

# Breast Cancer Analysis

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## Reading and Displaying the dataset:

```
> #Reading the dataset
> breast_cancer <- read.csv("C:\\Users\\APEKSHA\\Downloads\\wisc_bc_data.csv")
> #Displaying the dataset using head function
> head(breast_cancer)
```

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean
1	87139402	B	12.32	12.39	78.85	464.1	0.10280
2	8910251	B	10.60	18.95	69.28	346.4	0.09688
3	905520	B	11.04	16.83	70.92	373.2	0.10770
4	868871	B	11.28	13.39	73.00	384.8	0.11640
5	9012568	B	15.19	13.21	97.65	711.8	0.07963
6	906539	B	11.57	19.04	74.20	409.7	0.08546

```
compactness_mean concavity_mean points_mean symmetry_mean dimension_mean radius_se texture_se
1 0.06981 0.03987 0.03700 0.1959 0.05955 0.2360 0.6656
2 0.11470 0.06387 0.02642 0.1922 0.06491 0.4505 1.1970
3 0.07804 0.03046 0.02480 0.1714 0.06340 0.1967 1.3870
4 0.11360 0.04635 0.04796 0.1771 0.06072 0.3384 1.3430
5 0.06934 0.03393 0.02657 0.1721 0.05544 0.1783 0.4125
6 0.07722 0.05485 0.01428 0.2031 0.06267 0.2864 1.4400
```

	perimeter_se	area_se	smoothness_se	compactness_se	concavity_se	points_se	symmetry_se
1	1.670	17.43	0.008045	0.011800	0.01683	0.012410	0.01924
2	3.430	27.10	0.007470	0.035810	0.03354	0.013650	0.03504
3	1.342	13.54	0.005158	0.009355	0.01056	0.007483	0.01718
4	1.851	26.33	0.011270	0.034980	0.02187	0.019650	0.01580
5	1.338	17.72	0.005012	0.014850	0.01551	0.009155	0.01647
6	2.206	20.30	0.007278	0.020470	0.04447	0.008799	0.01868

```
dimension_worst radius_worst texture_worst perimeter_worst area_worst smoothness_worst
1 0.002248 13.50 15.64 86.97 549.1 0.1385
2 0.003318 11.88 22.94 78.28 424.8 0.1213
3 0.002198 12.41 26.44 79.93 471.4 0.1369
4 0.003442 11.92 15.77 76.53 434.0 0.1367
5 0.001767 16.20 15.73 104.50 819.1 0.1126
6 0.003339 13.07 26.98 86.43 520.5 0.1249
```

	compactness_worst	concavity_worst	points_worst	symmetry_worst	dimension_worst
1	0.1266	0.12420	0.09391	0.2827	0.06771
2	0.2515	0.19160	0.07926	0.2940	0.07587
3	0.1482	0.10670	0.07431	0.2998	0.07881
4	0.1822	0.08669	0.08611	0.2102	0.06784
5	0.1737	0.13620	0.08178	0.2487	0.06766
6	0.1937	0.25600	0.06664	0.3035	0.08284

```
> |
```

## Generate Frequency Table:

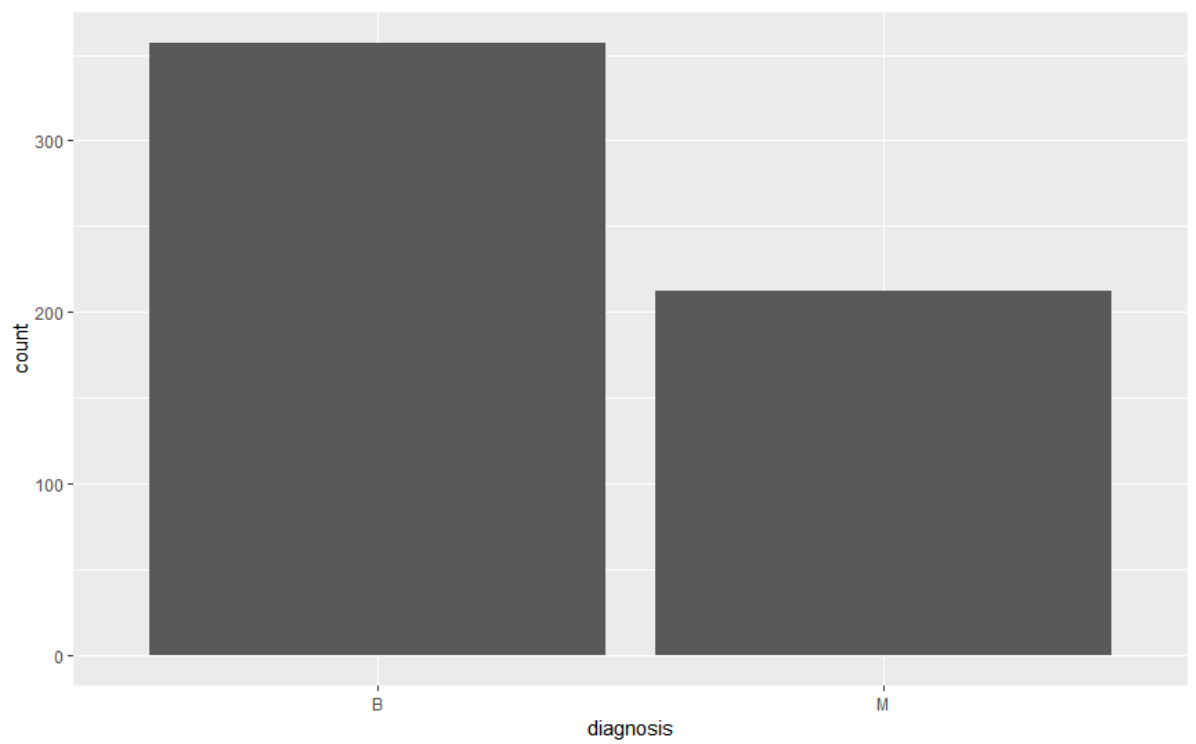
- This shows the frequency of two type of diagnosis categories:
  1. Benign(B) - 357
  2. Malignant(M) – 212

```
> diagnosis.table <- table(breast_cancer$diagnosis)
> diagnosis.table
```

```
  B    M
357 212
```

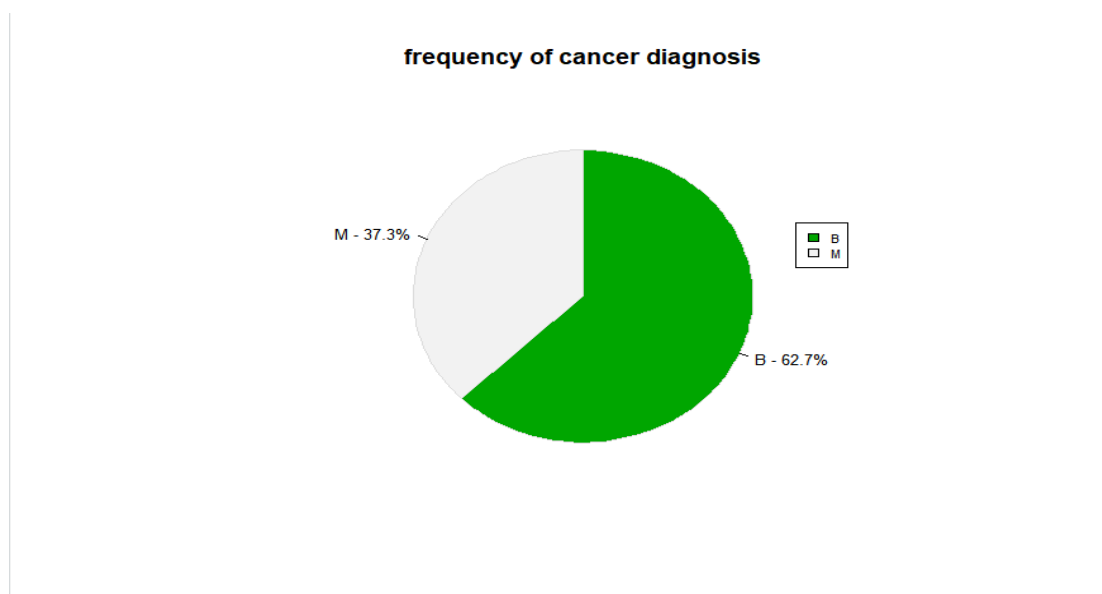
### Bar plot:

- The above frequency of benign and malignant is shown using bar plot.
- It is seen that the patients are more diagnosed as benign compared to malignant.



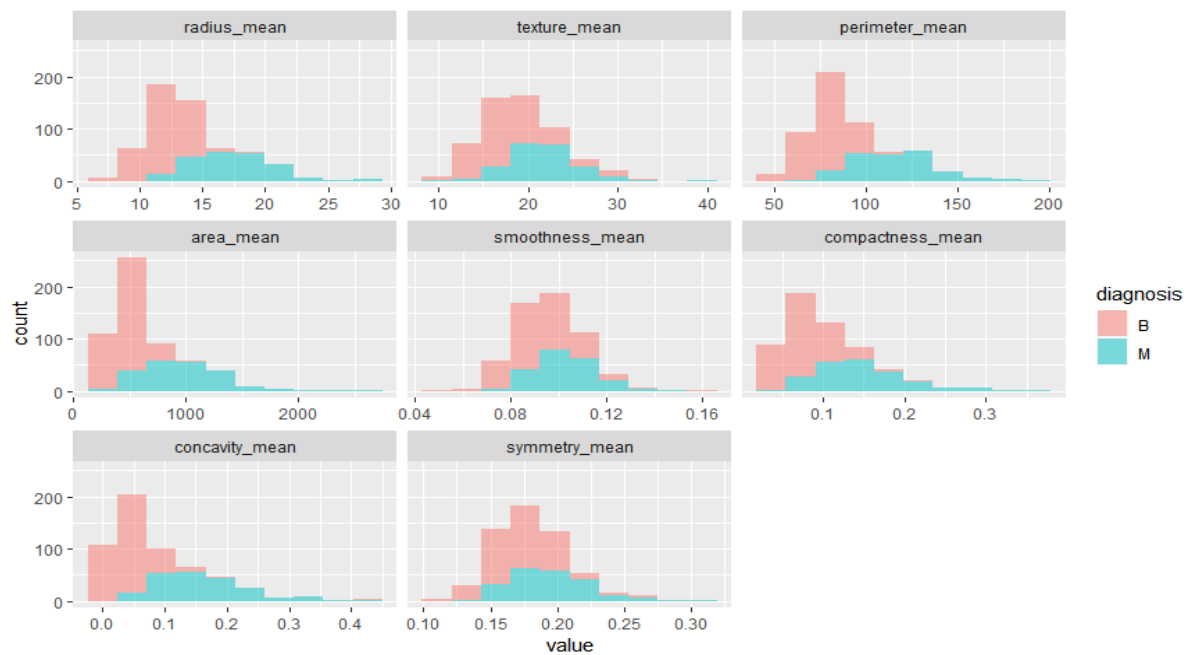
### Pie Chart:

- Pie Chart gives us the frequency of the two categories on the basis of percentage.  
Benign - 62.7%  
Malignant – 37.3%



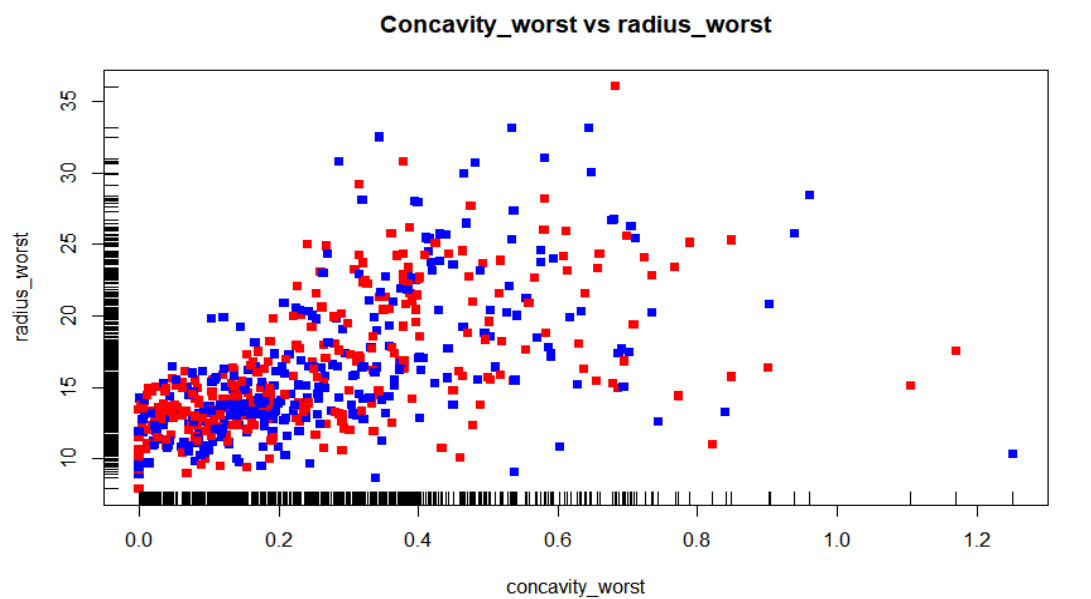
## Histogram:

- Using mean values of the dataset we plot histogram for the given data.
- In this plot, the histogram of two categories(B & M) is generated in one graph for better comparison and for visualization.



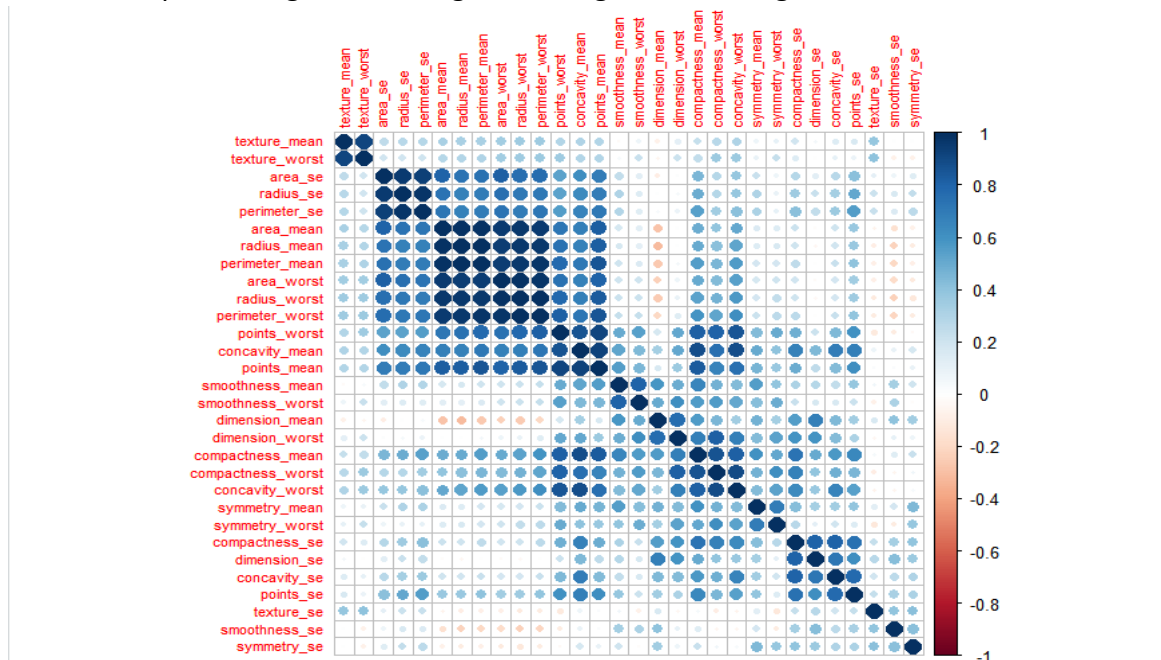
## Scatterplot:

- The fig. shows the relation between two variables ie. concavity\_worst vs radius\_worst.
- This represents that as concavity and radius increases, the patient can be more prone towards breast cancer.



## Correlation Matrix:

- Correlation Matrix establishes a relationship or connection between two or more measures statistically speaking tells you interdependence of variable quantities.
- The color key on right side gives you the values of the correlation.
- The dark blue color represents number one strong positive correlation whereas dark red representing number negative one gives weak negative correlation.



## Scatterplot Matrix:

- Scatterplot Matrix is a table of scatter plots. It is used when we have to visualize several plots together.
- The names in the row represent Y-axis and the names in the columns represent X-axis.

