: ", r2_tr)
print("r2 score for testing set: ", r2_te, "\n")

print("accuracy score for training set: ", accuracy_score(y_train, pred_tr))
print("accuracy score for testing set: ", accuracy_score(y_test, pred_te), "\n")

print("confusion matrices are in the format: ")
print("[[benign,    predicted benign correctly    ",
      " benign,    predicted malignant falsely", " ]")
print(" [malignant, predicted benign falsely      ",
      " malignant, predicted malignant correctly]]", "\n")

print("training set confusion matrix")
print(confusion_matrix(y_train, pred_tr))

print("testing set confusion matrix")
print(confusion_matrix(y_test, pred_te))
```

```
r2 score for training set:  1.0
r2 score for testing set:  0.8512276321265085 

accuracy score for training set:  1.0
accuracy score for testing set:  0.965034965034965 

confusion matrices are in the format: 
[[benign,    predicted benign correctly      benign,    predicted malignant falsely  ]
 [malignant, predicted benign falsely        malignant, predicted malignant correctly]] 

training set confusion matrix
[[268   0]
 [  0 158]]
testing set confusion matrix
[[87  2]
 [ 3 51]]
```

The model results are good. on the testing data set, the random forest model predicted 96.5% correctly, and performing well in predicting both benign and malignant tumors, as seen in the confusion matrix.

With some more data (we only had 569 patients total), **the model would likely perform even better**.

In [ ]: