# Capstone Project 1: Final Report

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If breast cancer is left untreated, the cancer spreads out to other parts of the body if it is a malignant cell growth. Benign cells are usually localized and do not spread to other parts. The average 5-year survival rate for women with invasive breast cancer is 91%. The average 10-year survival rate for women with invasive breast cancer is 84%. This year, an estimated 276,480 women in the United States will be diagnosed with invasive breast cancer, and It is estimated that 42,690 deaths (42,170 women and 520 men) from breast cancer will occur this year.I will predict if a given cancer cell is benign or malignant to be able to treat the cancer cells in a timely manner. The clients for this project would be hospitals and medical institutions. They care about this problem because using a highly accurate prediction model can reduce lives lost due to cancer by taking necessary preventive actions on malignant cancer cells.

## The Dataset

I use the University of California, Irvine Machine Learning repository Breast cancer diagnostic data set. I acquire the data set through Kaggle website, which can be found at this link:https://www.kaggle.com/uciml/breast-cancer-wisconsin-data

The dataset has 33 columns with 569 rows. There are ten computed real-valued features for each cell nucleus in the data set: radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry, fractal dimensions.  The mean, standard error and "worst" or largest (mean of the three largest values) of these features are also computed resulting in 30 features. There are a total of 357 Benign and 212 malignant points in the data set.

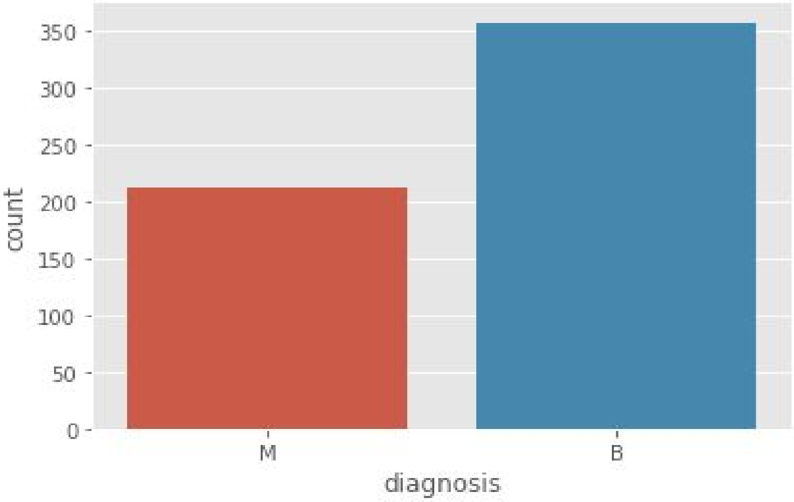


Figure 1 Benign and malignant groups

## Reducing Features

As each feature has 3 corresponding columns - worst, mean, and standard error, I thought it prudent to reduce those features down to mitigate multicollinearity. As such, I used logistic regression to select the best predictor in each group of features between worst, mean, and standard error.

Then, since I don't want to assume that there were no good features in each group other than the "best" one, I also calculate the correlation between the best feature and the other two features in the same group to confirm that multicollinearity was an issue. If the correlations were smaller than .5 between the two features I would also add it to my best features list. The final list consists of 13 features:  radius worst, texture worst, perimeter worst, area worst, smoothness worst, compactness mean, concavity mean, concave points worst, symmetry worst, fractal dimension worst. radius worst, texture worst, perimeter worst, area worst, smoothness worst, compactness mean, concavity mean, concave points worst, symmetry worst, fractal dimension worst.

## Exploratory Data Analysis

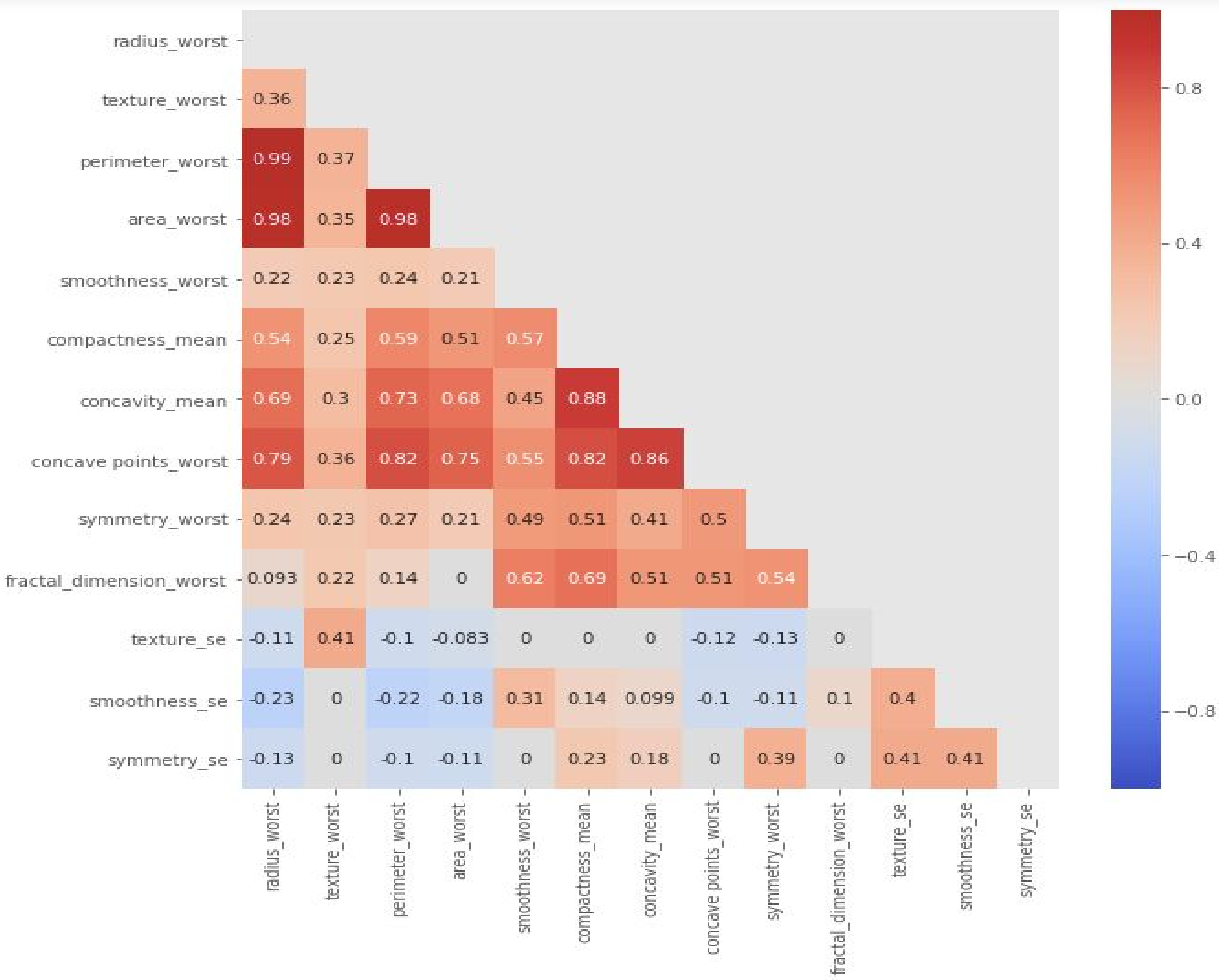


Figure 2 Correlation matrix of the best features

Above, you can see the correlation matrix of the best features. I have grayed out non-significant correlations between each two features group combinations. Correlation matrix shows that perimeter_worst,area_worst and radius_worst is highly correlated with .99, it is concerning. Also concavity_mean is highly correlated with concave_points_worst and compactness_worst.

## Comparing Malignant vs Benign

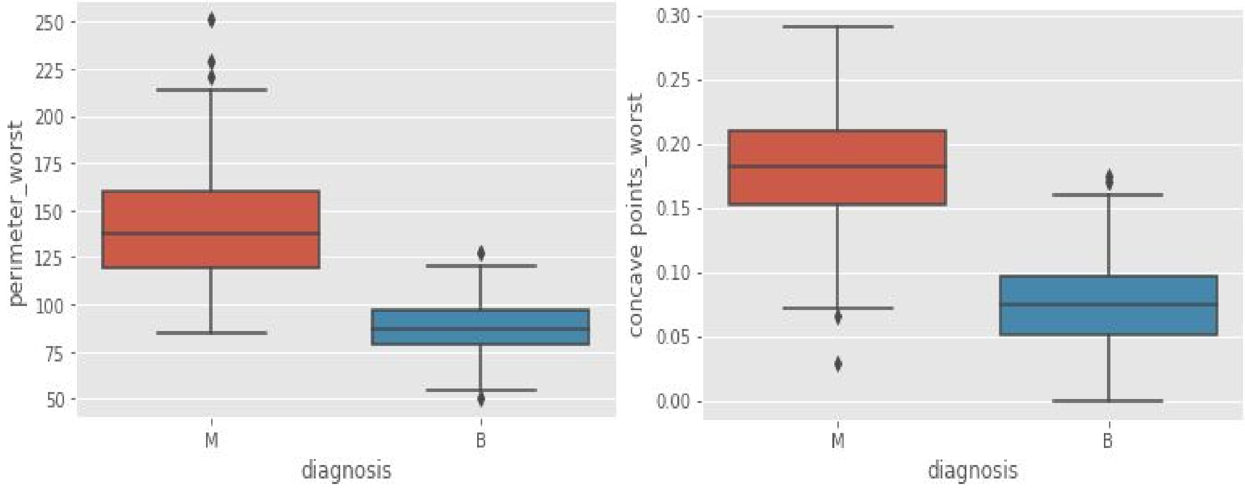


**Figure 3 Perimeter and Concave points box plots**

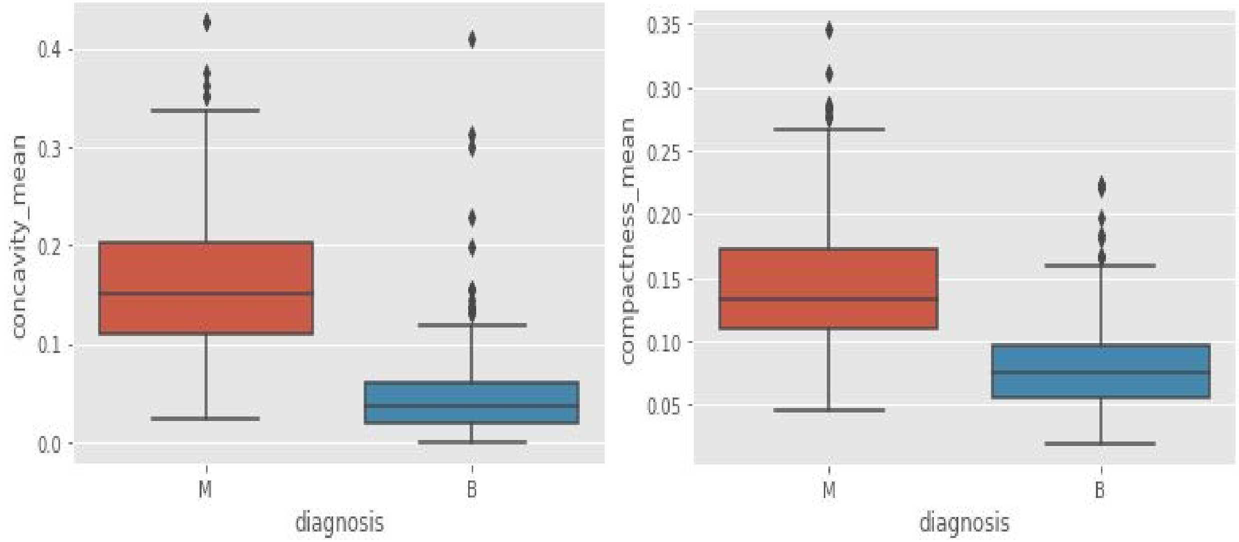
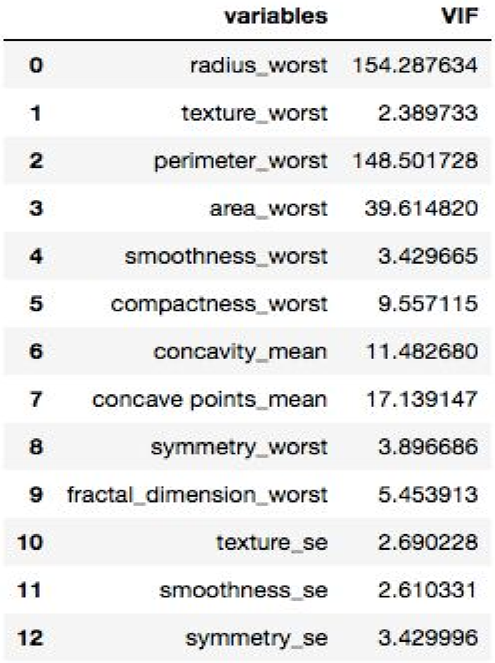


**Figure 4 Concavity and compactness box plots**

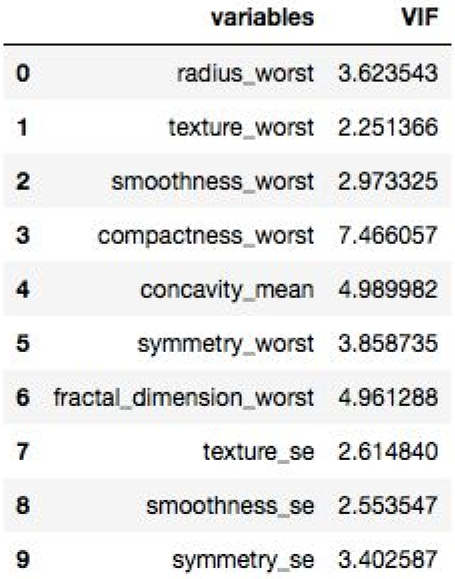
As the boxplots above show, Malignant and Benign cells tend to have different characteristics which makes it seem promising that they can be distinguished with a predictive model. In particular, concavity, perimeter, compactness, and number of concave points are all larger in Malignant cells than in Benign cells. Statistical testing using a t-test confirms that this relationship is statistically significant across all of these features with p < .05.

## Investigating Effect of Features on Malignancy

I start investigating the effect of features by detecting multicollinearity with Variance Inflation Factor(VIF). To be able to calculate VIF scores, I need to standardize all the features using StandardScaler. As we can see on the VIF table on the left below, radius_worst, perimeter_worst and area_worst have high variation inflation factor because they explain same variance.I drop the two features that has the highest two variance.Also,concavity_mean and concave points_mean are highly correlated and they have high vif so I drop the concave points_mean as well.



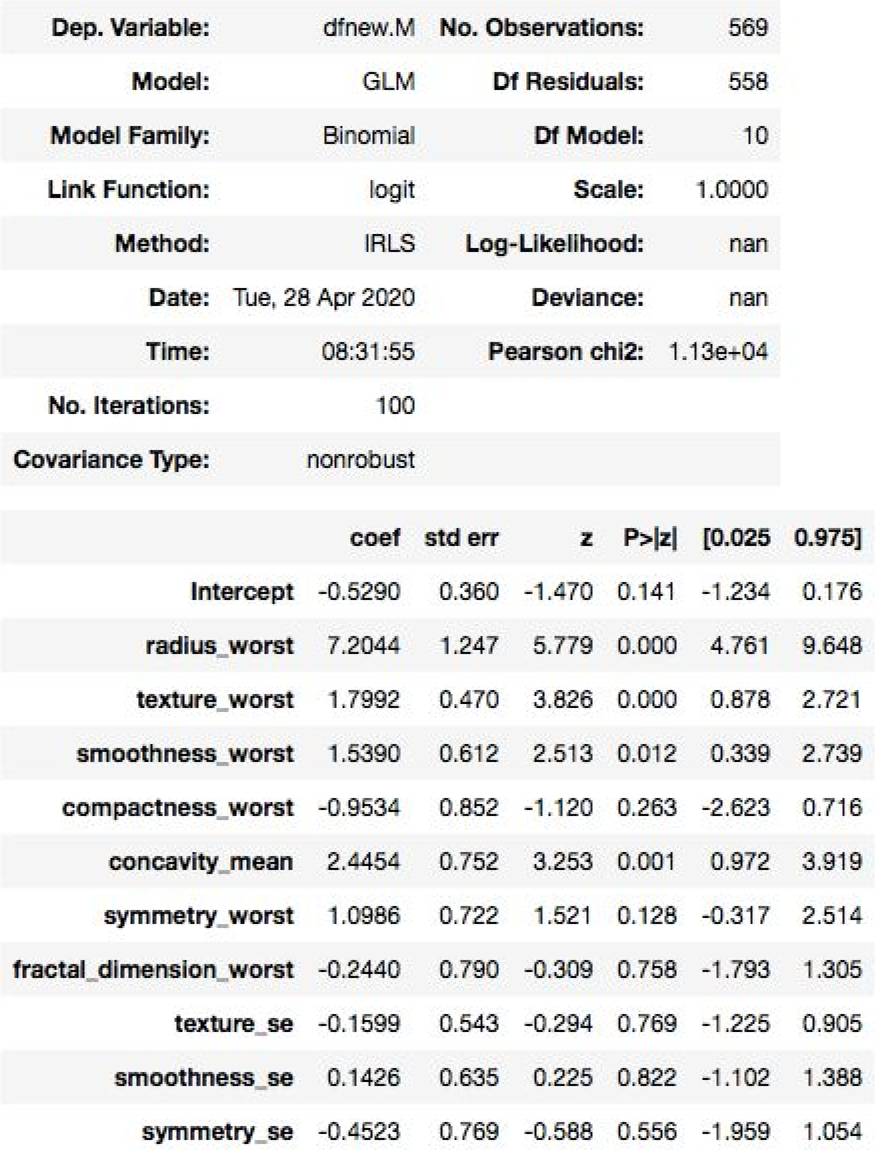
|  | variables | VIF |
|---|---|---|
| 0 | radius_worst | 154.287634 |
| 1 | texture_worst | 2.389733 |
| 2 | perimeter_worst | 148.501728 |
| 3 | area_worst | 39.614820 |
| 4 | smoothness_worst | 3.429665 |
| 5 | compactness_worst | 9.557115 |
| 6 | concavity_mean | 11.482680 |
| 7 | concave points_mean | 17.139147 |
| 8 | symmetry_worst | 3.896686 |
| 9 | fractal_dimension_worst | 5.453913 |
| 10 | texture_se | 2.690228 |
| 11 | smoothness_se | 2.610331 |
| 12 | symmetry_se | 3.429996 |



|  | variables | VIF |
|---|---|---|
| 0 | radius_worst | 3.623543 |
| 1 | texture_worst | 2.251366 |
| 2 | smoothness_worst | 2.973325 |
| 3 | compactness_worst | 7.466057 |
| 4 | concavity_mean | 4.989982 |
| 5 | symmetry_worst | 3.858735 |
| 6 | fractal_dimension_worst | 4.961288 |
| 7 | texture_se | 2.614840 |
| 8 | smoothness_se | 2.553547 |
| 9 | symmetry_se | 3.402587 |

After dropping area_worst,perimeter_worst and concave points_mean features from the data set, VIF scores decreased notably.Above on the right can be seen in the VIF table without those features.

After narrowing down the features using VIF scores, I then run them through a statsmodels logistic regression.Below we can see the summary report of our logistic regression.



| | | | |
|---|---|---|---|
| Dep. Variable: | dfnew.M | No. Observations: | 569 |
| Model: | GLM | Df Residuals: | 558 |
| Model Family: | Binomial | Df Model: | 10 |
| Link Function: | logit | Scale: | 1.0000 |
| Method: | IRLS | Log-Likelihood: | nan |
| Date: | Tue, 28 Apr 2020 | Deviance: | nan |
| Time: | 08:31:55 | Pearson chi2: | 1.13e+04 |
| No. Iterations: | 100 | | |
| Covariance Type: | nonrobust | | |

| | coef | std err | z | P>\|z\| | [0.025 | 0.975] |
|---|---|---|---|---|---|---|
| Intercept | -0.5290 | 0.360 | -1.470 | 0.141 | -1.234 | 0.176 |
| radius_worst | 7.2044 | 1.247 | 5.779 | 0.000 | 4.761 | 9.648 |
| texture_worst | 1.7992 | 0.470 | 3.826 | 0.000 | 0.878 | 2.721 |
| smoothness_worst | 1.5390 | 0.612 | 2.513 | 0.012 | 0.339 | 2.739 |
| compactness_worst | -0.9534 | 0.852 | -1.120 | 0.263 | -2.623 | 0.716 |
| concavity_mean | 2.4454 | 0.752 | 3.253 | 0.001 | 0.972 | 3.919 |
| symmetry_worst | 1.0986 | 0.722 | 1.521 | 0.128 | -0.317 | 2.514 |
| fractal_dimension_worst | -0.2440 | 0.790 | -0.309 | 0.758 | -1.793 | 1.305 |
| texture_se | -0.1599 | 0.543 | -0.294 | 0.769 | -1.225 | 0.905 |
| smoothness_se | 0.1426 | 0.635 | 0.225 | 0.822 | -1.102 | 1.388 |
| symmetry_se | -0.4523 | 0.769 | -0.588 | 0.556 | -1.959 | 1.054 |

Based on this analysis, it seems clear that radius is the most important feature with a coefficient more than 3x greater than the next most important feature, concavity, when everything is scaled. Looking at the p-values, the variables 'radius_worst',’texture_worst’', 'smoothness_worst', and ‘concavity_mean’ ’ seem to be the only significant predictors since their p-values are smaller than 0.05. All the other variables have their p-values larger than 0.05, and are, therefore, not significant.

The fitted model says that one unit increase in the radius_worst increases having a malignant cell by %133800 then having bening cell holding other features constant since exp(7.2) is 133.9. The coefficient for concavity_mean says that, holding other features constant,we see %1000 increases in the odds of having a malignant class for one-unit increase in concavity_mean since exp(2.44) is 11.

## Machine Learning

Machine Learning was performed on the dataset including only the best features as determined in the prior section. The training data was 55% of the data. The remaining 45% was my hold-out set that was left untouched until the final model has been selected and tuned. Before using different supervised machine learning approaches I performed hyperparameter tuning to find out what estimators worked most effectively. I used roc_auc as our metric to determine the best parameters for each model, grid searching over 5-fold cross-validation. The resulting best parameters for each model are below:

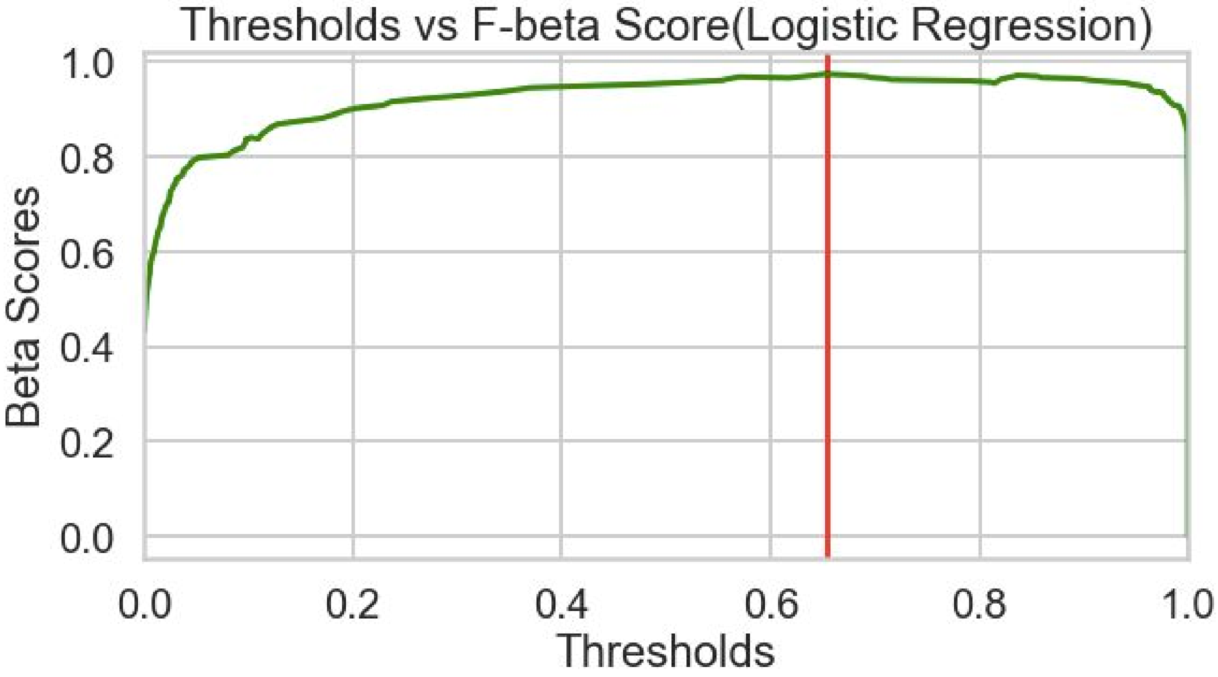
| Model | Parameters | Roc-Auc Score |
|---|---|---|
| Logistic Regression | C : 31 | 0.988 |
| KNN | N_neighbors : 39 | 0.970 |
| Random Forest | Max_depth : 19<br>Max_features : 4<br>N_estimators : 118 | 0.986 |

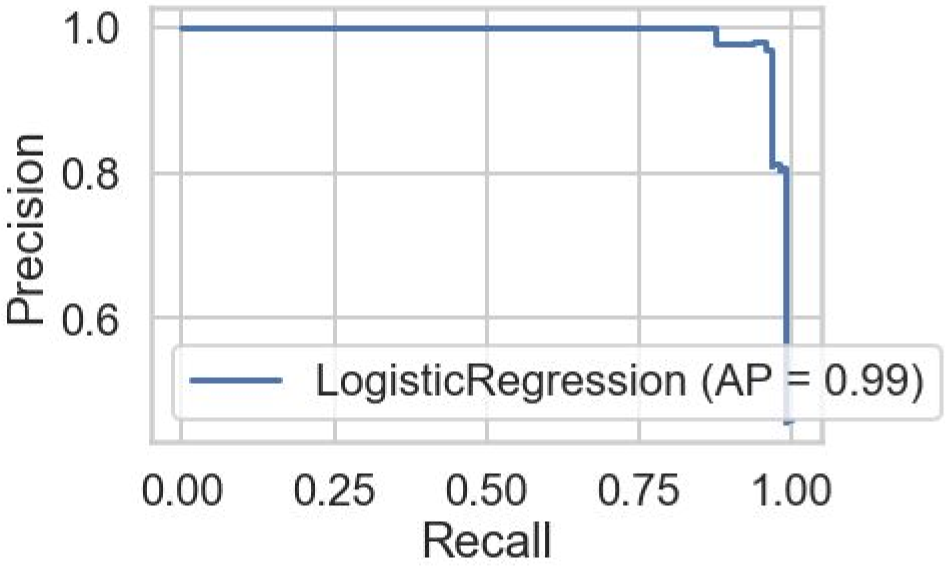
### Picking the Optimal Threshold

Since this is a cancer diagnostic project, it is much more important to get diagnosed correctly when a person has cancer to start treatment as early as possible. For that reason maximizing recall is important.I choose 1.5 as a beta score to be able to maximize the recall.

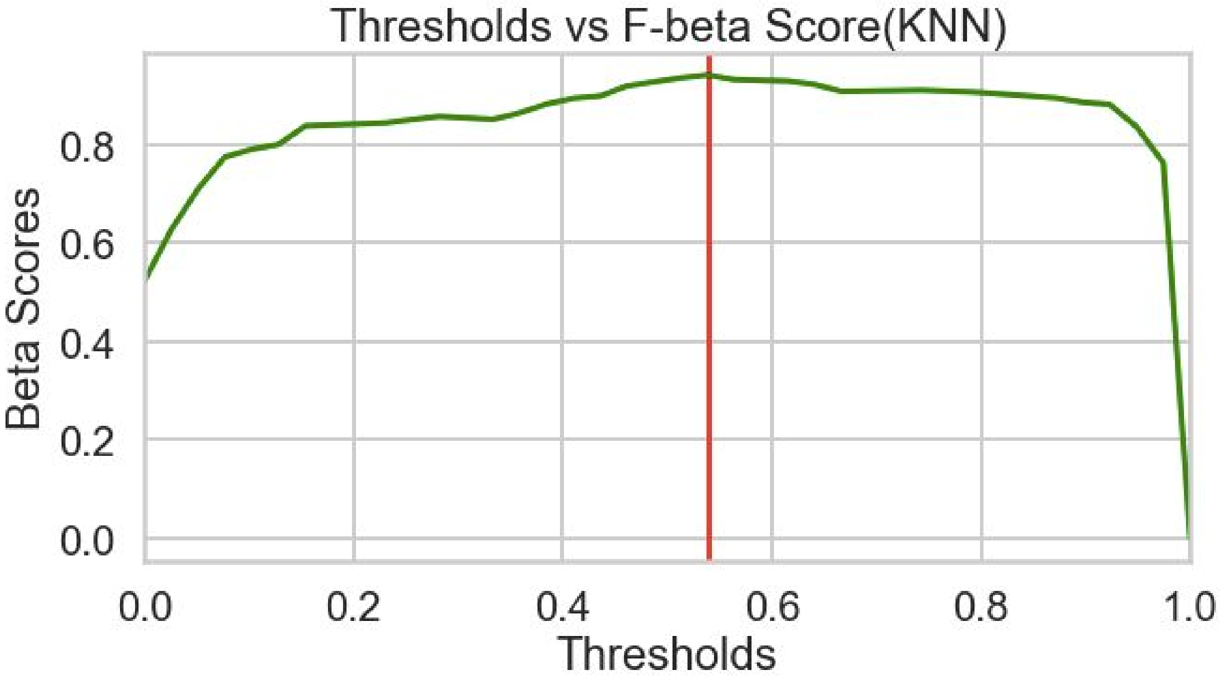
After hyperparameter tuning, We fit our model on the train set and predicted probabilities using the test set and then calculated different thresholds for our model. We have calculated different accuracy scores by looping over the different thresholds. Below graphs show all the scores and thresholds and the vertical line indicates  the best score and best threshold.

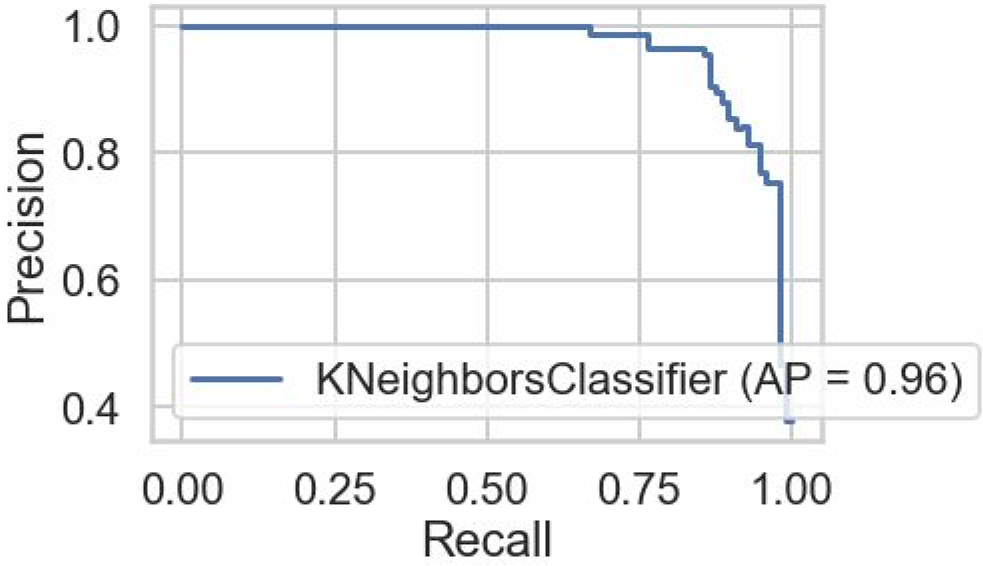
```
best threshold is: 0.6529148381619775
best score is: 0.9748427672955976
```

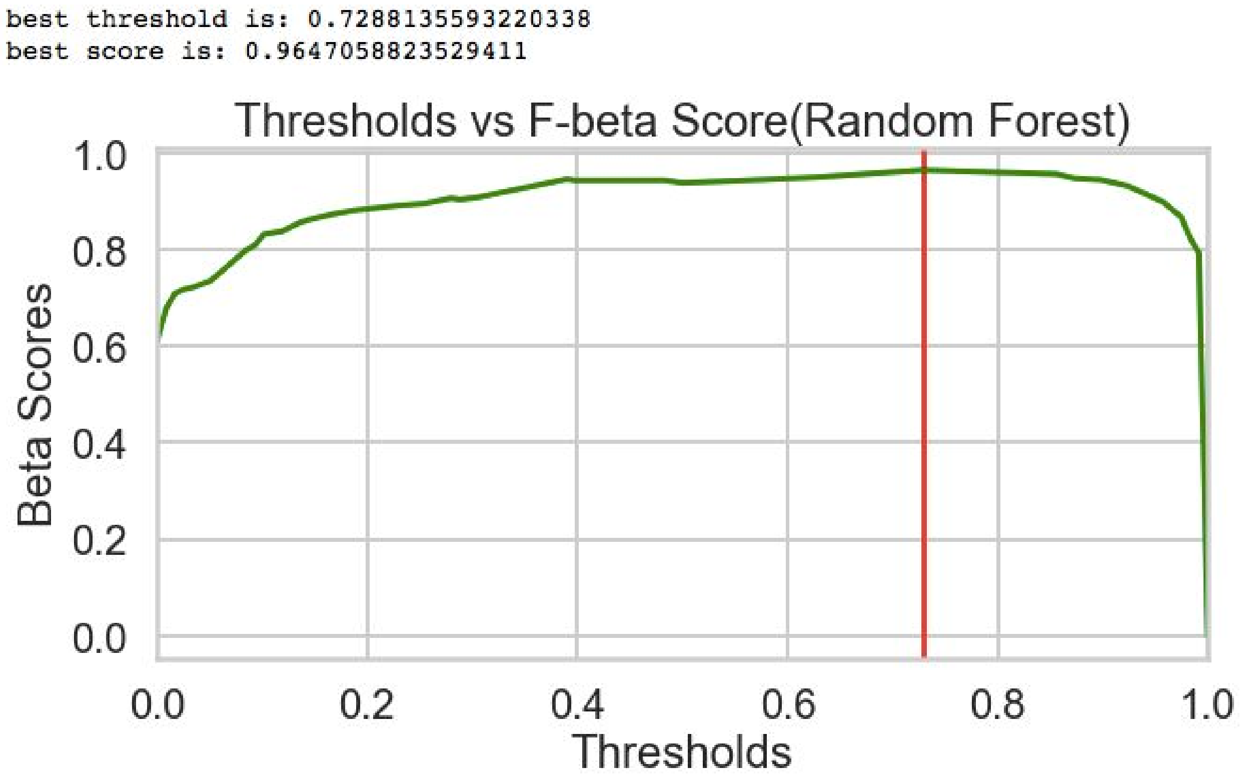




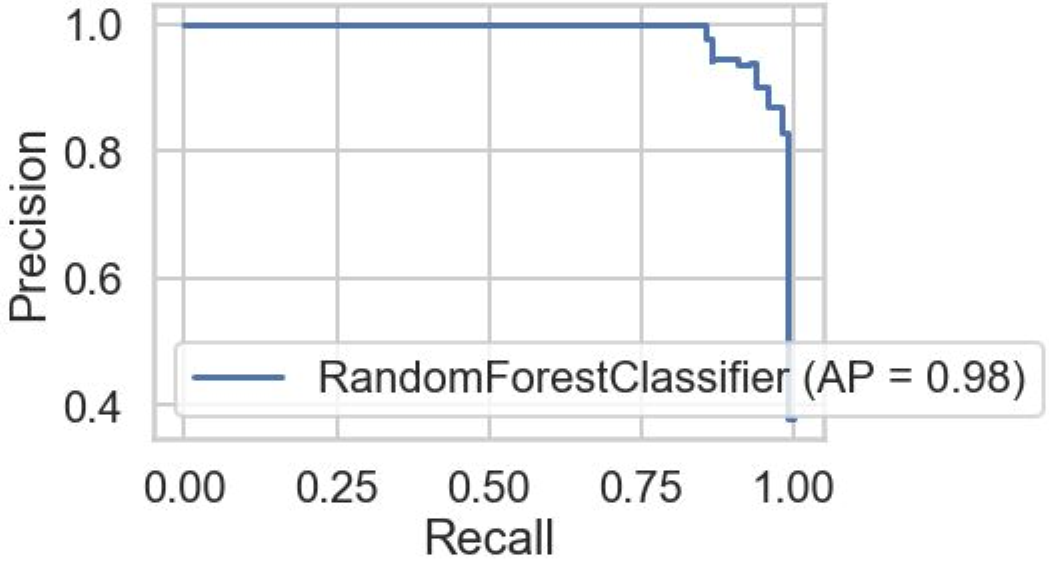
```
best threshold is: 0.5384615384615384
best score is: 0.9410430839002267
```



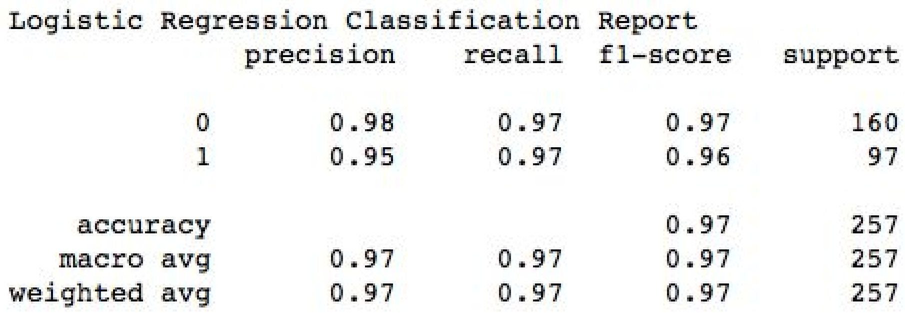




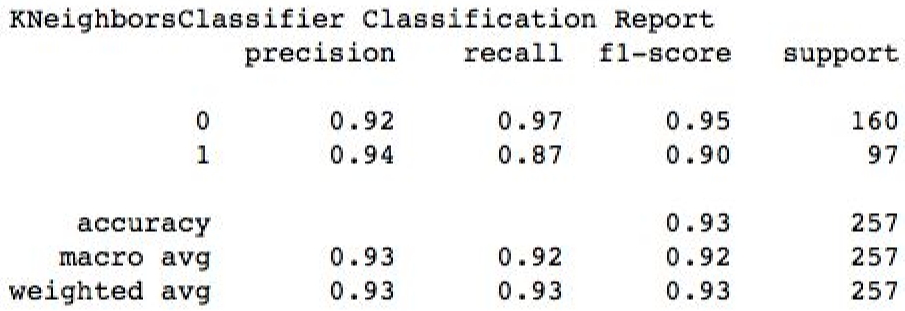
```
best threshold is: 0.7288135593220338
best score is: 0.9647058823529411
```



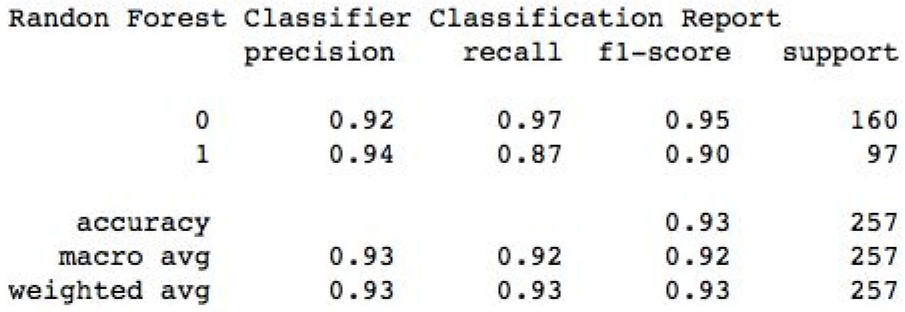
**Classification Reports of the Classifiers**



```
Logistic Regression Classification Report
              precision    recall  f1-score   support

           0       0.98      0.97      0.97       160
           1       0.95      0.97      0.96        97

    accuracy                           0.97       257
   macro avg       0.97      0.97      0.97       257
weighted avg       0.97      0.97      0.97       257
```



```
KNeighborsClassifier Classification Report
              precision    recall  f1-score   support

           0       0.92      0.97      0.95       160
           1       0.94      0.87      0.90        97

    accuracy                           0.93       257
   macro avg       0.93      0.92      0.92       257
weighted avg       0.93      0.93      0.93       257
```



```
Randon Forest Classifier Classification Report
              precision    recall  f1-score   support

           0       0.92      0.97      0.95       160
           1       0.94      0.87      0.90        97

    accuracy                           0.93       257
   macro avg       0.93      0.92      0.92       257
weighted avg       0.93      0.93      0.93       257
```

### Results

After building and testing over 3 models, I have concluded that the best one is using Logistic Regression Classifier with tuned hyperparameters. With the 98.8% it correctly labels the cells.

### Conclusion and Further Thoughts

Highly accurate prediction cancer data can save life. In this project, I tried to show the importance of feature selection and data visualization and model selection. Default data includes 33 features but after feature selection we drop this number from 33 to 13. Our model has accurately labeled 98.8% of the test data. We could try to increase the accuracy even higher by using different algorithms.