PROJECT REPORT

Breast Cancer Wisconsin (Diagnostic) Prediction

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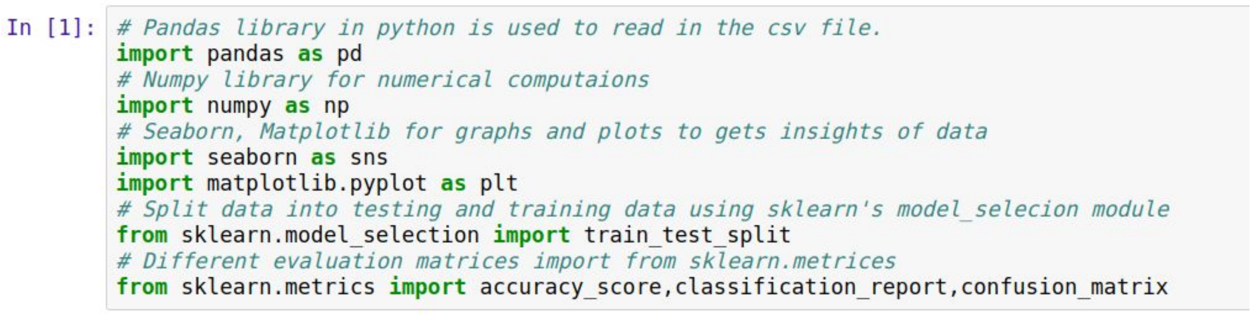
Problem Statement:

Our aim is to diagnose patients with breast cancer by analyzing the data of patients and classifying them into two categories, having diagnosis results as : (1) Benign (**B)** and (2) Malignant (**M).**

Libraries used:



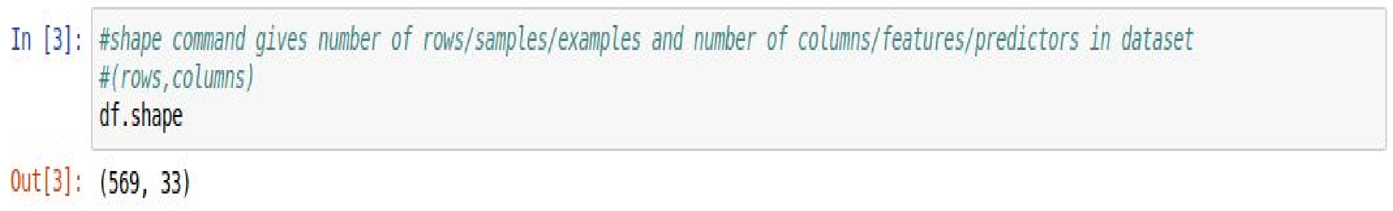
```
In [1]: # Pandas library in python is used to read in the csv file.
        import pandas as pd
        # Numpy library for numerical computaions
        import numpy as np
        # Seaborn, Matplotlib for graphs and plots to gets insights of data
        import seaborn as sns
        import matplotlib.pyplot as plt
        # Split data into testing and training data using sklearn's model_selecion module
        from sklearn.model_selection import train_test_split
        # Different evaluation matrices import from sklearn.metrices
        from sklearn.metrics import accuracy_score,classification_report,confusion_matrix
```

1) NumPy : The fundamental package for scientific computing with Python
2) Pandas : An open source, BSD-licensed library providing high-performance, easy-to-use data structures and data analysis tools for the Python programming language.
3) sklearn.model_selection :
   - Split arrays or matrices into random train and test subsets
   - Selecting optimal features
4) matplotlib.pyplot : Provides a MATLAB-like plotting framework.
5) Seaborn : Seaborn is a Python data visualization library based on matplotlib. It provides a high-level interface for drawing attractive and informative statistical Graphics.
6) XGBoost : XGBoost is an optimized distributed gradient boosting library designed to be highly efficient, flexible and portable.
7) sklearn.metrics :
   - Accuracy score: In multilabel classification, this function computes subset accuracy: the set of labels predicted for a sample must *exactly* match the corresponding set of labels in y_true.
   - Classification report:Build a report showing the main classification metrics
   - Confusion matrix: Compute confusion matrix to evaluate the accuracy of classification.

Details of Data:

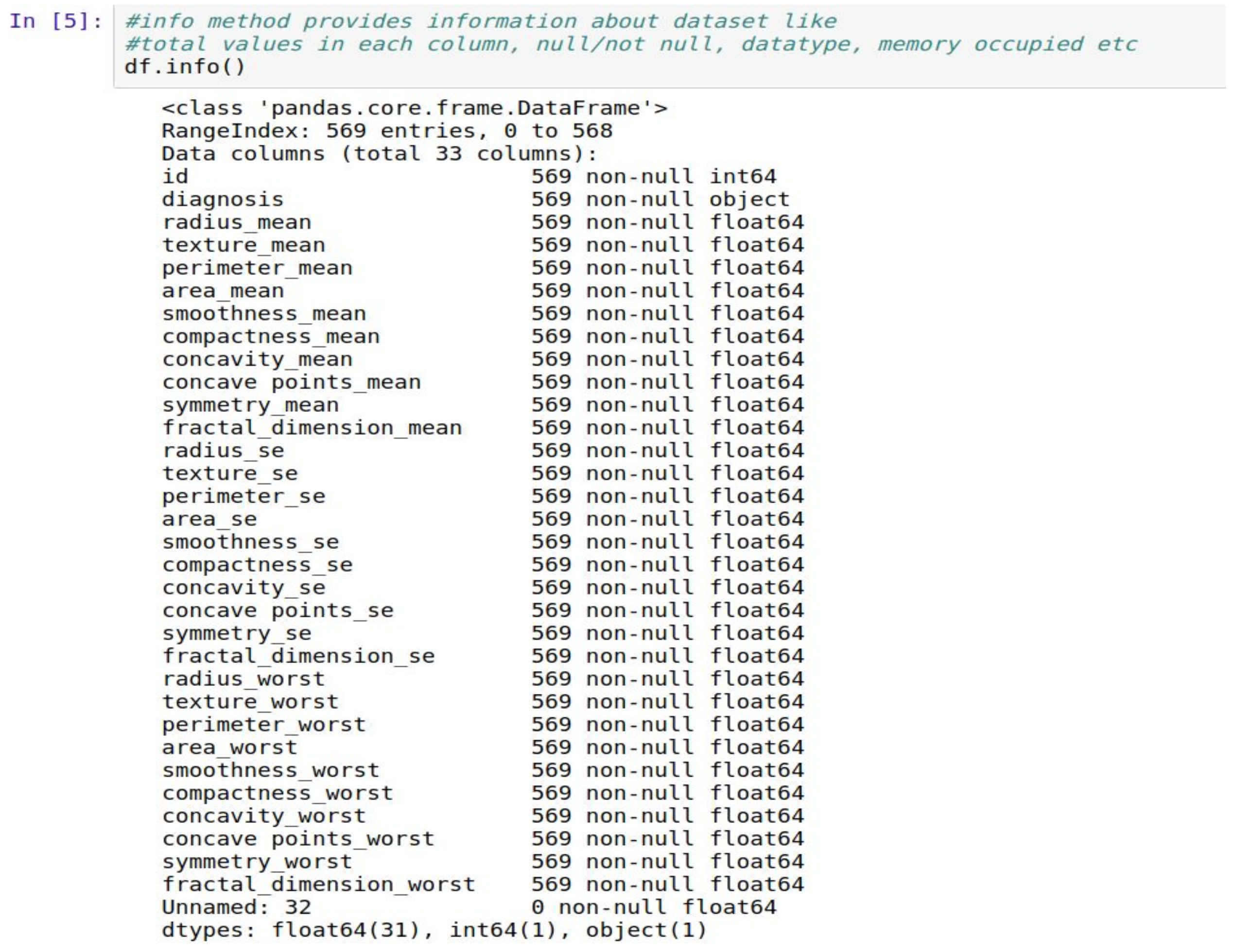
The data was collected from Kaggle:
https://www.kaggle.com/uciml/breast-cancer-wisconsin-data

No. of rows : 569
No. of columns : 33



```
In [3]: #shape command gives number of rows/samples/examples and number of columns/features/predictors in dataset
        #(rows,columns)
        df.shape

Out[3]: (569, 33)
```

Attributes:



```
In [5]: #info method provides information about dataset like
        #total values in each column, null/not null, datatype, memory occupied etc
        df.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 33 columns):
id                         569 non-null int64
diagnosis                  569 non-null object
radius_mean                569 non-null float64
texture_mean               569 non-null float64
perimeter_mean             569 non-null float64
area_mean                  569 non-null float64
smoothness_mean            569 non-null float64
compactness_mean           569 non-null float64
concavity_mean             569 non-null float64
concave points_mean        569 non-null float64
symmetry_mean              569 non-null float64
fractal_dimension_mean     569 non-null float64
radius_se                  569 non-null float64
texture_se                 569 non-null float64
perimeter_se               569 non-null float64
area_se                    569 non-null float64
smoothness_se              569 non-null float64
compactness_se             569 non-null float64
concavity_se               569 non-null float64
concave points_se          569 non-null float64
symmetry_se                569 non-null float64
fractal_dimension_se       569 non-null float64
radius_worst               569 non-null float64
texture_worst              569 non-null float64
perimeter_worst            569 non-null float64
area_worst                 569 non-null float64
smoothness_worst           569 non-null float64
compactness_worst          569 non-null float64
concavity_worst            569 non-null float64
concave points_worst       569 non-null float64
symmetry_worst             569 non-null float64
fractal_dimension_worst    569 non-null float64
Unnamed: 32                0 non-null float64
dtypes: float64(31), int64(1), object(1)
```

1) ID number

The unique ID allotted to each patient to differentiate between them.

2) Diagnosis (M = malignant, B = benign)

The target variable .i.e the conclusion if the tumour is malignant or benign.

3-33) Ten real-valued features are computed for each cell nucleus:

a) Radius

The mean of distances from center to points on the perimeter.

b) Texture

The standard deviation of gray-scale values.

c) Perimeter

d) Area

e) Smoothness

The local variation in radius lengths.

f) Compactness

Perimeter^2 / Area - 1.0

g) Concavity

The severity of concave portions of the contour.

h) Concave Points

Number of concave portions of the contour.

i) Symmetry

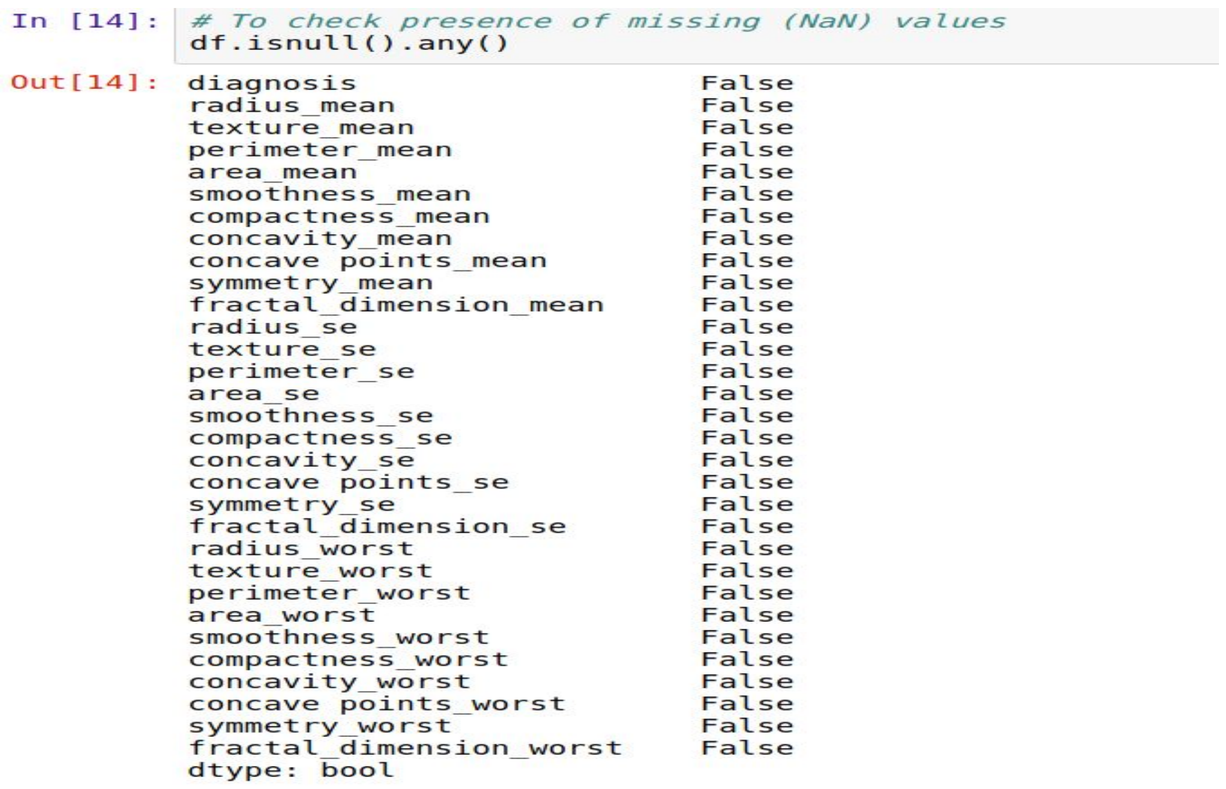
j) Fractal Dimension

Coastline approximation - 1

The mean, standard error and "worst" or largest (mean of the three largest values) of these features were computed for each image, resulting in 30 features.
For instance, field 3 is Mean Radius, field 13 is Radius SE, field 23 is Worst Radius.

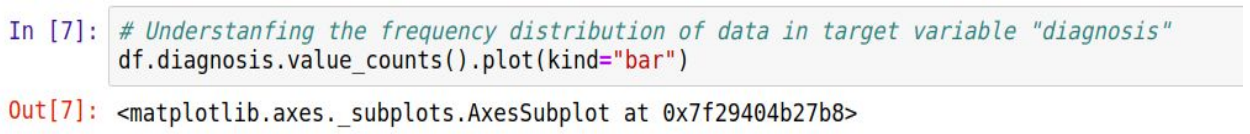
All feature values are recorded with four significant digits.

Missing attribute values: There are no missing values in the dataset.

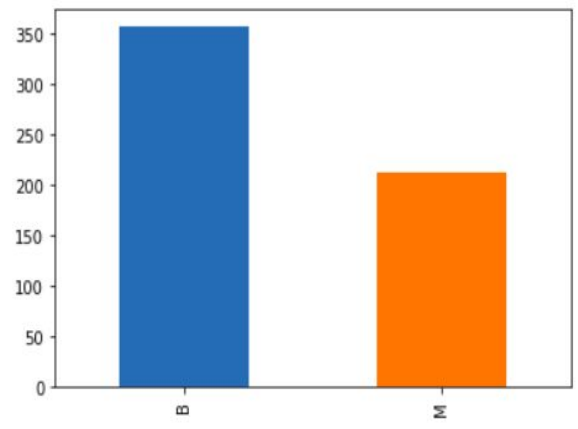


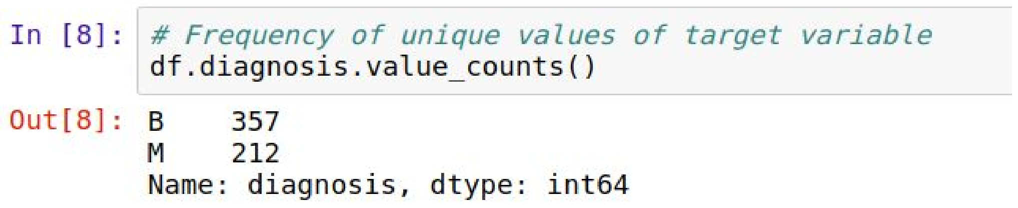
```
In [14]: # To check presence of missing (NaN) values
         df.isnull().any()

Out[14]: diagnosis                  False
         radius_mean                False
         texture_mean               False
         perimeter_mean             False
         area_mean                  False
         smoothness_mean            False
         compactness_mean           False
         concavity_mean             False
         concave points_mean        False
         symmetry_mean              False
         fractal_dimension_mean     False
         radius_se                  False
         texture_se                 False
         perimeter_se               False
         area_se                    False
         smoothness_se              False
         compactness_se             False
         concavity_se               False
         concave points_se          False
         symmetry_se                False
         fractal_dimension_se       False
         radius_worst               False
         texture_worst              False
         perimeter_worst            False
         area_worst                 False
         smoothness_worst           False
         compactness_worst          False
         concavity_worst            False
         concave points_worst       False
         symmetry_worst             False
         fractal_dimension_worst    False
         dtype: bool
```

Class distribution: 357 benign, 212 malignant



```
In [7]: # Understanfing the frequency distribution of data in target variable "diagnosis"
        df.diagnosis.value_counts().plot(kind="bar")

Out[7]: <matplotlib.axes._subplots.AxesSubplot at 0x7f29404b27b8>
```



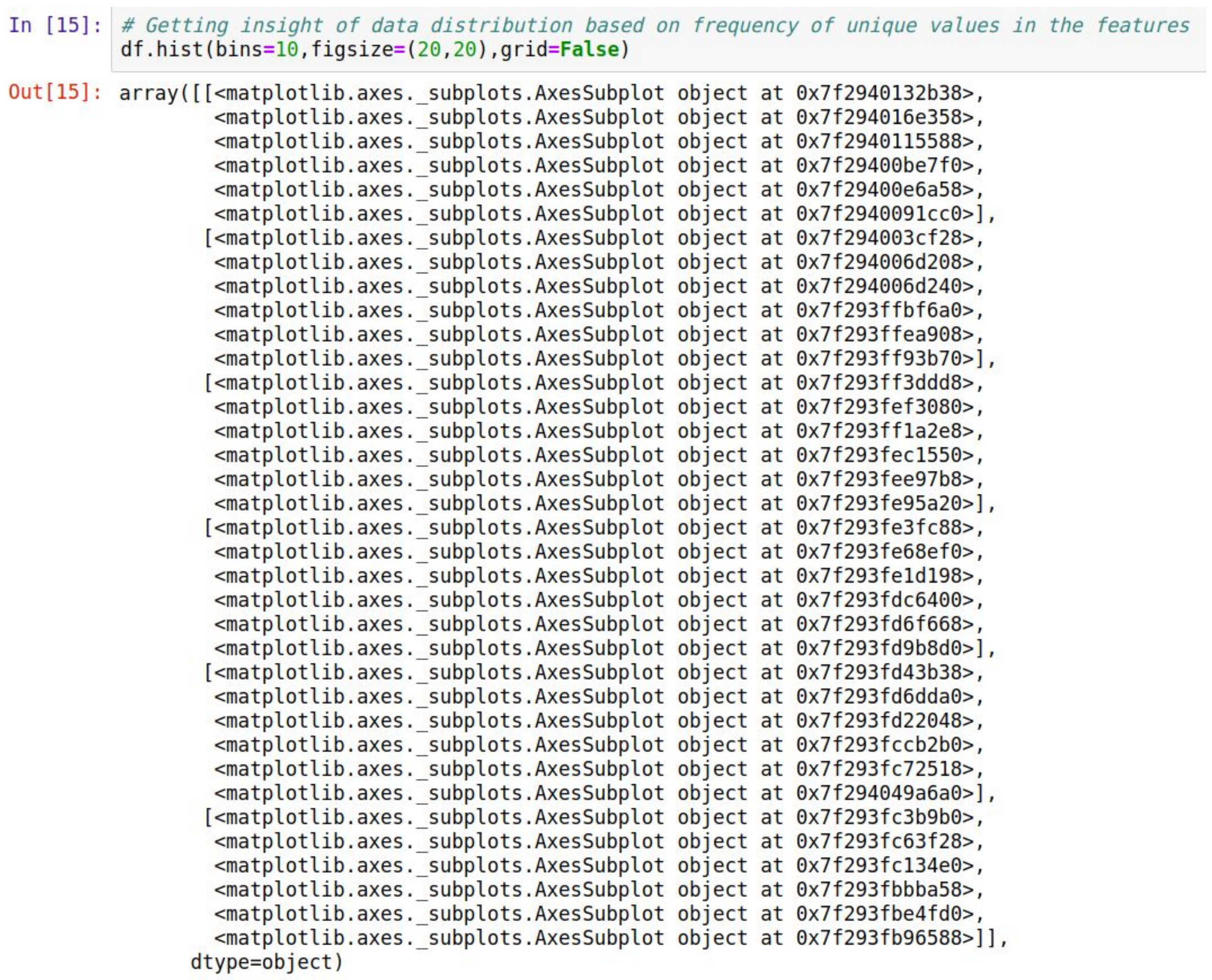


```
In [8]: # Frequency of unique values of target variable
        df.diagnosis.value_counts()

Out[8]: B    357
        M    212
        Name: diagnosis, dtype: int64
```

Preprocessing of Data:

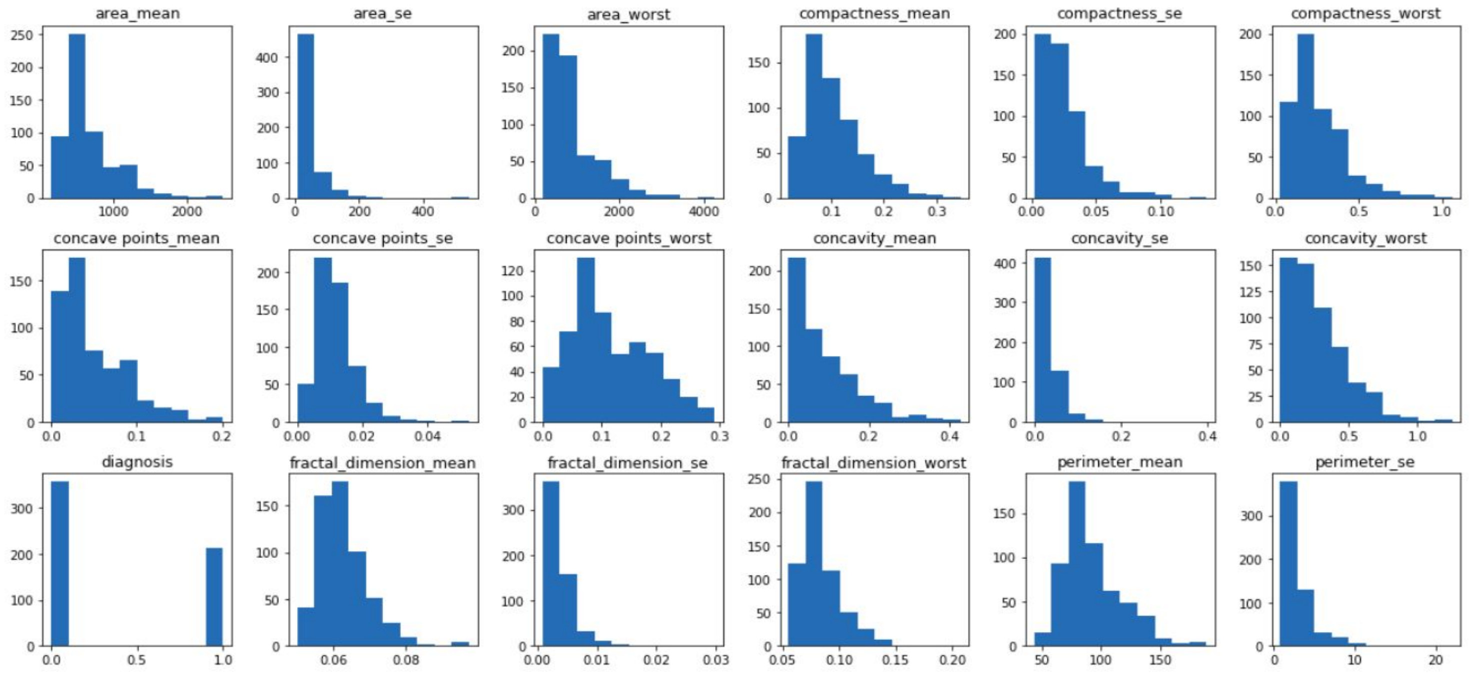
1. Visualization

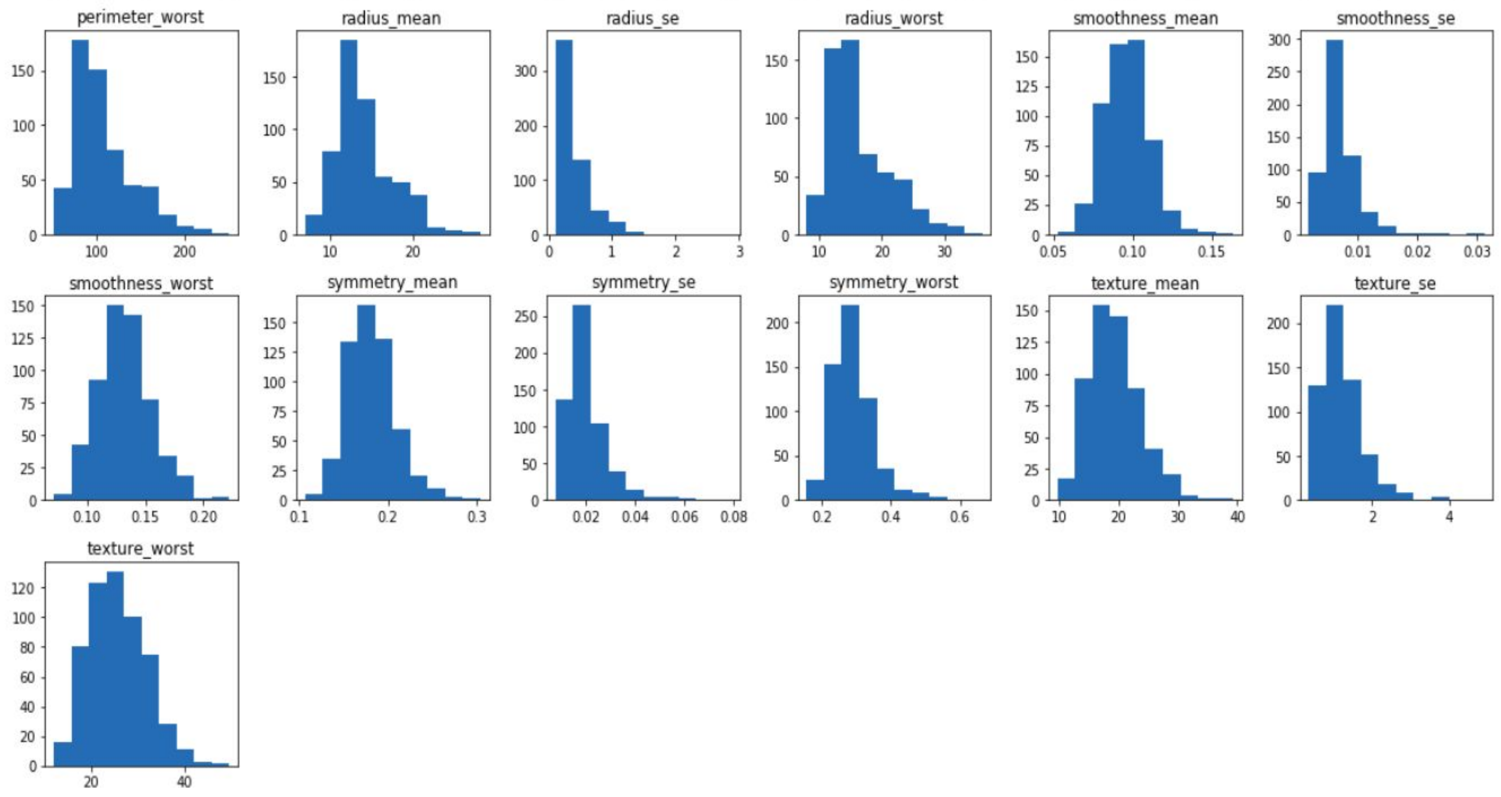
Visual representation of data using histograms for each feature to get insights about the frequency of various feature values in data.



```
In [15]: # Getting insight of data distribution based on frequency of unique values in the features
         df.hist(bins=10,figsize=(20,20),grid=False)

Out[15]: array([[<matplotlib.axes._subplots.AxesSubplot object at 0x7f2940132b38>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f294016e358>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f2940115588>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f29400be7f0>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f29400e6a58>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f2940091cc0>],
                [<matplotlib.axes._subplots.AxesSubplot object at 0x7f294003cf28>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f294006d208>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f294006d240>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293ffbf6a0>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293ffea908>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293ff93b70>],
                [<matplotlib.axes._subplots.AxesSubplot object at 0x7f293ff3ddd8>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293fef3080>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293ff1a2e8>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293fec1550>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293fee97b8>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293fe95a20>],
                [<matplotlib.axes._subplots.AxesSubplot object at 0x7f293fe3fc88>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293fe68ef0>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293fe1d198>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293fdc6400>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293fd6f668>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293fd9b8d0>],
                [<matplotlib.axes._subplots.AxesSubplot object at 0x7f293fd43b38>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293fd6dda0>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293fd22048>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293fccb2b0>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293fc72518>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f294049a6a0>],
                [<matplotlib.axes._subplots.AxesSubplot object at 0x7f293fc3b9b0>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293fc63f28>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293fc134e0>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293fbbba58>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293fbe4fd0>,
                 <matplotlib.axes._subplots.AxesSubplot object at 0x7f293fb96588>]],
               dtype=object)
```

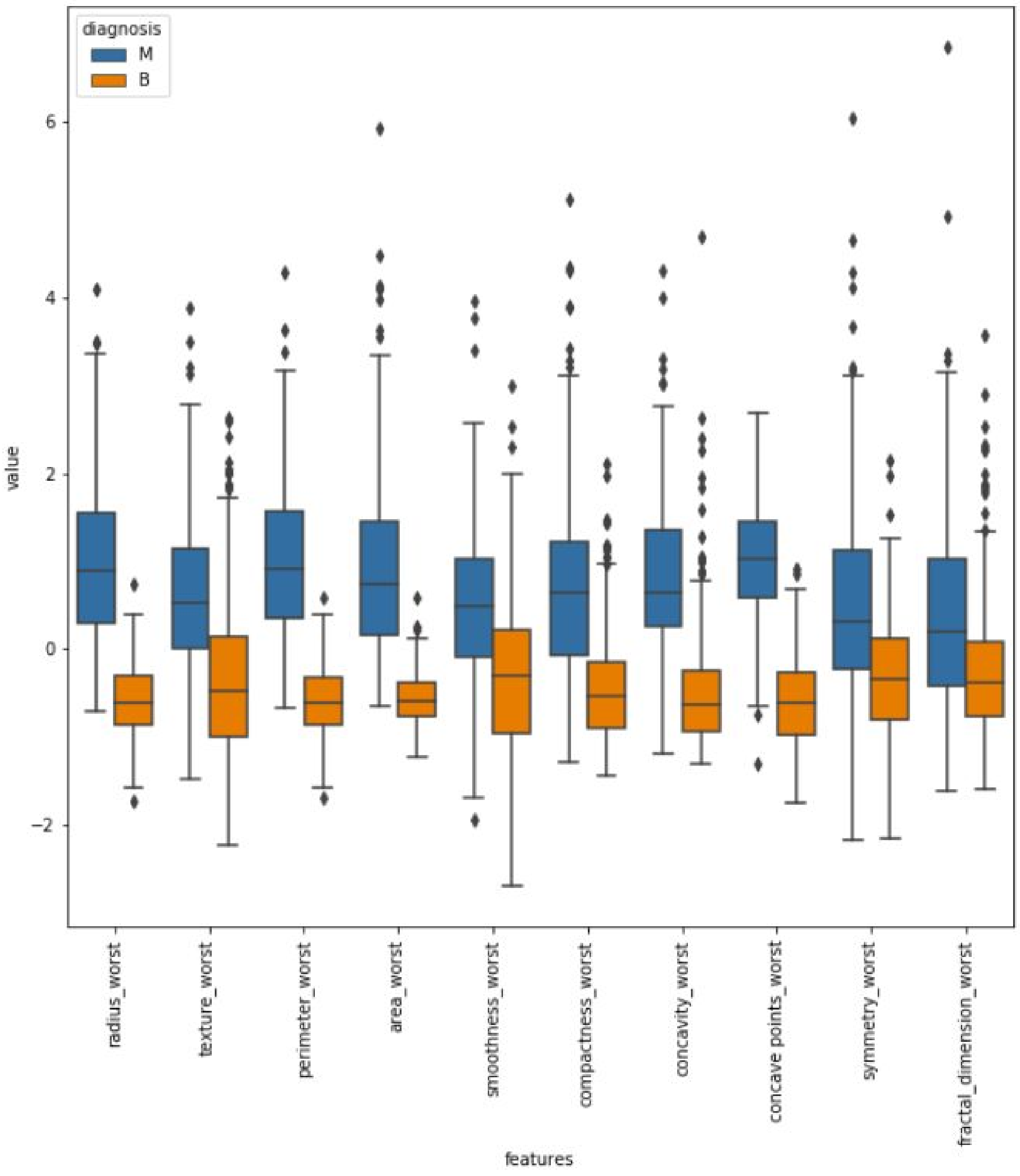
Breast Cancer Diagnosis Wisconsin Data Set



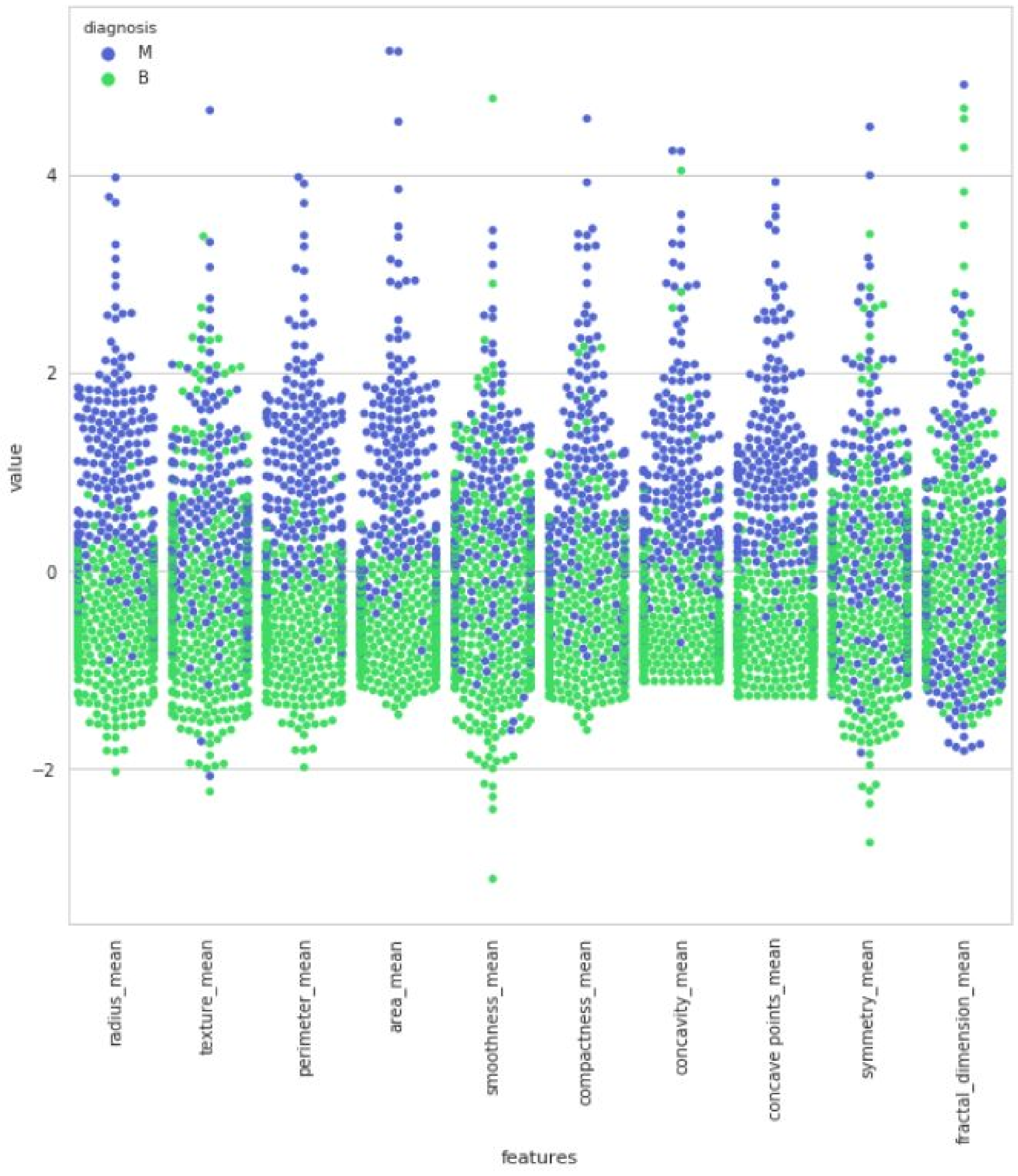


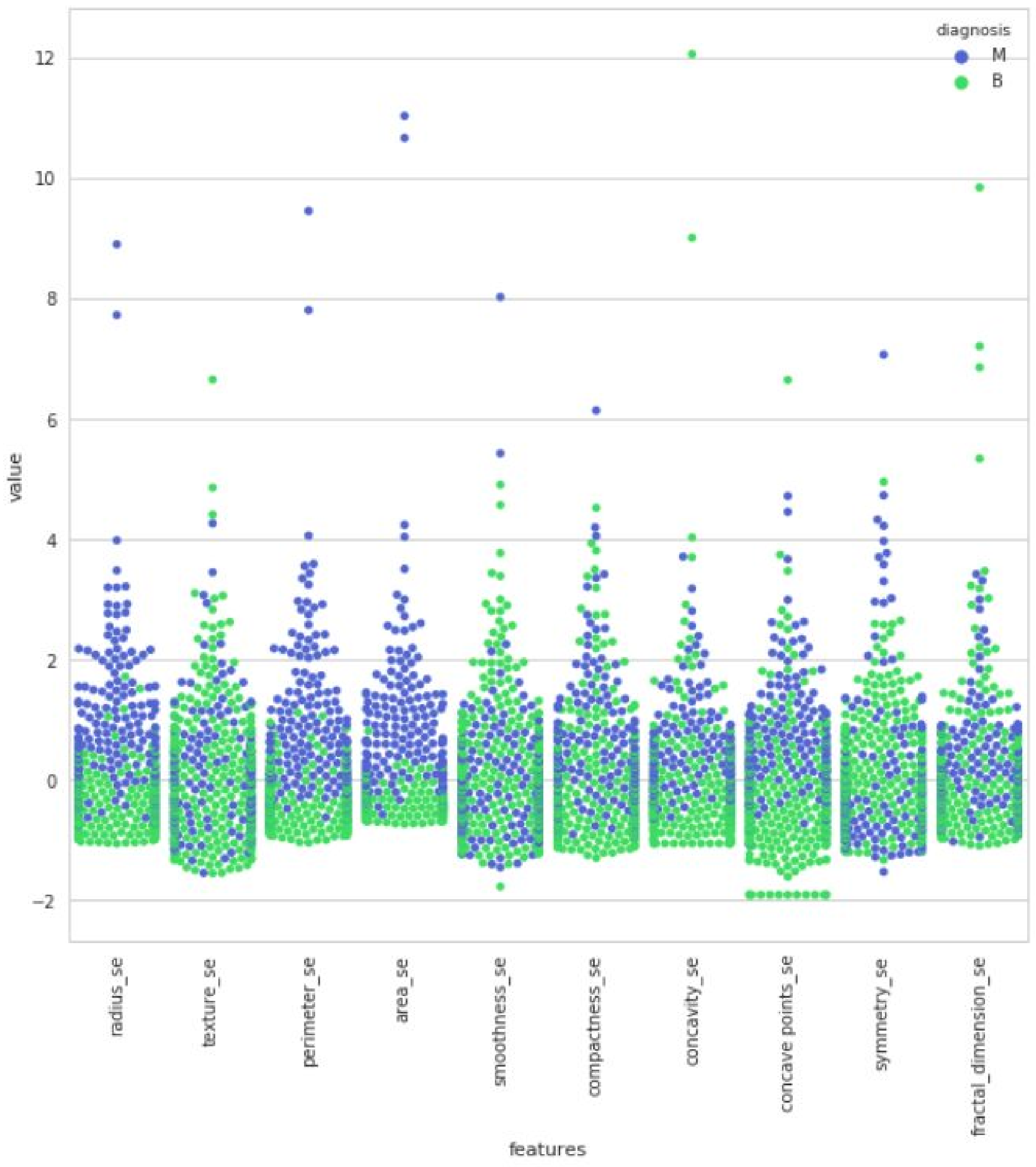
Box Plots for attributes:

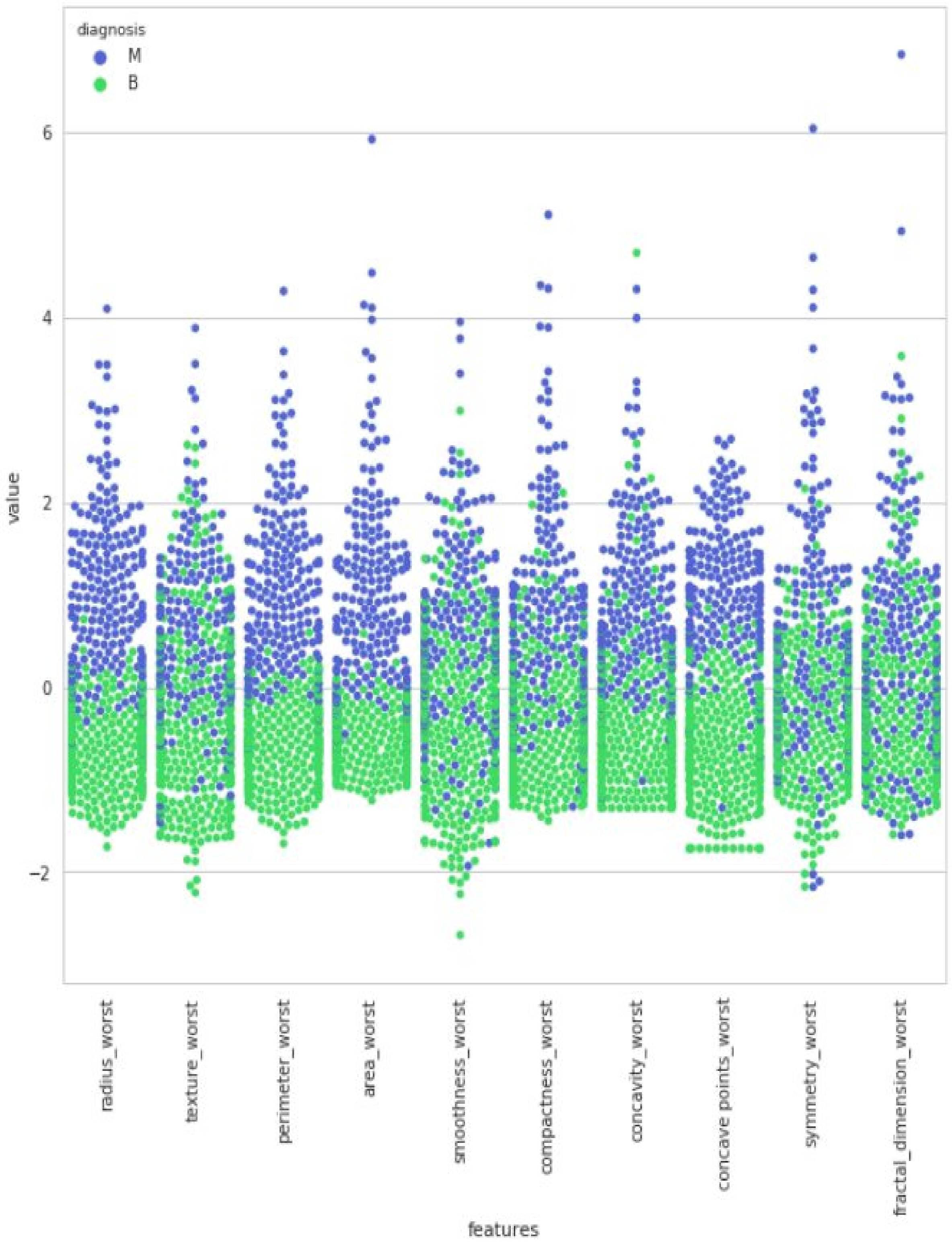
It is used to visualize the distribution of values of attributes and to see the outliers. As an example, we have plotted box plots for few of the attributes.



Swarm Plots:

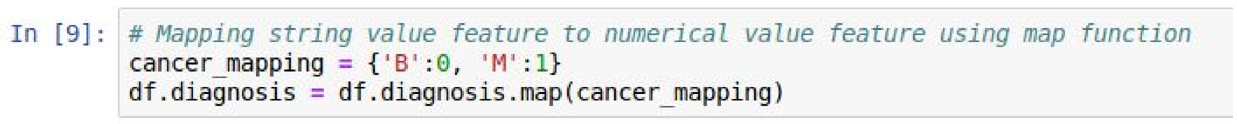

diagnosis
M
B
value
4
2
0
−2
radius_mean
texture_mean
perimeter_mean
area_mean
smoothness_mean
compactness_mean
concavity_mean
concave points_mean
symmetry_mean
fractal_dimension_mean
features


diagnosis
M
B
value
12
10
8
6
4
2
0
−2
radius_se
texture_se
perimeter_se
area_se
smoothness_se
compactness_se
concavity_se
concave points_se
symmetry_se
fractal_dimension_se
features


diagnosis
M
B
6
4
2
0
−2
value
radius_worst
texture_worst
perimeter_worst
area_worst
smoothness_worst
compactness_worst
concavity_worst
concave points_worst
symmetry_worst
fractal_dimension_worst
features

2. Mapping string to numeric data

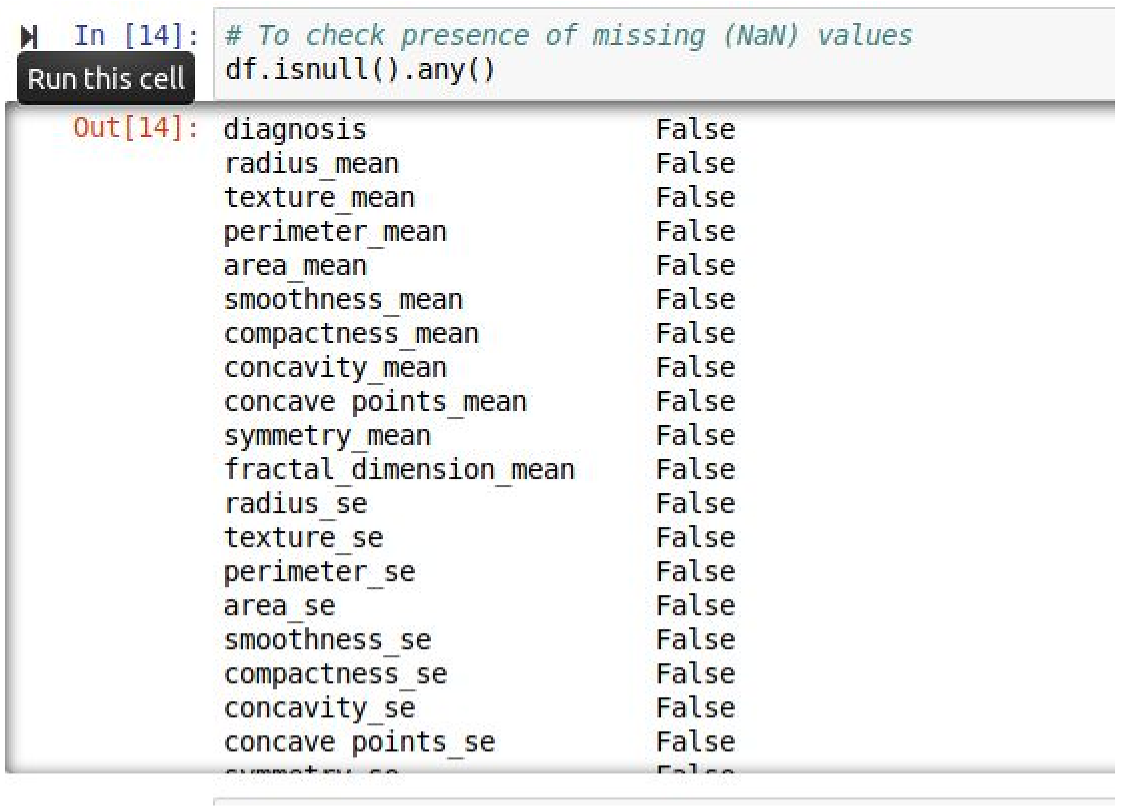
The feature “diagnosis” has values in the form of string (‘object’) which is mapped to numeric form for analysis.
The mapping function is:
‘B’ → 0
‘M’ → 1



```
In [9]: # Mapping string value feature to numerical value feature using map function
        cancer_mapping = {'B':0, 'M':1}
        df.diagnosis = df.diagnosis.map(cancer_mapping)
```

3. Missing values

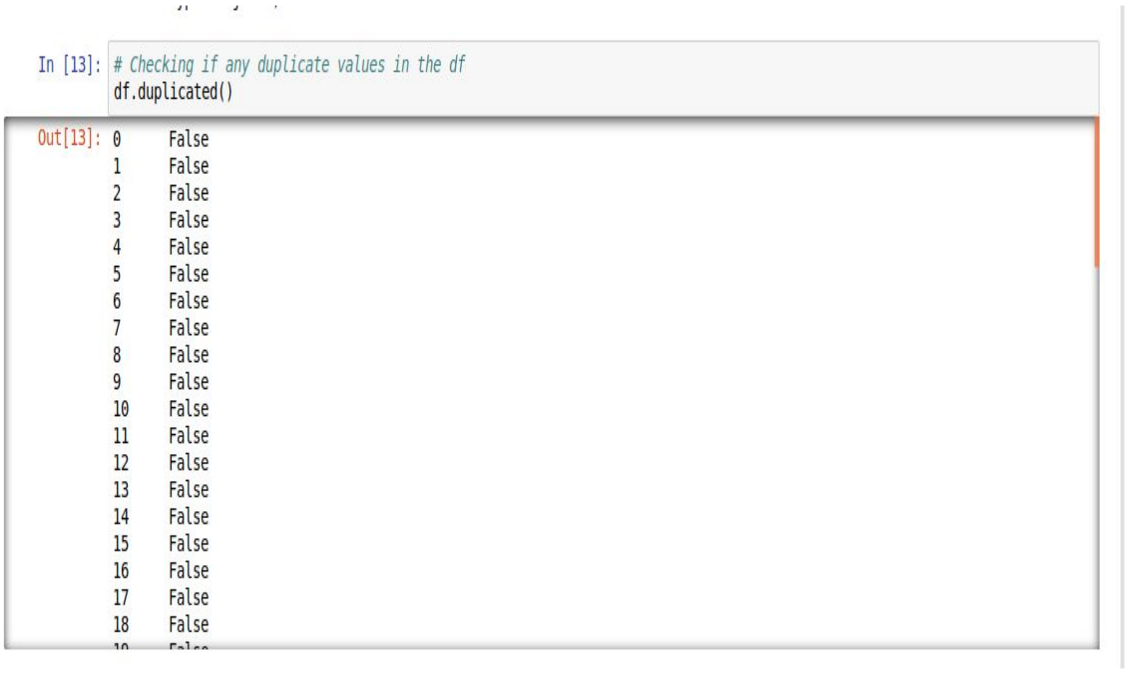
The data contains no missing values for any of the attributes as inferred from the in the figure below. So, we don’t have to deal with them.



```
In [14]: # To check presence of missing (NaN) values
         df.isnull().any()

Out[14]: diagnosis                  False
         radius_mean                False
         texture_mean               False
         perimeter_mean             False
         area_mean                  False
         smoothness_mean            False
         compactness_mean           False
         concavity_mean             False
         concave points_mean        False
         symmetry_mean              False
         fractal_dimension_mean     False
         radius_se                  False
         texture_se                 False
         perimeter_se               False
         area_se                    False
         smoothness_se              False
         compactness_se             False
         concavity_se               False
         concave points_se          False
```

4. Duplicate data

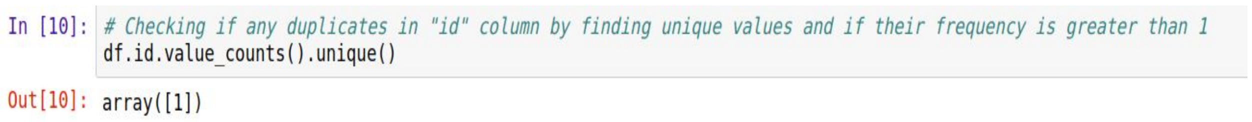
The data contains no duplicate instances of patient data.



```
In [13]: # Checking if any duplicate values in the df
         df.duplicated()

Out[13]: 0      False
         1      False
         2      False
         3      False
         4      False
         5      False
         6      False
         7      False
         8      False
         9      False
         10     False
         11     False
         12     False
         13     False
         14     False
         15     False
         16     False
         17     False
         18     False
```

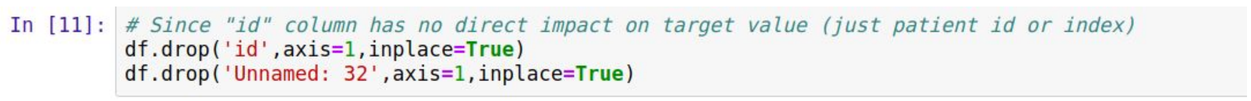
5. Feature subset selection

The feature "id" is a unique attribute for each patient and it is irrelevant to the process of classification, so it can be eliminated.



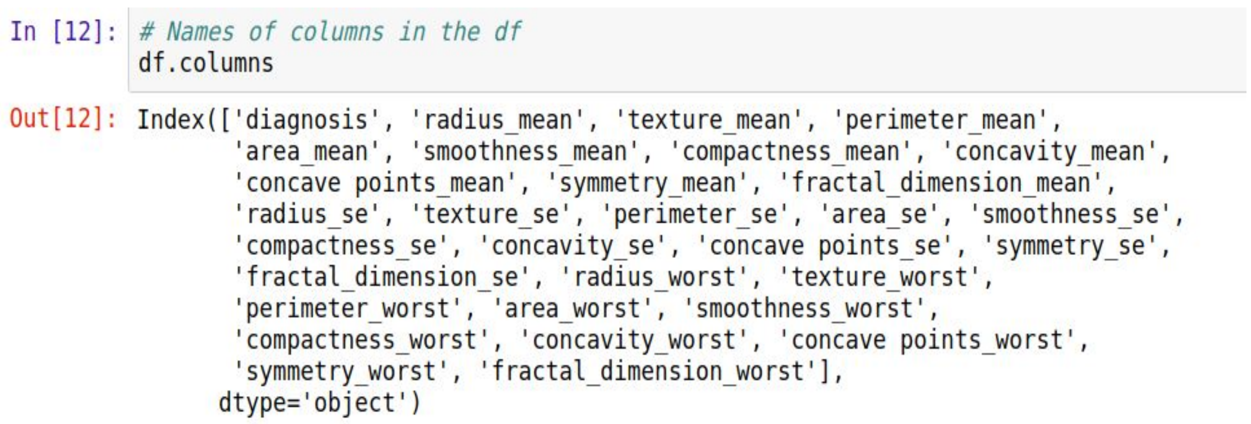
```
In [10]: # Checking if any duplicates in "id" column by finding unique values and if their frequency is greater than 1
         df.id.value_counts().unique()

Out[10]: array([1])
```

This gives that all instances in dataset have unique id. Meaning it has little impact on the prediction of target value.



```
In [11]: # Since "id" column has no direct impact on target value (just patient id or index)
         df.drop('id',axis=1,inplace=True)
         df.drop('Unnamed: 32',axis=1,inplace=True)
```

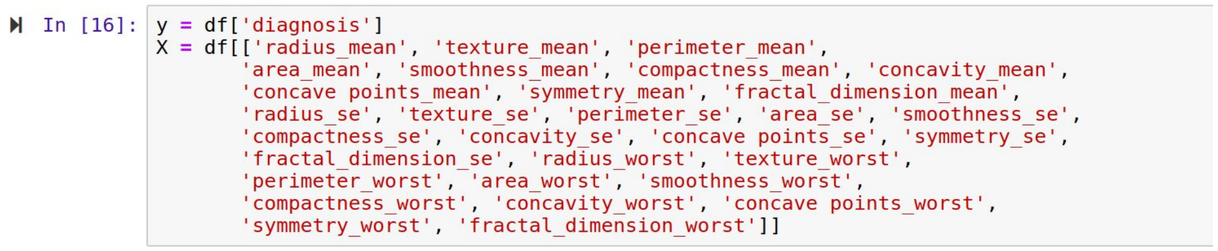
So, we drop the features : ‘id’ and ‘unnamed 32’
Resultant columns in the data :



```
In [12]: # Names of columns in the df
         df.columns

Out[12]: Index(['diagnosis', 'radius_mean', 'texture_mean', 'perimeter_mean',
                'area_mean', 'smoothness_mean', 'compactness_mean', 'concavity_mean',
                'concave points_mean', 'symmetry_mean', 'fractal_dimension_mean',
                'radius_se', 'texture_se', 'perimeter_se', 'area_se', 'smoothness_se',
                'compactness_se', 'concavity_se', 'concave points_se', 'symmetry_se',
                'fractal_dimension_se', 'radius_worst', 'texture_worst',
                'perimeter_worst', 'area_worst', 'smoothness_worst',
                'compactness_worst', 'concavity_worst', 'concave points_worst',
                'symmetry_worst', 'fractal_dimension_worst'],
               dtype='object')
```

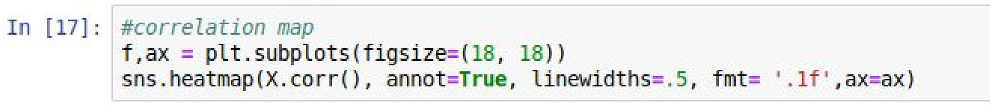
6. <u>Dimensionality reduction</u>

The features which are highly correlated (show dependency) with the target variable (‘diagnosis’) are highly relevant for our classification problem.
We can remove irrelevant attributes in order to reduce the size of data for easier computation.
Here, **y** stores the target or class variable & **x** stores the non-class attributes

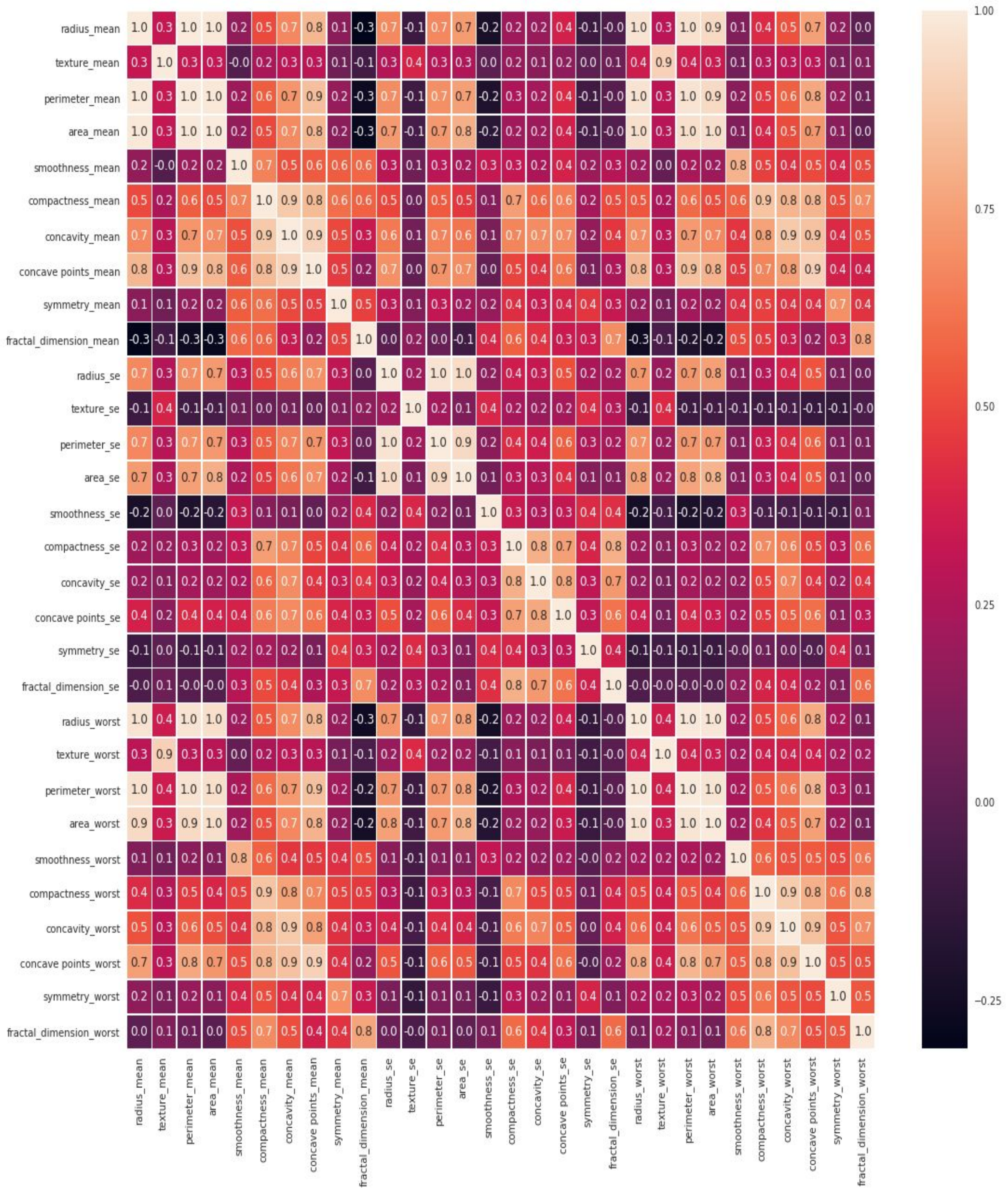


```
In [16]: y = df['diagnosis']
         X = df[['radius_mean', 'texture_mean', 'perimeter_mean',
                'area_mean', 'smoothness_mean', 'compactness_mean', 'concavity_mean',
                'concave points_mean', 'symmetry_mean', 'fractal_dimension_mean',
                'radius_se', 'texture_se', 'perimeter_se', 'area_se', 'smoothness_se',
                'compactness_se', 'concavity_se', 'concave points_se', 'symmetry_se',
                'fractal_dimension_se', 'radius_worst', 'texture_worst',
                'perimeter_worst', 'area_worst', 'smoothness_worst',
                'compactness_worst', 'concavity_worst', 'concave points_worst',
                'symmetry_worst', 'fractal_dimension_worst']]
```

The irrelevant attributes can be found by computing the correlation among non-class attributes, and then we can reduce a subset of highly co-relevant non-class attributes to a single or less number of attributes which would reduce the size of data.
Therefore, we create a heatmap to display the correlation between all the features:



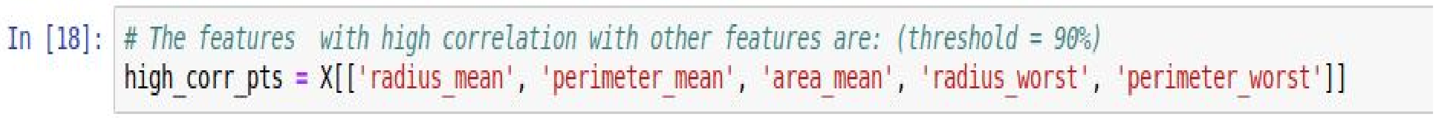
```
In [17]: #correlation map
         f,ax = plt.subplots(figsize=(18, 18))
         sns.heatmap(X.corr(), annot=True, linewidths=.5, fmt= '.1f',ax=ax)
```


radius_mean
texture_mean
perimeter_mean
area_mean
smoothness_mean
compactness_mean
concavity_mean
concave points_mean
symmetry_mean
fractal_dimension_mean
radius_se
texture_se
perimeter_se
area_se
smoothness_se
compactness_se
concavity_se
concave points_se
symmetry_se
fractal_dimension_se
radius_worst
texture_worst
perimeter_worst
area_worst
smoothness_worst
compactness_worst
concavity_worst
concave points_worst
symmetry_worst
fractal_dimension_worst
1.00
0.75
0.50
0.25
0.00
−0.25

This heatplot visualizes the correlation between each pair of attribute in the dataset. We can select those attributes which have high correlation with each other according to a threshold value, and then we will implement the classification algorithm with a reduced set of attributes by taking various smaller subsets of the these highly correlated (dependent) attributes, and compare the results.

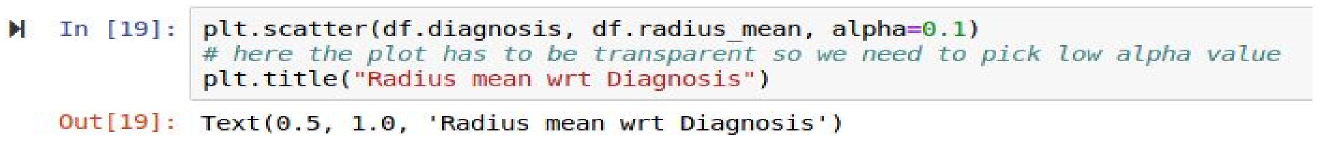
Here, we take **threshold value: 0.90**
From the heat plot we infer that the following features are the most related (corr>9) to the other features:

1. Radius_mean
2. Perimeter_mean
3. Area_mean
4. Radius_worst
5. Perimeter_worst

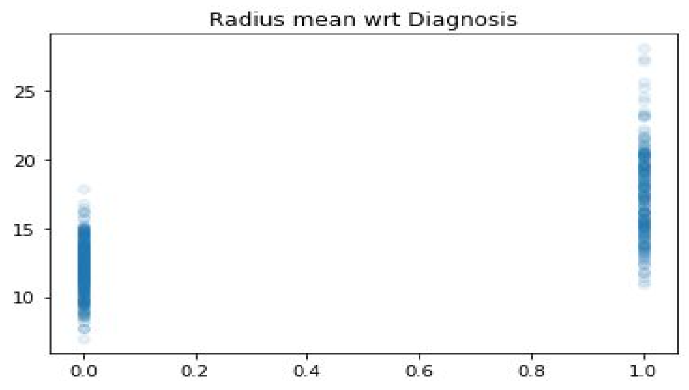


```
In [18]: # The features  with high correlation with other features are: (threshold = 90%)
         high_corr_pts = X[['radius_mean', 'perimeter_mean', 'area_mean', 'radius_worst', 'perimeter_worst']]
```

Then we plot scatter plots for all the high correlation features with respect to the target feature(diagnosis):

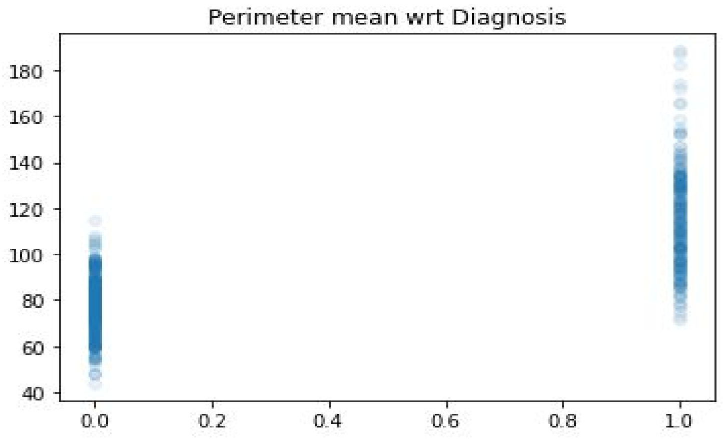


```
In [19]: plt.scatter(df.diagnosis, df.radius_mean, alpha=0.1)
         # here the plot has to be transparent so we need to pick low alpha value
         plt.title("Radius mean wrt Diagnosis")

Out[19]: Text(0.5, 1.0, 'Radius mean wrt Diagnosis')
```



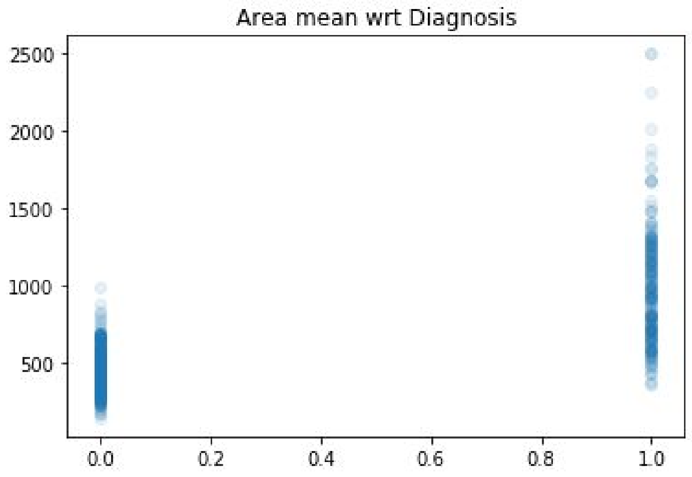
In [20]:
```
plt.scatter(df.diagnosis, df.perimeter_mean, alpha=0.1)
# here the plot has to be transparent so we need to pic low alpha value
plt.title("Perimeter mean wrt Diagnosis")
```

Out[20]:
```
Text(0.5, 1.0, 'Perimeter mean wrt Diagnosis')
```

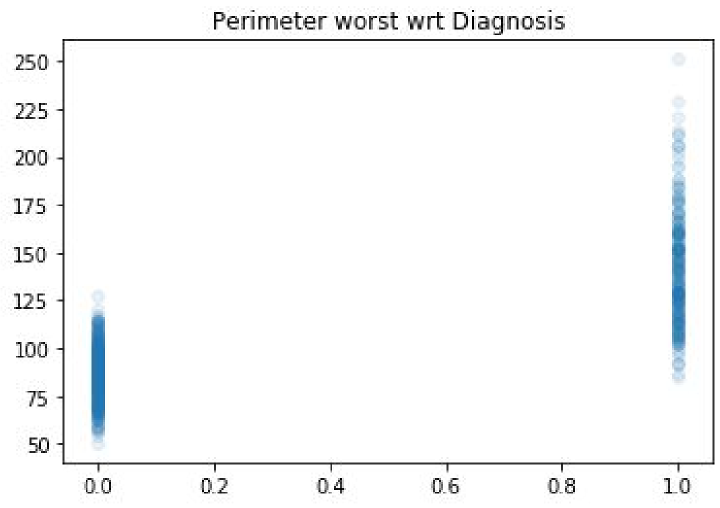


In [22]:
```
plt.scatter(df.diagnosis, df.area_mean, alpha=0.1)
# here the plot has to be transparent so we need to pic low alpha value
plt.title("Area mean wrt Diagnosis")
```

Out[22]:
```
Text(0.5, 1.0, 'Area mean wrt Diagnosis')
```



```
In [23]: plt.scatter(df.diagnosis, df.perimeter_worst, alpha=0.1)
         # here the plot has to be transparent so we need to pic low alpha value
         plt.title("Perimeter worst wrt Diagnosis")

Out[23]: Text(0.5, 1.0, 'Perimeter worst wrt Diagnosis')
```



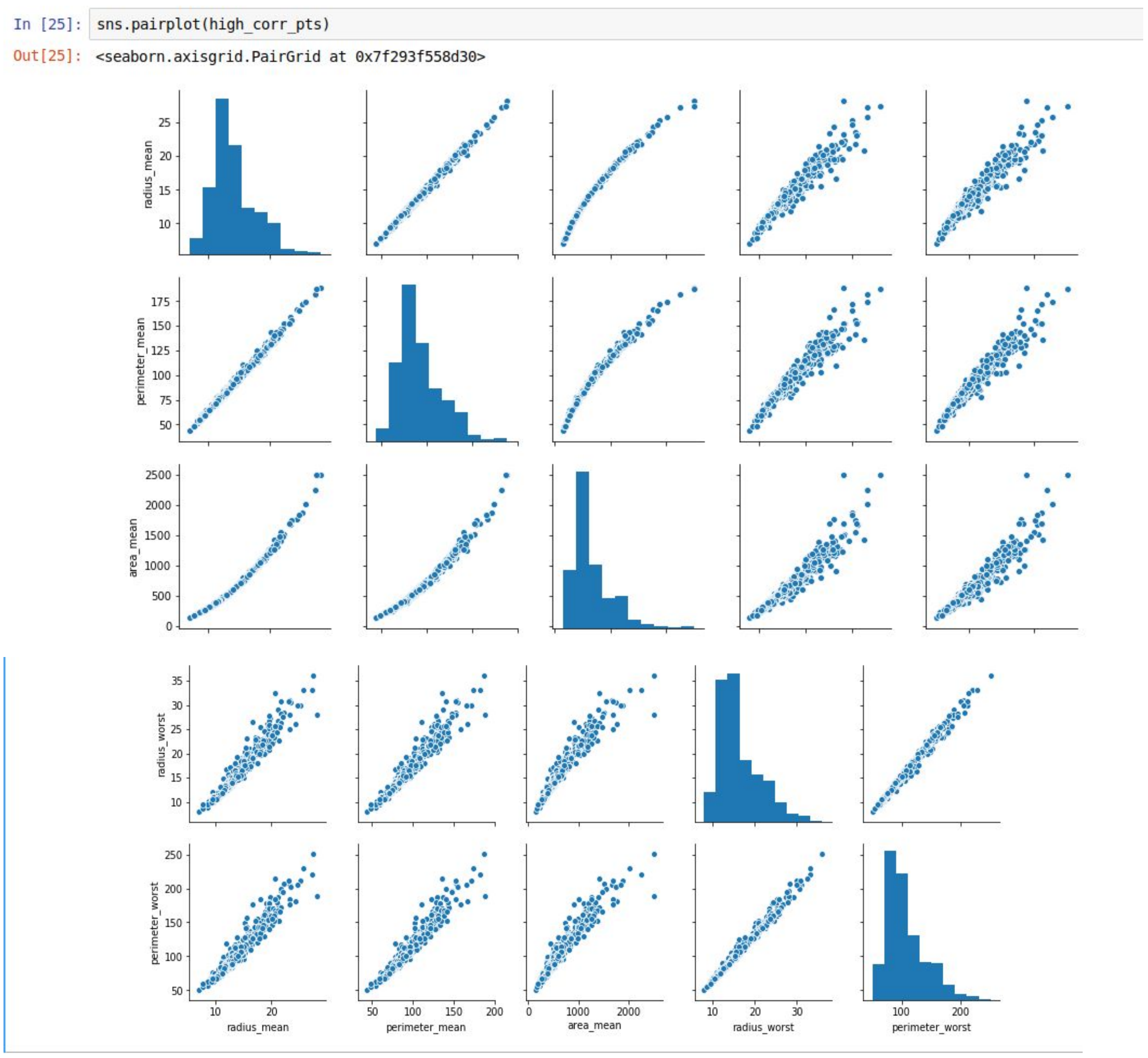
Splitting of data into test and train sets

We now split the data into a test set and a training set.

```
In [24]: # Splitting data with 40% test data and rest 60% is training data
         X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.4)
```

The test set size is chosen to be 40% of the whole data.

We then make a pairplot between all the high correlation features:



```
In [25]: sns.pairplot(high_corr_pts)
Out[25]: <seaborn.axisgrid.PairGrid at 0x7f293f558d30>
```

Training the model and predicting the target variable:

We are using a gradient boosting framework provided by XGBoost to train the model. XGBoost is short for eXtreme gradient boosting. It is a library designed and optimized for boosted tree algorithms.

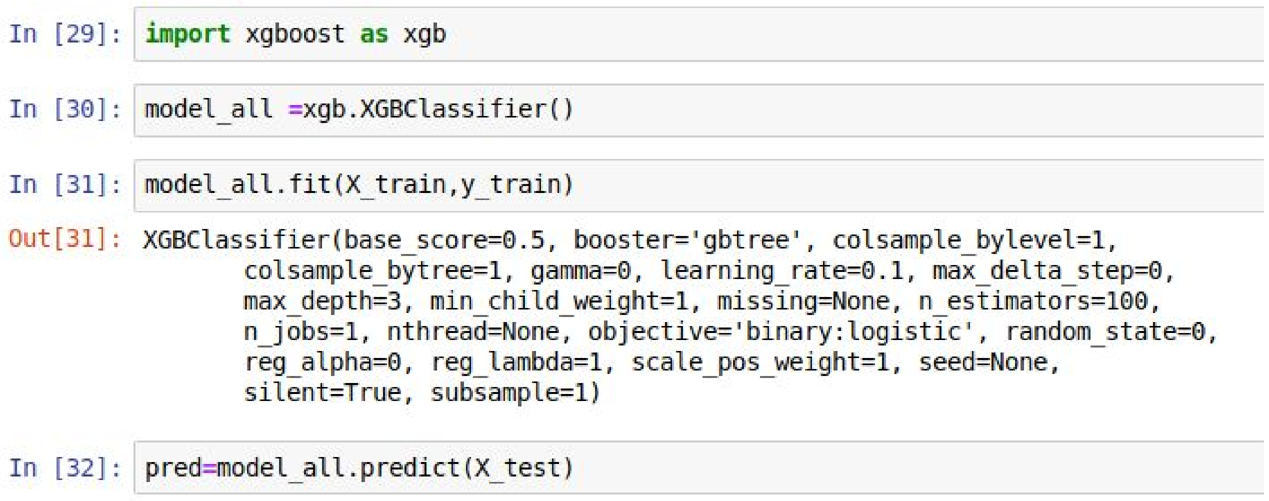
It's main goal is to push the extreme of the computation limits of machines to provide a ***scalable***, ***portable*** and ***accurate*** for large scale tree boosting.

Features:

- Speed: it can automatically do parallel computation on Windows and Linux, with OpenMP. It is generally over 10 times faster than the classical gbm.
- Input Type: it takes several types of input data:
- Dense Matrix: R’s dense matrix, i.e. matrix ;
- Sparse Matrix: R’s sparse matrix, i.e. Matrix::dgCMatrix ;
- Data File: local data files ;
- xgb.DMatrix: its own class (recommended).
- Sparsity: it accepts sparse input for both tree booster and linear booster, and is optimized for sparse input ;
- Customization: it supports customized objective functions and evaluation functions.

Gradient boosting involves three elements:

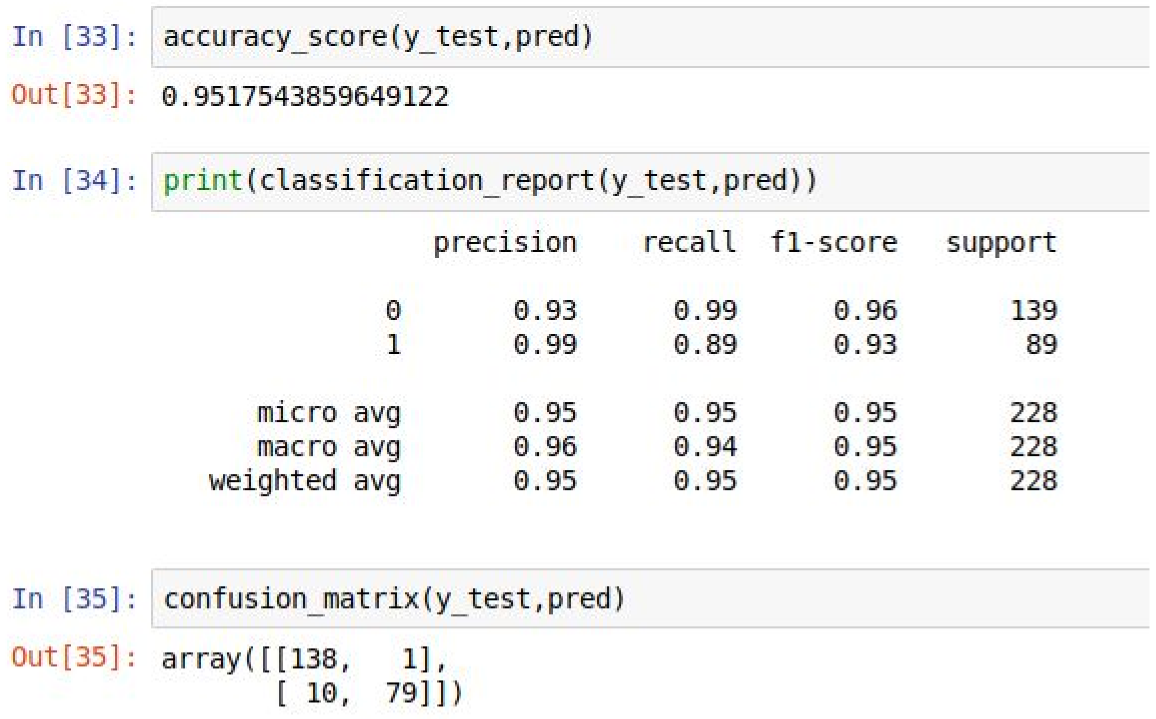
1. A loss function to be optimized.
2. A weak learner to make predictions.
3. An additive model to add weak learners to minimize the loss function.



```
In [29]: import xgboost as xgb

In [30]: model_all =xgb.XGBClassifier()

In [31]: model_all.fit(X_train,y_train)

Out[31]: XGBClassifier(base_score=0.5, booster='gbtree', colsample_bylevel=1,
                colsample_bytree=1, gamma=0, learning_rate=0.1, max_delta_step=0,
                max_depth=3, min_child_weight=1, missing=None, n_estimators=100,
                n_jobs=1, nthread=None, objective='binary:logistic', random_state=0,
                reg_alpha=0, reg_lambda=1, scale_pos_weight=1, seed=None,
                silent=True, subsample=1)

In [32]: pred=model_all.predict(X_test)
```

Analyzing the predictions:

We find the accuracy and confusion matrix of the predictions:



```
In [33]: accuracy_score(y_test,pred)

Out[33]: 0.9517543859649122

In [34]: print(classification_report(y_test,pred))

                  precision    recall  f1-score   support

               0       0.93      0.99      0.96       139
               1       0.99      0.89      0.93        89

       micro avg       0.95      0.95      0.95       228
       macro avg       0.96      0.94      0.95       228
    weighted avg       0.95      0.95      0.95       228

In [35]: confusion_matrix(y_test,pred)

Out[35]: array([[138,   1],
                [ 10,  79]])
```

We get an accuracy of 0.9517.

Finding the optimal features:

Now we find the optimal number of features and what those features are. We do this by using RFECV.

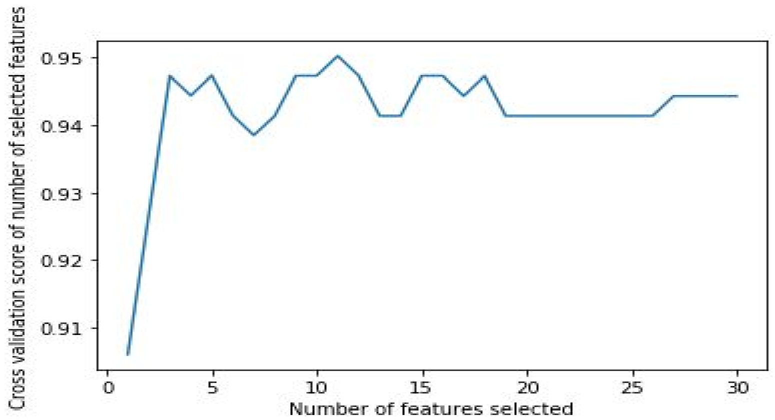
```
In [37]: from sklearn.feature_selection import RFECV

         # The "accuracy" scoring is proportional to the number of correct classifications
         clf = xgb.XGBClassifier()
         rfecv = RFECV(estimator=clf, step=1, cv=4,scoring='accuracy')   #5-fold cross-validation
         rfecv = rfecv.fit(X_train, y_train)

         print('Optimal number of features :', rfecv.n_features_)
         print('Best features :', X_train.columns[rfecv.support_])
```

```
Optimal number of features : 11
Best features : Index(['concave points_mean', 'area_se', 'compactness_se',
       'fractal_dimension_se', 'radius_worst', 'texture_worst',
       'perimeter_worst', 'area_worst', 'concavity_worst',
       'concave points_worst', 'symmetry_worst'],
      dtype='object')
```

<u>11 optimal features</u> are selected.

We now plot the number of features VS. cross-validation scores to see how it affects the predication:

```
In [38]: # Plot number of features VS. cross-validation scores
         import matplotlib.pyplot as plt
         plt.figure()
         plt.xlabel("Number of features selected")
         plt.ylabel("Cross validation score of number of selected features")
         plt.plot(range(1, len(rfecv.grid_scores_) + 1), rfecv.grid_scores_)
         plt.show()
```



The graph shows how the score varies with varying number of features. The score is highest when the number of features is 11.

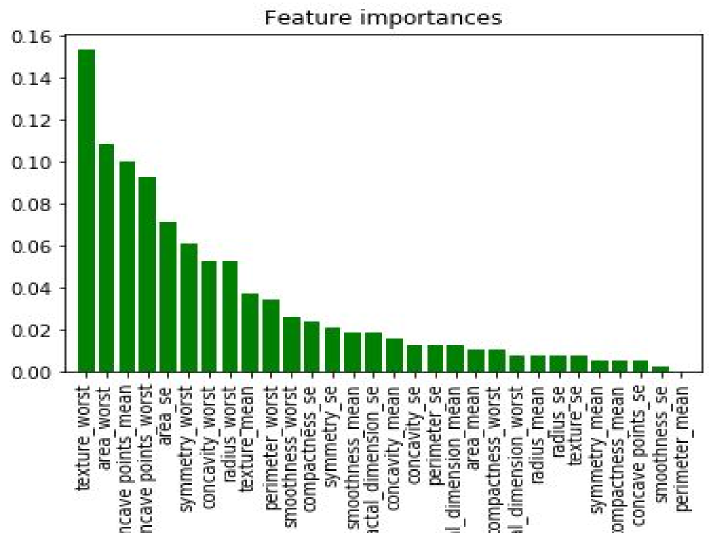
We now rank the features by their importance:

```
In [39]: # Feature ranking with recursive feature elimination and cross-validated selection of the best number of features.
         importances = (model_all.feature_importances_)
         indices = np.argsort(importances)[::-1]
         print("Feature ranking:")
         for f in range(X_train.shape[1]):
             print("%d. feature %d (%f)" % (f + 1, indices[f], importances[indices[f]]))
```

```
Feature ranking:
1. feature 21 (0.153439)
2. feature 23 (0.108466)
3. feature 7 (0.100529)
4. feature 27 (0.092593)
5. feature 13 (0.071429)
6. feature 28 (0.060847)
7. feature 26 (0.052910)
8. feature 20 (0.052910)
9. feature 1 (0.037037)
10. feature 22 (0.034392)
11. feature 24 (0.026455)
12. feature 15 (0.023810)
13. feature 18 (0.021164)
14. feature 4 (0.018519)
15. feature 19 (0.018519)
16. feature 6 (0.015873)
17. feature 16 (0.013228)
18. feature 12 (0.013228)
19. feature 9 (0.013228)
20. feature 3 (0.010582)
21. feature 25 (0.010582)
22. feature 29 (0.007937)
```

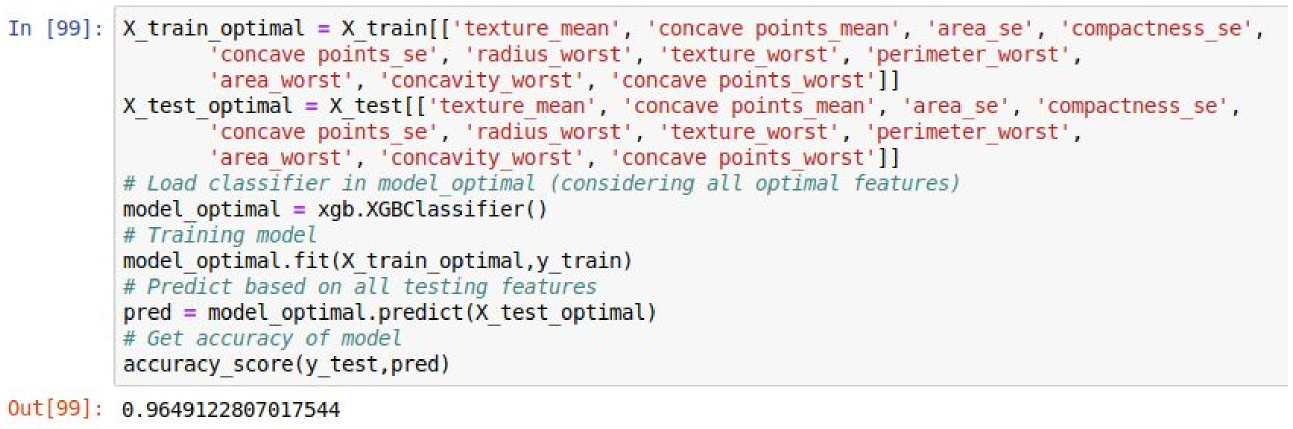
We then plot the importances of the features:

```
In [40]: # plot
         plt.title("Feature importances")

         plt.bar(range(X_train.shape[1]), importances[indices],
                color="g", align="center")

         plt.xticks(range(X_train.shape[1]), X_train.columns[indices],rotation=90)
         plt.xlim([-1, X_train.shape[1]])
         plt.show()
         plt.show()
```



Training and analyzing the model with only the optimal features:

We train the model and predict the target variable using only the selected optimal features (11) and get an **accuracy of 0.9649**



```
In [99]: X_train_optimal = X_train[['texture_mean', 'concave points_mean', 'area_se', 'compactness_se',
                'concave points_se', 'radius_worst', 'texture_worst', 'perimeter_worst',
                'area_worst', 'concavity_worst', 'concave points_worst']]
         X_test_optimal = X_test[['texture_mean', 'concave points_mean', 'area_se', 'compactness_se',
                'concave points_se', 'radius_worst', 'texture_worst', 'perimeter_worst',
                'area_worst', 'concavity_worst', 'concave points_worst']]
         # Load classifier in model_optimal (considering all optimal features)
         model_optimal = xgb.XGBClassifier()
         # Training model
         model_optimal.fit(X_train_optimal,y_train)
         # Predict based on all testing features
         pred = model_optimal.predict(X_test_optimal)
         # Get accuracy of model
         accuracy_score(y_test,pred)

Out[99]: 0.9649122807017544
```

Why we chose this algorithm:

1. A benefit of the gradient boosting framework is that a new boosting algorithm does not have to be derived for each loss function that may want to be used, instead, it is a generic enough framework that any differentiable loss function can be used.
2. Regression trees are used that output real values for splits and whose output can be added together, allowing subsequent models outputs to be added and “correct” the residuals in the predictions. Trees are constructed in a greedy manner, choosing the best split points based on purity scores like Gini or to minimize the loss.
3. Instead of parameters, we have weak learner sub-models or more specifically decision trees.
4. After calculating the loss, to perform the gradient descent procedure, we must add a tree to the model that reduces the loss (i.e. follow the gradient). We do this by parameterizing the tree, then modify the parameters of the tree and move in the right direction by (reducing the residual loss.

5. Xgboost manages only numeric vectors. What to do when you have categorical data? A simple method to convert categorical variable into numeric vector is One Hot Encoding.
6. Xgboost can scale with hundreds of workers (with each worker utilizing multiple processors) smoothly and solve machine learning problems involving Terabytes of real world data.

Other four enhancements to basic gradient boosting:

1. Tree Constraints
2. Shrinkage
3. Random sampling
4. Penalized Learning

Conclusion:

- We started by exploring the data with EDA(*exploratory data analysis)* methods. We analyzed the data types of the features and converted the string data type to integer(using hot encoding).
- We then checked for missing values and duplicates and dealt with them.
- After performing preliminary analysis, we plotted the data to get more insights.
- Further we dropped certain features that, upon analysis, we found to be irrelevant to the target variable.
- We found the correlation of all the features with the target variable as well as among each other. We then found the 11 most optimal feature.

As we can observe, we have *reduced the number of features from 30 to 11*, and have also *increased the accuracy of our model from 95.17% To 96.49%* during the process.