
Comparison of three machine learning predictors on diagnostic cancer data

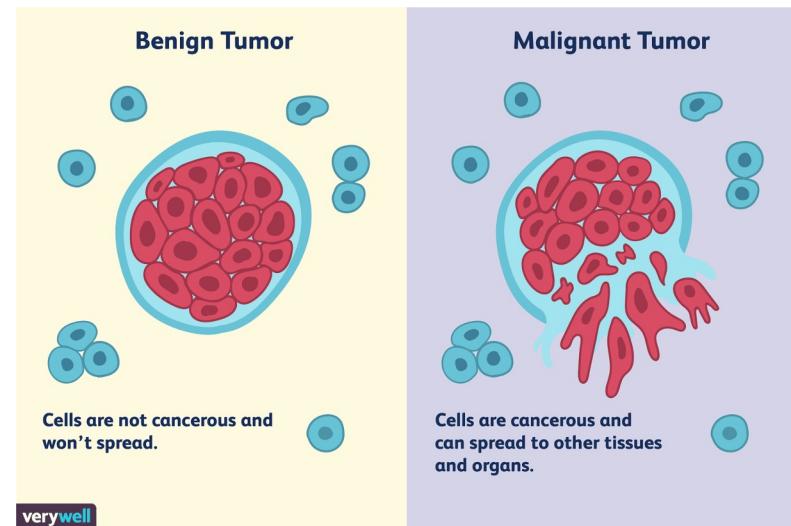
— By Thomas Griffin, Mehak Kapoor,
and Onyeka Onyenememezu —

Talk Overview

- Data Set
- Problem Data
- Three Machine Learning Predictor- hyperparameters, visual graphs, accuracy results.
 - Decision Tree
 - Logistic Regression
 - KNN
- Comparison of Accuracy

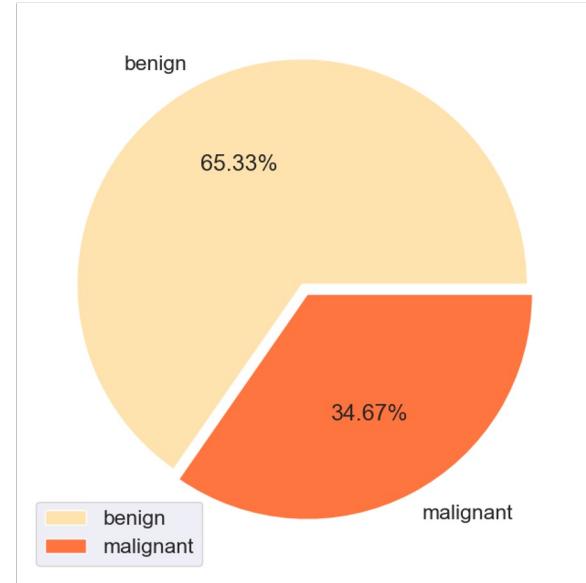
Introduction- Breast cancer

- Most common cause of death in women worldwide.
- Early detection is the most effective way to reduce the breast cancer deaths.
- Benign and Malignant tumors
- Nine real-valued features are computed for each cell nucleus:
 - Clump Thickness
 - Uniformity of Cell Size
 - Uniformity of Cell Shape
 - Marginal Adhesion
 - Single Epithelial
 - Bare Nuclei
 - Bland Chromatin
 - Normal Nucleoli
 - Mitosis

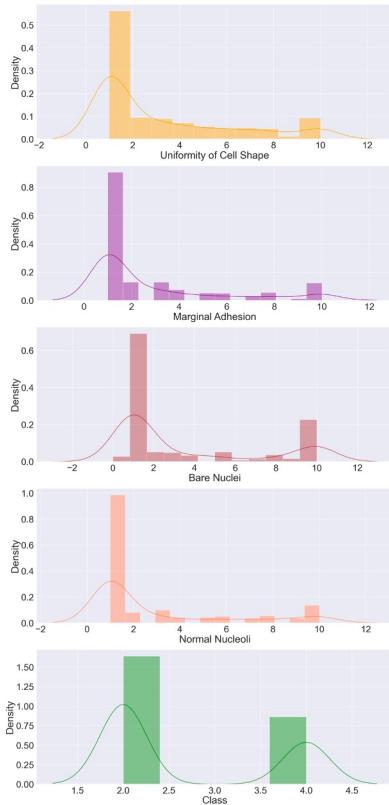
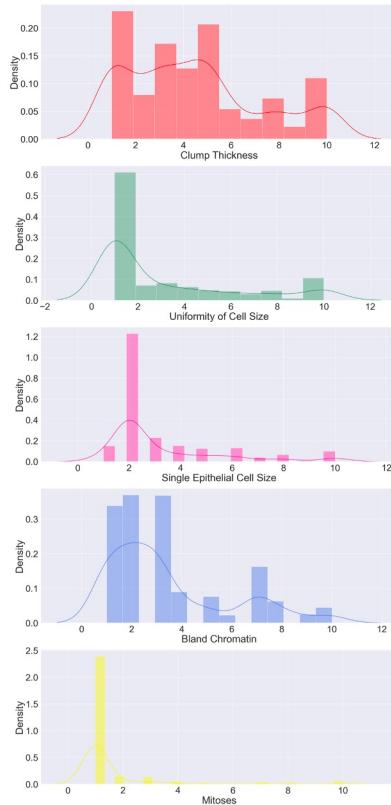


More about the data!

- 699 instances
- 9 features + 1 class
- Missing values - 16 denoted by '?'
- Distribution of class:
 - Benign - 458
 - Malignant - 241



Data Visualization



	Correlation between different attributes									
Clump Thickness	1	0.64	0.65	0.49	0.52	0.59	0.56	0.54	0.35	0.72
Uniformity of Cell Size	0.64	1	0.91	0.71	0.75	0.68	0.76	0.72	0.46	0.82
Uniformity of Cell Shape	0.65	0.91	1	0.68	0.72	0.7	0.74	0.72	0.44	0.82
Marginal Adhesion	0.49	0.71	0.68	1	0.6	0.67	0.67	0.6	0.42	0.7
Single Epithelial Cell Size	0.52	0.75	0.72	0.6	1	0.58	0.62	0.63	0.48	0.68
Bare Nuclei	0.59	0.68	0.7	0.67	0.58	1	0.67	0.57	0.34	0.82
Bland Chromatin	0.56	0.76	0.74	0.67	0.62	0.67	1	0.67	0.34	0.76
Normal Nucleoli	0.54	0.72	0.72	0.6	0.63	0.57	0.67	1	0.43	0.71
Mitoses	0.35	0.46	0.44	0.42	0.48	0.34	0.34	0.43	1	0.42
Class	0.72	0.82	0.82	0.7	0.68	0.82	0.76	0.71	0.42	1
Clump Thickness										
Uniformity of Cell Size										
Uniformity of Cell Shape										
Marginal Adhesion										
Single Epithelial Cell Size										
Bare Nuclei										
Bland Chromatin										
Normal Nucleoli										
Mitoses										
Class										



Handling missing data

- Method of corrections
 - Average dataset : Filled in the missing data points with the average of the column
 - Removed column : All missing data were in the Bare nuclei column so we removed this column
 - Removed Row : All rows with missing data were deleted



Data Split

- Average Dataset
 - Train = 499 samples
 - Test = 100 samples
 - Validation = 100 samples
- Removed Column
 - Train = 499 samples
 - Test = 100 samples
 - Validation = 100 samples
- Removed Row
 - Train = 489 samples
 - Test = 97 samples
 - Validation = 97 samples

For all three predictors we used the same splitting of the data.



Decision Tree - Hyperparameter Tuning

We chose to use depth of 4 as higher depth was overfitting our training data. Dataset was “small” enough to not worry about node sizes.

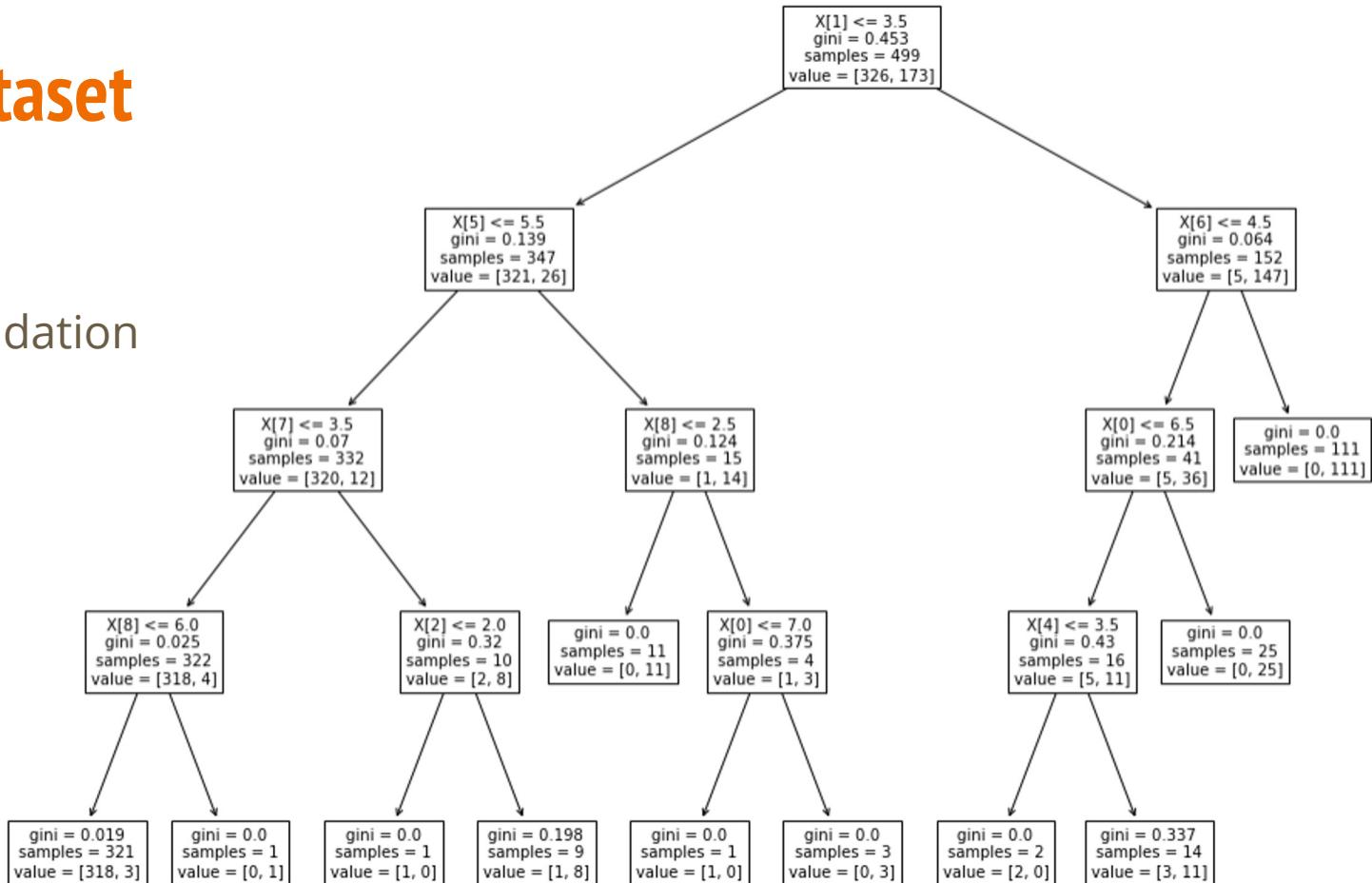
Depth of Tree	Accuracy of Test Data (100 points)
1	.87
2	.89
3	.90
4	.91
5	.9
6	.89
7	.89

Average Dataset

Depth=4

Accuracy on Validation

Data set = 92%

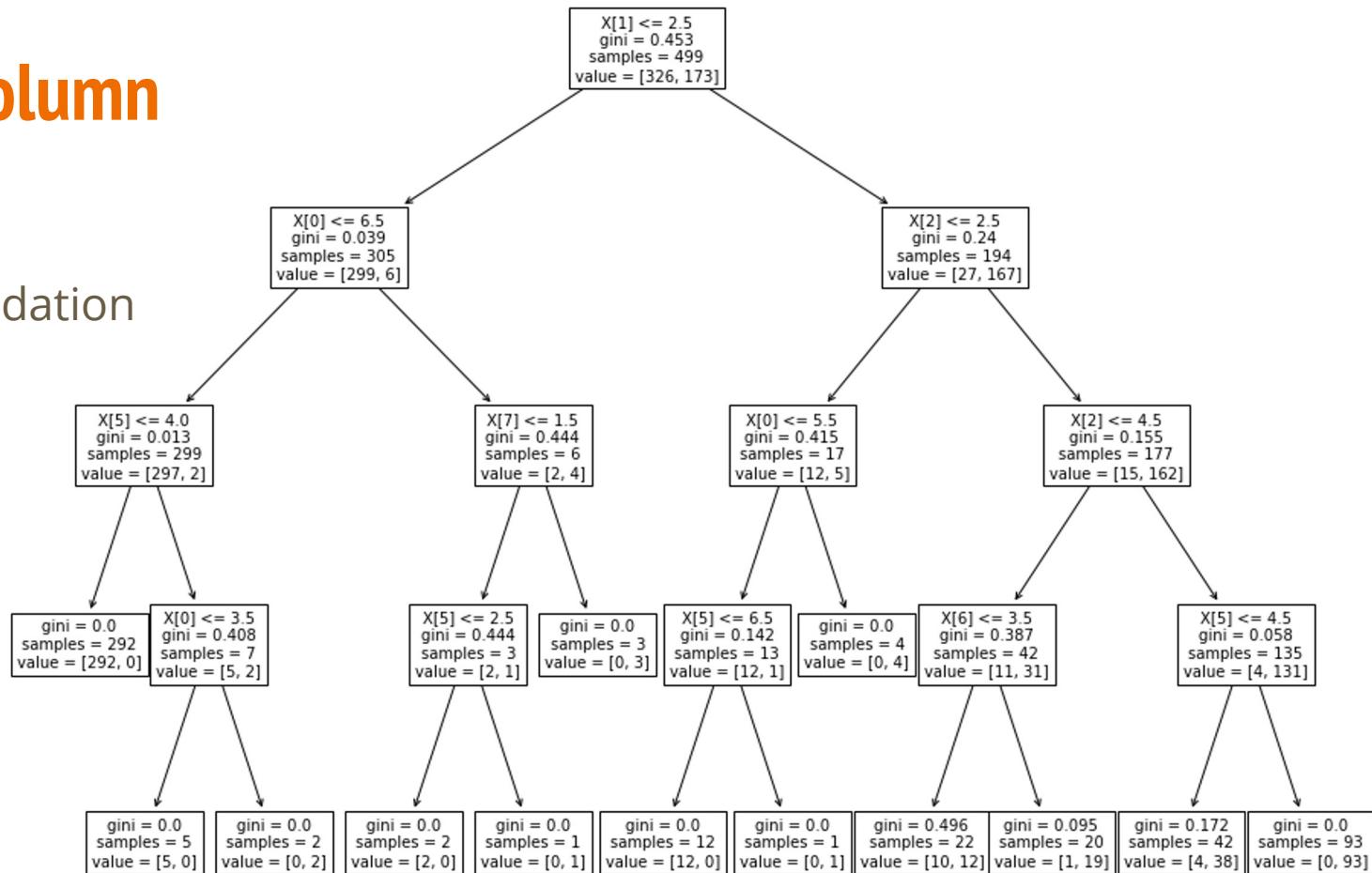


Removed Column

Depth=4

Accuracy on Validation

Data set = 94%



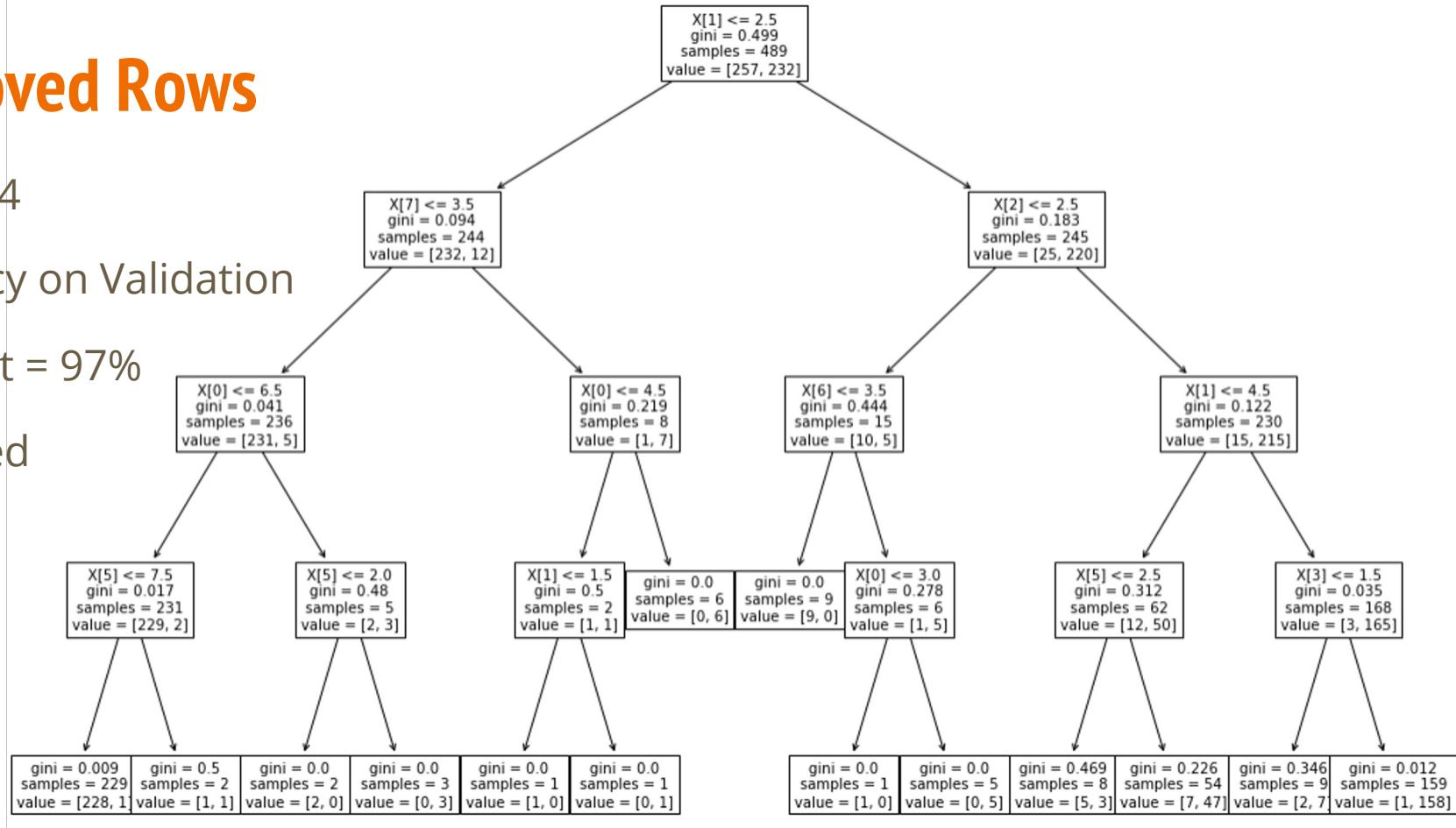
Removed Rows

Depth=4

Accuracy on Validation

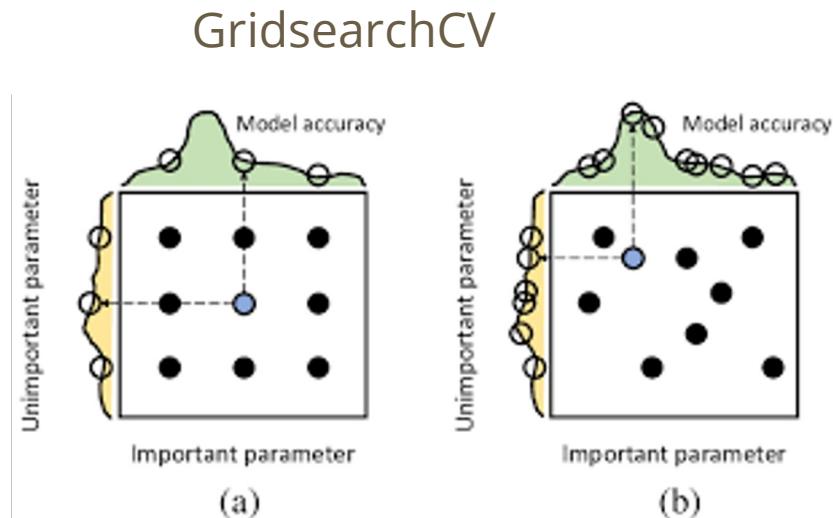
Data set = 97%

Rounded



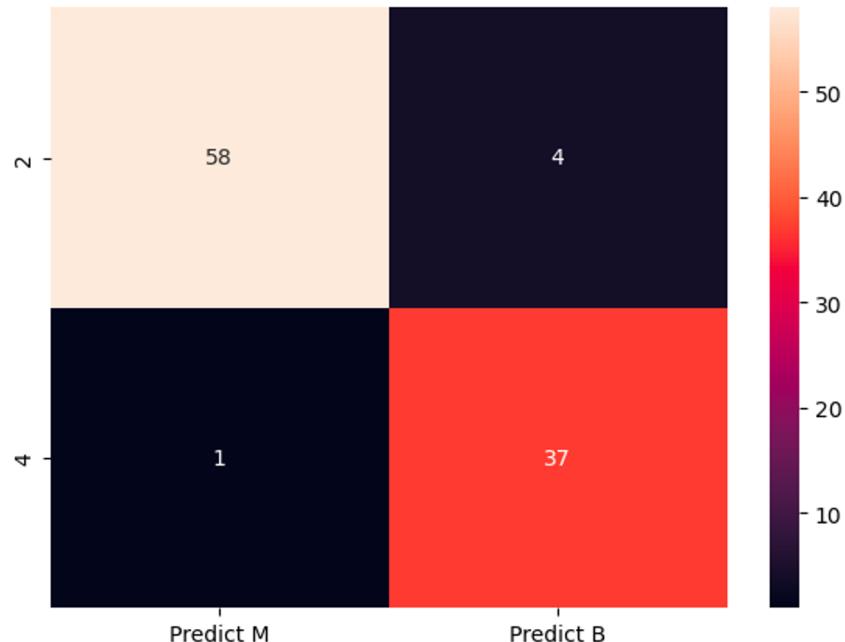
Logistic Regression - Hyperparameter Tuning

- Penalty
 - L2
 - L1
- C : regularization strength
 - 0.000001
 - 0.001
 - 0.01
 - 0.1
 - 1
 - 10
 - 100
 - 1000



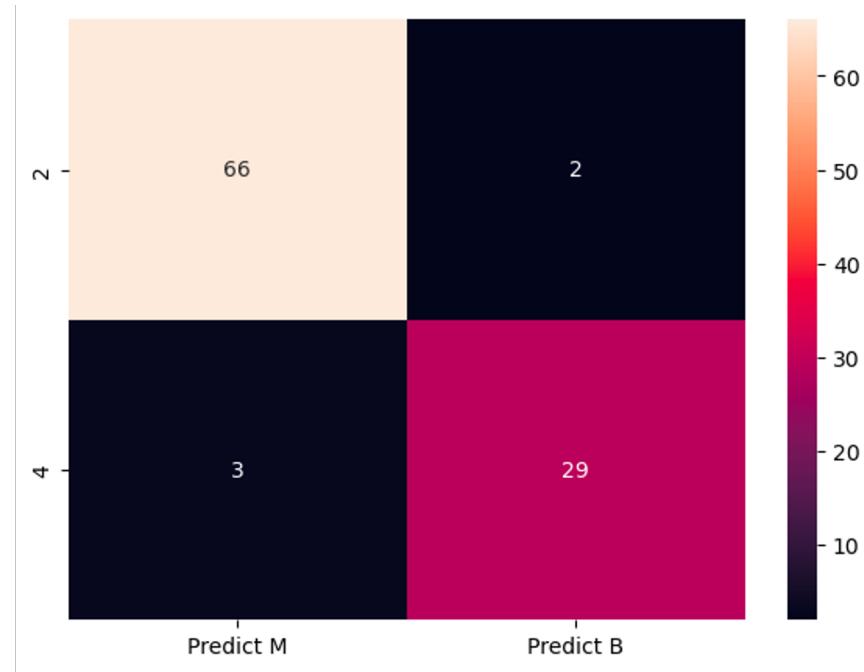
Average Dataset

- Accuracy : 95%
- Best parameters
 - $C = 10$
 - l2 penalty



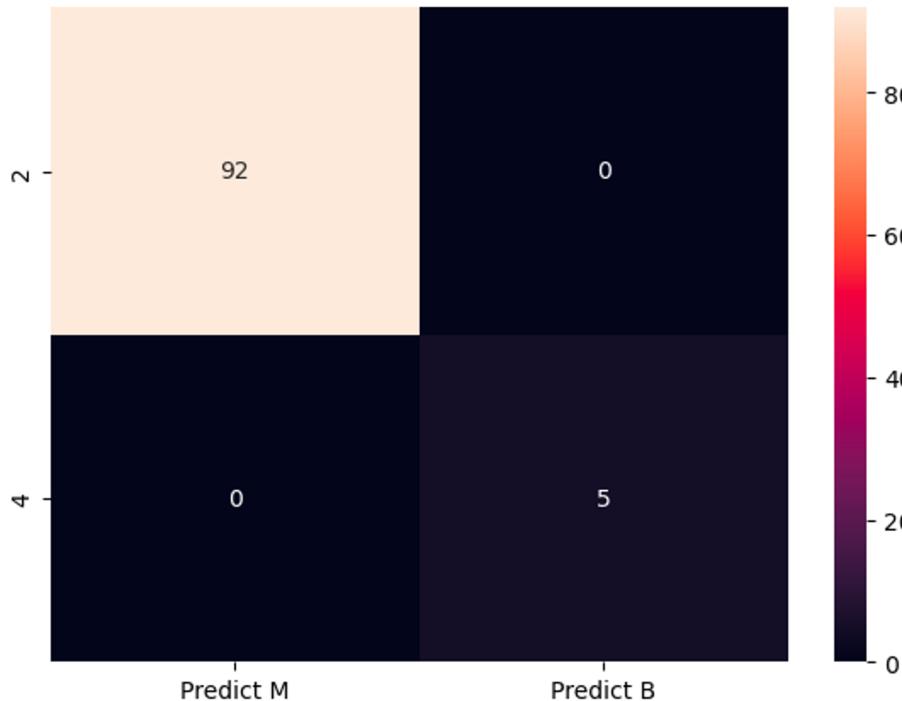
Removed Column

- Accuracy : 95%
- Best parameters:
 - $C=0.1$
 - l2 penalty



Removed Rows

- Accuracy : 100%
- Best parameters
 - $C = 0.01$
 - $L2$ penalty



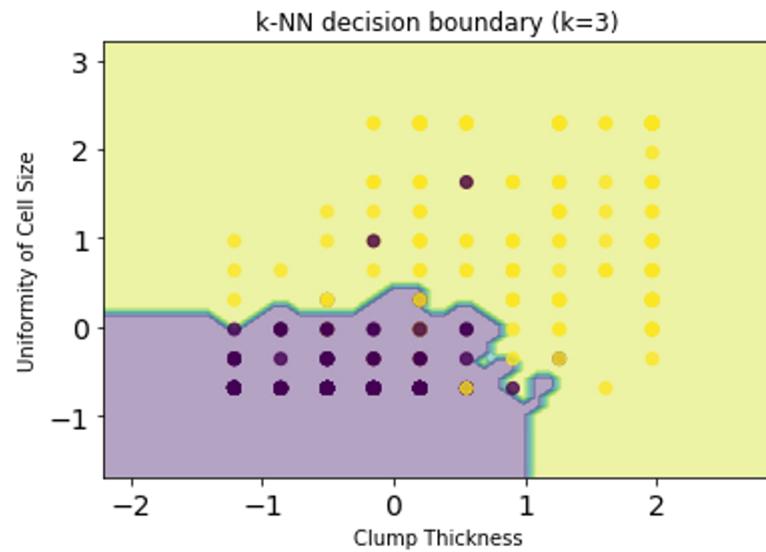
Hyperparameter tuning - KNN

Using GridsearchCV found the best combination of parameters for :

- n_neighbors
 - Range 1 to 21
- weights
 - Uniform
 - Distance
- metric
 - Euclidean
 - Manhattan
 - Minkowski

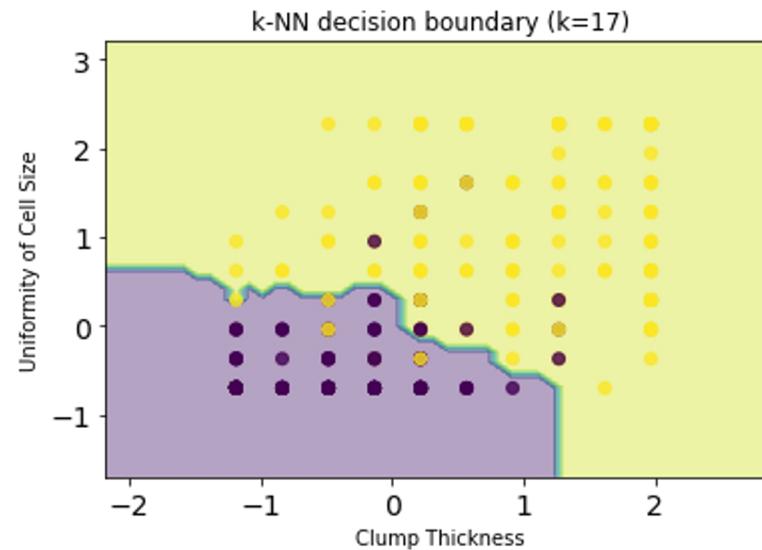
Average Dataset

Accuracy = 96%



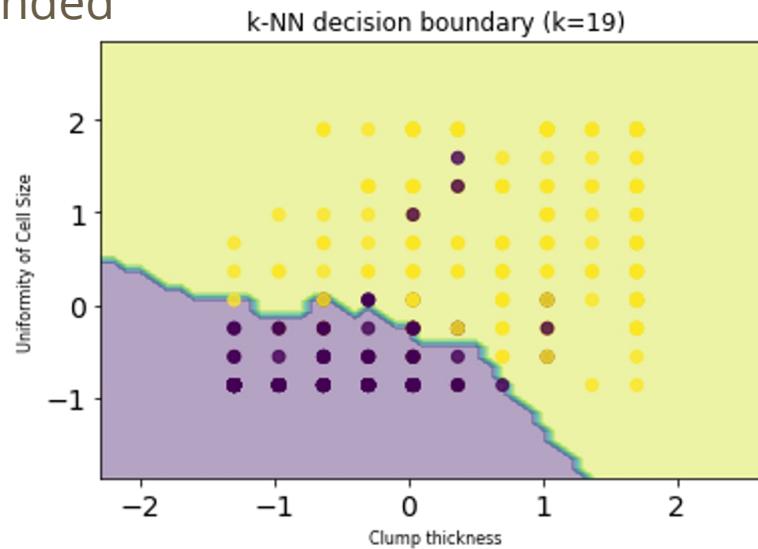
Removed Column

Accuracy = 95%



Removed Rows

Accuracy : 99% Rounded



Conclusion : Accuracy table/matrix

Comparing the results we see a slight increase in accuracy for Logistic Regression and KNN over the Decision Tree models.

	Average	Removed Column	Removed Row
Logistic Regression	95%	95%	100%
Decision Tree	92%	94%	97%
KNN	96%	95%	99%

Possible Future Work

- Testing out different ways to handle the missing values.
 - Median
 - Mode
- Un-Scale the data
 - Currently the categories are scaled 1-10 on different metrics, we could instead use the raw unsorted data.
- Other Predictors
 - Neural Networks
 - Random Forests
 - Gradient Boost

Dataset

Creators:

1. Dr. William H. Wolberg, General Surgery Dept.
University of Wisconsin, Clinical Sciences Center
Madison, WI 53792
wolberg '@' eagle.surgery.wisc.edu

2. W. Nick Street, Computer Sciences Dept.
University of Wisconsin, 1210 West Dayton St., Madison, WI 53706
street '@' cs.wisc.edu 608-262-6619

3. Olvi L. Mangasarian, Computer Sciences Dept.
University of Wisconsin, 1210 West Dayton St., Madison, WI 53706
olvi '@' cs.wisc.edu

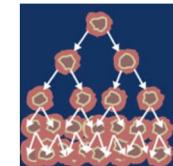


Check out the [beta version](#) of the new UCI Machine Learning Repository we are currently testing! [Contact us](#) if you have any

Breast Cancer Wisconsin (Diagnostic) Data Set

[Download](#): [Data Folder](#), [Data Set Description](#)

Abstract: Diagnostic Wisconsin Breast Cancer Database



Data Set Characteristics:	Multivariate	Number of Instances:	569	Area:	Life
Attribute Characteristics:	Real	Number of Attributes:	32	Date Donated	1995-11-01
Associated Tasks:	Classification	Missing Values?	No	Number of Web Hits:	1976500

Source:

Creators:

1. Dr. William H. Wolberg, General Surgery Dept.
University of Wisconsin, Clinical Sciences Center
Madison, WI 53792
wolberg '@' eagle.surgery.wisc.edu

2. W. Nick Street, Computer Sciences Dept.
University of Wisconsin, 1210 West Dayton St., Madison, WI 53706
street '@' cs.wisc.edu 608-262-6619

3. Olvi L. Mangasarian, Computer Sciences Dept.
University of Wisconsin, 1210 West Dayton St., Madison, WI 53706
olvi '@' cs.wisc.edu

THANKS

