

## **Project Report -1 Adult Census Data**

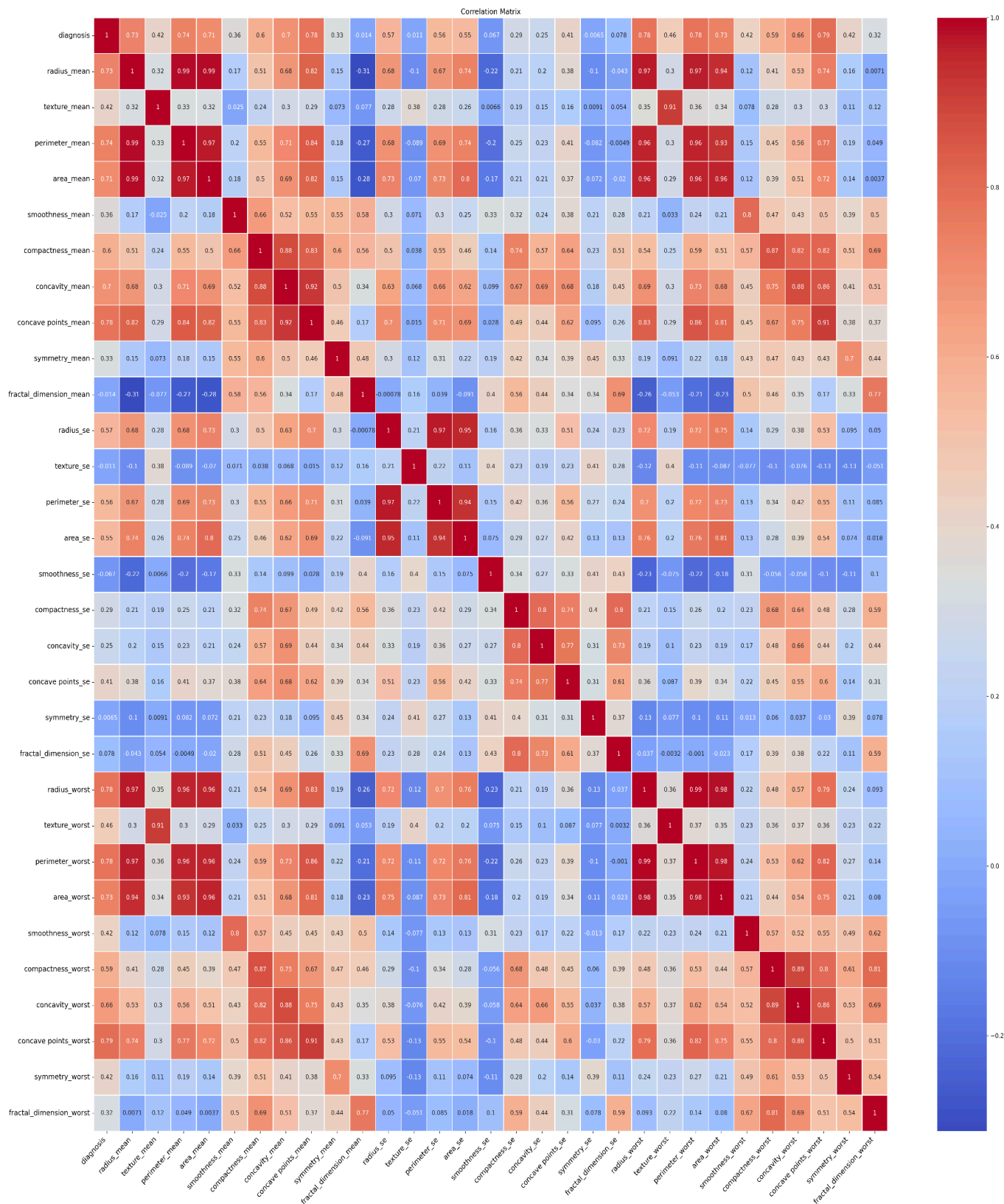
**1. Provide brief details about the nature of your dataset. What is it about? What type of data are we encountering? How many entries and variables does the dataset comprise?**

1. The WDBC dataset represent the characteristics of the cell nuclei present in the image of breast tissue . The end goal is to find whether it is benign or malignant
2. We are encountering with 31 numerical features like size , shape and texture of the cell , smoothness and 1 categorical features with B or M .
3. The dataset contains 569 entries and 32 columns .

**2. Provide the main statistics about the dataset entries (mean, std, number of missing values, etc.)**

data.describe().T									
	count	mean	std	min	25%	50%	75%	max	
diagnosis	569.0	0.372583	0.483918	0.000000	0.000000	0.000000	1.000000	1.00000	
radius_mean	569.0	14.127292	3.524049	6.981000	11.700000	13.370000	15.780000	28.11000	
texture_mean	569.0	19.289649	4.301036	9.710000	16.170000	18.840000	21.800000	39.28000	
perimeter_mean	569.0	91.845255	24.091002	43.790000	75.210000	86.180000	103.800000	188.50000	
area_mean	569.0	654.889104	351.914129	143.500000	420.300000	551.100000	782.700000	2501.00000	
smoothness_mean	569.0	0.096404	0.014038	0.052630	0.086410	0.095920	0.105300	0.16340	
compactness_mean	569.0	0.104341	0.052813	0.019380	0.064920	0.092630	0.130400	0.34540	
concavity_mean	569.0	0.088799	0.079720	0.000000	0.029560	0.061540	0.130700	0.42680	
concave points_mean	569.0	0.048919	0.038803	0.000000	0.020310	0.033500	0.074000	0.20120	
symmetry_mean	569.0	0.181131	0.027428	0.106000	0.161900	0.179200	0.195700	0.30400	
fractal_dimension_mean	569.0	0.062790	0.007065	0.049960	0.057690	0.061540	0.066120	0.09744	
radius_se	569.0	0.405172	0.277313	0.111500	0.232400	0.324200	0.478900	2.87300	
texture_se	569.0	1.215555	0.551626	0.360200	0.833900	1.108000	1.473000	4.88500	
perimeter_se	569.0	2.866059	2.021855	0.757000	1.606000	2.287000	3.357000	21.98000	
area_se	569.0	40.337079	45.491006	6.802000	17.850000	24.530000	45.190000	542.20000	
smoothness_se	569.0	0.007041	0.003003	0.001713	0.005169	0.006380	0.008146	0.03113	
compactness_se	569.0	0.025449	0.017918	0.002252	0.012950	0.020420	0.032450	0.13540	
concavity_se	569.0	0.031841	0.030226	0.000000	0.014980	0.025890	0.042050	0.39600	
concave points_se	569.0	0.011796	0.006170	0.000000	0.007638	0.010930	0.014710	0.05279	
symmetry_se	569.0	0.020542	0.008266	0.007882	0.015160	0.018730	0.023480	0.07895	
fractal_dimension_se	569.0	0.003795	0.002646	0.000895	0.002248	0.003187	0.004558	0.02984	
radius_worst	569.0	16.269190	4.833242	7.930000	13.010000	14.970000	18.790000	36.04000	
texture_worst	569.0	25.677223	6.146258	12.020000	21.080000	25.410000	29.720000	49.54000	
perimeter_worst	569.0	107.261213	33.602542	50.410000	84.110000	97.660000	125.400000	251.20000	
area_worst	569.0	880.583128	569.356993	185.200000	515.300000	686.500000	1084.000000	4254.00000	
smoothness_worst	569.0	0.132369	0.022832	0.071170	0.116600	0.131300	0.146000	0.22260	
compactness_worst	569.0	0.254265	0.157336	0.027290	0.147200	0.211900	0.339100	1.05800	
concavity_worst	569.0	0.272188	0.208624	0.000000	0.114500	0.226700	0.382900	1.25200	
concave points_worst	569.0	0.114606	0.065732	0.000000	0.064930	0.099930	0.161400	0.29100	
symmetry_worst	569.0	0.290076	0.061867	0.156500	0.250400	0.282200	0.317900	0.66380	
fractal_dimension_worst	569.0	0.083946	0.018061	0.055040	0.071460	0.080040	0.092080	0.20750	

3. Provide the correlation matrix and write your inference about it.



1.Features like radius\_mean, texture\_mean, perimeter\_mean, and area\_mean show higher mean values compared to other features.

2.In the correlation matrix concave\_point\_worst , concavity\_point\_mean are highly correlated with diagnosis . That is it strongly predict the malignancy .

3.Other than concave\_point\_worst, perimeter\_mean , radius\_mean, area\_mean ,area\_worst, perimeter\_worst,radius worst are strongly correlated with malignancy .

4. From the row radius\_mean the perimeter\_mean , area\_mean are highly correlated to each other . This indicates that it contains the redundant values .

To reduce the redundancy we need to take PCA to combine into one feature .

5. These redundant data contains in perimeter\_mean , area\_mean,radius\_worst,perimeter\_worst columns respectively .

6.concavity\_se , compactness\_se show weak correlations with diagnosis.

7. fractional\_dimension\_mean is likely associated with benign tumors .