

# Breast Cancer Data Analysis

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# Executive Summary (project and project goals)

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Create accurate and reliable models to predict if somebody has breast cancer and which type of breast cancer they have.

Data Sets:

Breast Cancer Wisconsin - UC Irvin:

- (<https://archive.ics.uci.edu/dataset/17/breast+cancer+wisconsin+diagnostic>)

BRCA – Kaggle

- (<https://www.kaggle.com/datasets/amandam1/breastcancerdataset>)

# BC Dataset - Selected Models

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Breast Cancer Wisconsin - UC Irvine

1. Neural Network
2. XGB Classifier
3. Logistic Regression
4. Support Vector Machine

# BRCA Dataset - Selected Model

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## BRCA – Kaggle

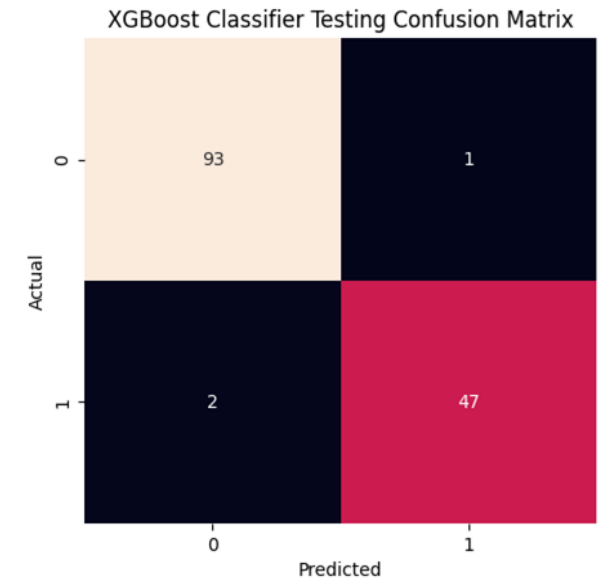
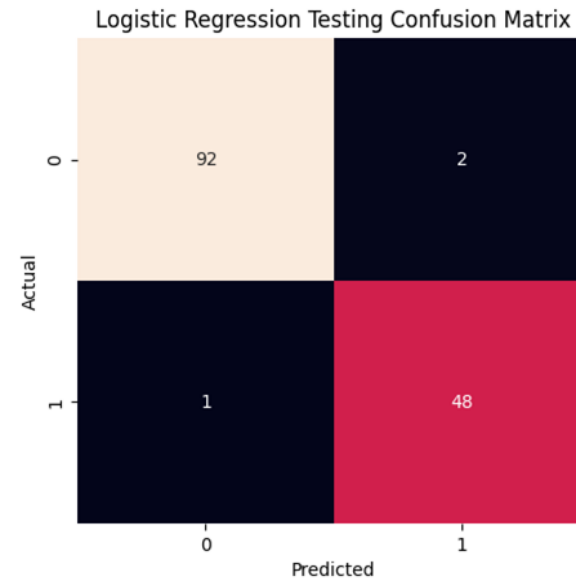
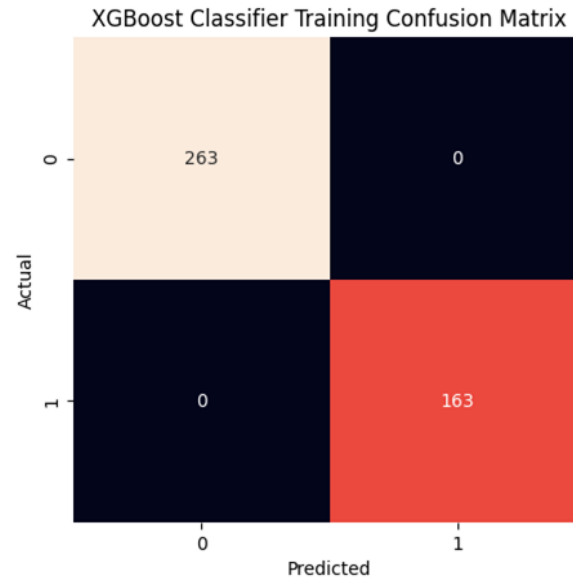
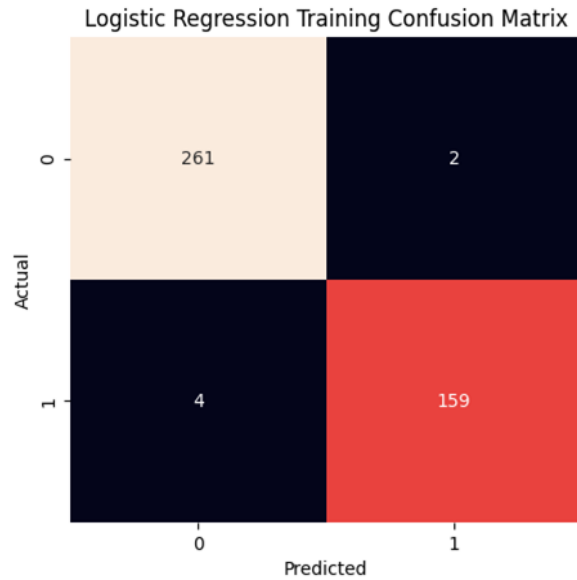
1. Neural Network
2. Sequential Neural Network
3. Support Vector Machine
4. K-Nearest Neighbors- KNN

# Data Preparation Process

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- Describe the source of your data and why you chose it for your project.
  - Kaggle is well known source for data sets.
  - we choose the BC data because of its large set of features to predict a cancer cell.
- Describe the collection, cleanup, and preparation process.
  - Collection searching on Kaggle for usable datasets
  - Identifying feature and target wanted, dropping unwanted columns, transforming data into format the models will work with using One Hot Encoder, Label Encoder, and to categorical, then Standard Scaler to scale the sets.
- Describe the training process.
  - Separating the features and target into training and testing datasets, scaling the datasets, fitting the data into the models, predicting results based on the testing data.

# BC Dataset – Logistic Regression vs. XGBoost Classifier



# BC Dataset – Classification Reports

Logistic Regression Model Training Classification Report

	precision	recall	f1-score	support
0	0.98	0.99	0.99	263
1	0.99	0.98	0.98	163
accuracy			0.99	426
macro avg	0.99	0.98	0.99	426
weighted avg	0.99	0.99	0.99	426

Logistic Regression Model Testing Classification Report

	precision	recall	f1-score	support
0	0.99	0.98	0.98	94
1	0.96	0.98	0.97	49
accuracy			0.98	143
macro avg	0.97	0.98	0.98	143
weighted avg	0.98	0.98	0.98	143

XGB Classifier Model Training Classification Report

	precision	recall	f1-score	support
0	1.00	1.00	1.00	263
1	1.00	1.00	1.00	163
accuracy			1.00	426
macro avg	1.00	1.00	1.00	426
weighted avg	1.00	1.00	1.00	426

XGB Classifier Model Testing Classification Report

	precision	recall	f1-score	support
0	0.98	0.99	0.98	94
1	0.98	0.96	0.97	49
accuracy			0.98	143
macro avg	0.98	0.97	0.98	143
weighted avg	0.98	0.98	0.98	143

# BC Dataset Neural Network

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## Setup

### Layers

- `nn.add(Dense(units=16, input_dim=31, activation="relu"))`
- `nn.add(Dense(units=8, activation="relu"))`
- `nn.add(Dense(units=1, activation="sigmoid"))`

### Compilation

- `nn.compile(loss="binary_crossentropy", optimizer="adam", metrics=["accuracy"])`

### Fitting the model

- `nn.fit(X_train_scaled, y_train, epochs=200)`

## Results

### Evaluation

- loss: 0.1247
- categorical\_accuracy: 0.9650

### Predictions

- Benign (0.0) - 88
- malignant (1.0) - 55

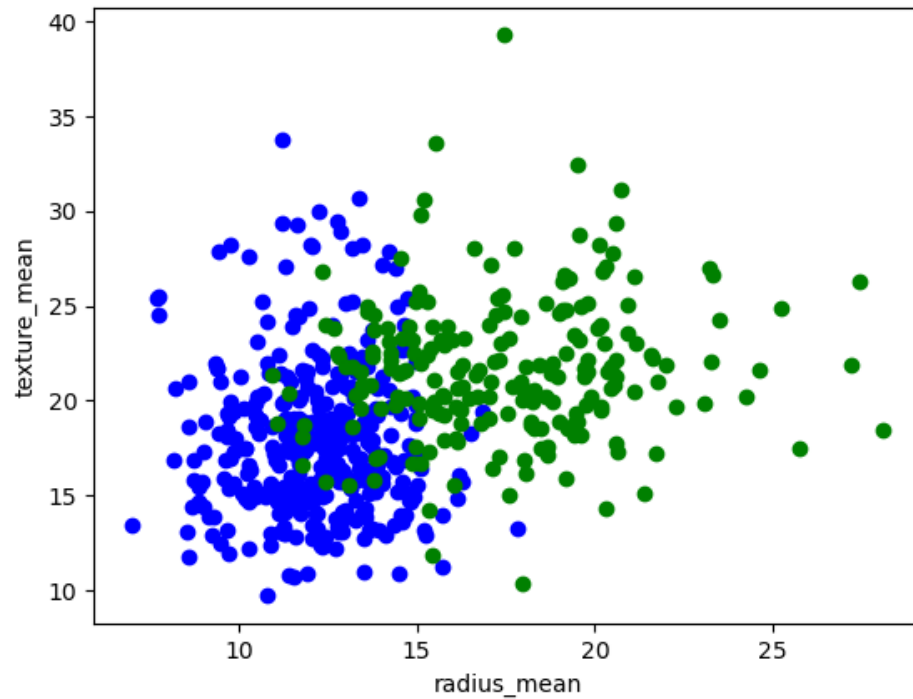


# BC Dataset

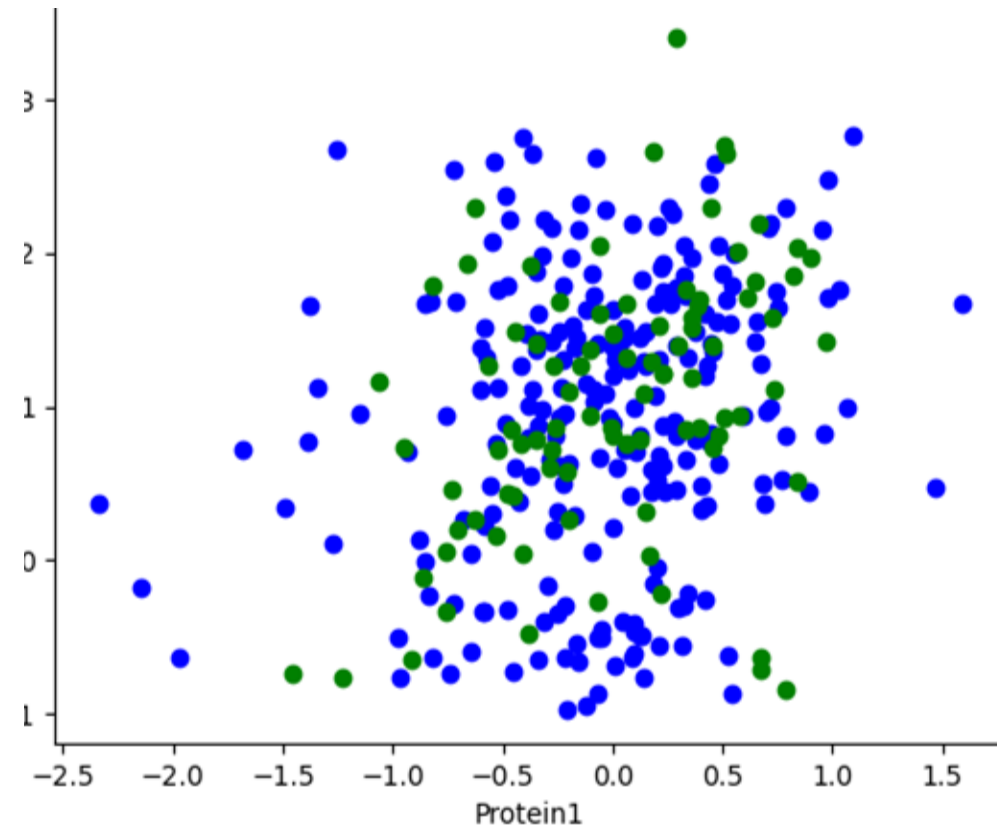
## svm

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BC data



BRCA data



# Data Preprocessing

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## BC Data

559 rows/31 columns

no nulls

y= diagnosis

x= drop diagnosis

## BRCA Data

Dropped 6 columns

one hot encoder(histology)

nan after encoding

y= histology

x= drop histology

# SVM

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## BC Data

- Kernel selection - Linear
- Parameter Tuning- N
- 80% train set
- random state=1
- Acc score = 0.96

## BRCA Data

- imbalanced data?
- Parameter Tuning- N
- 80% train set
- random state=1
- Acc score = 0.58

# ann/knn

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BC Data

ANN

Tuning- N

BRCA Data

KNN

Tuning- y

neighbor classifier- 2,3,4

2 accuracy= 0.51

3 accuracy= 0.46

4 accuracy= 0.55

# BRCA Dataset Neural Network

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## Setup

### Layers

- `nn.add(Dense(units=7, input_dim=14, activation="relu"))`
- `nn.add(Dense(units=4, activation="relu"))`
- `nn.add(Dense(units=2, activation="relu"))`
- `nn.add(Dense(units=1, activation="relu"))`
- `nn.add(Dense(units=1, activation="relu"))`

### Compilation

- `nn.compile(loss="binary_crossentropy", optimizer="adam", metrics=["accuracy"])`

### Fitting the model

- `nn.fit(X_train_scaled, y_train, epochs=50)`

## Results

### Evaluation

- `loss: (NaN)`
- `categorical_accuracy: 0.6429`

### Predictions

- Infiltrating Ductal Carcinoma (0.0) - 54
- Mucinous Carcinoma (1.0) - 4
- Infiltrating Lobular Carcinoma (2.0) - 20
- No Prediction (NaN) - 6

# BRCA Dataset

## Sequential Neural Network

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### Setup

#### Layers

- `(Dense(25, input_dim = number_of_predictors, activation = 'relu'))`
- `(Dense(25, activation = 'relu'))`
- `(Dense(25, activation = 'tanh'))`
- `(Dense(25, activation = 'tanh'))`
- `(Dropout(.1))`
- `(Dense(number_of_classes, activation='softmax'))`

#### Compilation

- `(loss="categorical_focal_crossentropy", optimizer= "adam", metrics=['categorical_accuracy'])`

#### Fitting the model

- `number_of_epochs = 200`
- `nn.fit(X_train_scaled, y_train, epochs = number_of_epochs, shuffle = True)`

### Results

#### Evaluation

- `loss: 0.1370`
- `categorical_accuracy: 0.6875`

#### Predictions

- Infiltrating Ductal Carcinoma - 80

# Group Approach to Achieve Project Goals

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## Evaluation Methods

- .evaluate (Neural Networks)
- confusion matrix, classification report(Logistic Regression/XGB Classifier)

## Unanticipated Problems

- NaNs in y\_test (Neural Network BRCA)
- Low accuracy score for the BRCA model.
- How to display the Confusion Matrix.

# Results / Conclusions

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Almost perfectly predict if somebody had cancer.

- BC Dataset
  - 96.5% Accurate (Neural Network)
  - 99% training, 98% testing Accuracy (LR Model)
  - 100% training, 98% testing Accuracy (XGB Classifier Model)
  - 95.6% accurate (SVM)

Not able to predict the type of cancer based on the provided data with enough accuracy.

- BRCA Dataset
  - 68.75% Accurate (Sequential Neural Network)
  - 64.29% Accurate (Neural Network)
  - 58.20% Accurate(SVM)
  - 55% Accurate(KNN)



# Next Steps

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- BC Dataset
  - Find more testing data
  - Testing Accuracy >98%
- BRCA Dataset
  - Deeper analysis of model failure.
  - Try to determine which features are necessary to predict cancer type
  - Find Larger dataset for training
  - Try over sampling or SMOTE to account for imbalanced targets.