

# Wisconsin Breast Cancer Diagnosis Model

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## Overview

The purpose of this machine learning project is to build a breast cancer diagnostic model based on analysis of the University of Wisconsin's Breast Cancer (Diagnostic) dataset. The dataset is a collection of features computed from digitized images of a fine needle aspirate(FNA) of breast mass. These features describe the cell nuclei captured in the image. The diagnostic machine learning model's goal is to predict the mass as benign or malignant. The dataset was split into test and train datasets with the best model selected based on accuracy.

Attribute information in the dataset as described at <https://www.kaggle.com/uciml/breast-cancer-wisconsin-data> (<https://www.kaggle.com/uciml/breast-cancer-wisconsin-data>):

1. ID number 2) Diagnosis (M = malignant, B = benign) 3-32)

Ten real-valued features are computed for each cell nucleus: a) radius (mean of distances from center to points on the perimeter) b) texture (standard deviation of gray-scale values) c) perimeter d) area e) smoothness (local variation in radius lengths) f) compactness ( $\text{perimeter}^2 / \text{area} - 1.0$ ) g) concavity (severity of concave portions of the contour) h) concave points (number of concave portions of the contour) i) symmetry j) fractal dimension ("coastline approximation" - 1)

The mean, standard error and "worst" or largest (mean of the three largest values) of these features were computed for each image, resulting in 30 features. For instance, field 3 is Mean Radius, field 13 is Radius SE, field 23 is Worst Radius.

All feature values are recoded with four significant digits.

Missing attribute values: none

Class distribution: 357 benign, 212 malignant

NOTE: The class distribution is not balanced. When comparing model results, 'Balanced Accuracy' calculations are used to compensate for the significantly large majority of benign class instances.

## Pre-Processing

During Pre-Processing, NULLs were checked and removed, the id column was removed, and the Caret library zero variance check function was run against the predictors to scan for non-descriptive features. No non-variant features were identified by the zero variance check function:

```
## integer(0)
```

# Analysis

Dataset Structure:

```
## 'data.frame': 569 obs. of 31 variables:
## $ diagnosis      : Factor w/ 2 levels "B","M": 2 2 2 2 2 2 2 2 2 2 ...
## $ radius_mean    : num 18 20.6 19.7 11.4 20.3 ...
## $ texture_mean    : num 10.4 17.8 21.2 20.4 14.3 ...
## $ perimeter_mean  : num 122.8 132.9 130 77.6 135.1 ...
## $ area_mean       : num 1001 1326 1203 386 1297 ...
## $ smoothness_mean : num 0.1184 0.0847 0.1096 0.1425 0.1003 ...
## $ compactness_mean : num 0.2776 0.0786 0.1599 0.2839 0.1328 ...
## $ concavity_mean  : num 0.3001 0.0869 0.1974 0.2414 0.198 ...
## $ concave.points_mean : num 0.1471 0.0702 0.1279 0.1052 0.1043 ...
## $ symmetry_mean   : num 0.242 0.181 0.207 0.26 0.181 ...
## $ fractal_dimension_mean : num 0.0787 0.0567 0.06 0.0974 0.0588 ...
## $ radius_se       : num 1.095 0.543 0.746 0.496 0.757 ...
## $ texture_se       : num 0.905 0.734 0.787 1.156 0.781 ...
## $ perimeter_se     : num 8.59 3.4 4.58 3.44 5.44 ...
## $ area_se          : num 153.4 74.1 94 27.2 94.4 ...
## $ smoothness_se    : num 0.0064 0.00522 0.00615 0.00911 0.01149 ...
## $ compactness_se   : num 0.049 0.0131 0.0401 0.0746 0.0246 ...
## $ concavity_se     : num 0.0537 0.0186 0.0383 0.0566 0.0569 ...
## $ concave.points_se : num 0.0159 0.0134 0.0206 0.0187 0.0188 ...
## $ symmetry_se      : num 0.03 0.0139 0.0225 0.0596 0.0176 ...
## $ fractal_dimension_se : num 0.00619 0.00353 0.00457 0.00921 0.00511 ...
## $ radius_worst     : num 25.4 25 23.6 14.9 22.5 ...
## $ texture_worst     : num 17.3 23.4 25.5 26.5 16.7 ...
## $ perimeter_worst  : num 184.6 158.8 152.5 98.9 152.2 ...
## $ area_worst       : num 2019 1956 1709 568 1575 ...
## $ smoothness_worst : num 0.162 0.124 0.144 0.21 0.137 ...
## $ compactness_worst : num 0.666 0.187 0.424 0.866 0.205 ...
## $ concavity_worst  : num 0.712 0.242 0.45 0.687 0.4 ...
## $ concave.points_worst : num 0.265 0.186 0.243 0.258 0.163 ...
## $ symmetry_worst   : num 0.46 0.275 0.361 0.664 0.236 ...
## $ fractal_dimension_worst : num 0.1189 0.089 0.0876 0.173 0.0768 ...
```

Dataset Summary Statistics:

```

## diagnosis radius_mean texture_mean perimeter_mean
## B:357 Min. : 6.981 Min. : 9.71 Min. : 43.79
## M:212 1st Qu.:11.700 1st Qu.:16.17 1st Qu.: 75.17
## Median :13.370 Median :18.84 Median : 86.24
## Mean :14.127 Mean :19.29 Mean : 91.97
## 3rd Qu.:15.780 3rd Qu.:21.80 3rd Qu.:104.10
## Max. :28.110 Max. :39.28 Max. :188.50
## area_mean smoothness_mean compactness_mean concavity_mean
## Min. : 143.5 Min. :0.05263 Min. :0.01938 Min. :0.00000
## 1st Qu.: 420.3 1st Qu.:0.08637 1st Qu.:0.06492 1st Qu.:0.02956
## Median : 551.1 Median :0.09587 Median :0.09263 Median :0.06154
## Mean : 654.9 Mean :0.09636 Mean :0.10434 Mean :0.08880
## 3rd Qu.: 782.7 3rd Qu.:0.10530 3rd Qu.:0.13040 3rd Qu.:0.13070
## Max. :2501.0 Max. :0.16340 Max. :0.34540 Max. :0.42680
## concave.points_mean symmetry_mean fractal_dimension_mean
## Min. :0.00000 Min. :0.1060 Min. :0.04996
## 1st Qu.:0.02031 1st Qu.:0.1619 1st Qu.:0.05770
## Median :0.03350 Median :0.1792 Median :0.06154
## Mean :0.04892 Mean :0.1812 Mean :0.06280
## 3rd Qu.:0.07400 3rd Qu.:0.1957 3rd Qu.:0.06612
## Max. :0.20120 Max. :0.3040 Max. :0.09744
## radius_se texture_se perimeter_se area_se
## Min. :0.1115 Min. :0.3602 Min. : 0.757 Min. : 6.802
## 1st Qu.:0.2324 1st Qu.:0.8339 1st Qu.: 1.606 1st Qu.: 17.850
## Median :0.3242 Median :1.1080 Median : 2.287 Median : 24.530
## Mean :0.4052 Mean :1.2169 Mean : 2.866 Mean : 40.337
## 3rd Qu.:0.4789 3rd Qu.:1.4740 3rd Qu.: 3.357 3rd Qu.: 45.190
## Max. :2.8730 Max. :4.8850 Max. :21.980 Max. :542.200
## smoothness_se compactness_se concavity_se
## Min. :0.001713 Min. :0.002252 Min. :0.00000
## 1st Qu.:0.005169 1st Qu.:0.013080 1st Qu.:0.01509
## Median :0.006380 Median :0.020450 Median :0.02589
## Mean :0.007041 Mean :0.025478 Mean :0.03189
## 3rd Qu.:0.008146 3rd Qu.:0.032450 3rd Qu.:0.04205
## Max. :0.031130 Max. :0.135400 Max. :0.39600
## concave.points_se symmetry_se fractal_dimension_se
## Min. :0.000000 Min. :0.007882 Min. :0.0008948
## 1st Qu.:0.007638 1st Qu.:0.015160 1st Qu.:0.0022480
## Median :0.010930 Median :0.018730 Median :0.0031870
## Mean :0.011796 Mean :0.020542 Mean :0.0037949
## 3rd Qu.:0.014710 3rd Qu.:0.023480 3rd Qu.:0.0045580
## Max. :0.052790 Max. :0.078950 Max. :0.0298400
## radius_worst texture_worst perimeter_worst area_worst
## Min. : 7.93 Min. :12.02 Min. : 50.41 Min. : 185.2
## 1st Qu.:13.01 1st Qu.:21.08 1st Qu.: 84.11 1st Qu.: 515.3
## Median :14.97 Median :25.41 Median : 97.66 Median : 686.5
## Mean :16.27 Mean :25.68 Mean :107.26 Mean : 880.6
## 3rd Qu.:18.79 3rd Qu.:29.72 3rd Qu.:125.40 3rd Qu.:1084.0

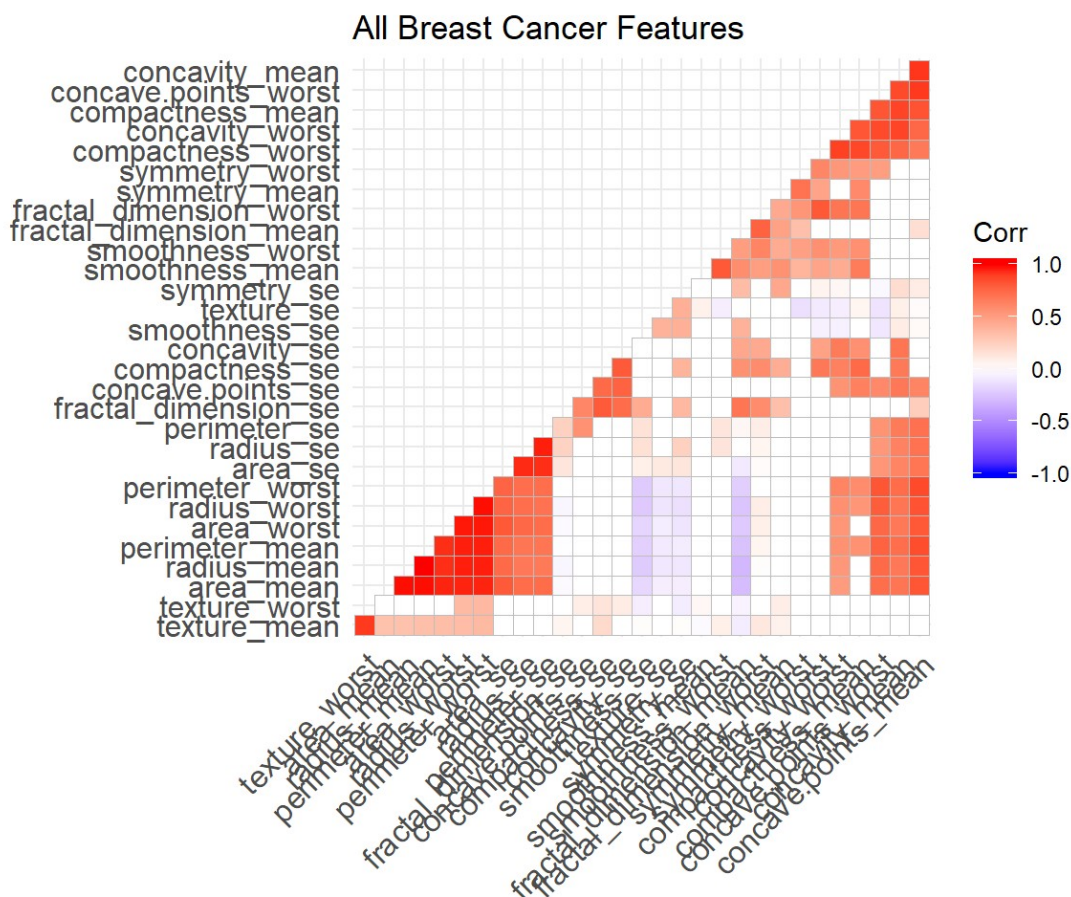
```

```

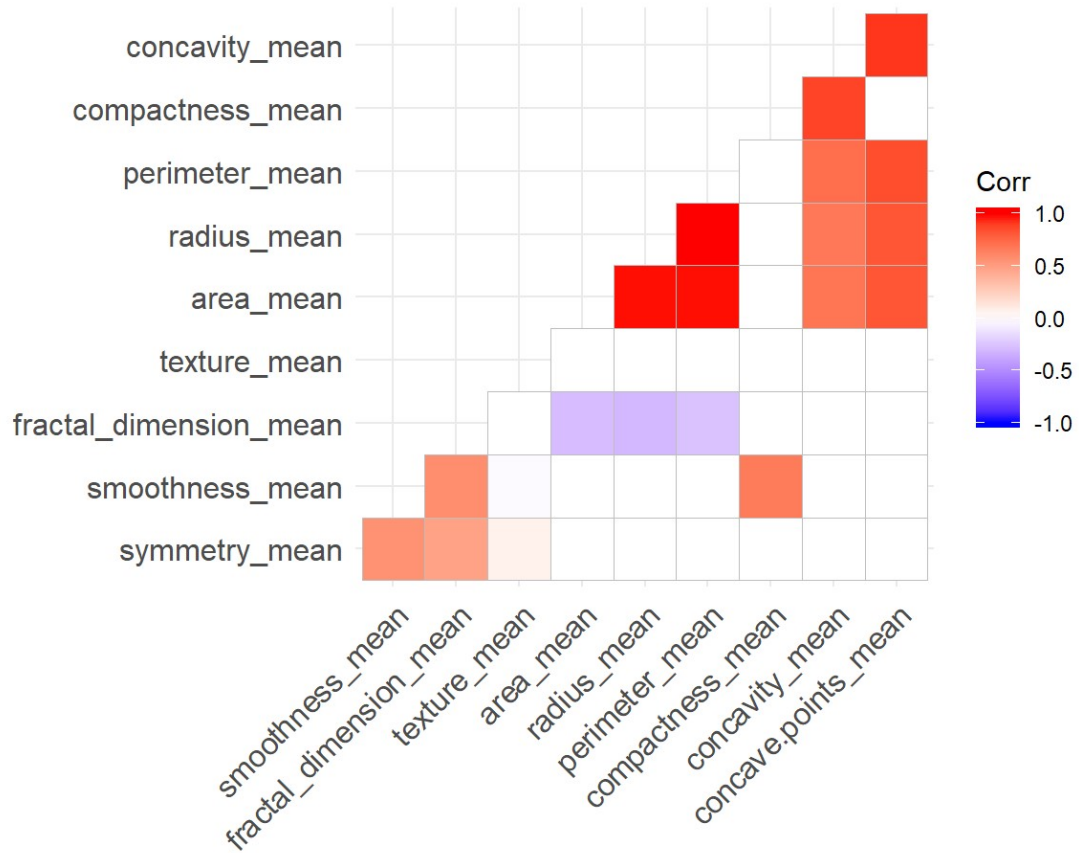
## Max.      :36.04    Max.      :49.54    Max.      :251.20    Max.      :4254.0
## smoothness_worst compactness_worst concavity_worst concave.points_worst
## Min.      :0.07117  Min.      :0.02729  Min.      :0.00000  Min.      :0.00000
## 1st Qu.:0.11660    1st Qu.:0.14720    1st Qu.:0.1145    1st Qu.:0.06493
## Median :0.13130    Median :0.21190    Median :0.2267    Median :0.09993
## Mean     :0.13237    Mean     :0.25427    Mean     :0.2722    Mean     :0.11461
## 3rd Qu.:0.14600    3rd Qu.:0.33910    3rd Qu.:0.3829    3rd Qu.:0.16140
## Max.     :0.22260    Max.     :1.05800    Max.     :1.2520    Max.     :0.29100
## symmetry_worst fractal_dimension_worst
## Min.      :0.1565    Min.      :0.05504
## 1st Qu.:0.2504    1st Qu.:0.07146
## Median :0.2822    Median :0.08004
## Mean     :0.2901    Mean     :0.08395
## 3rd Qu.:0.3179    3rd Qu.:0.09208
## Max.     :0.6638    Max.     :0.20750

```

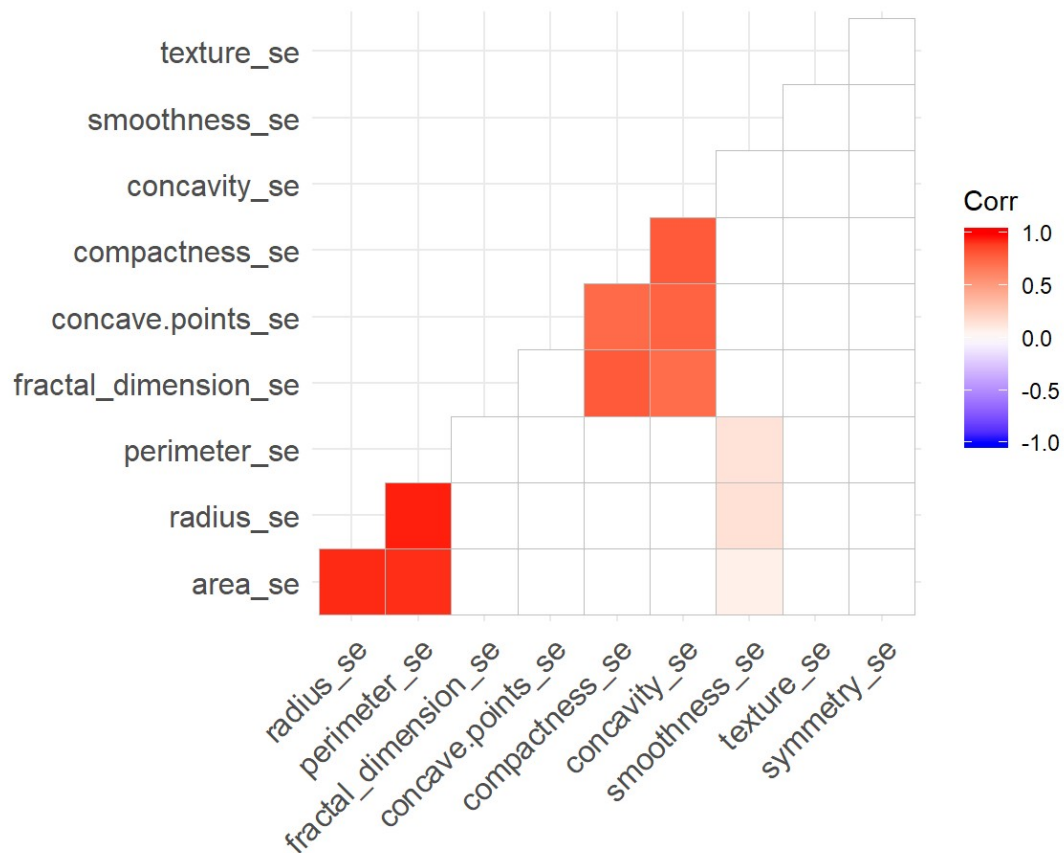
Features were analyzed for correlations. Plots were split by type of feature (mean, sd, or 'worst') to improve visual. Insignificant features were removed from the triangle matrix. Some correlations are expected due to geometry (i.e. radius and area). Of interest are correlations of concavity and compactness across the four plots.

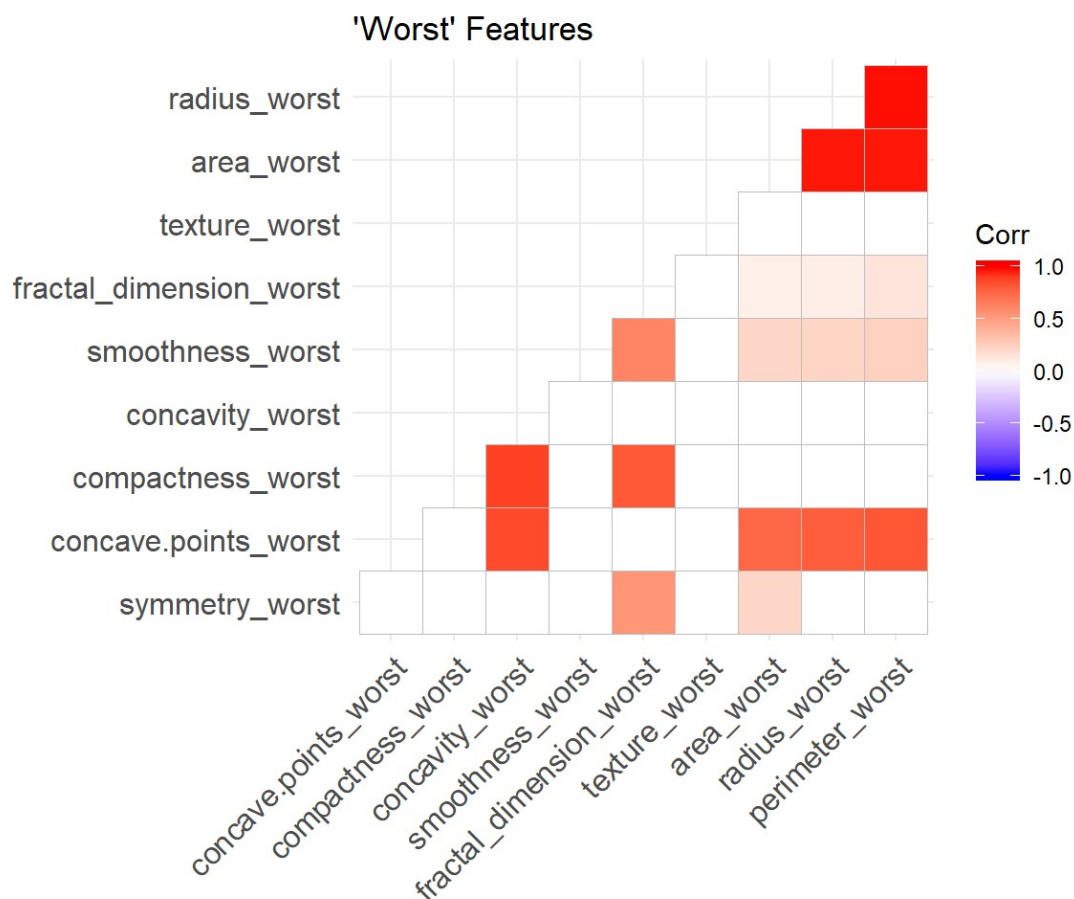


Mean Features



### Std. Dev. Features





## Modeling

The dataset was split into train and test datasets with a 60/40 ratio. Train and Test dataset diagnosis (B/M) column proportions were approximately equal. However the B and M class ratio is not balanced.

```
##
##          B          M
## 0.627566 0.372434
```

```
##
##          B          M
## 0.627193 0.372807
```

The following models were evaluated in order of increasing Balanced Accuracy. A Confusion Matrix (cm function) was used to rely on the function's calculation of Balanced Accuracy. Balanced Accuracy was chosen as the deciding metric vs simple Accuracy given Benign (B) class instances greatly outnumber Malignant (M) instances in the dataset.

1. Decision Tree (rpart)
2. Random Forest
3. SVM Linear

#### 4. SVM Radial

Confusion Matrix for Decision Tree (rpart):

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  B    M
##           B 138  10
##           M   5  75
##
##           Accuracy : 0.9342
##           95% CI : (0.8938, 0.9627)
##    No Information Rate : 0.6272
##    P-Value [Acc > NIR] : <2e-16
##
##           Kappa : 0.8576
##  McNemar's Test P-Value : 0.3017
##
##           Sensitivity : 0.9650
##           Specificity : 0.8824
##           Pos Pred Value : 0.9324
##           Neg Pred Value : 0.9375
##           Prevalence : 0.6272
##           Detection Rate : 0.6053
##    Detection Prevalence : 0.6491
##           Balanced Accuracy : 0.9237
##
##           'Positive' Class : B
##
```

Confusion Matrix for Random Forest shows a significant bump in Balanced Accuracy to over .95:



```

## Confusion Matrix and Statistics
##
##           Reference
## Prediction  B    M
##           B 141    7
##           M   2   78
##
##           Accuracy : 0.9605
##           95% CI : (0.9264, 0.9818)
##           No Information Rate : 0.6272
##           P-Value [Acc > NIR] : <2e-16
##
##           Kappa : 0.9146
##           McNemar's Test P-Value : 0.1824
##
##           Sensitivity : 0.9860
##           Specificity : 0.9176
##           Pos Pred Value : 0.9527
##           Neg Pred Value : 0.9750
##           Prevalence : 0.6272
##           Detection Rate : 0.6184
##           Detection Prevalence : 0.6491
##           Balanced Accuracy : 0.9518
##
##           'Positive' Class : B
##

```

Confusion Matrix for SVM Linear increases Balanced Accuracy just slightly:

```

## Confusion Matrix and Statistics
##
##           Reference
## Prediction  B    M
##           B 142    7
##           M   1   78
##
##           Accuracy : 0.9649
##           95% CI : (0.932, 0.9847)
##           No Information Rate : 0.6272
##           P-Value [Acc > NIR] : <2e-16
##
##           Kappa : 0.9239
##           McNemar's Test P-Value : 0.0771
##
##           Sensitivity : 0.9930
##           Specificity : 0.9176
##           Pos Pred Value : 0.9530
##           Neg Pred Value : 0.9873
##           Prevalence : 0.6272
##           Detection Rate : 0.6228
##           Detection Prevalence : 0.6535
##           Balanced Accuracy : 0.9553
##
##           'Positive' Class : B
##

```

Confusion Matrix for SVM Radial gives another bump to Balanced Accuracy to over .97. This reflects how the dataset predictors better fit a non-linear SVM model providing for 3 more accurate predictions and accurately predicts *all* Benign tumors!

```

## Confusion Matrix and Statistics
##
##           Reference
## Prediction  B    M
##           B 143    5
##           M   0   80
##
##           Accuracy : 0.9781
##           95% CI : (0.9496, 0.9928)
##           No Information Rate : 0.6272
##           P-Value [Acc > NIR] : < 2e-16
##
##           Kappa : 0.9525
##           McNemar's Test P-Value : 0.07364
##
##           Sensitivity : 1.0000
##           Specificity : 0.9412
##           Pos Pred Value : 0.9662
##           Neg Pred Value : 1.0000
##           Prevalence : 0.6272
##           Detection Rate : 0.6272
##           Detection Prevalence : 0.6491
##           Balanced Accuracy : 0.9706
##
##           'Positive' Class : B
##

```

## Conclusion

The Balanced Accuracy for a SVM Radial model against the entire Wisconsin Breast Cancer (Diagnosis) dataset is over .98:

```

## Confusion Matrix and Statistics
##
##           Reference
## Prediction  B    M
##           B 357    8
##           M   0 204
##
##           Accuracy : 0.9859
##           95% CI : (0.9725, 0.9939)
##           No Information Rate : 0.6274
##           P-Value [Acc > NIR] : < 2e-16
##
##           Kappa : 0.9697
##           McNemar's Test P-Value : 0.01333
##
##           Sensitivity : 1.0000
##           Specificity : 0.9623
##           Pos Pred Value : 0.9781
##           Neg Pred Value : 1.0000
##           Prevalence : 0.6274
##           Detection Rate : 0.6274
##           Detection Prevalence : 0.6415
##           Balanced Accuracy : 0.9811
##
##           'Positive' Class : B
##

```

Like during testing, all benign (B) tumors were accurately predicted using the SVM Radial model. SVM Radial was over 96% accurate in identifying malignant (M) tumors, 204 out of 212 malignancies were predicted.