Breast cancer prediction with supervised machine learning algorithm

My chosen dataset is the Breast Cancer Wisconsin Diagnostic dataset (https://www.kaggle.com/code/pratikkgandhi/predicting-breast-cancer-with-random-forest-95 accessed 21 Oct 2024) which includes 33 features, that are computed from a digitized image of a fine needle aspirate (FNA) of a breast mass. The mean, standard error and "worst" or largest (mean of the three largest values) of these features were computed for each image. It has 569 observations and no missing values.

The objective of this project is to compare different supervised machine learning models in terms of accurately predicting breast cancer. A high accuracy model would be beneficial as a backend platform to a business whose focus is on improving health with new technology.

First, the raw data is imported with the pandas package and inspected for size, weather there are any null values present, for the column types and then it goes through a series of data cleaning and visualisation techniques to ensure that the correct features are used for prediction. To train the ML model, the features that describe the size of the nuclei are chosen alongside the column that stores the values of the actual diagnosis. With the help of the correlation matrix from sklearn and visualisation from seaborn packages, the number of columns are narrowed down again (only highly correlated columns are taken forward).

```
In [16]: import numpy as np
    import pandas as pd
    import matplotlib.pyplot as plt
    import seaborn as sns
    from sklearn import preprocessing
    from sklearn import metrics
    from sklearn.model_selection import train_test_split, RandomizedSearchCV
    from sklearn.linear_model import LogisticRegression
    from sklearn.ensemble import RandomForestClassifier
    from sklearn.metrics import confusion_matrix
In [17]: data = pd.read_csv('data.csv')
In [18]: data.shape
Out[18]: (569, 33)
In [19]: data.describe()
```

Out[19]:

smootnnes	area_mean	perimeter_mean	texture_mean	radius_mean	Ia	
569	569.000000	569.000000	569.000000	569.000000	5.690000e+02	count
С	654.889104	91.969033	19.289649	14.127292	3.037183e+07	mean
(351.914129	24.298981	4.301036	3.524049	1.250206e+08	std
С	143.500000	43.790000	9.710000	6.981000	8.670000e+03	min
C	420.300000	75.170000	16.170000	11.700000	8.692180e+05	25%
C	551.100000	86.240000	18.840000	13.370000	9.060240e+05	50%
(782.700000	104.100000	21.800000	15.780000	8.813129e+06	75%
(2501.000000	188.500000	39.280000	28.110000	9.113205e+08	max

8 rows × 32 columns

In [20]: 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		float64		
19	concave points_se	569	non-null	float64		
20	symmetry_se	569	non-null	float64		
21	<pre>fractal_dimension_se</pre>	569		float64		
22	radius_worst	569		float64		
23	texture_worst	569	non-null	float64		
24	perimeter_worst	569		float64		
25	area_worst	569		float64		
26	smoothness_worst	569		float64		
27	compactness_worst	569		float64		
28	concavity_worst	569		float64		
29	concave points_worst	569		float64		
30	symmetry_worst		non-null	float64		
31	<pre>fractal_dimension_worst</pre>		non-null	float64		
32	Unnamed: 32		on-null	float64		
<pre>dtypes: float64(31), int64(1), object(1)</pre>						
memory usage: 146.8+ KB						

memory usage: 146.8+ KB

Out[21]: 0 1 2

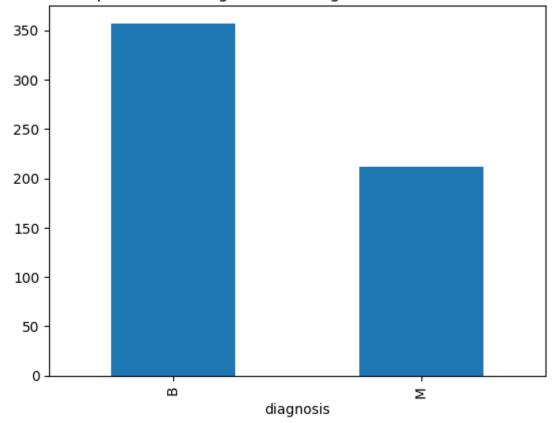
id	842302	842517	84300903
diagnosis	М	М	М
radius_mean	17.99	20.57	19.69
texture_mean	10.38	17.77	21.25
perimeter_mean	122.8	132.9	130.0
area_mean	1001.0	1326.0	1203.0
smoothness_mean	0.1184	0.08474	0.1096
compactness_mean	0.2776	0.07864	0.1599
concavity_mean	0.3001	0.0869	0.1974
concave points_mean	0.1471	0.07017	0.1279
symmetry_mean	0.2419	0.1812	0.2069
fractal_dimension_mean	0.07871	0.05667	0.05999
radius_se	1.095	0.5435	0.7456
texture_se	0.9053	0.7339	0.7869
perimeter_se	8.589	3.398	4.585
area_se	153.4	74.08	94.03
smoothness_se	0.006399	0.005225	0.00615
compactness_se	0.04904	0.01308	0.04006
concavity_se	0.05373	0.0186	0.03832
concave points_se	0.01587	0.0134	0.02058
symmetry_se	0.03003	0.01389	0.0225
fractal_dimension_se	0.006193	0.003532	0.004571
radius_worst	25.38	24.99	23.57
texture_worst	17.33	23.41	25.53
perimeter_worst	184.6	158.8	152.5
area_worst	2019.0	1956.0	1709.0
smoothness_worst	0.1622	0.1238	0.1444
compactness_worst	0.6656	0.1866	0.4245
concavity_worst	0.7119	0.2416	0.4504
concave points_worst	0.2654	0.186	0.243
symmetry_worst	0.4601	0.275	0.3613
fractal_dimension_worst	0.1189	0.08902	0.08758
Unnamed: 32	NaN	NaN	NaN

Remove the unnecessary columns from the dataframe

```
In [22]: data.drop('Unnamed: 32', axis = 1, inplace = True)
data.drop('id', axis = 1, inplace = True)

What are the values in the diagnosis column?
```

Proportion of malignant or benign cases in the dataset



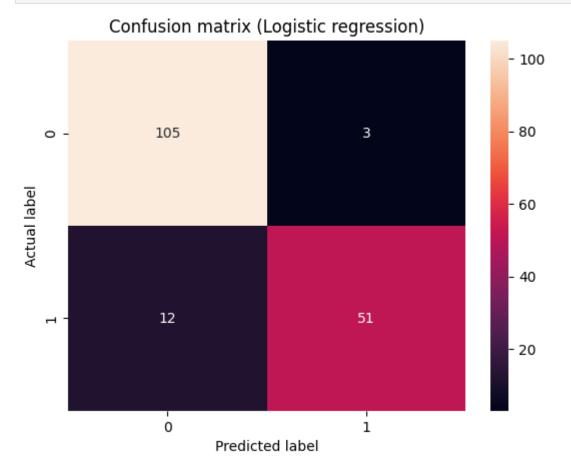
```
In [26]: data['diagnosis'] = data['diagnosis'].replace({'B': 0, 'M': 1})
```

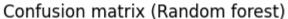
/var/folders/3c/5q4qt7wd2zbgbqznjhttqttm0000gn/T/ipykernel_20497/276317377 1.py:1: FutureWarning: Downcasting behavior in `replace` is deprecated and will be removed in a future version. To retain the old behavior, explicitly call `result.infer_objects(copy=False)`. To opt-in to the future behavior, set `pd.set_option('future.no_silent_downcasting', True)` data['diagnosis'].replace({'B': 0, 'M': 1})

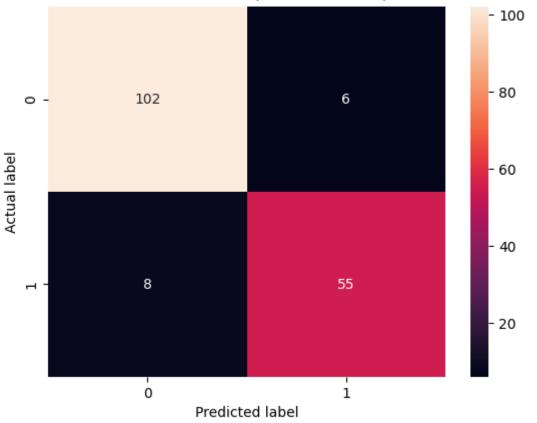
What is the influence of the feature on the diagnosis?

```
In [27]: mean_data = data[['diagnosis','radius_mean','texture_mean','perimeter_mean'
In [28]: heatmap = sns.heatmap(mean_data.corr(), annot=True)
           heatmap
Out[28]: <Axes: >
                                                                                              - 1.0
                                        0.73 0.42 0.74 0.71 0.36 0.6 0.7 0.78 0.33-0.013
                         diagnosis - 1
                      radius mean -0.73
                                         1
                                             0.32
                                                       0.99 0.17 0.51 0.68 0.82 0.15 -0.31
                                                                                              - 0.8
                     texture_mean -0.42 0.32 1
                                                  0.33 0.32-0.0230.24 0.3 0.29 0.0710.076
                   perimeter_mean -0.74 1 0.33 1 0.99 0.21 0.56 0.72 0.85 0.18 -0.26
                                                                                              - 0.6
                        area_mean -0.71 0.99 0.32 0.99 1
                                                           0.18 0.5 0.69 0.82 0.15 -0.28
                                                                                              - 0.4
                 smoothness_mean -0.36 0.17-0.0230.21 0.18
                                                            1
                                                                0.66 0.52 0.55 0.56 0.58
                compactness mean - 0.6 0.51 0.24 0.56 0.5 0.66
                                                                 1 0.88 0.83 0.6 0.57
                                                                                              - 0.2
                   concave points_mean - 0.78 0.82 0.29 0.85 0.82 0.55 0.83 0.92 1
                                                                               0.46 0.17
                                                                                              - 0.0
                   symmetry_mean -0.33 0.15 0.071 0.18 0.15 0.56 0.6 0.5 0.46
                                                                                1
                                                                                    0.48
                                                                                                 -0.2
           fractal_dimension_mean -0.013-0.31-0.076-0.26-0.28 0.58 0.57 0.34 0.17 0.48
                                                                           concave points_mean
                                                                                symmetry_mean
                                                                                     fractal dimension mean
                                              texture mean
                                                             smoothness_mean
                                                                  compactness_mean
                                                                      concavity_mean
                                                   perimeter_mean
                                                        area_mean
                                          adius_mean
In [29]: features = data[['radius mean', 'perimeter mean', 'area mean', 'compactness m
           target = data['diagnosis']
           X = features
           y = target
           X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.3, r
```

The dataset is split into training and test sets, in 70:30 ratio. Then Logistic Regression, a supervised machine learning model is applied and the accuracy of the predicted and true results are compared. Another model, Random Forest is used, which is an ensemble model. As the two models gave the same accuracy percentages, I used RandomSearchCV to optimise the parameters.





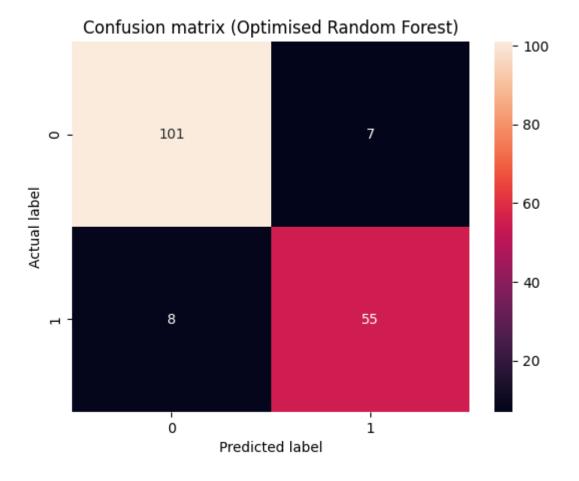


```
In [36]: from sklearn.metrics import accuracy_score
acc_logreg = accuracy_score(y_test, y_pred_logreg)
acc_rf = accuracy_score(y_test, y_pred_rf)
```

```
Accuracy of Logistic Regression model: 0.9122807017543859
         Accuracy of Random Forest model: 0.9181286549707602
         As the more complex model did not result in better prediction, let's perform
         hyperparameter tuning on the Random Forest Classifier
In [37]: #Hyperparameter tuning using RandomizedSearchCV
         param_dist = {'n_estimators': (10,20,30,40,50), 'max_depth': (1,5,10,15,20)}
         rand search = RandomizedSearchCV(rf, param distributions = param dist, n ite
         rand_search.fit(X_train, y_train)
Out[37]:
                  RandomizedSearchCV ① ②
          ▶ estimator: RandomForestClassifier
               ► RandomForestClassifier
In [38]: rand_search.best_params_
Out[38]: {'n estimators': 40, 'max depth': 5}
In [39]: #Optimised parameters for Random Forest
         rf_best= RandomForestClassifier(n_estimators=50, max_depth=5)
         rfc_best = rf_best.fit(X_train, y_train)
         y pred rf best= rf best.predict(X test)
         cm_rf_best= metrics.confusion_matrix(y_test, y_pred_rf_best)
In [40]: cm_rf_best
Out[40]: array([[101,
                       7],
                [ 8, 55]])
In [41]: cm_rf_best_heatmap = sns.heatmap(pd.DataFrame(cm_rf_best), annot=True, fmt='
         plt.title('Confusion matrix (Optimised Random Forest)')
         plt.ylabel('Actual label')
         plt.xlabel('Predicted label')
         plt.show()
```

print("Accuracy of Logistic Regression model:", acc_logreg)

print("Accuracy of Random Forest model:", acc_rf)



Final results:

```
In [42]: acc_rf_best = accuracy_score(y_test, y_pred_rf_best)

print("Accuracy of Logistic Regression model:", acc_logreg)
print("Accuracy of Random Forest model:", acc_rf)
print("Accuracy of Optimised Random Forest model:", acc_rf_best)
```

Accuracy of Logistic Regression model: 0.9122807017543859 Accuracy of Random Forest model: 0.9181286549707602

Accuracy of Optimised Random Forest model: 0.9122807017543859

Conclusion

All three machine learning models gave a very promising score predicting breast cancer, achieving 91% accuracy. This could be explained by the nature of the dataset, where the features are well separated. Logistic Regression, as a linear model, works well with these linear datasets. Random Forest Classifier, on the other hand, may have overfitted, as it is a non-linear ensemble model. Key insights from this analysis revealed that some features highly influenced whether the tumor was malignant or benign. Applying RandomSearchCV hyperparameter tuning improved the computation time but at the same time did not compromise accuracy. One way to improve this metric would be to evaluate a bigger dataset. Also other feature engineering techniques, such as PCA dimensionality reduction could be beneficial. Furthermore, other machine learning

models such as Gradient Boosting might provide improvements. This project confirms, that with limited data, Logistic Regression model is as accurate as a more complex Random Forest Classifier.