

# Breast Cancer Prediction Analysis

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# Overview

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  - a. Principal Component Analysis (PCA)
3. Feature Selection with LASSO
4. Prediction of Malignant Tumors
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# Introduction and Motivations

# Motivations

- Breast cancer is a serious and prevalent disease
  - 1 out of 8 women develop breast cancer in the US<sup>1</sup>
  - 1 out of 3 new cancer cases in women are breast cancer<sup>1</sup>
- Most biopsied tumors are benign (non-cancerous)—only 20% are malignant (cancerous)<sup>2</sup>
- Accordingly, identifying characteristics of malignant tumors is important to avoid mistreatment of cancer (e.g., unnecessary chemotherapy)
- Highly accurate classification models may support healthcare decision making and tumor identification

<sup>1</sup><https://www.cancer.org/cancer/breast-cancer/about/how-common-is-breast-cancer.html>

<sup>2</sup><https://cancer.stonybrookmedicine.edu/breast-cancer-team/patients/bse/breastlumps>

# Introduction to Dataset

- Wisconsin Tumor Dataset with tumor information collected from **N=569** individuals<sup>3</sup>
- “Features are computed from a digitized image of a fine needle aspirate (FNA) of a breast mass. They describe characteristics of the cell nuclei present in the image.”
- Outcome variable was tumor diagnosis: **benign** (coded as 0, **N=357**, ~63%) **malignant** (coded as 1, **N=212**, ~37%)
- **Variables:**
  1. **radius** (mean of distances from center to points on the perimeter)
  2. **texture** (standard deviation of gray-scale values)
  3. **perimeter**
  4. **area**
  5. **smoothness** (local variation in radius lengths)
  6. **compactness** ( $\text{perimeter}^2 / \text{area} - 1.0$ )
  7. **concavity** (severity of concave portions of the contour)
  8. **concave points** (number of concave portions of the contour)
  9. **symmetry**
  10. **fractal dimension** ("coastline approximation" - 1)
- Mean, standard error, and “worst” value for each feature calculated, totalling 10\*3=30 variables

<sup>3</sup><https://www.kaggle.com/datasets/uciml/breast-cancer-wisconsin-data>

# Exploratory Data Analysis

# Exploratory Data Analysis

- Looked at missing values, data types, number of unique values in each column
- Checked the distribution of the variables
- Encode target variable (M = malignant, B = benign) to 1, 0

```
1 # Check for missing values
2 print(df.isna().sum())
```

```
✓ 0.2s
```

```
id
diagnosis
radius_mean
texture_mean
perimeter_mean
area_mean
smoothness_mean
compactness_mean
concavity_mean
concave_points_mean
symmetry_mean
fractal_dimension_mean
radius_se
texture_se
perimeter_se
area_se
smoothness_se
compactness_se
concavity_se
concave_points_se
symmetry_se
fractal_dimension_se
radius_worst
texture_worst
perimeter_worst
area_worst
smoothness_worst
compactness_worst
concavity_worst
concave_points_worst
symmetry_worst
fractal_dimension_worst
Unnamed: 32
dtype: int64
```

```
1 # Print the data types of the columns
2 print(df.dtypes)
```

```
✓ 0.2s
```

```
id int64
diagnosis int64
radius_mean float64
texture_mean float64
perimeter_mean float64
area_mean float64
smoothness_mean float64
compactness_mean float64
concavity_mean float64
concave_points_mean float64
symmetry_mean float64
fractal_dimension_mean float64
radius_se float64
texture_se float64
perimeter_se float64
area_se float64
smoothness_se float64
compactness_se float64
concavity_se float64
concave_points_se float64
symmetry_se float64
fractal_dimension_se float64
radius_worst float64
texture_worst float64
perimeter_worst float64
area_worst float64
smoothness_worst float64
compactness_worst float64
concavity_worst float64
concave_points_worst float64
symmetry_worst float64
fractal_dimension_worst float64
Unnamed: 32 float64
dtype: object
```

```
1 # Print the number of unique values in each column
2 print(df.nunique())
```

```
✓ 0.2s
```

```
id 569
diagnosis 2
radius_mean 456
texture_mean 479
perimeter_mean 522
area_mean 539
smoothness_mean 474
compactness_mean 537
concavity_mean 537
concave_points_mean 542
symmetry_mean 432
fractal_dimension_mean 499
radius_se 540
texture_se 519
perimeter_se 533
area_se 528
smoothness_se 547
compactness_se 541
concavity_se 533
concave_points_se 507
symmetry_se 498
fractal_dimension_se 545
radius_worst 457
texture_worst 511
perimeter_worst 514
area_worst 544
smoothness_worst 411
compactness_worst 529
concavity_worst 539
concave_points_worst 492
symmetry_worst 500
fractal_dimension_worst 535
Unnamed: 32 0
dtype: int64
```

```
1 df.describe()
```

```
✓ 0.7s
```

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	...	texture_worst	perimeter_worst	area_worst	smoothness_worst	compactness_worst	concavity_worst	concave points_worst	symmetry_worst	fractal_dimension_worst
count	5.690000e+02	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	...	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000
mean	3.037183e+07	0.372583	14.127292	19.289649	91.969033	654.889104	0.096360	0.104341	0.088799	0.048919	...	25.677223	107.261213	860.583128	0.132369	0.264265	0.271188	0.114606	0.290076	0.083946
std	1.260206e+08	0.483918	3.524049	4.301036	24.299891	351.914129	0.014064	0.052813	0.079720	0.038803	...	6.146258	33.602542	569.356993	0.022832	0.157336	0.208624	0.065732	0.061867	0.018061
min	8.670000e+03	0.000000	6.981000	9.710000	43.790000	143.500000	0.052630	0.019380	0.000000	0.000000	...	12.020000	50.410000	185.200000	0.071170	0.027290	0.000000	0.000000	0.156500	0.056040
25%	8.692180e+05	0.000000	11.700000	16.170000	75.170000	420.300000	0.086370	0.064920	0.029560	0.020310	...	21.080000	84.110000	515.300000	0.116600	0.147200	0.114500	0.064930	0.250400	0.071460
50%	9.060240e+05	0.000000	13.370000	18.840000	86.240000	551.100000	0.095870	0.092630	0.061540	0.033500	...	25.410000	97.660000	686.500000	0.131300	0.219100	0.226700	0.099930	0.282200	0.080040
75%	8.813129e+06	1.000000	15.780000	21.800000	104.100000	782.700000	0.105300	0.130400	0.130700	0.074000	...	29.720000	125.400000	1084.000000	0.146000	0.339100	0.382900	0.161400	0.317900	0.092080
max	9.113205e+08	1.000000	28.110000	39.280000	188.500000	2501.000000	0.163400	0.345400	0.426800	0.201200	...	49.540000	251.200000	4254.000000	0.222600	1.058000	1.252000	0.291000	0.663800	0.207500

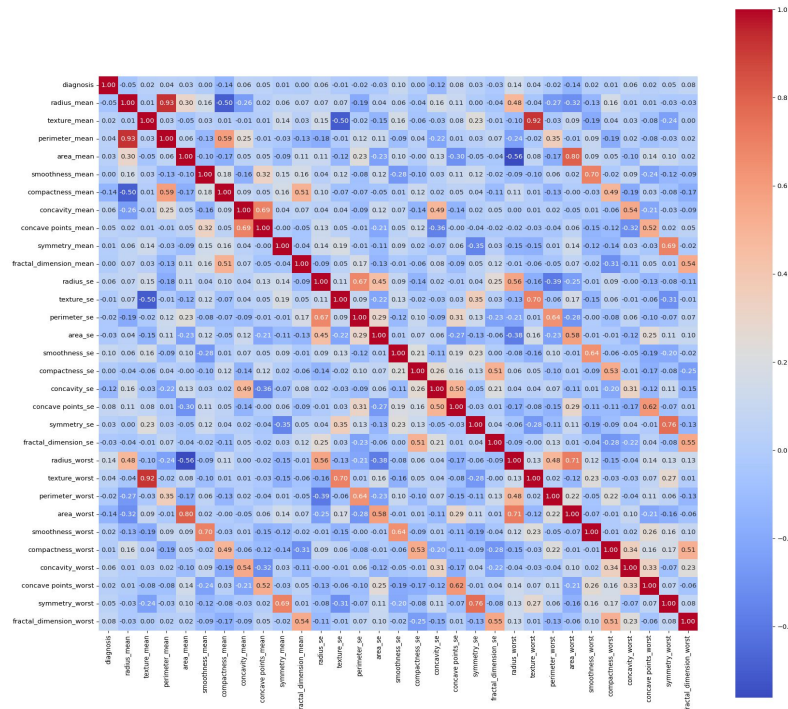
# Exploratory Data Analysis

- Partial correlation plot: measures the strength of the linear relationship between two variables while controlling for the effects of one or more additional variables
- Help remove the influence of confounding factors and produce a more accurate prediction model
- The variables that are highly correlated with the diagnosis may have low correlation values in the partial correlation plot due to the effects of other variables

Top 21 Variables Correlated with Diagnosis:

concavity_worst	0.95
symmetry_se	0.94
fractal_dimension_worst	0.94
compactness_worst	0.93
compactness_se	0.93
concavity_se	0.93
concavity_mean	0.92
smoothness_worst	0.92
symmetry_worst	0.90
fractal_dimension_se	0.90
perimeter_se	0.88
concave points_worst	0.87
compactness_mean	0.86
perimeter_worst	0.85
radius_se	0.85
radius_worst	0.85
concave points_mean	0.84
perimeter_mean	0.82
symmetry_mean	0.82
concave points_se	0.81
fractal_dimension_mean	0.80

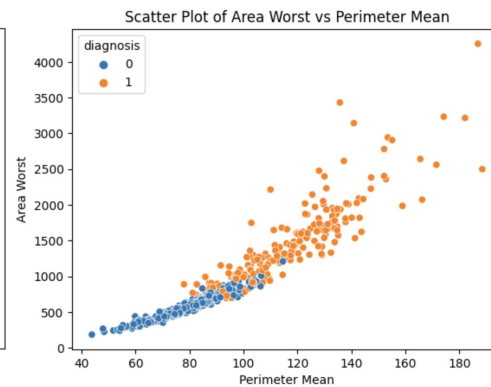
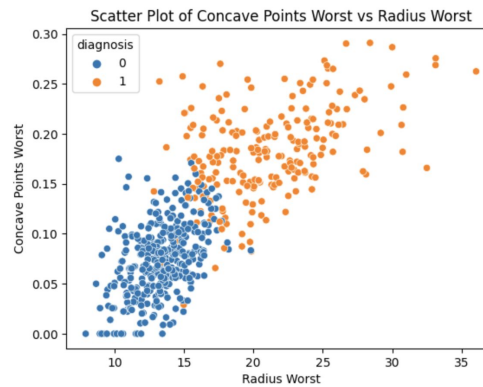
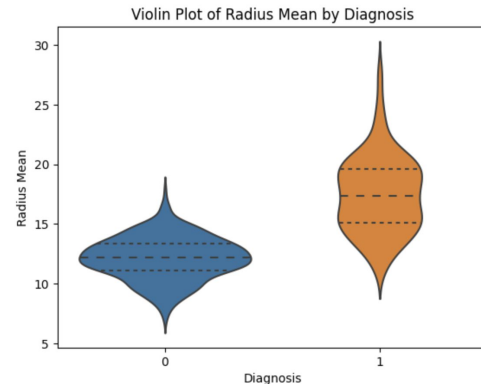
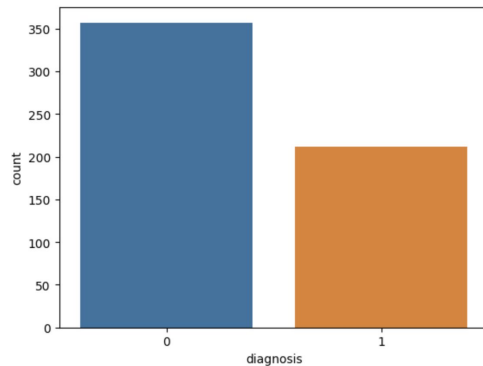
Name: diagnosis, dtype: object



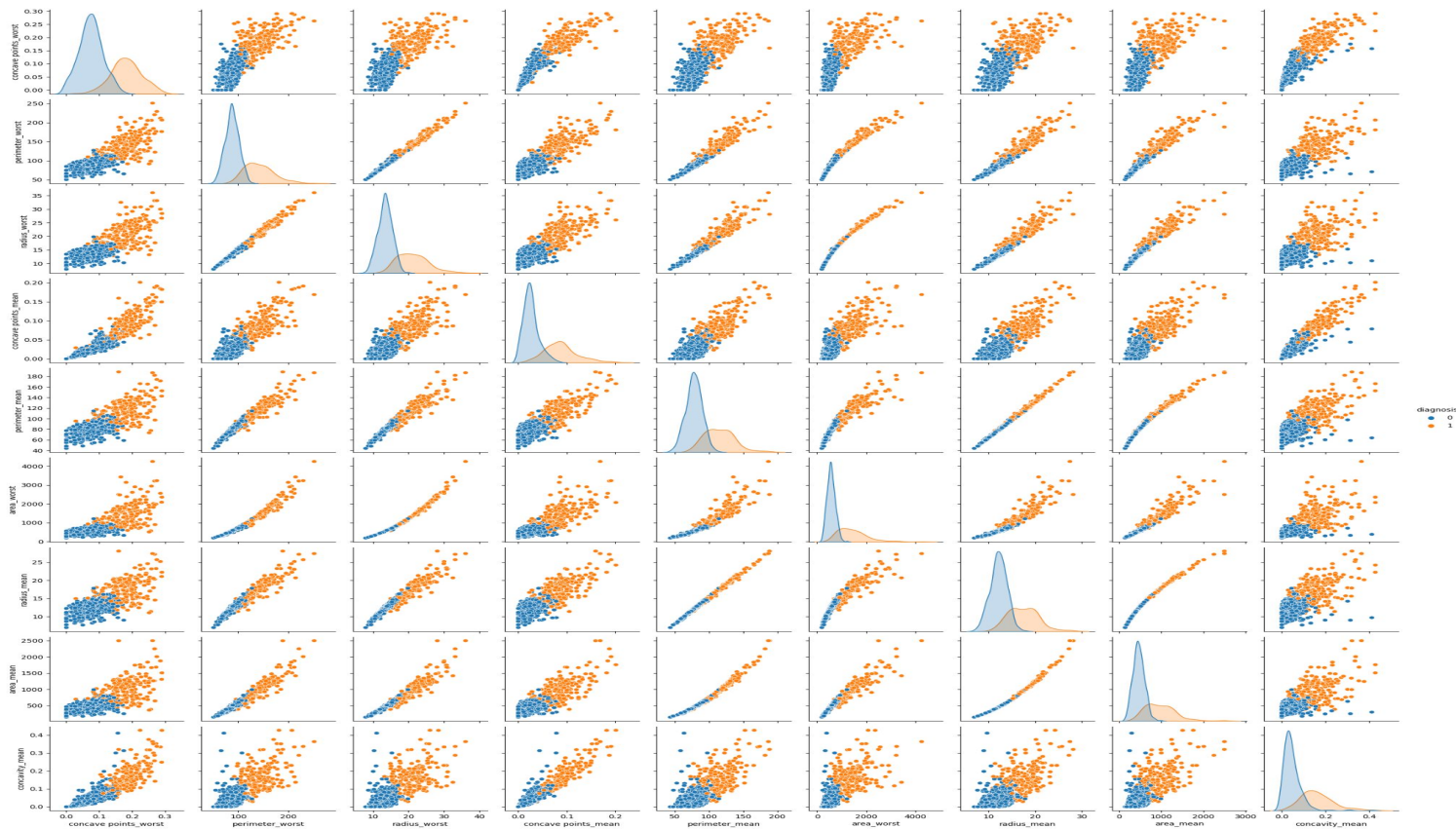


# Exploratory Data Analysis

- Balanced dataset
- Clear separation between the diagnosis groups in the scatter plot of concave points\_worst vs radius\_worst
- The mean radius for malignant tumors tends to be larger than that for benign tumors in the violin plot of radius\_mean by diagnosis

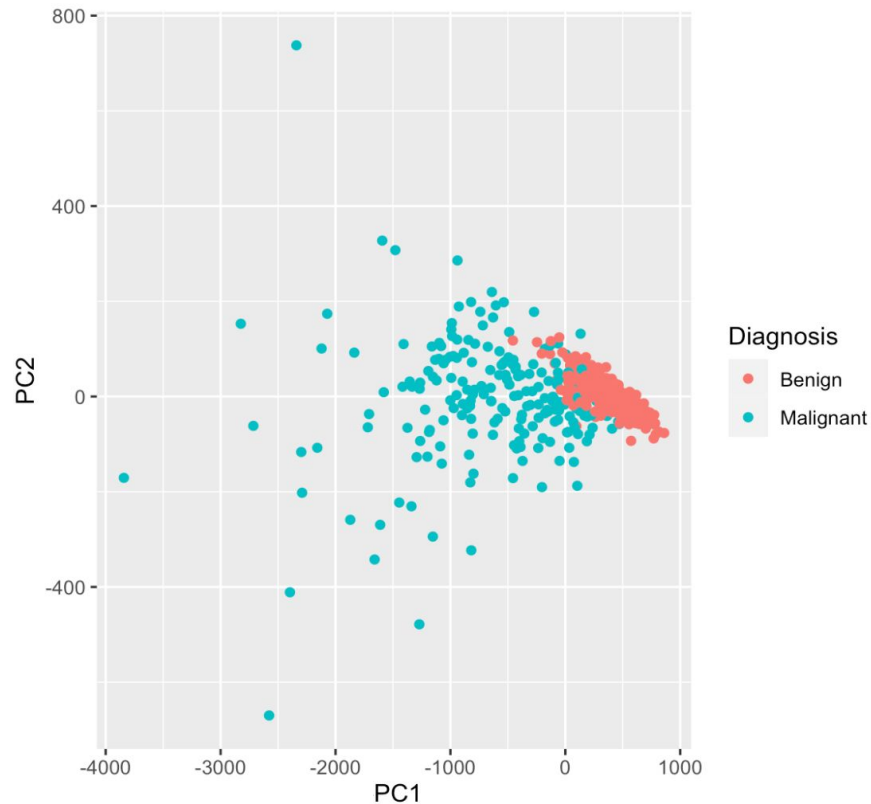
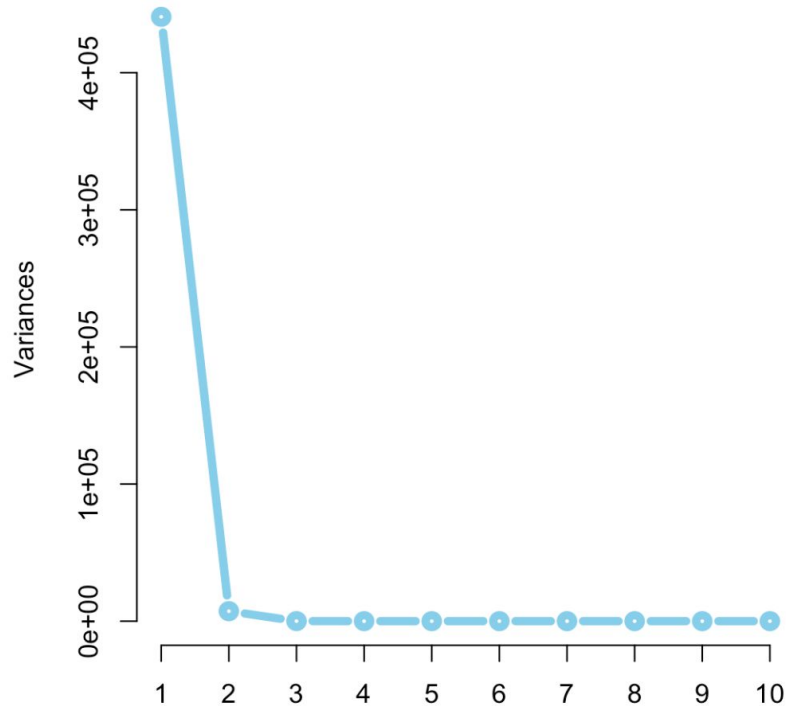


# Exploratory Data Analysis



# Principal Component Analysis (PCA)

Variances of the First Ten Principle Components



# Feature Selection: LASSO

# LASSO Regression with Cross Validation

- We scaled the dataset using MinMax Scaling algorithm. Ensuring that all the features are on similar scale, thereby preventing any bias in the model. Since some machine learning algorithms tend to be impacted by numerical instability, using this transformation we eliminate those issues.
- Scaled data was passed into Lasso regression model with 5 fold cross validation to avoid data leakage, and overfitting.
- From 30 variables, 21 variables were selected by the regression model, with an Accuracy of 0.963.

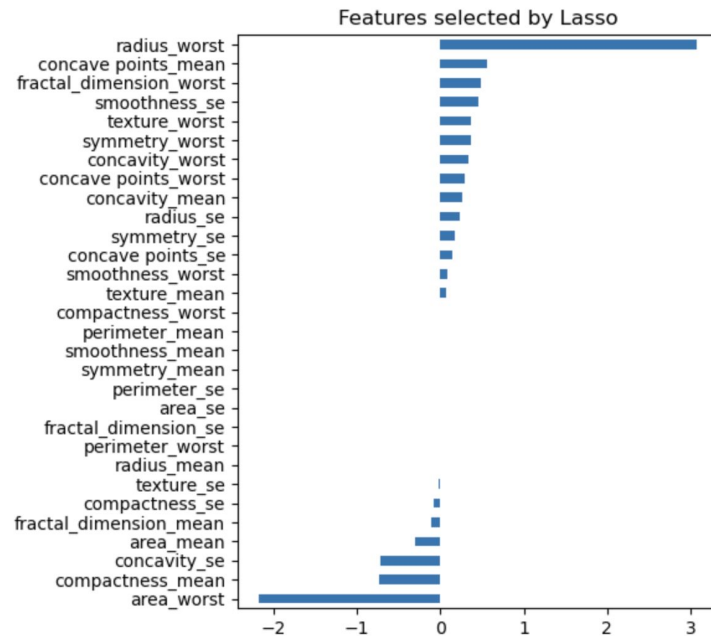
```
#Using LassoCV  
  
lasso_model = LassoCV(cv=5, random_state=40)  
lasso_model.fit(xtrain, ytrain)
```

$$x' = \frac{x - \min(x)}{\max(x) - \min(x)}$$

```
In [9]: from sklearn.metrics import f1_score  
  
coef = pd.Series(lasso_model.coef_, index=breast_data.columns[2:])  
best_cols = coef[coef != 0].index.tolist()  
  
ypred = lasso_model.predict(xtest)  
  
# calculate the accuracy of the predictions  
accuracy = f1_score(ytest, ypred.round())  
  
# print the selected columns and the accuracy of the predictions  
print("Selected columns: " + ", ".join(best_cols))  
print("Accuracy:", round(accuracy, 4))  
  
Selected columns: texture_mean, area_mean, compactness_mean, concavity_mean, concave points_mean, fractal_dimension_m  
ean, radius_se, texture_se, smoothness_se, compactness_se, concavity_se, concave points_se, symmetry_se, radius_wors  
t, texture_worst, area_worst, smoothness_worst, concavity_worst, concave points_worst, symmetry_worst, fractal_dimens  
ion_worst  
Accuracy: 0.963
```

# Features selected by Lasso

- After analyzing the data on 5 fold cross-validation set, we found that 21 features were important for further analysis, since their estimates weren't reduced to zero.
- The model also explains relationship between different columns and the outcome variable, ex. Columns like concavity\_se, area\_worst negatively influence the outcome of cancer, whereas columns like smoothness, radius\_worst, positively influence the outcome.



# Prediction Models

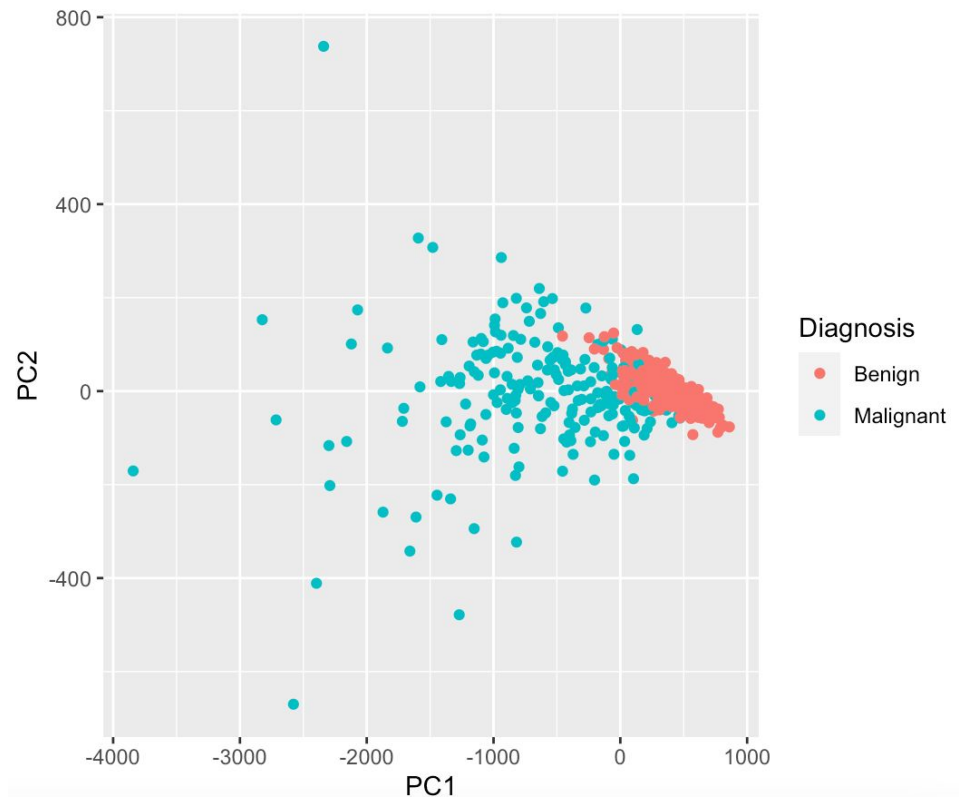
# K-Means Clustering

- Used k-means clustering and compared to given labels (malignant vs. benign)
- Used  $k = 2$  since the actual outcome is binary
- In the table, 1 = benign, 2 = malignant for the clusters
- K-means algorithm over classifies individuals into the benign group
- Accuracy of 85%, silhouette score 0.70

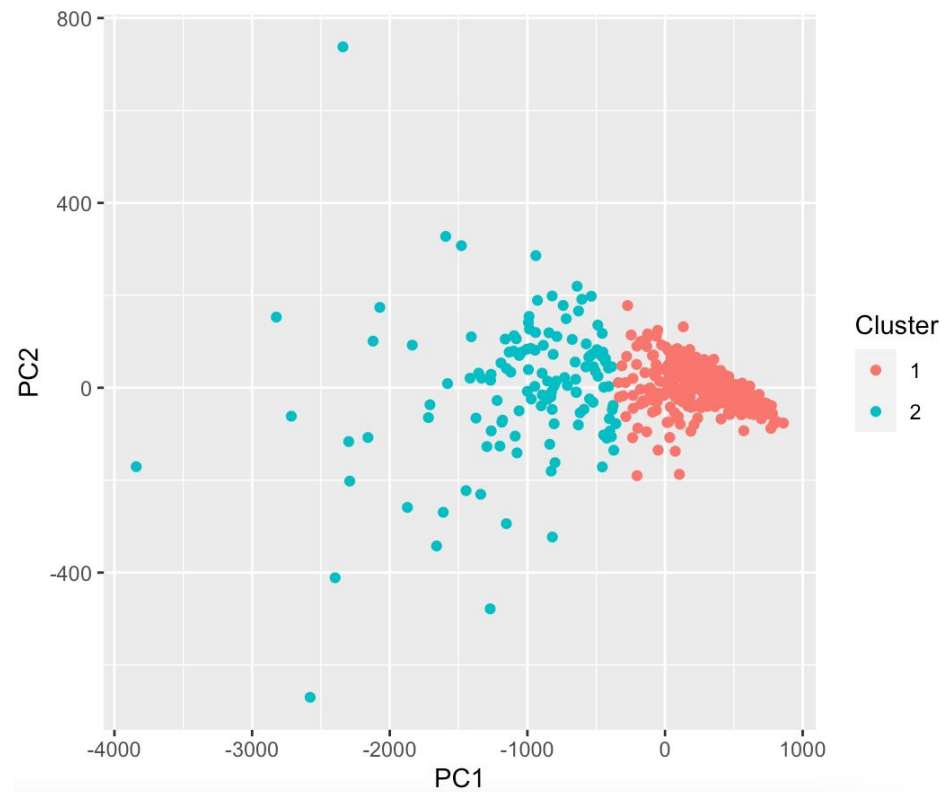
	Benign	Malignant
1	356	82
2	1	130



# Labels From Dataset



# K-Means clustering



# Linear Discriminant Analysis (LDA)

- Supervised classification method
- LDA projects the data onto a subspace
  - Minimize variance within classes, maximize distance between classes

Approach:

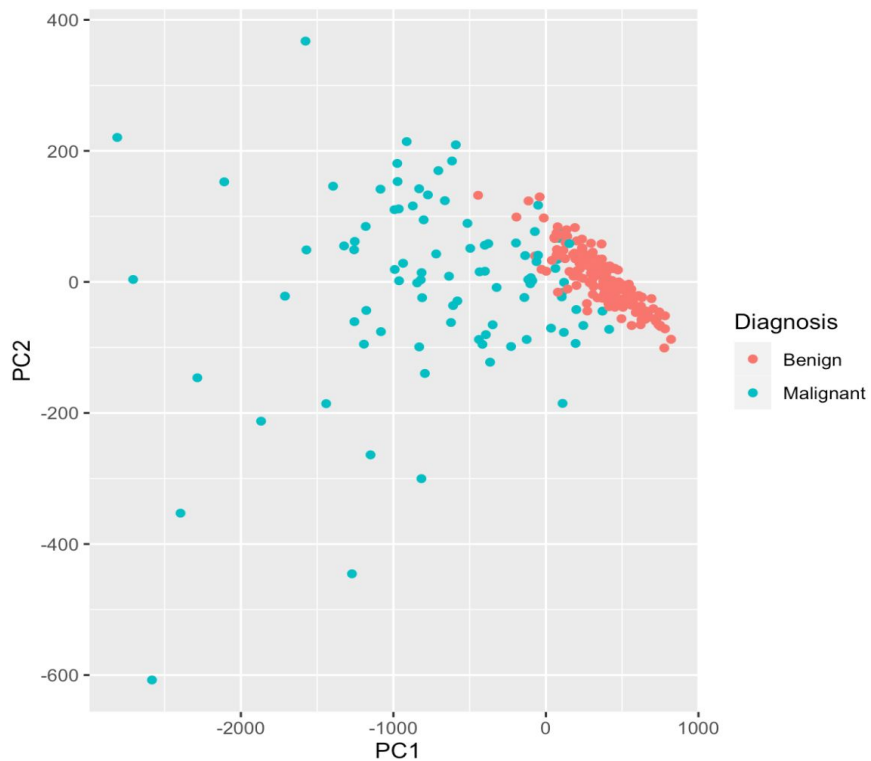
- Train vs test split
- Fit to training data, predict on testing data
- Compared the fitted labels to the actual labels
- Accuracy of 96%
- Higher accuracy than k-means

		B	M
Training Accuracy:	B	286	1
	M	16	152
96%			

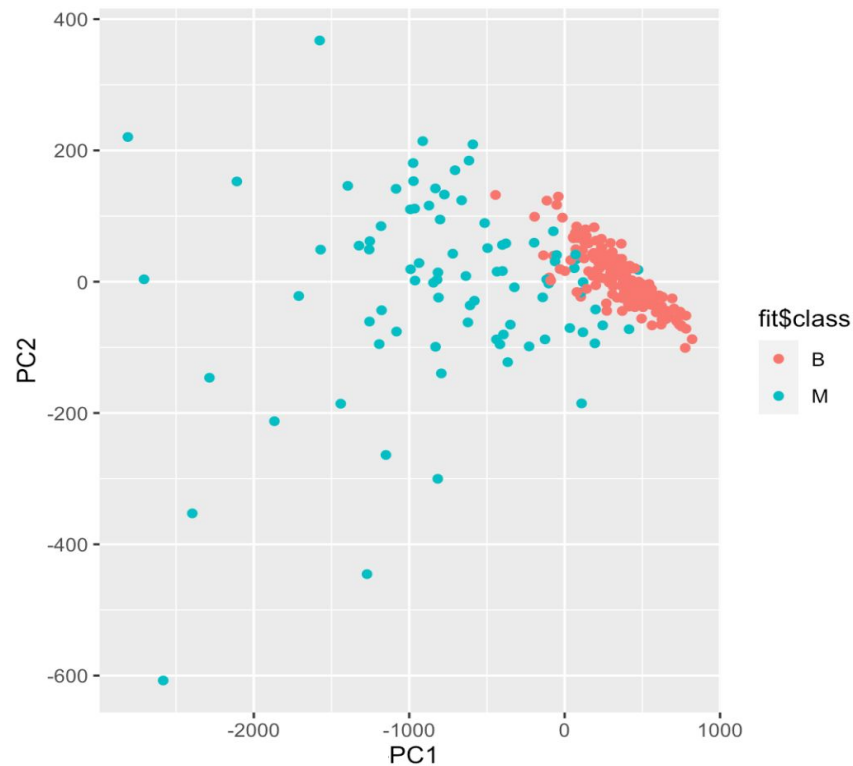
		B	M
Testing Accuracy:	B	167	2
	M	8	84
96%			

# LDA

## Original Labels

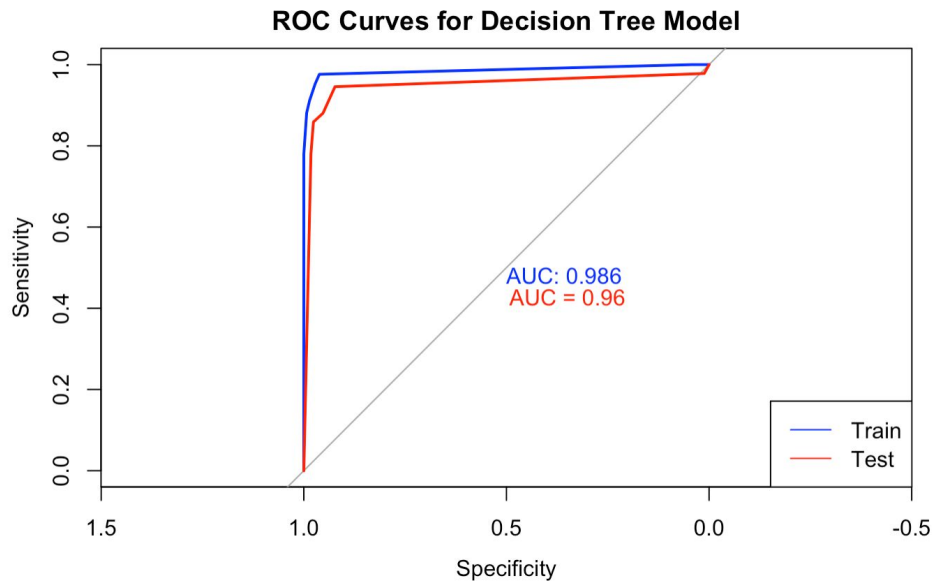


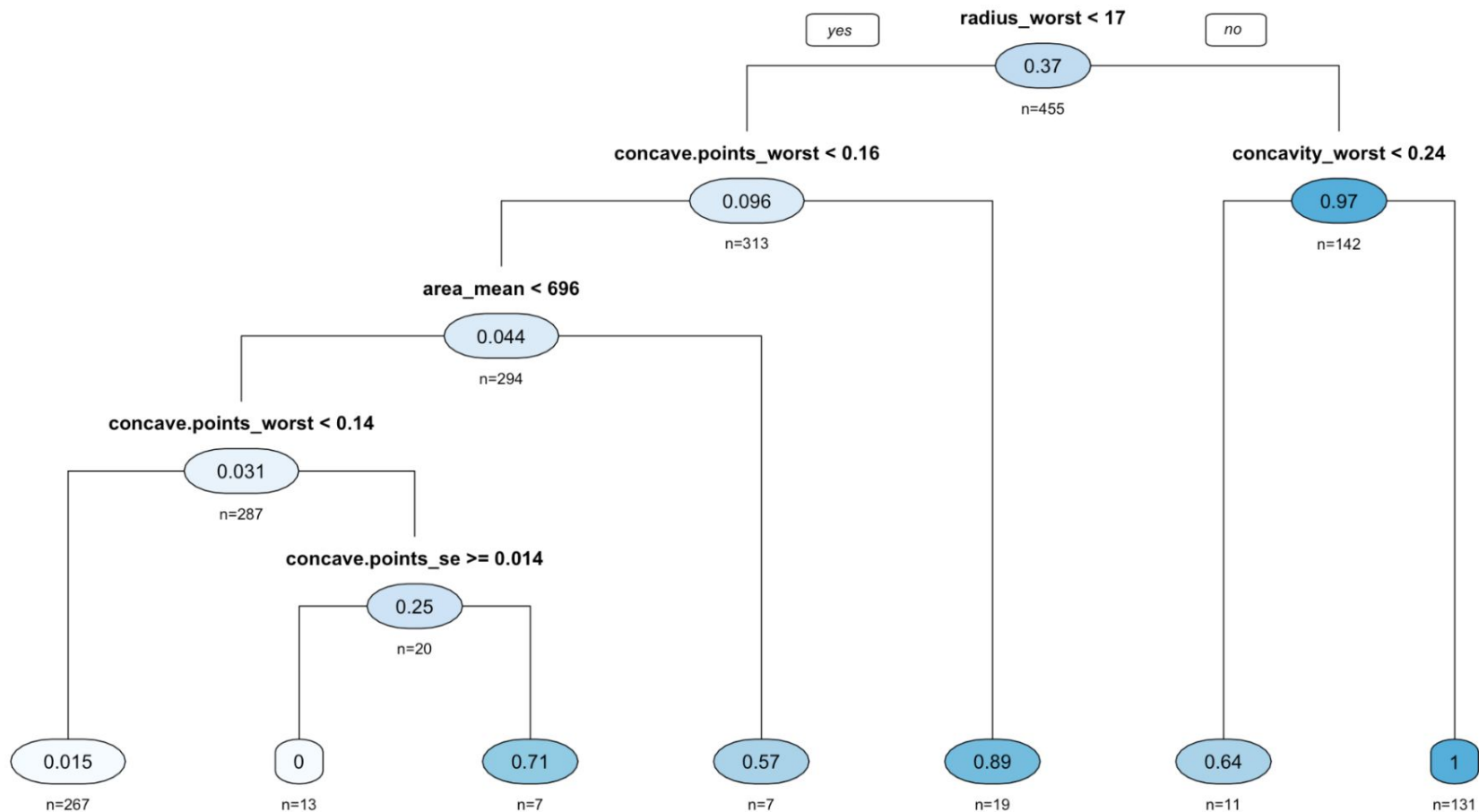
## LDA fit on test subset



# Decision Tree

- Used 80%/20% train/test split to subset data
- `rpart()` function in R used with default parameters to fit model on train set, then predict on test

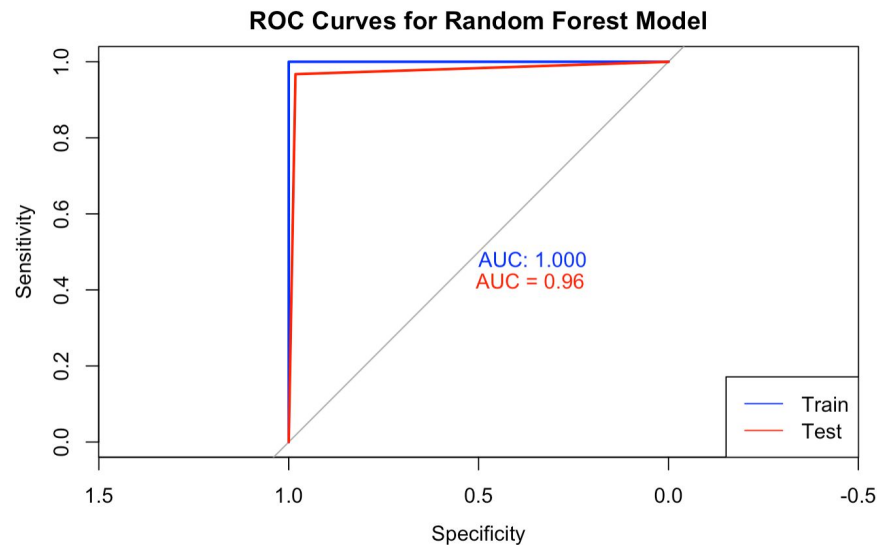




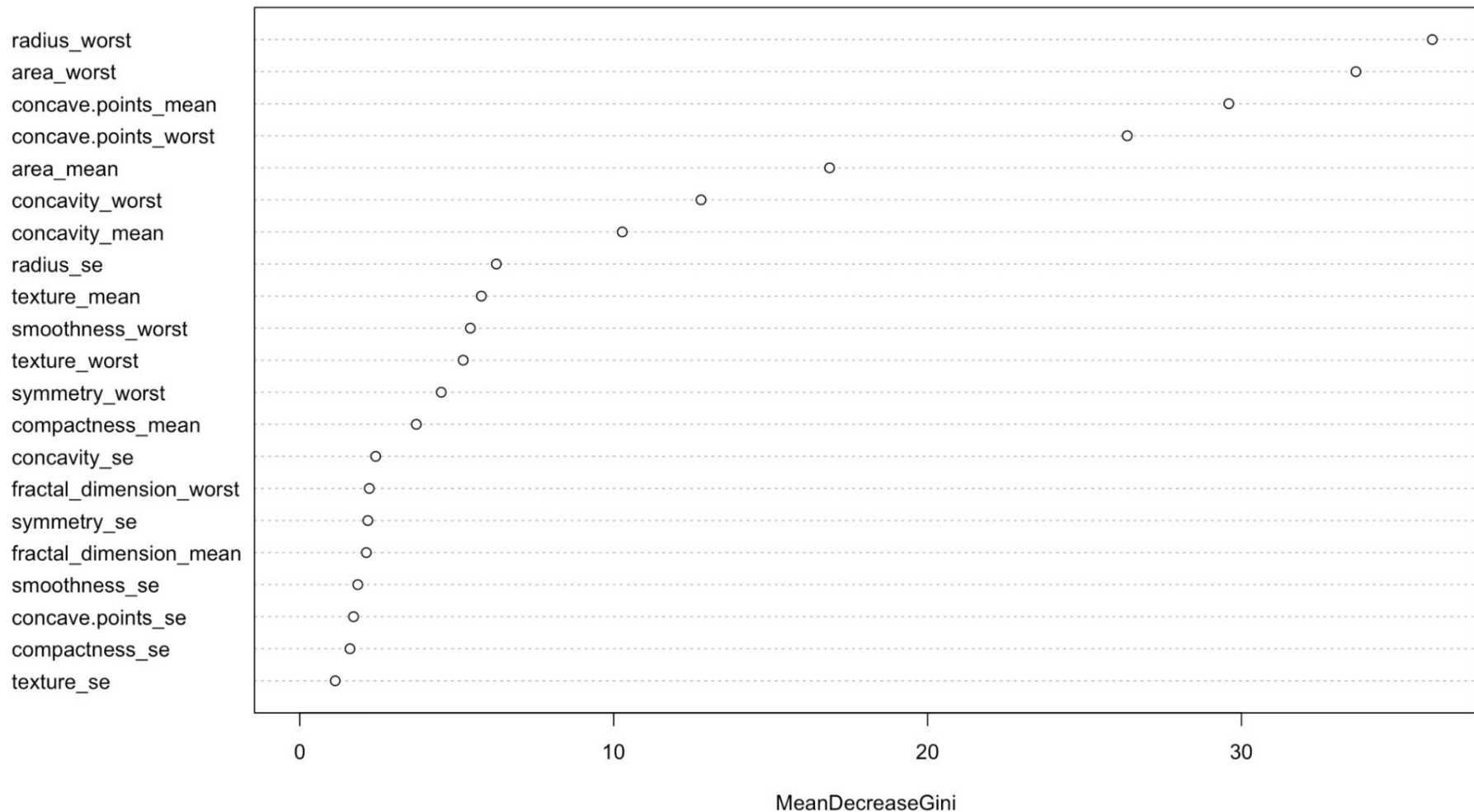
# Random Forest

- Used RandomForest() in R to fit model on 80% train set
- Number of trees = 500, features per split = sqrt(p) (p=21)

pred_rf_te	0	1
0	166	3
1	3	89

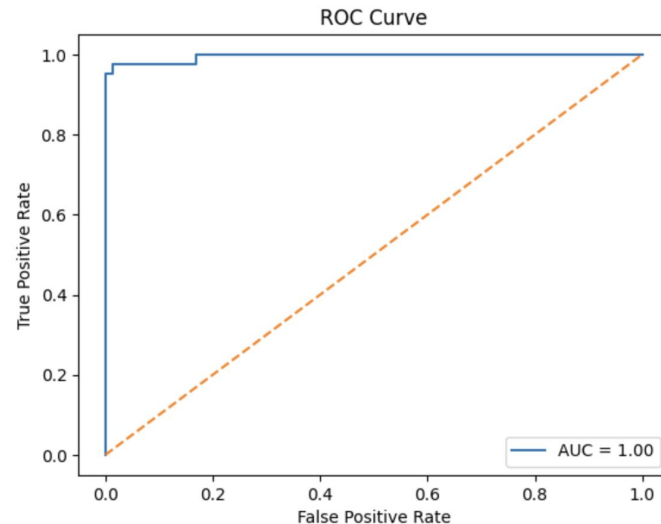


Feature Importance of Random Forest Model



# Neural Network

- 1 input layer, 1 hidden layer, and 1 output layer of 1 neuron, with ReLU activation functions for the input and hidden layers (simple, computationally efficient), and sigmoid activation function for the output layer (used when output layer of binary classification problems)
- 50 epochs (number of times the entire dataset is passed through the neural network during the training process)
- batch size of 32 (the model updates its weights and biases based on 32 training examples at a time.)



Test loss: 0.069, Test accuracy: 0.982

ReLU:  $f(x) = \max(0, x)$

Sigmoid:  $f(x) = 1 / (1 + \exp(-x))$



# Discussion

# Discussion of Model Results

- PCA able to explain majority of variance in data & visualize diagnosis clusters
- Out of 30 variables, Lasso Regression model identifies 21 as most informative; these variables were included in all classification models
- All classifications obtained high performance ( $AUC > 0.95$ )
  - Neural network had the best performance
  - Decision tree likely the best model for clinical interpretability
- Variables for tumor radius, concavity points, and area were among most informative predictors



Thank you!

