Breast Cancer Classification Prediction

A project by Rafif

Project Overview

Goal

To predict whether a breast cancer case is benign or malignant based on the available features.

Dataset

This dataset is obtained from the Breast Cancer Wisconsin Dataset (Kaggle), and it is also one of the standard datasets in Scikit-learn.

Focus

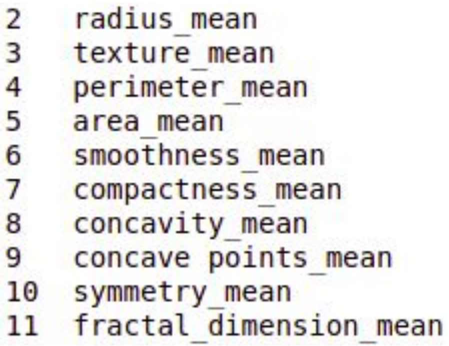
This project focuses on standard data cleaning and EDA pipeline, hyperparameter tuning using grid search, dimensionality reduction using PCA, and classification using logistic regression and SVM.

Dataset

Contains 33 columns:

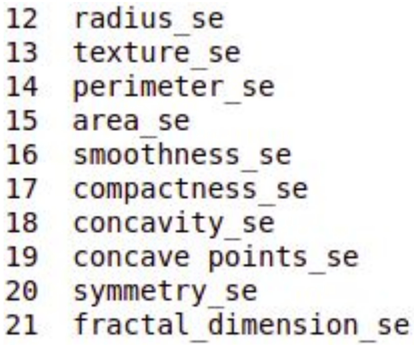
- 1 ID column and 1 NaN column
- 30 features:
  - 10 unique features: radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry, and fractal dimension
  - 3 measurements: mean, standard error, worst
- The target `diagnosis`: 357 benign, 212 malignant

10 'mean' columns



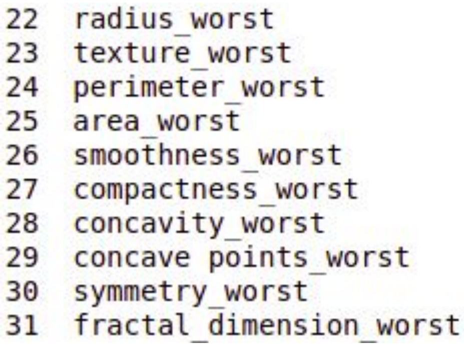
```
2    radius_mean
3    texture_mean
4    perimeter_mean
5    area_mean
6    smoothness_mean
7    compactness_mean
8    concavity_mean
9    concave points_mean
10   symmetry_mean
11   fractal_dimension_mean
```

10 'standard error' columns



```
12   radius_se
13   texture_se
14   perimeter_se
15   area_se
16   smoothness_se
17   compactness_se
18   concavity_se
19   concave points_se
20   symmetry_se
21   fractal_dimension_se
```

10 'worst' columns



```
22   radius_worst
23   texture_worst
24   perimeter_worst
25   area_worst
26   smoothness_worst
27   compactness_worst
28   concavity_worst
29   concave points_worst
30   symmetry_worst
31   fractal_dimension_worst
```

Features were directly computed from the cell nucleus

Preprocessing

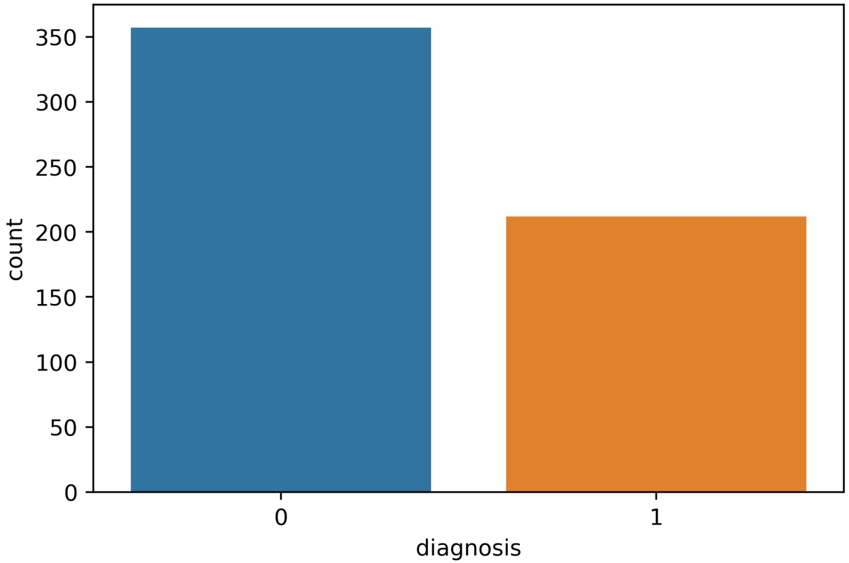
- Dropping unimportant columns: `id` and `Unnamed: 32`

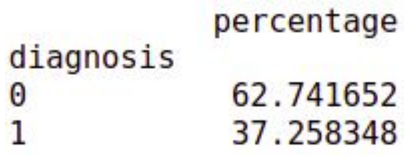
- No duplicated rows

- Binary encoding for `diagnosis`: benign (0), malignant (1)

EDA

- Check the distribution of `diagnosis`





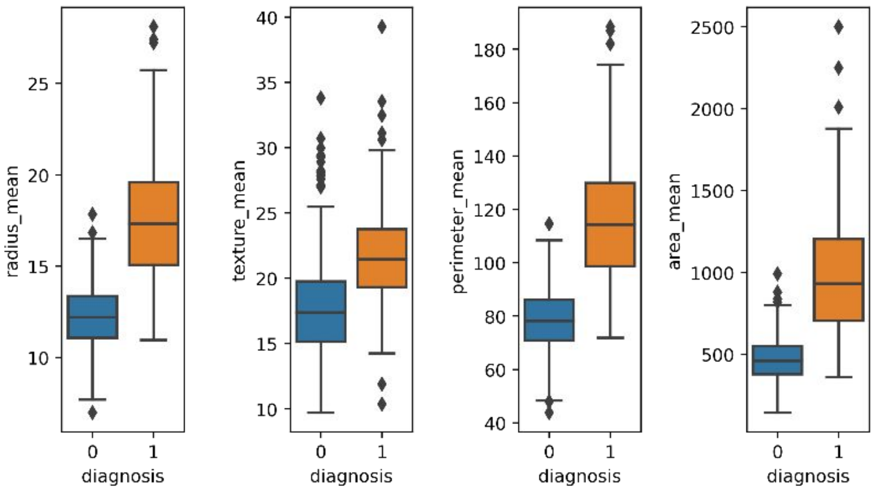
```
           percentage
diagnosis
0           62.741652
1           37.258348
```

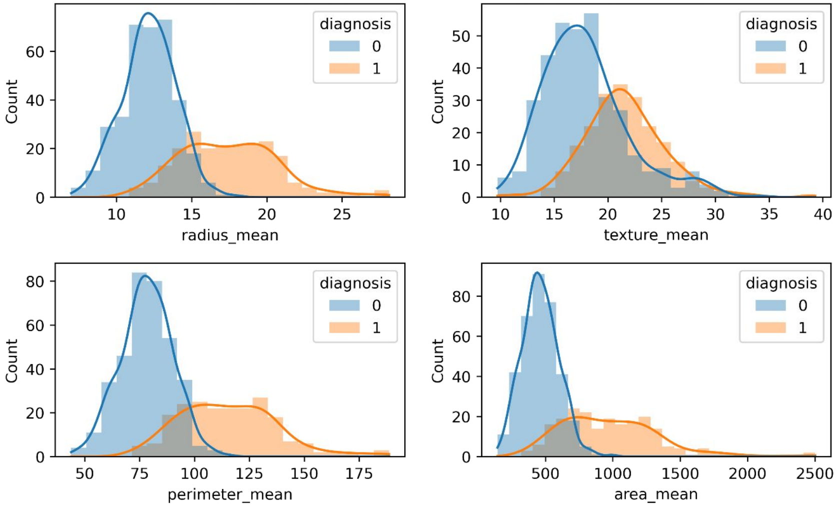
- More benign cases (1.5 times) than malignant cases → severe cases are rarer

- Slightly imbalanced, but not too extreme → balancing not needed

EDA

- Visualize distribution and check outliers with boxplot and histogram

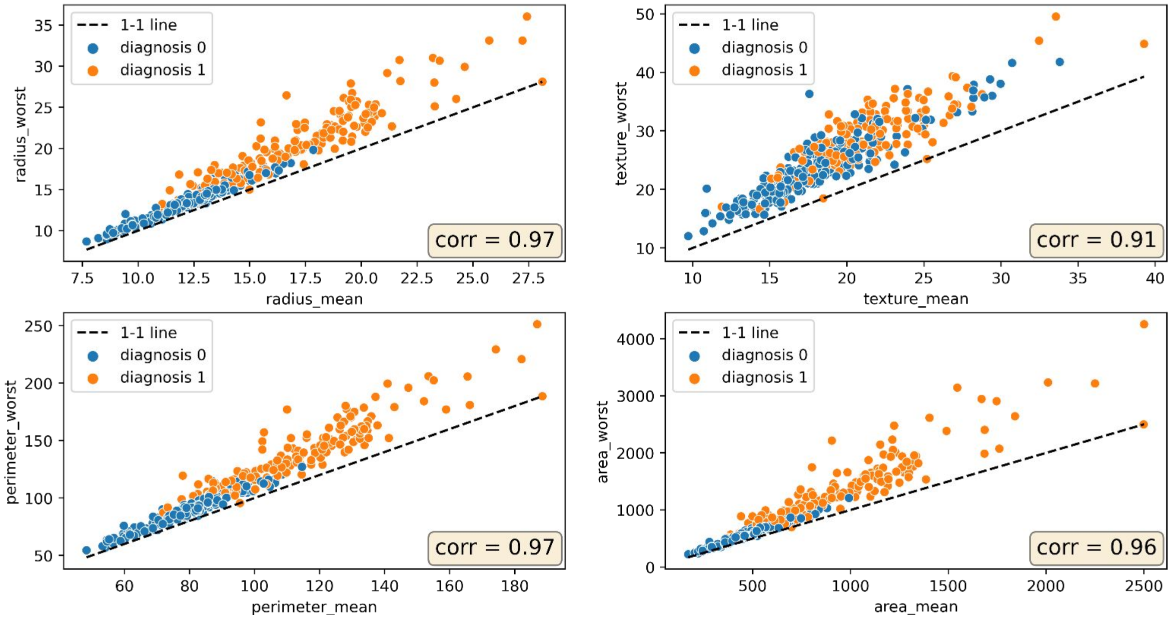




- Malignant cases have systematically larger values for the features
- No extreme outliers in the dataset

Feature Selection

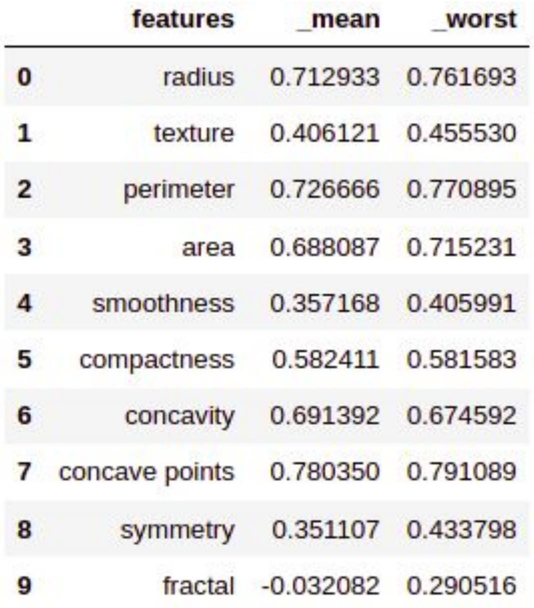
- Train-test split to prevent information leakage (70:30 ratio)
- Checking the correlation between `_mean` and `_worst` features



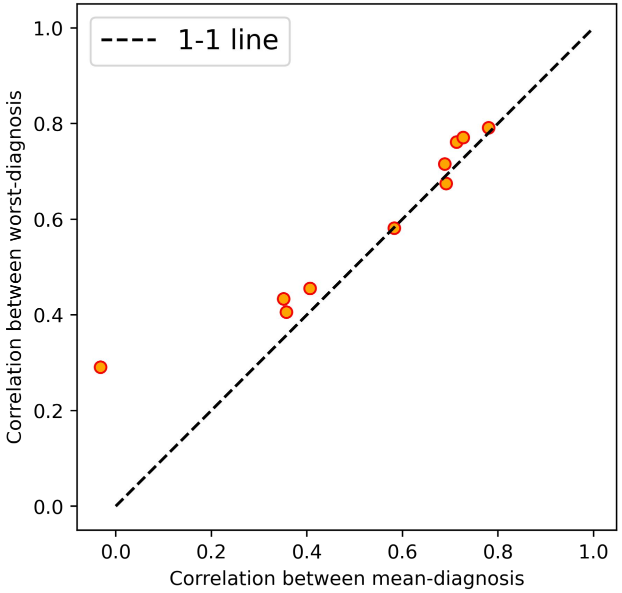
- High correlation (as expected)
- Have to pick one as predictors: `_mean` or `_worst`

Feature Selection

- Picking the one that has overall higher correlation with `diagnosis`
- Using point-biserial correlation (special case of Pearson correlation)



	features	_mean	_worst
0	radius	0.712933	0.761693
1	texture	0.406121	0.455530
2	perimeter	0.726666	0.770895
3	area	0.688087	0.715231
4	smoothness	0.357168	0.405991
5	compactness	0.582411	0.581583
6	concavity	0.691392	0.674592
7	concave points	0.780350	0.791089
8	symmetry	0.351107	0.433798
9	fractal	-0.032082	0.290516



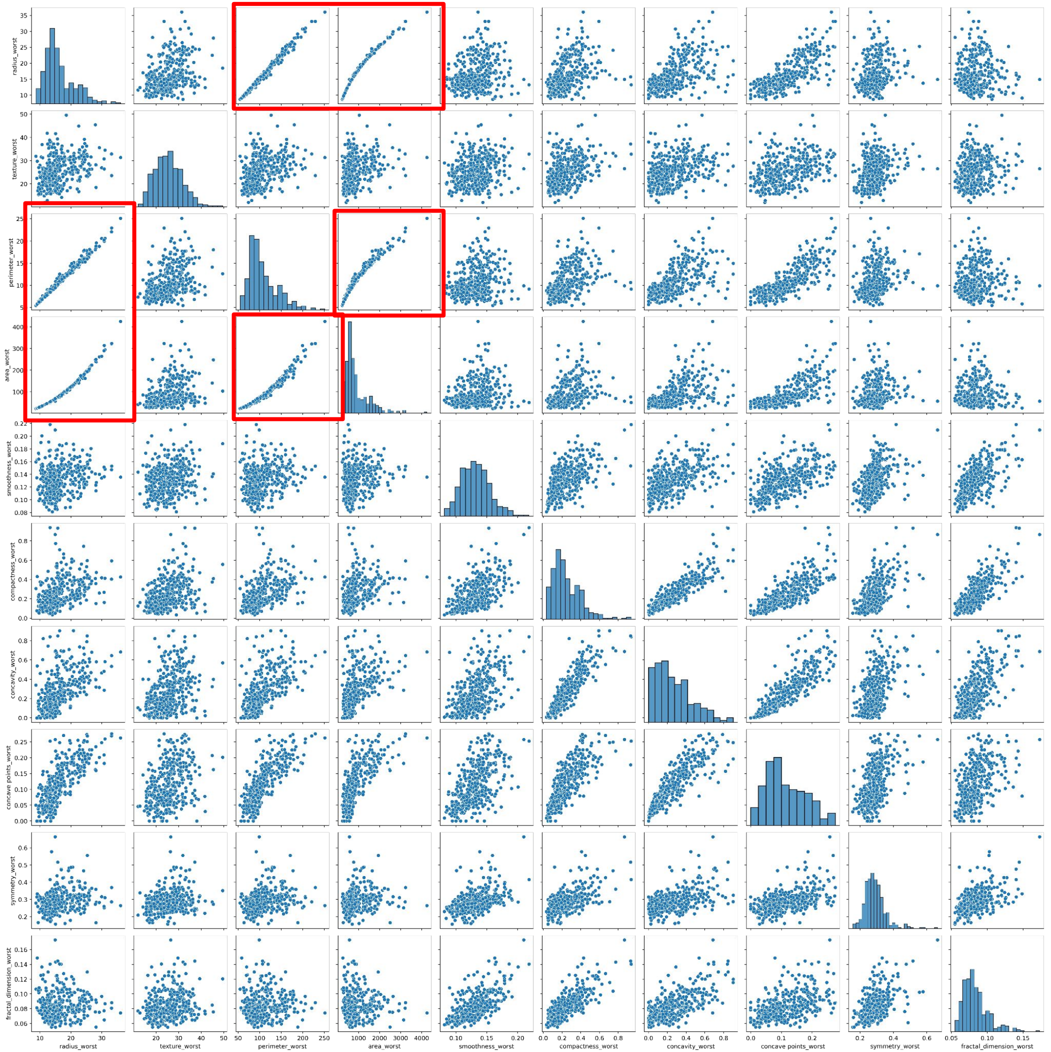
- Overall, `_worst` features have higher correlation with `diagnosis`
- Dropping all `_mean` features

Feature Selection

- Check correlations within `_worst` features

- `radius` is correlated with `perimeter` and `area` (also expected)

- `perimeter` has the largest correlation with `perimeter` diagnosis → dropping `radius` and `area`



Building the Model: Logistic Regression

- Linearly separable case → using logistic regression and support vector machine (SVM).

- Employing the grid search method to optimize the hyperparameters.

- For logistic regression, the best hyperparameters are:
  - ❑ C = 100
  - ❑ Penalty = l2
  - ❑ Solver = newton-cg

Evaluating the Model: Logistic Regression

Recall as metric → as few false negatives as possible

- Better to falsely diagnose someone as having a malignant cancer (more treatment, potentially saving lives) than falsely diagnose a cancer as benign (less treatment, potentially losing lives).

Test data = 171		Prediction	
		0	1
Actual	0	105	3
	1	1	62

Recall score = 98%

The model performs very well

Building the Model: SVM

For SVM, the best hyperparameters are:

- C = 100
- gamma = 1
- kernel = linear

Evaluating the Model: SVM

Test data = 171		Prediction	
		0	1
Actual	0	104	4
	1	2	61

Recall score = 97% → slightly lower since there is 1 more false negative.

Overall, logistic regression performs better.

Dimensionality Reduction with PCA

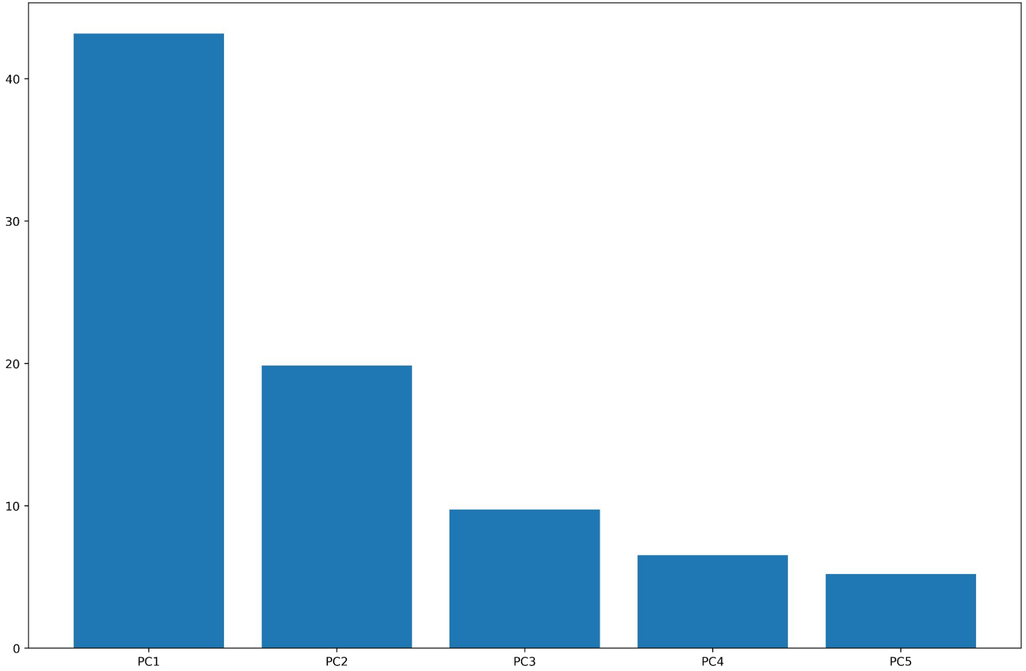
- Using PCA to reduce feature dimensions, and see if the results can be improved.

- Using the whole dataset again (minus `id` and `Unnamed: 32`) → train-test split to prevent information leakage.

- Scaling the features with sklearn's `StandardScaler` → mean 0, variance 1 for all features.

Dimensionality Reduction with PCA

Skree plot:

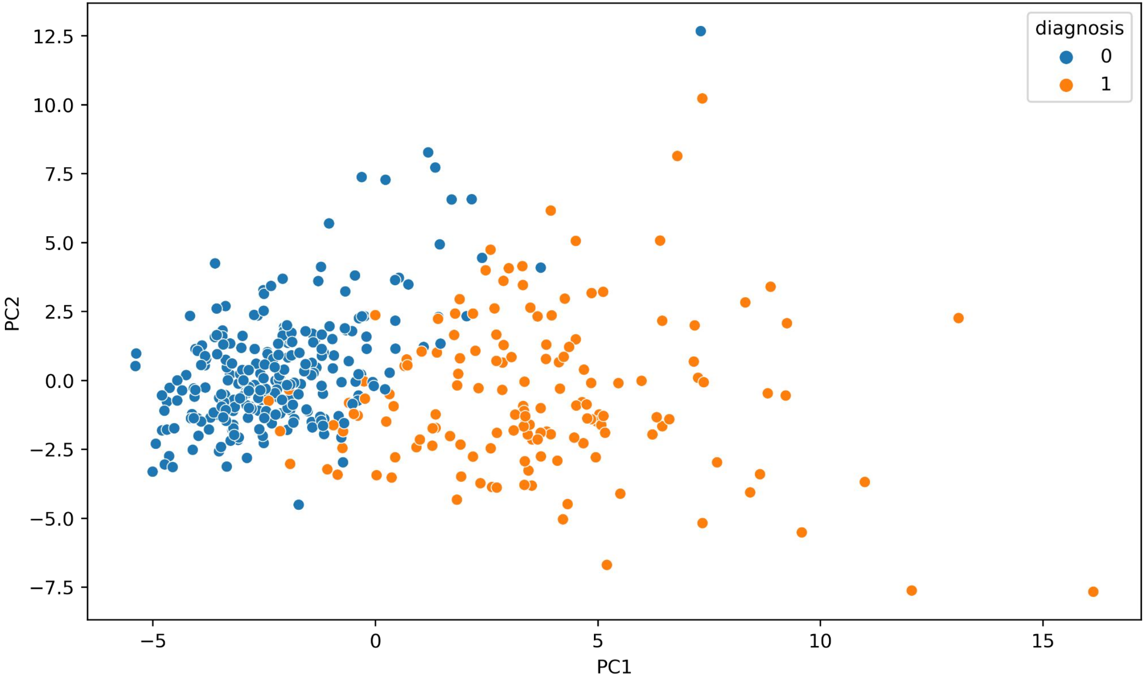


- Needs at least 5 PC's to preserve 80% information in the data.

- But is it really necessary to use 5 PC's?

Dimensionality Reduction with PCA

Plot the data in 2 PC's



- The separation between the cases is very clear
- Two PC's are all we need!

Building the Model: PCA + Logistic Regression

- Using only 2 PC’s and transform the features into PC coordinates.

- Building the model again with similar method (grid search).

- For logistic regression, the best hyperparameters are:
    - C = 0.1
    - penalty = l1
    - solver = liblinear

Evaluating the Model: PCA + Logistic Regression

Test data = 171		Prediction	
		0	1
Actual	0	106	2
	1	1	62

- The recall score has not improved.
- Accuracy increases to 98% since one false positive is removed.

Building the Model: PCA + SVM

- For SVM, the best hyperparameters are:
  - ❑ C = 1
  - ❑ gamma = 1
  - ❑ Kernel = linear

Evaluating the Model: PCA + SVM

Test data = 171		Prediction	
		0	1
Actual	0	106	2
	1	3	60

- The recall score has slightly dropped to 95% (more false negatives).
- Accuracy increases to 97% (more correct predictions).
- Overall, logistic regression still performs better.

Conclusion

1. There are more benign cases than malignant cases in this dataset → normal since severe cases should be rarer.
2. Malignant cases have larger values on all of the features.
3. The _`mean` features are highly correlated with the `_worst` features, but `_worst` have higher correlations with `diagnosis`.
4. The target `diagnosis` in this dataset is linearly separable. Therefore, logistic regression and SVM perform very well.
5. Using PCA to reduce the dimension of the data does not improve model performance significantly, but it is very time-efficient and easy to implement for this dataset.