Breast Cancer Prediction Milestone: Data Collection, Data Visualization, Data Exploration and Data Processing

Group 25

Student 1: Siva Vasantha Harika Mangu
Student 2: Raaga Sindhu Mangalagiri

mangu.s@northeastern.edu
mangalagiri.r@northeastern.edu

Percentage of Effort Contributed by Student 1: 50%

Percentage of Effort Contributed by Student 2: 50%

Signature of Student 1: Siva Vasantha Harika Mangu

Signature of Student 2: Raaga Sindhu Mangalagiri

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Project Proposal

IE 7275: Data Mining in Engineering

Problem Statement:

About 1 in 8 women will develop invasive breast cancer over the course of their lifetime. And every year around 40,000 women in United States alone, are dying from breast cancer. It starts when cells in breast begin to grow out of control. These cells usually form tumors that can be seen via X-ray often felt as lumps in the breast area. And one of the shocking revelations can be said that it is found in women who don't show any symptoms. It is mostly occurring disease among women and in specific elderly age groups. They cannot prevent or control their risk of cancer, and it cannot even be recognized at early stage due to lack of symptoms and abnormalities they face.

Hence, by building a machine learning model, we can be able to predict the risks of breast cancer among women at early age, based on different attributes acting as a contributing factor to the disease.

Problem Definition:

Given a set of patient data including demographic information, medical history, and medical imaging results, the goal is to develop a model or system that can accurately predict the likelihood of a patient developing breast cancer. The challenge is to classify these tumors into malignant(cancerous) or benign(non-cancerous). The model should be able to handle missing or incomplete data and be able to generalize well to new unseen cases. Additionally, the model should be interpretable and provide insights on the most important features/variables that contribute to the prediction. The goal is to improve the early detection and prevention of breast cancer by identifying high-risk individuals and providing them with the necessary interventions, resulting in better outcomes for patients.

Data Sources:

Kaggle

[Breast Cancer Dataset | Kaggle]

Data Description:

Breast cancer data set consists of 32 attributes and 570 records in total, in which 30 attributes are contributing as predictors and the attribute diagnosis is the response variable which predicts whether the patient is Benign or malignant. The Unique ID is the primary key which is the not the predictor either or a response variable. The predictors such as radius_mean,texture_mean,perimeter_mean,area_mean,smoothness_mean,compactness_mean,concavity_mean,concavepoints_mean,symmetry_mean,fractal_dimension_mean,radius_se,texture_se,perimeter_se,area_se,smoothness_se,compactness_worst,concavity_worst,concavepoints_worst,symmetry_worst,fractal_dimension_worst.Some of the other risk factors which can be considered as predictors are age, family history, certain genetic mutations, and certain lifestyle factors such as alcohol consumption and lack of physical activity. Symptoms of breast cancer include a lump or thickening in the breast tissue, changes in the size or shape of the breast, and changes to the skin on the breast such as redness or dimpling.

Insights

List of Predictors:

The dataset we are working on contains various measurements related to breast cancer diagnosis. Here is an overview of the attributes(columns) we have in the dataset:

1. radius_mean: mean of distances from the center to points on the perimeter of the tumor.
2. texture_mean: standard deviation of gray-scale values
3. perimeter_mean: perimeter of the tumor
4. area_mean: area of the tumor
5. smoothness_mean: local variation in radius lengths
6. compactness_mean: perimeter^2/area – 1.0
7. concave points_mean: number of concave portions of the contour
8. symmetry_mean: symmetry of the tumor
9. fractal_dimension_mean: “coastline approximation” - 1
10. radius_se: standard error of the mean of distances from the center to points on the perimeter

11. texture_se: standard error of gray-scale values
12. perimeter_se: standard error of the perimeter
13. area_se: standard error of the area
14. smoothness_se: standard error of local variation in radius lengths
15. compactness_se: standard error of perimeter^2/area – 1.0
16. concavity_se: standard error of number of concave portions of the contour
17. concave points_se: standard error of number of concave portions of the contour
18. symmetry_se: standard error of symmetry of the tumor
19. fractal_dimension_se: standard error of "coastline approximation" – 1
20. radius_worst: "worst" or largest mean value from the mean of distances from the center to points on the perimeter
21. texture_worst: "worst" or largest standard deviation of gray-scale values
22. perimeter_worst: "worst" or largest perimeter of the tumor
23. area_worst: "worst" or largest area of the tumor
24. smoothness_worst: "worst" or largest local variation in radius lengths
25. compactness_worst: "worst" or largest perimeter^2/area – 1.0
26. concavity_worst: "worst" or largest number of concave portions of the contour
27. concave_points_worst: "worst" or largest number of concave portions of the contour
28. symmetry_worst: "worst" or largest symmetry of the tumor
29. fractal_dimension_worst: "worst" or largest "coastline approximation" – 1

Each attribute provides different information about the tumor, such as its size, texture, shape, and smoothness. Understanding what each attribute represents helps make decision about feature selection and model performance evaluation.

Exploratory Data Analysis

To determine which attributes are highly correlated and could be useful in predicting breast cancer, we can calculate the correlation matrix of the dataset. The correlation matrix shows the correlation coefficient between each pair of attributes and find potential attributes for the better prediction, where a values of 1 indicates a positive correlation, 0 indicates no correlation, and -1 indicates a perfect negative correlation. The values greater than 0.7 are considered as highly correlated. Next,

we found the correlation of these highly correlated variables with the response variable(diagnosis) to determine the targeted variables responsible for our prediction.

Dividing the dataset for better understanding and visualization:

The first 10 attributes (radius mean, texture mean, perimeter mean, area mean, smoothness mean, compactness mean, concavity mean, concave points mean, symmetry mean, and fractal dimension) are measures of the tumor's size, shape, and texture based on a digital image of a biopsy. The next 10 attributes (radius se, texture se, perimeter se, area se, smoothness se, compactness se, concavity se, concave points se, symmetry se, and fractal dimension se) are the standard errors of these same measurements, which indicate the variability or uncertainty of the estimates. The last 10 attributes (radius worst, texture worst, area worst, smoothness worst, concavity worst, concave points worst, symmetry worst, and fractal dimension worst) are the "worst" or largest values of these measurements observed in the biopsy, which indicate the aggressiveness or malignancy of the tumor. These features can be used to build a machine learning model for breast cancer prediction diagnosis. Therefore, we are concentrating on finding the most correlated attributes on 3 different sets i.e., first 10, second 10 and the last, inorder to build a machine learning model for breast can cer prediction or diagnosis.

We are finding Correlation matrix in order to find the relation between individual attributes and hence able to scale down with attributes which have high correlation, thus helping us to understand what attributes we must focus on to predict breast cancer. We have used inbuilt corr() function to find the correlation matrix of first 10 attributes. Below is the correlation matrix We have mapped the correlation values in a heatmap using seaborn in order to recognize highly correlated attributes. And then, have segregated values which are above 0.7 as highly correlated

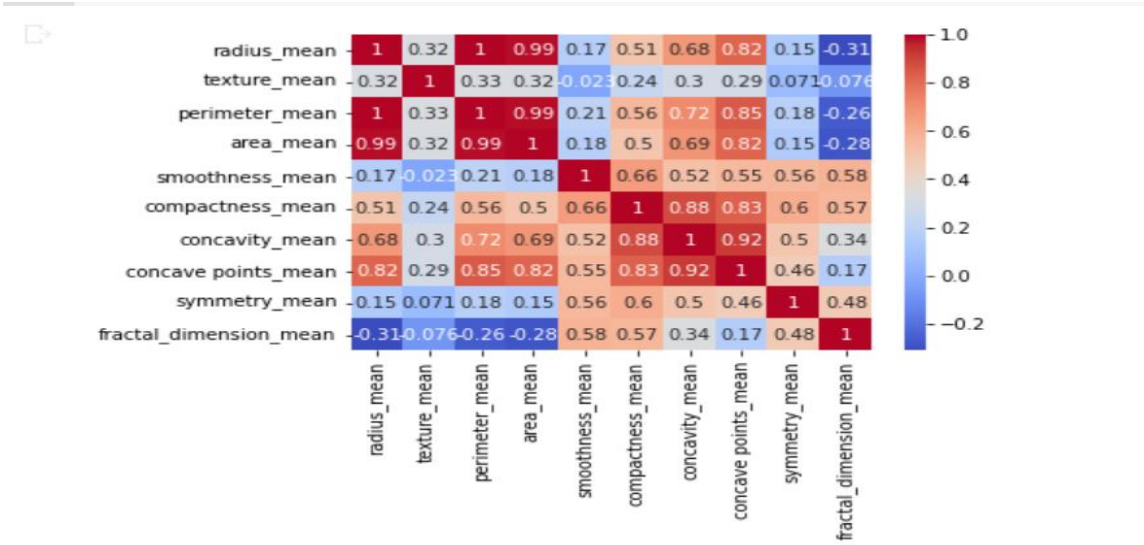


Figure1: Heatmap of correlation values of first 10 attributes

The above steps such as finding the correlation matrix and finding the attributes which are highly correlated has been repeated and plotted a heatmap and segregated the values which are above 0.7 as highly correlated values.

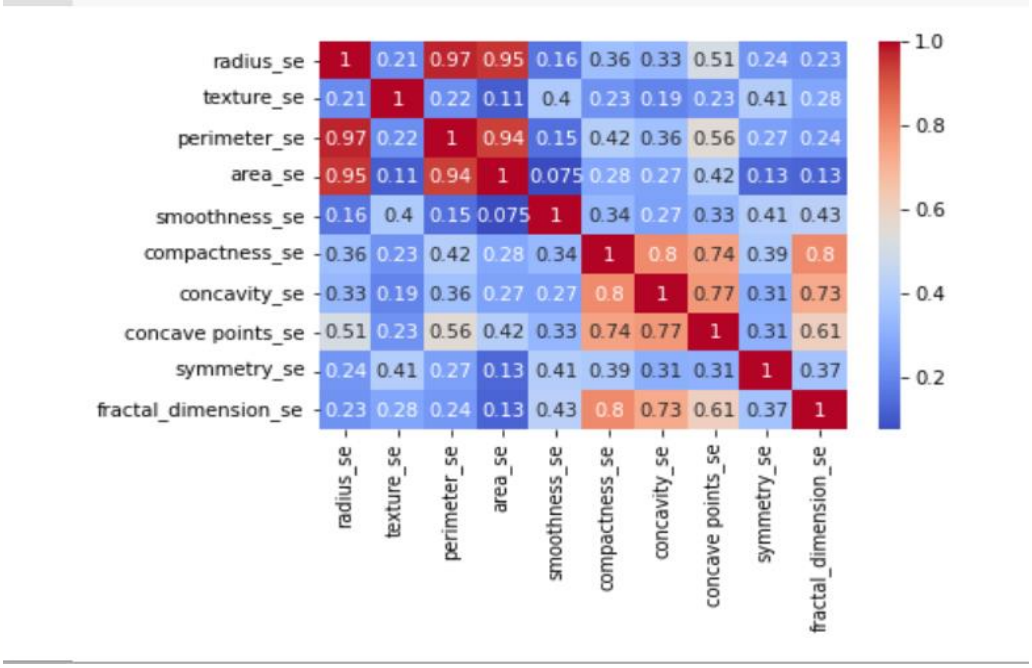


Figure 2: Heatmap of Correlation matrix of next 10 attributes

Again, the above steps such as finding the correlation matrix and finding the attributes which are highly correlated has been repeated and plotted a heatmap and segregated the values which are above 0.7 as highly correlated values.

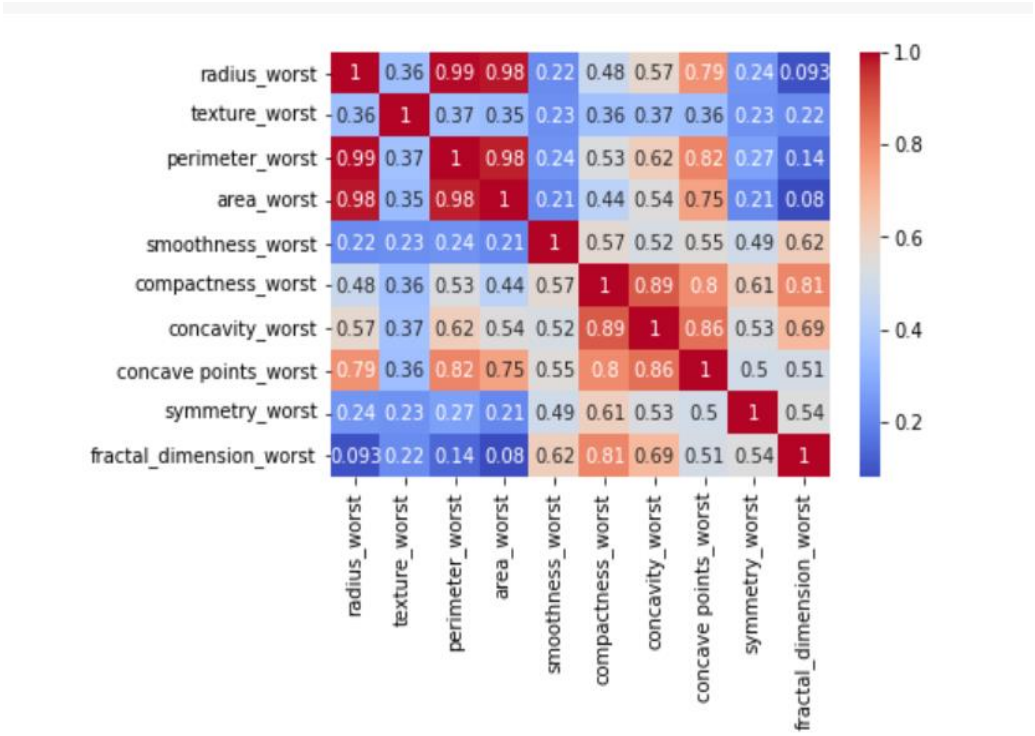


Figure 3: Heatmap of Correlation values of last 10 attributes

After comparing all the values, the columns which have highest correlation values among first 10 attributes are “perimeter_mean” and “concave points_mean”. Hence, we have plotted a pair plot of these columns to check the malignant and benign data points, in order to crosscheck the correlation concept.

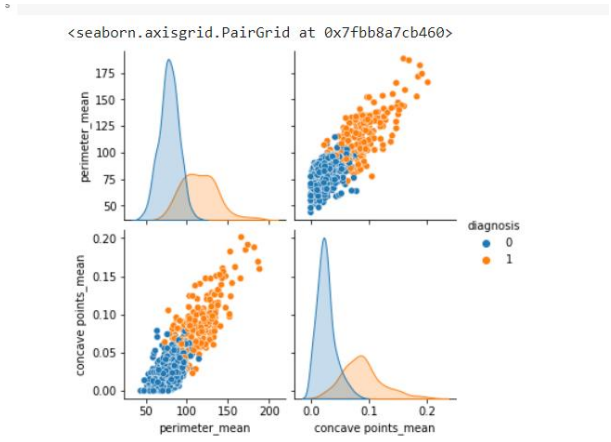


Figure 4: Pair plot of highly correlated values from first 10 attributes

After comparing all the values, the columns which have highest correlation values among next 10 attributes are “perimeter_se”, “radius_se”, “concave points_se” and “concavity_se”. Hence, we have plotted a pair plot of these columns to check the malignant and benign data points, in order to crosscheck the correlation concept.

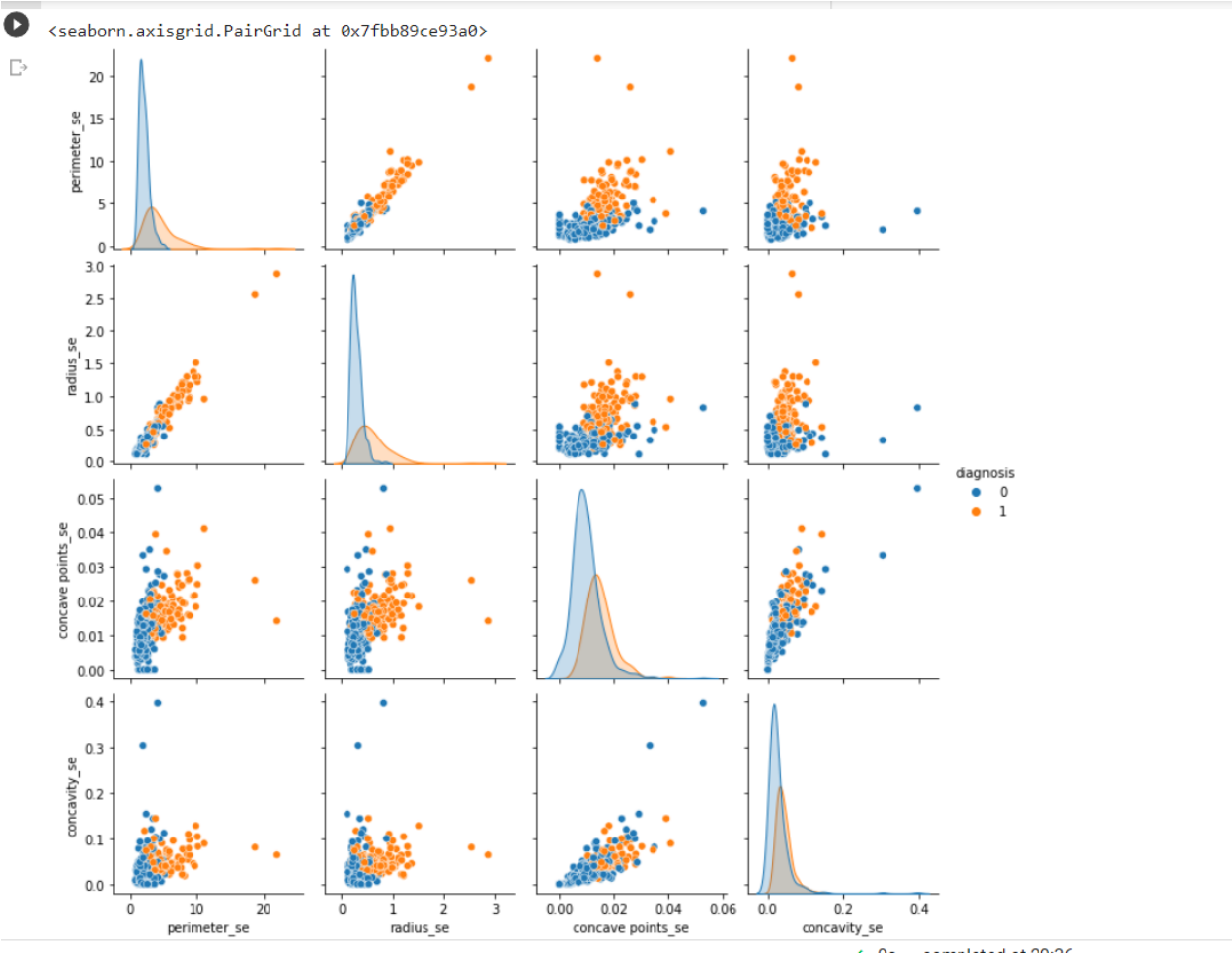


Figure 5: Pair plot of highly correlated values from next 10 attributes

After comparing all the values, the columns which have highest correlation values among last 10 attributes are “perimeter_worst”, “radius_worst”,” concavity_worst” and “concave points_worst”. Hence, we have plotted a pair plot of these columns to check the malignant and benign data points, in order to crosscheck the correlation concept.

Figure 6: Pair plot of highly correlated values of last 10 attributes

Data Preprocessing:

Plotting box plots for the most important attributes contributing towards building a machine learning model to predict Breast cancer prediction.

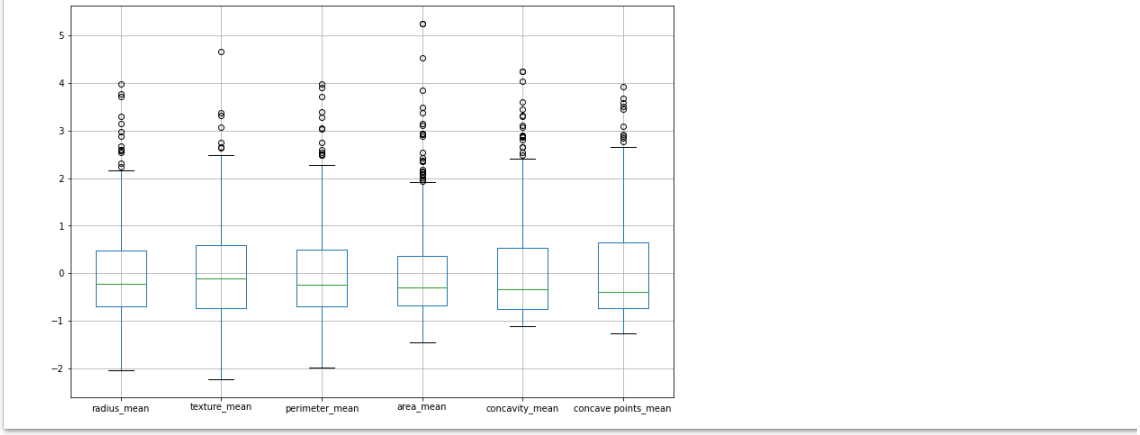
df.describe() – This function helps us understand the arithmetical attributions of the attributes present in the dataset.

```
df.describe()
```

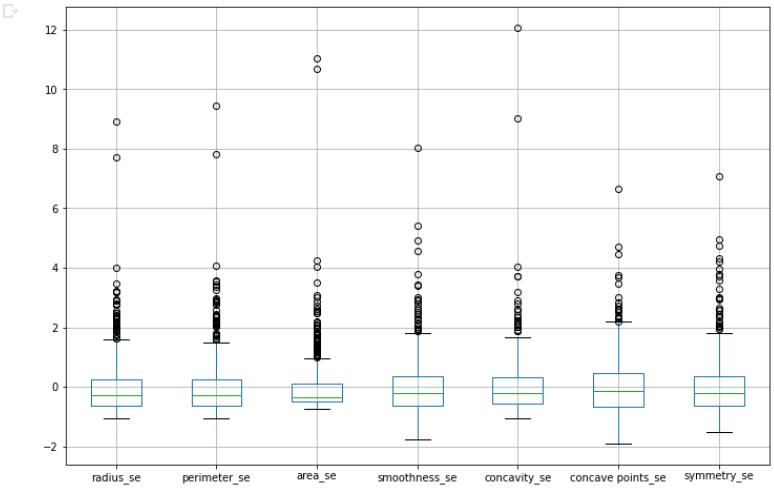
	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	...	radius_worst	texture_worst	perimeter_worst	area_worst	smoothness_worst
count	5.690000e+02	569.000000	5.690000e+02	5.690000e+02	5.690000e+02	5.690000e+02	5.690000e+02	5.690000e+02	5.690000e+02	5.690000e+02	...	5.690000e+02	5.690000e+02	5.690000e+02	569.000000	569.000000
mean	3.037183e+07	0.372583	6.243785e-18	1.248757e-17	1.248757e-17	6.243785e-18	2.497514e-17	1.248757e-17	2.497514e-17	-1.248757e-17	...	-1.248757e-17	1.248757e-17	1.248757e-17	880.583128	0.132369
std	1.250206e+08	0.483918	1.000880e+00	1.000880e+00	1.000880e+00	1.000880e+00	1.000880e+00	1.000880e+00	1.000880e+00	1.000880e+00	...	1.000880e+00	1.000880e+00	1.000880e+00	569.356993	0.022832
min	8.670000e+03	0.000000	-2.029648e+00	-2.229249e+00	-1.984504e+00	-1.454443e+00	-3.112085e+00	-1.610136e+00	-1.114873e+00	-1.261820e+00	...	-1.726901e+00	-2.223994e+00	-1.693361e+00	185.200000	0.071170
25%	8.692180e+05	0.000000	-6.893853e-01	-7.259631e-01	-6.919555e-01	-6.671955e-01	-7.109628e-01	-7.470860e-01	-7.437479e-01	-7.379438e-01	...	-6.749213e-01	-7.486293e-01	-6.895783e-01	515.300000	0.116600
50%	9.060240e+05	0.000000	-2.150816e-01	-1.046362e-01	-2.359800e-01	-2.951869e-01	-3.489108e-02	-2.219405e-01	-3.422399e-01	-3.977212e-01	...	-2.690395e-01	-4.351564e-02	-2.859802e-01	686.500000	0.131300
75%	8.813129e+06	1.000000	4.693926e-01	5.841756e-01	4.996769e-01	3.635073e-01	6.361990e-01	4.938569e-01	5.260619e-01	6.469351e-01	...	5.220158e-01	6.583411e-01	5.402790e-01	1084.000000	0.146000
max	9.113205e+08	1.000000	3.971288e+00	4.651889e+00	3.976130e+00	5.250529e+00	4.770911e+00	4.568425e+00	4.243589e+00	3.927930e+00	...	4.094189e+00	3.885905e+00	4.287337e+00	4254.000000	0.222600

8 rows × 32 columns

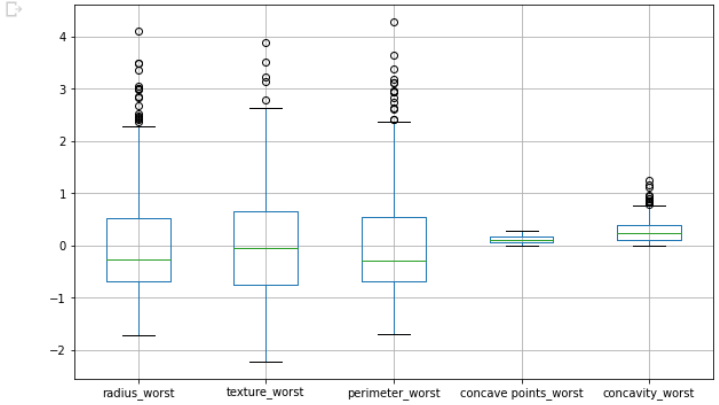
```
boxplot1=df.boxplot(column=['radius_mean','texture_mean','perimeter_mean','area_mean','concavity_mean','concave points_mean'],figsize=(12,8))
```




```
[81] boxplot2=df.boxplot(column=['radius_se','perimeter_se','area_se','smoothness_se','concavity_se','concave points_se','symmetry_se'],figsize=(12,8))
```



```
[80] boxplot3=df.boxplot(column=['radius_worst','texture_worst','perimeter_worst','concave points_worst','concavity_worst'],figsize=(10,6))
```



Data Cleaning

The breast cancer dataset consists of 30 predictors and one response variable and when we uploaded our dataset, we found no null values. So, we did not drop or impute any value to the attributes. Data cleaning is not necessary because our dataset is consistent, and no missing values and we are not standardizing the data and we checked the outliers.

```
breast_cancer.isnull().sum()

id                         0
diagnosis                  0
radius_mean                0
texture_mean               0
perimeter_mean             0
area_mean                  0
smoothness_mean            0
compactness_mean           0
concavity_mean             0
concave points_mean        0
symmetry_mean              0
fractal_dimension_mean     0
radius_se                  0
texture_se                 0
perimeter_se               0
area_se                    0
smoothness_se              0
compactness_se             0
concavity_se               0
concave points_se          0
symmetry_se                0
fractal_dimension_se       0
radius_worst               0
texture_worst              0
perimeter_worst            0
area_worst                 0
smoothness_worst           0
compactness_worst          0
concavity_worst            0
concave points_worst       0
symmetry_worst             0
```

Dimension Reduction:

Dimensionality reduction for a dataset depends on various factors such as the number of variables, the level of correlation among variables, the nature of the problem, the computational resources available, and the desired level of accuracy.

In the case of Breast cancer prediction dataset with 30 attributes, performing dimensionality reduction may not be necessary as the number of attributes is not very high. However, if some of the attributes are highly correlated, and there is a concern about overfitting, then performing dimensionality reduction can be beneficial.
Hence, we are not performing any dimensional reduction steps on the dataset, as all the attributes contribute to prediction of breast cancer.

Conclusion:

From the above observations we can find all the attributes that we selected for the feature selection are highly correlated and Perimeter mean, concave points mean, radius se, perimeter se, concave points se, concavity se, perimeter worst, radius worst, concave points worst, concavity worst are the attributes which are contributing more towards our prediction breast cancer. We can observe most of the data points to be malignant. We can conclude that the above selected attributes will play a major role for a better machine learning model.
Therefore, we conclude any predictive model developed using the dataset should consider role of these attributes and their relations.