# final report

2023-12-19

# Abstract

## Introduction

## Data and Methods

# Descriptive Data

### **Data Cleaning and Preparation**

The dataset utilized in this study was derived from a comprehensive breast cancer database. The initial step in data preparation involved the standardization of variable names to ensure consistency. In addition, we converted several categorical variables into factors with defined levels. Specifically, we recoded the survival status variable into a binary format with Dead as 1 and Alive as 0. Finally, a new variable node\_positive\_prop was created and calculated based on the ratio of reginol\_node\_positive to regional\_node\_examined. This variable represents the proportion of examined nodes that were found to be positive.

#### Variable and Model Selection Procedures

After preprocessing the dataset, we subdivided our dataset into categorical and numerical variables in order to have a general outline data patterns. In **Table 1**, we summarized the essential statistics of all the categorical variables, which includes variable names, number of missing values, unique and top counts.

For numerical variables, we employed boxplot visualizations to effectively represent their distribution patterns. As illustrated in **Figure 1**, these boxplots serve as a comprehensive visualization, which include potential outliers, important quartiles, and medians of all the numerical variables. # Assumption Checking

#### Result

Variable Selection

Model Selection

#### Conclusion

# Appendix

#### **Table**

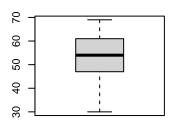
Table 1: Summary Statistics of Categorical Variables

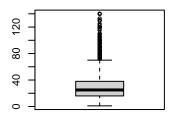
| Variable       | Missing | Unique Counts | Top Counts                              |
|----------------|---------|---------------|---|
| race           | 0       | 3             | Whi: 3413, Oth: 320, Bla: 291           |
| marital_status | 0       | 5             | Mar: 2643, Sin: 615, Div: 486, Wid: 235 |

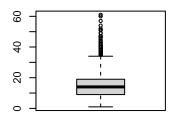
| Variable               | Missing | Unique Counts | Top Counts                                |
|------------------------|---------|---------------|---|
| t_stage                | 0       | 4             | T2: 1786, T1: 1603, T3: 533, T4: 102      |
| n_stage                | 0       | 3             | N1: 2732, N2: 820, N3: 472                |
| x6th_stage             | 0       | 5             | IIA: 1305, IIB: 1130, III: 1050, III: 472 |
| differentiate          | 0       | 4             | Mod: 2351, Poo: 1111, Wel: 543, Und: 19   |
| grade                  | 0       | 4             | 2: 2351, 3: 1111, 1: 543, ana: 19         |
| a_stage                | 0       | 2             | Reg: 3932, Dis: 92                        |
| estrogen_status        | 0       | 2             | Pos: 3755, Neg: 269                       |
| progesterone_status    | 0       | 2             | Pos: 3326, Neg: 698                       |
| status                 | 0       | 2             | 0: 3408, 1: 616                           |
| $node\_positive\_prop$ | 0       | NA            | NA  |

# Figure

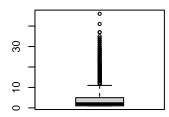
Figure 1: Numerical Variables Distribution
Tumor Size Node Examined



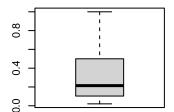




**Positive Node** 



# **Proportion of Positive Nodes**



# Contribution