Predicting Alzheimer's Disease Using Machine Learning: A Data-Driven Approach to Early Diagnosis and Risk Factor Identification

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Abstract

Alzheimer's disease (AD) is a progressive neurodegenerative disorder with rising global prevalence, posing a significant burden on public health systems. Early diagnosis is essential for effective intervention but remains challenging due to the disease's complex etiology. This study develops a predictive classification model using data from the Kaggle Alzheimer's Disease Classification dataset. The dataset comprises over 2,000 patient records, including demographic, clinical, and cognitive variables. Employing machine learning techniques, the model identifies significant predictors associated with AD onset. Results demonstrate the utility of data-driven methods in improving diagnostic accuracy and underscore the potential of integrating multimodal data—such as neuroimaging and genetic information—to enhance predictive performance. These findings contribute to the development of early screening strategies aimed at reducing the clinical and societal impact of AD.

Key Words: Alzheimer's Disease, Early Diagnosis, Machine Learning, Random Forest, Feature Selection, Cognitive Assessment

1 Introduction

Alzheimer's disease (AD) is an irreversible, progressive neurodegenerative disorder characterized by neuronal loss, cerebral atrophy, and cognitive decline, ultimately impairing the capacity to perform daily activities. Affecting over 50 million individuals worldwide, its prevalence is projected to rise markedly due to global population aging. This growing burden presents significant challenges not only for patients and caregivers but also for healthcare systems facing increasing demands for clinical and long-term care resources.

Early-stage AD is often asymptomatic or presents with subtle cognitive impairment, complicating timely diagnosis. Enhancing diagnostic accuracy at this stage is therefore critical for effective clinical and therapeutic intervention. Recent advances in machine learning have demonstrated considerable potential in identifying latent patterns within complex, high-dimensional health data. This study applies machine learning algorithms to a publicly available dataset comprising demographic, clinical, lifestyle, and cognitive variables, with the objective of identifying predictors of early-stage AD. In addition to classification modeling, the study explores statistical associations between selected features and diagnostic outcomes, thereby contributing to risk stratification, early screening strategies, and evidence-based public health decision-making.

2 Methods

2.1 Data Preprocessing and Feature Engineering

The dataset underwent rigorous preprocessing to ensure quality and compatibility with machine learning algorithms. Missing values were visualized using the `Amelia` package to identify patterns and gaps. For numerical variables, median imputation was employed due to its robustness to outliers. Categorical variables were imputed using mode values to preserve underlying class distributions.

To address multicollinearity, pairwise correlations were evaluated using the `corrplot` package, and highly correlated features were reviewed for exclusion. Categorical variables such as `Gender` and `Smoking` were encoded using one-hot encoding to ensure model compatibility. Continuous variables, including `BMI` and `CholesterolLevels`, were normalized using the `caret::preProcess` function to standardize scales and facilitate algorithmic convergence.

2.2 Data Loading and Cleaning

The dataset was partitioned into training (train.csv) and testing (test.csv) sets, both of which were cleaned and preprocessed. Non-informative variables (e.g., `PatientID` and `DoctorInCharge`) were removed, and categorical variables were consistently formatted and converted to factor types to ensure compatibility with modeling algorithms.

2.3 Exploratory Data Analysis

Prior to model training, exploratory data analysis (EDA) was conducted to uncover underlying patterns and gain an initial understanding of the dataset. Both univariate and bivariate analyses were performed to examine variable distributions and interrelationships.

Univariate analysis involved plotting histograms for numerical varialbes and bar charts for categorical variables (Figures 1 and 2). For example, the distribution of `MMSE` showed clear separation between diagnosed and non-diagnosed individuals, indicating strong predictive relevance. These visualizations also revealed that the majority of participants were between 60 and 90 years old, with notable variation in cognitive assessment scores.

Bivariate analysis included the use of correlation heatmaps (via the `corrplot` package) to assess relationships among numerical variables and detect potential multicollinearity. Furthermore, boxplots were employed to visualize the associations between selected predictors and diagnostic outcomes.

2.4 Machine Learning Models

This study employed multiple machine learning algorithms to classify early-stage Alzheimer's disease, including logistic regression, random forest, linear discriminant analysis (LDA), and Naive Bayes. Additionally, hyperparameter tuning was applied to op-

timize model performance. The following subsections provide a detailed explanation of each method:

Logistics Regression Logistic regression is a widely used classification technique that models the probability of a binary outcome as a function of input variables. A logistic regression model was fitted using the training data, and its performance was evaluated on a validation set using a confusion matrix. The model achieved an accuracy of 86.33%.

Random Forest Random forest is an ensemble learning method that constructs multiple decision trees and aggregates their predictions. To prevent overfitting and improve generalizability, 5-fold cross-validation was performed using the `caret` package. This strategy leveraged caret for training and hyperparameter tuning. A grid search was used to tune the key hyperparameter `mtry`, which defines the number of variables considered at each split. The final random forest model was then built using the optimized `mtry` value, ensuring strong predictive performance. The optimized model achieved an accuracy of 94.33%.

Linear Discriminant Analysis (LDA) LDA is a dimensionality reduction and classification method that identifies linear combinations of features that maximize inter-class differences while minimizing intra-class differences. The LDA model achieved an accuracy of 85.67% on the validation set.

Naive Bayes Naive Bayes is a probabilistic classifier that performs classification by calculating prior probabilities and conditional probabilities of variables for each category, based on Bayes' theorem. The model assumes independence among features. Despite this simplifying assumption, the model performed competitively, achieving an accuracy of 86.67%.

Hyperparameter Tuning Hyperparameter tuning method defines the range of candidate hyperparameter combinations by constructing a grid. In this study, hyperparameter tuning was performed using grid search to identify the optimal value of `mtry`, ranging from 10 to 25. The best-performing model fitted by this method (with `mtry` = 15), achieved the highest accuracy of 94.93%.

2.5 Feature Selection

Feature importance analysis was assessed using two methods: the Random Forest method and Recursive Feature Elimination (RFE). Both techniques revealed that Age, Cognitive Assessment Scores, and Family History of Alzheimer's were the most important predictors of early-stage Alzheimer's disease.

The **Random Forest** method evaluates variable importance by randomly shuffling the values of a specific feature and observing the resulting change in model performance. A significant performance drop indicates the feature's high importance. The feature importance results are visually represented in Figure 3 in the Appendix.

The **RFE** method selects the most predictive features by iteratively removing the least important ones and evaluating the model's performance after each elimination. The variable selection results from RFE were consistent with those obtained through the Random Forest method. Additionally, RFE suggested that a model including only five variables (`FunctionalAssessment`, `ADL`, `MMSE`, `MemoryComplaints`, `BehavioralProblems`) would outperform models incorporating additional variables.

2.6 Evaluation Metrics

The model was evaluated using a combination of metrics to assess its reliability and clinical relevance. **Accuracy** was the primary metric for measuring overall classification performance. **Precision** and **recall** were calculated to analyze the trade-offs between false positives and false negatives, with the **F1 score** capturing the balance between these two metrics. Additionally, the area under the Receiver Operating Characteristic curve (**ROC-AUC**), displayed in Figure 3 in the Appendix, provides a threshold-independent measure of the model's ability to distinguish between diagnosed and undiagnosed cases.

The models were assessed using several methods to see how well they predicted the diagnosis. **Logistic Regression** acheived an accuracy of 86.33%, **Linear Discriminant Analysis (LDA)** reached 85.67%, and **Naive Bayes** performed slightly better with an accuracy of 86.67%. However, **Random Forest** outperformed all other models, achieving an accuracy of 94.33%.

Precision and **Recall** were used to evaluate the models' ability to balance false positives and false negatives. **Recall**, or sensitivity, measures how well the model identifies undiagnosed cases. The Random Forest model excelled in this area, with a recall of 98.45%, meaning it missed very few undiagnosed cases. It also had a specificity of 86.79%, reflecting its ability to minimize false positives.

The **ROC-AUC** score, which measures the model's ability to distinguish between positive and negative cases, was also considered. The Random Forest model scored the highest at 96.16%, demonstrating its superior ability to differentiate between diagnosed and undiagnosed individuals compared to the other models.

Further improvements were made to the Random Forest model through **hyperparameter tuning**. This process fine-tuned the model's settings, resulting in a more accurate prediction. Cross-validation and the use of Synthetic Minority Over-sampling Technique (**SMOTE**) to handle imbalanced data helped identify the optimal number of variables to split on, with an `mtry` value of 15. This adjustment reduced the model's error rate, enhancing its reliability.

Finally, the **confusion matrix** confirmed that the Random Forest model was the best overall, achieving a balanced accuracy of 92.62%, indicating both precision and consistency.

In conclusion, the Random Forest model emerged as the most reliable and effective choice for this task. It demonstrated the highest accuracy, exceptional recall and specificity, and strong performance after hyperparameter tuning, making it a robust tool for predicting Alzheimer's diagnosis.

3 Results and Conclusion

The analysis commenced with comprehensive exploratory data analysis (EDA), including statistical summaries, correlation assessments, and visualizations of variable distributions and relationships with the diagnosis outcome. Missing data were handled through median imputation for numeric variables and conversion of relevant fields into factors, ensuring that the modeling phase started with a complete and consistent dataset.

Multiple classification models were trained and evaluated to

identify the most reliable predictor of early-stage Alzheimer's disease. Logistic regression served as the baseline model, providing interpretable coefficients and odds ratios, which are especially valuable in clinical settings. However, due to its linear assumptions and limited flexibility with complex interactions, its performance was outpaced by more sophisticated methods.

Additional models, including Linear Discriminant Analysis (LDA) and Naive Bayes, were also considered. While LDA is effective under assumptions of normally distributed features and equal class covariances, and Naive Bayes offers fast probabilistic classification under strong independence assumptions, neither model surpassed the performance of more flexible ensemble techniques in this study.

The Random Forest model was trained with 500 trees, leveraging its strength in handling high-dimensional data and capturing non-linear relationships without extensive feature engineering. Initial model evaluation on the validation set demonstrated significant improvements over logistic regression and other classical models.

To further enhance performance, hyperparameter tuning was conducted using a grid search across `mtry` values (10 to 25), combined with five-fold cross-validation via the `caret` package. Additionally, SMOTE (Synthetic Minority Over-sampling Technique) was applied to address class imbalance. The optimal value of `mtry` was determined to be 15. The final tuned Random Forest model achieved an out-of-bag (OOB) error rate of 4.43%, confirming the value of careful hyperparameter calibration.

External evaluation was conducted via Kaggle, providing a robust benchmark using an unseen test set. The final model achieved a prediction score of **90.705%**. This result affirms the model's generalizability and competitive performance under standardized evaluation criteria.

Stepwise logistic regression models based on AIC and BIC were also examined to assess whether simpler models could offer comparable performance. While these approaches helped identify a parsimonious subset of features, they did not yield substantial improvements on the validation set. In contrast, the Random Forest model retained superior predictive accuracy, particularly after tuning and accounting for class imbalance.

In conclusion, the tuned Random Forest model demonstrated superior performance compared to logistic regression, LDA, and Naive Bayes. Its strong performance was further validated by external benchmarking through Kaggle. Although simpler models offer interpretability, the complexity of the data and the nature of the classification task favored a flexible, ensemble-based approach. These findings suggest that the final model developed in this study serves as a reliable tool for predicting early-stage Alzheimer's disease.

4 Discussion

Although the modeling pipeline was comprehensive, several should be acknowledged. First, model evaluation was primarily based on accuracy and confusion matrices. While the codebase supported ROC and AUC computations, the final numeric values were not explicitly reported. Without a complete set of evaluation metrics, it is challenging to characterize performance in terms of sensitivity, specificity, or calibration. More nuanced metrics might offer greater insights, especially in a clinical context where misclassification costs differ between false positives and false negatives.

Second, the imputation and feature engineering strategies were relatively basic. Median imputation was used for missing numeric values, and categorical variables were encoded using standard methods without incorporating domain-specific transformations. Incorporating clinical expertise could facilitate more meaningful variable selection and improve model discriminability through the inclusion of interaction terms or derived variables.

Third, while internal validation via data splitting and cross-validation was methodologically sound, the absence of a fully independent clinical dataset limits the assessment of generalizability. Although the Kaggle evaluation provides a form of external validation, further validation on an entirely separate dataset would strengthen confidence in the applicability across diverse populations or settings.

Model interpretability presents another challenge. Although the Random Forest model offer excellent predictive performance, it is inherently less interpretable than linear models such as logistic regression. While variable importance plots offer some insight into predictor relevance, advanced explainability techniques such as SHAP (SHapley Additive exPlanations) values or partial dependence plots could provide more transparent, feature-level explanations of model decisions. This would be particularly valuable in healthcare applications, where transparency and interpretability are essential for clinical adoption.

Finally, while stepwise feature selection based on AIC or BIC aids in model parsimony, such approaches do not necessarily yield models with optimal generalization. Although these criteria help reduce model complexity, they do not always lead to improved predictive performance. More robust approaches, including regularization methods (e.g., LASSO or ridge regression) or hybrid feature selection guided by domain expertise, could offer a better balance between interpretability and predictive performance.

5 References

5.1 Dataset

The dataset used in this study was obtained from Kaggle: Classification of the Alzheimer's Disease.

5.2 Tool

All analyses and modeling were conducted using RStudio: RStudio - Posit Open Source Platform.

6 Appendix

Figure 1. EDA Plots (Univariate Analysis)

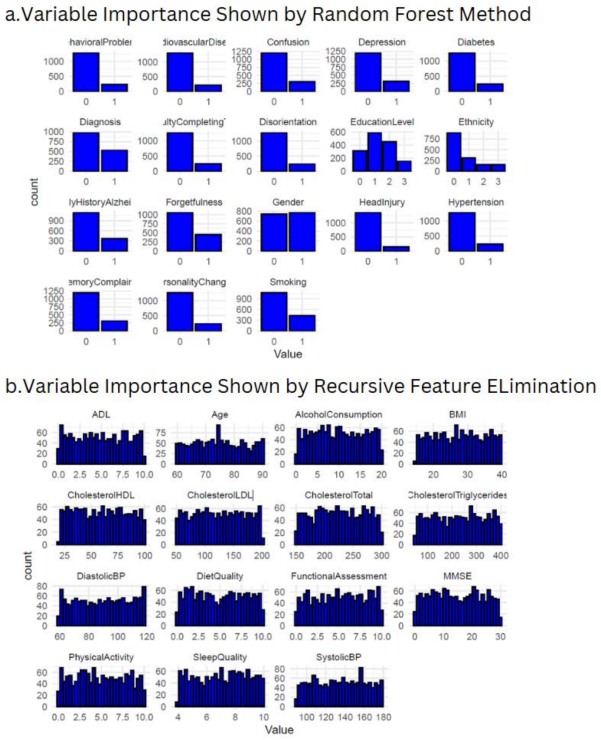


Figure 2. EDA Plots (Bivariate Analysis)

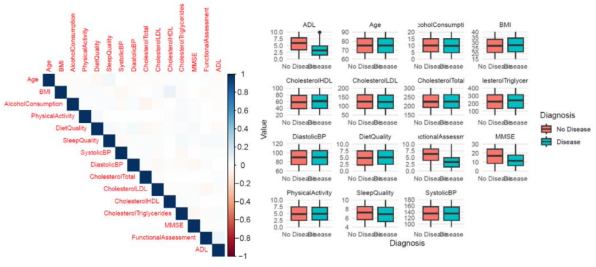


Figure 3. ROC Curves of the Models

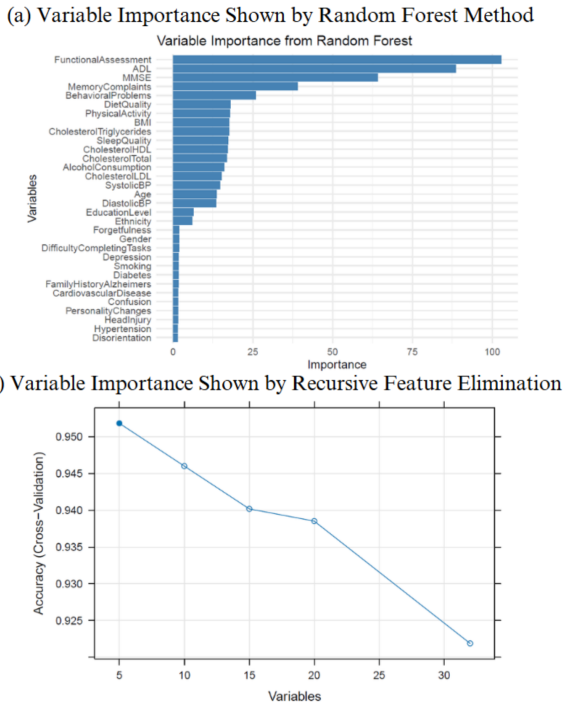
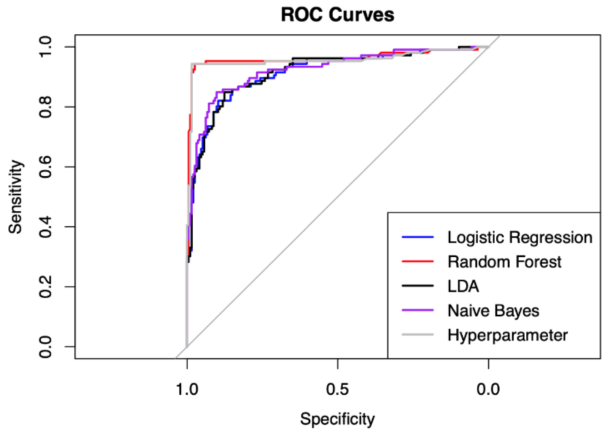


Figure 4. ROC Curves of the Models



7 Code

1. Exploratory Data Analysis (EDA)

1.1. Load the Data

```
# Install required packages if not already installed
install.packages(c('tidyverse', 'ggplot2', 'corrplot', 'caret', 'randomForest', 'e1071', 'leaps', 'pROC
```

```
## Installing packages into '/usr/local/lib/R/site-library'
## (as 'lib' is unspecified)
```

```
## also installing the dependencies 'RANN', 'ROSE'
```

```
# Load libraries
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.5.0     v tibble    3.2.1
## v lubridate 1.9.3     v tidyr     1.3.1
## v purrr     1.0.2
```

```
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become error
```

```
library(ggplot2)
library(corrplot)
```

```
## corrplot 0.92 loaded
```

```
library(caret)
```

```
## Loading required package: lattice
##
## Attaching package: 'caret'
##
## The following object is masked from 'package:purrr':
##
##     lift
```

```
library(randomForest)
```

```
## randomForest 4.7-1.1
## Type rfNews() to see new features/changes/bug fixes.
##
## Attaching package: 'randomForest'
##
## The following object is masked from 'package:dplyr':
##
```

```
##     combine
##
## The following object is masked from 'package:ggplot2':
##
##     margin
```

```
library(e1071)
library(leaps)
library(pROC)
```

```
## Type 'citation("pROC")' for a citation.
##
## Attaching package: 'pROC'
##
## The following objects are masked from 'package:stats':
##
##     cov, smooth, var
```

```
library(Amelia)
```

```
## Loading required package: Rcpp
## ##
## ## Amelia II: Multiple Imputation
## ## (Version 1.8.1, built: 2022-11-18)
## ## Copyright (C) 2005-2024 James Honaker, Gary King and Matthew Blackwell
## ## Refer to http://gking.harvard.edu/amelia/ for more information
## ##
```

```
library(themis)
```

```
## Loading required package: recipes
##
## Attaching package: 'recipes'
##
## The following object is masked from 'package:stringr':
##
##     fixed
##
## The following object is masked from 'package:stats':
##
##     step
```

```
# Load the datasets
train <- read.csv('train.csv', stringsAsFactors = FALSE)
test <- read.csv('test.csv', stringsAsFactors = FALSE)
```

1.2. Data Overview

1.2.1. Inspect Data Structure

```
# View the first few rows
head(train)
```

```
##   PatientID Age Gender Ethnicity EducationLevel      BMI Smoking
## 1         1  67      0         3              0 37.20518       0
## 2         2  65      1         0              0 35.14184       1
## 3         3  62      0         1              1 17.87510       0
## 4         4  67      0         0              1 37.50344       1
```

```
## 5         5  65      1         0              2 29.18786       1
## 6         6  88      1         0              1 25.67389       0
##   AlcoholConsumption PhysicalActivity DietQuality SleepQuality
## 1         12.2156770         7.780544    6.433890     6.744820
## 2         17.1114042         6.645284    1.112379     7.568751
## 3         13.5255456         9.585769    4.266008     8.247084
## 4         19.9520140         1.953946    6.797333     7.666498
## 5          0.5332093         8.759570    6.364302     6.231143
## 6         10.3799869         8.043196    2.354424     4.764378
##   FamilyHistoryAlzheimers CardiovascularDisease Diabetes Depression HeadInjury
## 1                       0                     0        0          0          0
## 2                       0                     0        0          1          0
## 3                       0                     0        1          0          0
## 4                       0                     1        1          1          0
## 5                       0                     1        0          0          0
## 6                       0                     0        0          0          1
##   Hypertension SystolicBP DiastolicBP CholesterolTotal CholesterolLDL
## 1            0        137         114         270.1677      118.89108
## 2            0        111          82         227.2657      100.58877
## 3            0        131         108         202.4197      184.97482
## 4            0        121          76         235.9426      150.74410
## 5            0        158         117         292.3378      125.42963
## 6            0        126          83         270.9545       85.93615
##   CholesterolHDL CholesterolTriglycerides       MMSE FunctionalAssessment
## 1       78.04944                272.80402  0.6946002             9.986441
## 2       21.15240                156.87964 23.7899987             6.197277
## 3       36.97303                288.78818  6.5920715             9.572719
## 4       62.16979                195.95458 25.3426163             2.487042
## 5       82.86545                295.68221  6.6277415             7.521358
## 6       65.78187                 59.47537 22.1699224             6.592334
##   MemoryComplaints BehavioralProblems      ADL Confusion Disorientation
## 1                1                  0 6.009376         0              0
## 2                0                  0 7.519209         0              0
## 3                0                  0 8.573933         0              0
## 4                0                  0 6.217530         0              0
## 5                1                  0 5.193683         1              0
## 6                0                  0 9.420887         0              1
##   PersonalityChanges DifficultyCompletingTasks Forgetfulness Diagnosis
## 1                  0                         1             1         0
## 2                  0                         0             1         0
## 3                  0                         0             0         0
## 4                  0                         0             1         0
## 5                  0                         0             1         0
## 6                  1                         0             0         0
##   DoctorInCharge
## 1      XXXConfid
## 2      XXXConfid
## 3      XXXConfid
## 4      XXXConfid
## 5      XXXConfid
## 6      XXXConfid
```

```r
# Get the structure of the data
str(train)
```

```
## 'data.frame':    1504 obs. of  35 variables:
##  $ PatientID                : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ Age                      : int  67 65 62 67 65 88 83 72 90 61 ...
##  $ Gender                   : int  0 1 0 0 1 1 1 1 1 1 ...
##  $ Ethnicity                : int  3 0 1 0 0 0 1 1 3 0 ...
##  $ EducationLevel           : int  0 0 1 1 2 1 3 1 2 0 ...
##  $ BMI                      : num  37.2 35.1 17.9 37.5 29.2 ...
##  $ Smoking                  : int  0 1 0 1 1 0 0 0 0 0 ...
##  $ AlcoholConsumption       : num  12.216 17.111 13.526 19.952 0.533 ...
##  $ PhysicalActivity         : num  7.78 6.65 9.59 1.95 8.76 ...
##  $ DietQuality              : num  6.43 1.11 4.27 6.8 6.36 ...
##  $ SleepQuality             : num  6.74 7.57 8.25 7.67 6.23 ...
##  $ FamilyHistoryAlzheimers  : int  0 0 0 0 0 0 0 1 1 0 ...
##  $ CardiovascularDisease    : int  0 0 0 1 1 0 0 0 0 0 ...
##  $ Diabetes                 : int  0 0 1 1 0 0 0 0 0 0 ...
##  $ Depression               : int  0 1 0 1 0 0 0 1 0 0 ...
##  $ HeadInjury               : int  0 0 0 0 0 1 0 0 0 0 ...
##  $ Hypertension             : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ SystolicBP               : int  137 111 131 121 158 126 165 117 115 126 ...
##  $ DiastolicBP              : int  114 82 108 76 117 83 91 102 90 70 ...
##  $ CholesterolTotal         : num  270 227 202 236 292 ...
##  $ CholesterolLDL           : num  119 101 185 151 125 ...
##  $ CholesterolHDL           : num  78 21.2 37 62.2 82.9 ...
##  $ CholesterolTriglycerides : num  273 157 289 196 296 ...
##  $ MMSE                     : num  0.695 23.79 6.592 25.343 6.628 ...
##  $ FunctionalAssessment     : num  9.99 6.2 9.57 2.49 7.52 ...
##  $ MemoryComplaints         : int  1 0 0 0 1 0 0 0 0 0 ...
##  $ BehavioralProblems       : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ ADL                      : num  6.01 7.52 8.57 6.22 5.19 ...
##  $ Confusion                : int  0 0 0 0 1 0 0 0 0 1 ...
##  $ Disorientation           : int  0 0 0 0 0 1 0 0 1 0 ...
##  $ PersonalityChanges       : int  0 0 0 0 0 1 0 0 0 0 ...
##  $ DifficultyCompletingTasks: int  1 0 0 0 0 0 0 0 0 1 ...
##  $ Forgetfulness            : int  1 1 0 1 1 0 0 0 0 1 ...
##  $ Diagnosis                : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ DoctorInCharge           : chr  "XXXConfid" "XXXConfid" "XXXConfid" "XXXConfid" ...
```

```r
# Summary statistics
summary(train)
```

```
##    PatientID           Age            Gender         Ethnicity
##  Min.   :   1.0   Min.   :60.00   Min.   :0.0000   Min.   :0.0000
##  1st Qu.: 376.8   1st Qu.:67.00   1st Qu.:0.0000   1st Qu.:0.0000
##  Median : 752.5   Median :75.00   Median :1.0000   Median :0.0000
##  Mean   : 752.5   Mean   :74.91   Mean   :0.5086   Mean   :0.7114
##  3rd Qu.:1128.2   3rd Qu.:83.00   3rd Qu.:1.0000   3rd Qu.:1.0000
##  Max.   :1504.0   Max.   :90.00   Max.   :1.0000   Max.   :3.0000
##  EducationLevel       BMI           Smoking       AlcoholConsumption
##  Min.   :0.000   Min.   :15.01   Min.   :0.0000   Min.   : 0.002003
##  1st Qu.:1.000   1st Qu.:21.37   1st Qu.:0.0000   1st Qu.: 5.204286
##  Median :1.000   Median :27.76   Median :0.0000   Median : 9.924320
##  Mean   :1.296   Mean   :27.55   Mean   :0.2839   Mean   :10.030205
##  3rd Qu.:2.000   3rd Qu.:33.78   3rd Qu.:1.0000   3rd Qu.:15.140505
##  Max.   :3.000   Max.   :39.93   Max.   :1.0000   Max.   :19.988291
##  PhysicalActivity    DietQuality        SleepQuality    FamilyHistoryAlzheimers
```

```
##  Min.   :0.003616   Min.   :0.009385   Min.   : 4.003   Min.   :0.0000
##  1st Qu.:2.538671   1st Qu.:2.302514   1st Qu.: 5.480   1st Qu.:0.0000
##  Median :4.790574   Median :4.979274   Median : 7.100   Median :0.0000
##  Mean   :4.914426   Mean   :4.937305   Mean   : 7.042   Mean   :0.2447
##  3rd Qu.:7.452197   3rd Qu.:7.576618   3rd Qu.: 8.550   3rd Qu.:0.0000
##  Max.   :9.987429   Max.   :9.998346   Max.   :10.000   Max.   :1.0000
##  CardiovascularDisease    Diabetes        Depression       HeadInjury
##  Min.   :0.0000        Min.   :0.0000   Min.   :0.0000   Min.   :0.00000
##  1st Qu.:0.0000        1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.00000
##  Median :0.0000        Median :0.0000   Median :0.0000   Median :0.00000
##  Mean   :0.1343        Mean   :0.1596   Mean   :0.2081   Mean   :0.09508
##  3rd Qu.:0.0000        3rd Qu.:0.0000   3rd Qu.:0.0000   3rd Qu.:0.00000
##  Max.   :1.0000        Max.   :1.0000   Max.   :1.0000   Max.   :1.00000
##   Hypertension      SystolicBP     DiastolicBP     CholesterolTotal
##  Min.   :0.0000   Min.   : 90.0   Min.   : 60.00   Min.   :150.1
##  1st Qu.:0.0000   1st Qu.:112.0   1st Qu.: 74.00   1st Qu.:190.5
##  Median :0.0000   Median :135.0   Median : 90.00   Median :224.4
##  Mean   :0.1516   Mean   :134.7   Mean   : 89.71   Mean   :225.2
##  3rd Qu.:0.0000   3rd Qu.:156.0   3rd Qu.:105.00   3rd Qu.:262.5
##  Max.   :1.0000   Max.   :179.0   Max.   :119.00   Max.   :300.0
##  CholesterolLDL   CholesterolHDL  CholesterolTriglycerides      MMSE
##  Min.   : 50.40   Min.   :20.00   Min.   : 50.41           Min.   : 0.0353
##  1st Qu.: 87.52   1st Qu.:39.15   1st Qu.:136.31           1st Qu.: 7.1155
##  Median :124.52   Median :59.59   Median :229.55           Median :14.3225
##  Mean   :124.88   Mean   :59.51   Mean   :226.90           Mean   :14.6491
##  3rd Qu.:161.96   3rd Qu.:78.91   3rd Qu.:313.06           3rd Qu.:21.8386
##  Max.   :199.97   Max.   :99.98   Max.   :399.94           Max.   :29.9914
##  FunctionalAssessment MemoryComplaints BehavioralProblems      ADL
##  Min.   :0.00046      Min.   :0.0000   Min.   :0.0000     Min.   :0.004354
##  1st Qu.:2.65883      1st Qu.:0.0000   1st Qu.:0.0000     1st Qu.:2.358590
##  Median :5.19113      Median :0.0000   Median :0.0000     Median :4.877862
##  Mean   :5.13989      Mean   :0.2055   Mean   :0.1516     Mean   :4.903536
##  3rd Qu.:7.61636      3rd Qu.:0.0000   3rd Qu.:0.0000     3rd Qu.:7.517219
##  Max.   :9.99647      Max.   :1.0000   Max.   :1.0000     Max.   :9.972663
##    Confusion      Disorientation   PersonalityChanges DifficultyCompletingTasks
##  Min.   :0.0000   Min.   :0.0000   Min.   :0.0000     Min.   :0.0000
##  1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.0000     1st Qu.:0.0000
##  Median :0.0000   Median :0.0000   Median :0.0000     Median :0.0000
##  Mean   :0.2028   Mean   :0.1562   Mean   :0.1569     Mean   :0.1622
##  3rd Qu.:0.0000   3rd Qu.:0.0000   3rd Qu.:0.0000     3rd Qu.:0.0000
##  Max.   :1.0000   Max.   :1.0000   Max.   :1.0000     Max.   :1.0000
##  Forgetfulness      Diagnosis      DoctorInCharge
##  Min.   :0.0000   Min.   :0.0000   Length:1504
##  1st Qu.:0.0000   1st Qu.:0.0000   Class :character
##  Median :0.0000   Median :0.0000   Mode  :character
##  Mean   :0.2999   Mean   :0.3537
##  3rd Qu.:1.0000   3rd Qu.:1.0000
##  Max.   :1.0000   Max.   :1.0000
```

1.2.2. Check for Missing Values

```
# Check for missing values in training data
sapply(train, function(x) sum(is.na(x)))
```

```
##                PatientID                      Age                   Gender
```

```
##                      0                      0                      0
##              Ethnicity        EducationLevel                    BMI
##                      0                      0                      0
##                Smoking     AlcoholConsumption      PhysicalActivity
##                      0                      0                      0
##            DietQuality          SleepQuality FamilyHistoryAlzheimers
##                      0                      0                      0
##  CardiovascularDisease               Diabetes             Depression
##                      0                      0                      0
##            HeadInjury           Hypertension             SystolicBP
##                      0                      0                      0
##           DiastolicBP      CholesterolTotal        CholesterolLDL
##                      0                      0                      0
##        CholesterolHDL CholesterolTriglycerides                   MMSE
##                      0                      0                      0
##   FunctionalAssessment       MemoryComplaints    BehavioralProblems
##                      0                      0                      0
##                   ADL              Confusion        Disorientation
##                      0                      0                      0
##     PersonalityChanges DifficultyCompletingTasks        Forgetfulness
##                      0                      0                      0
##              Diagnosis        DoctorInCharge
##                      0                      0
```

```r
# Load the Amelia library
library(Amelia)

# Visualize missing data
missmap(train, main = "Missing values in Training Data", col = c("yellow", "black"), legend = FALSE)
```

1.3. Data Cleaning

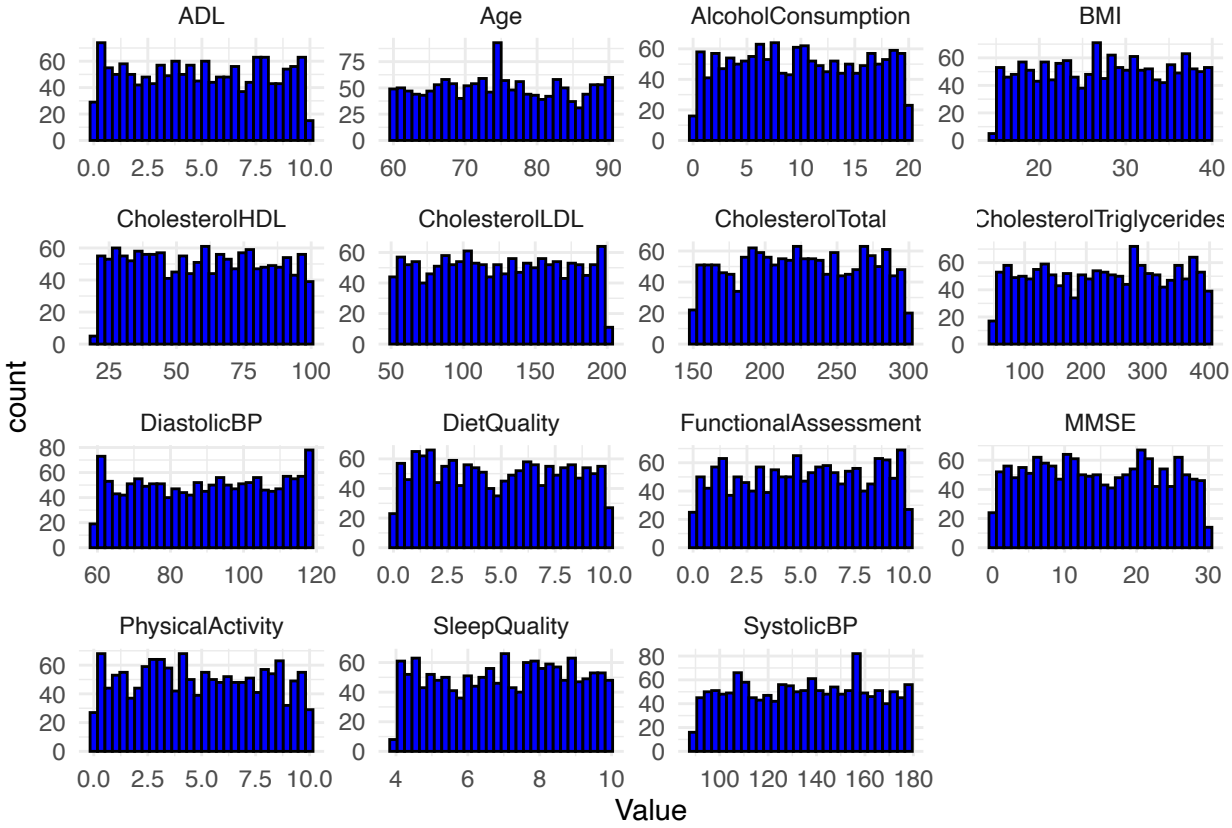
```
library(dplyr)
# Remove 'PatientID' and 'DoctorInCharge' from train
train <- train %>% select(-PatientID, -DoctorInCharge)
# Identify categorical variables
categorical_vars <- c('Gender', 'Ethnicity', 'EducationLevel', 'Smoking', 'MemoryComplaints',
                      'BehavioralProblems', 'FamilyHistoryAlzheimers', 'CardiovascularDisease',
                      'Diabetes', 'Depression', 'HeadInjury', 'Hypertension', 'Confusion',
                      'Disorientation', 'PersonalityChanges', 'DifficultyCompletingTasks',
                      'Forgetfulness', 'Diagnosis')

# Convert to factors
train[categorical_vars] <- lapply(train[categorical_vars], as.factor)
# For numerical variables, use median imputation
numerical_vars <- setdiff(names(train), categorical_vars)
train[numerical_vars] <- lapply(train[numerical_vars], function(x) ifelse(is.na(x), median(x, na.rm = T
```

1.4. Univariate Analysis

```
# Plot histograms for numerical variables
library(ggplot2)
library(tidyverse)

train %>%
  select(numerical_vars) %>%
  gather(key = "Variable", value = "Value") %>%
  ggplot(aes(x = Value)) +
```

```
  geom_histogram(bins = 30, fill = 'blue', color = 'black') +
  facet_wrap(~ Variable, scales = 'free') +
  theme_minimal()
```

```
## Warning: Using an external vector in selections was deprecated in tidyselect 1.1.0.
## i Please use `all_of()` or `any_of()` instead.
##   # Was:
##   data %>% select(numerical_vars)
##
##   # Now:
##   data %>% select(all_of(numerical_vars))
##
## See <https://tidyselect.r-lib.org/reference/faq-external-vector.html>.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

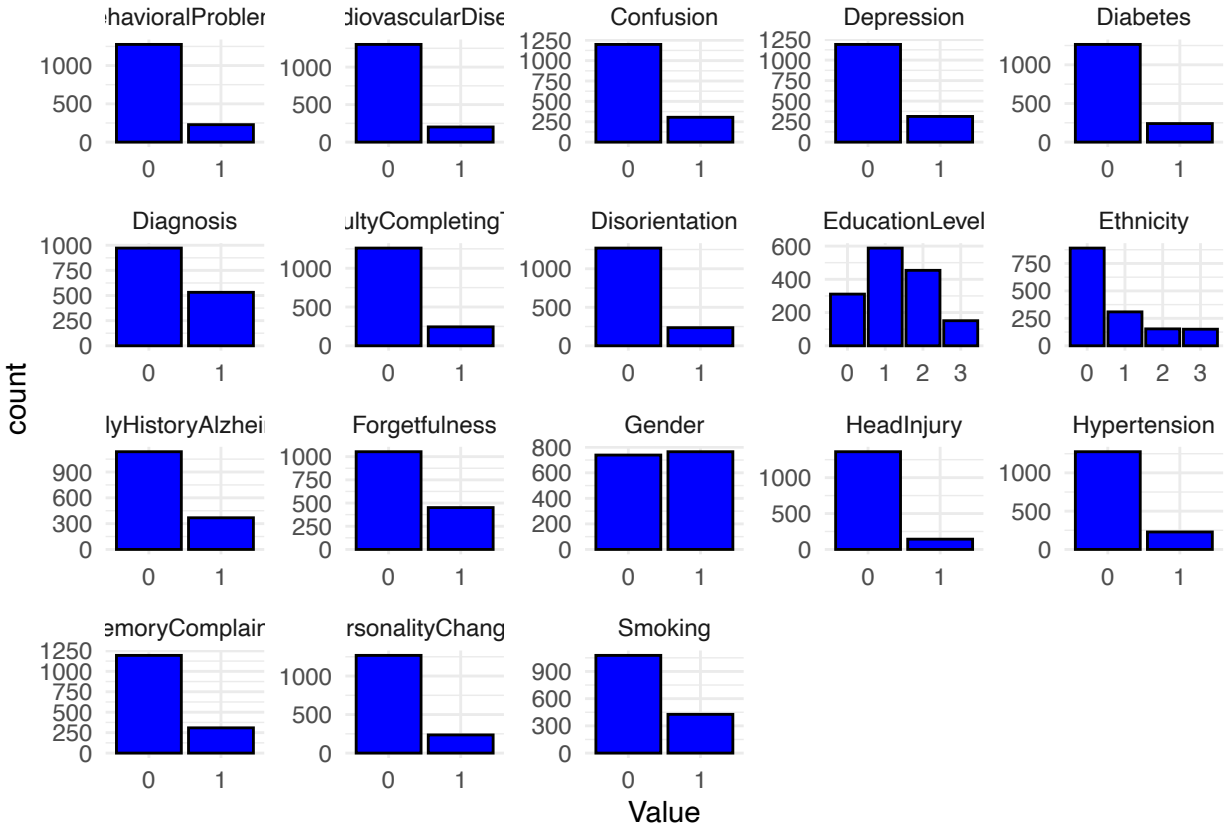



```
# Plot bar charts for categorical variables
train %>%
  select(categorical_vars) %>%
  gather(key = "Variable", value = "Value") %>%
  ggplot(aes(x = Value)) +
  geom_bar(fill = 'blue', color = 'black') +
  facet_wrap(~ Variable, scales = 'free') +
  theme_minimal()
```

```
## Warning: Using an external vector in selections was deprecated in tidyselect 1.1.0.
## i Please use `all_of()` or `any_of()` instead.
```

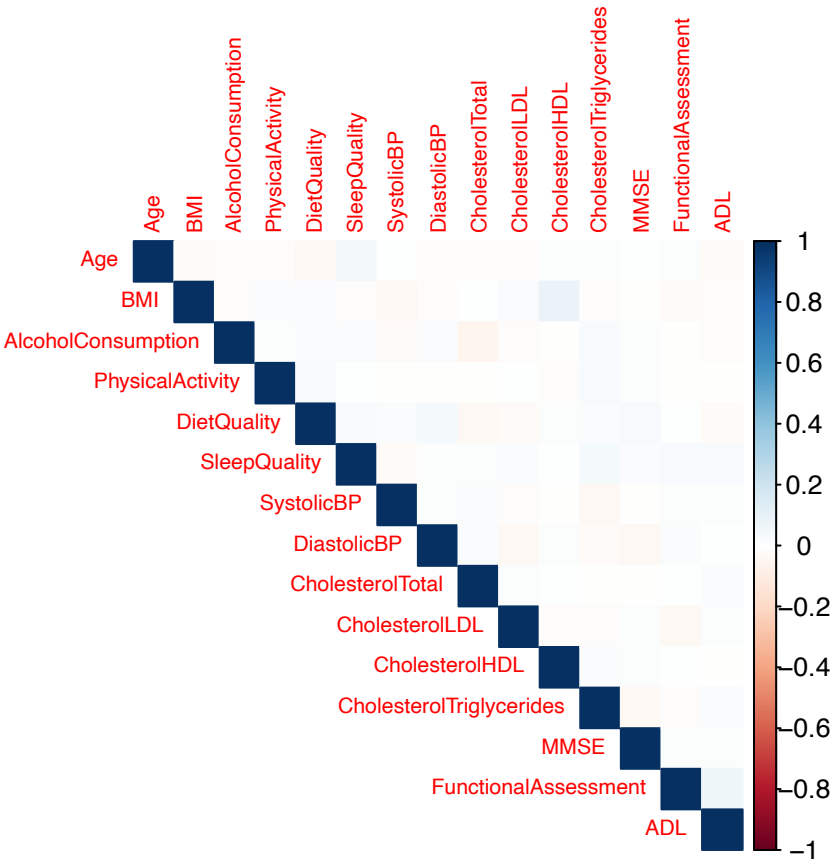
```
##   # Was:
##   data %>% select(categorical_vars)
##
##   # Now:
##   data %>% select(all_of(categorical_vars))
##
## See <https://tidyselect.r-lib.org/reference/faq-external-vector.html>.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
## Warning: attributes are not identical across measure variables; they will be
## dropped
```

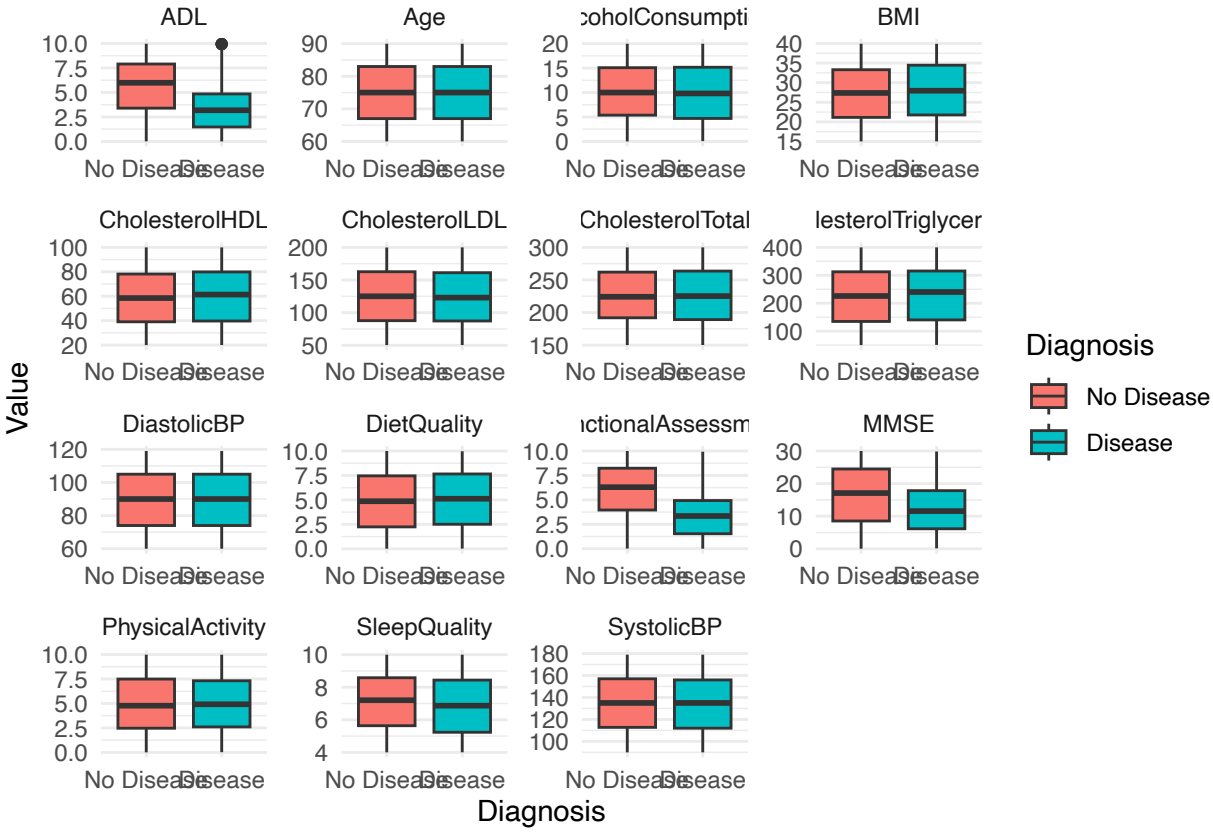


1.5. Bivariate Analysis

```r
# Calculate correlation matrix
corr_matrix <- cor(train %>% select(numerical_vars) %>% mutate_all(as.numeric))

# Plot correlation matrix
corrplot(corr_matrix, method = 'color', type = 'upper', tl.cex = 0.7)
```

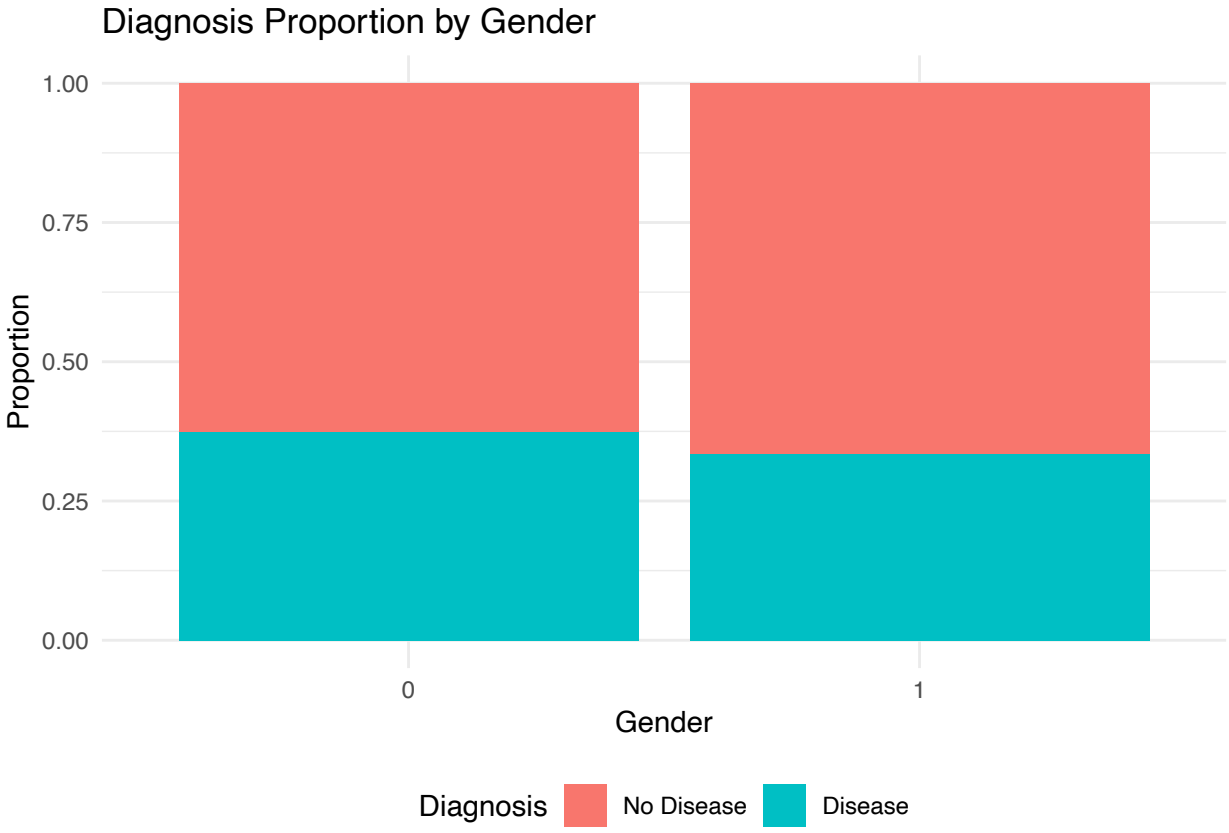



```r
# Boxplots for numerical variables vs Diagnosis
library(tidyr)
library(dplyr)
library(ggplot2)
train %>%
  select(numerical_vars, Diagnosis) %>%
  gather(key = "Variable", value = "Value", -Diagnosis) %>%
  ggplot(aes(x = Diagnosis, y = Value, fill = Diagnosis)) +
  geom_boxplot() +
  facet_wrap(~ Variable, scales = 'free') +
  theme_minimal()+
  scale_x_discrete(labels = c('0' = 'No Disease', '1' = 'Disease'))+
  scale_fill_discrete(labels = c('0' = 'No Disease', '1' = 'Disease'))
```

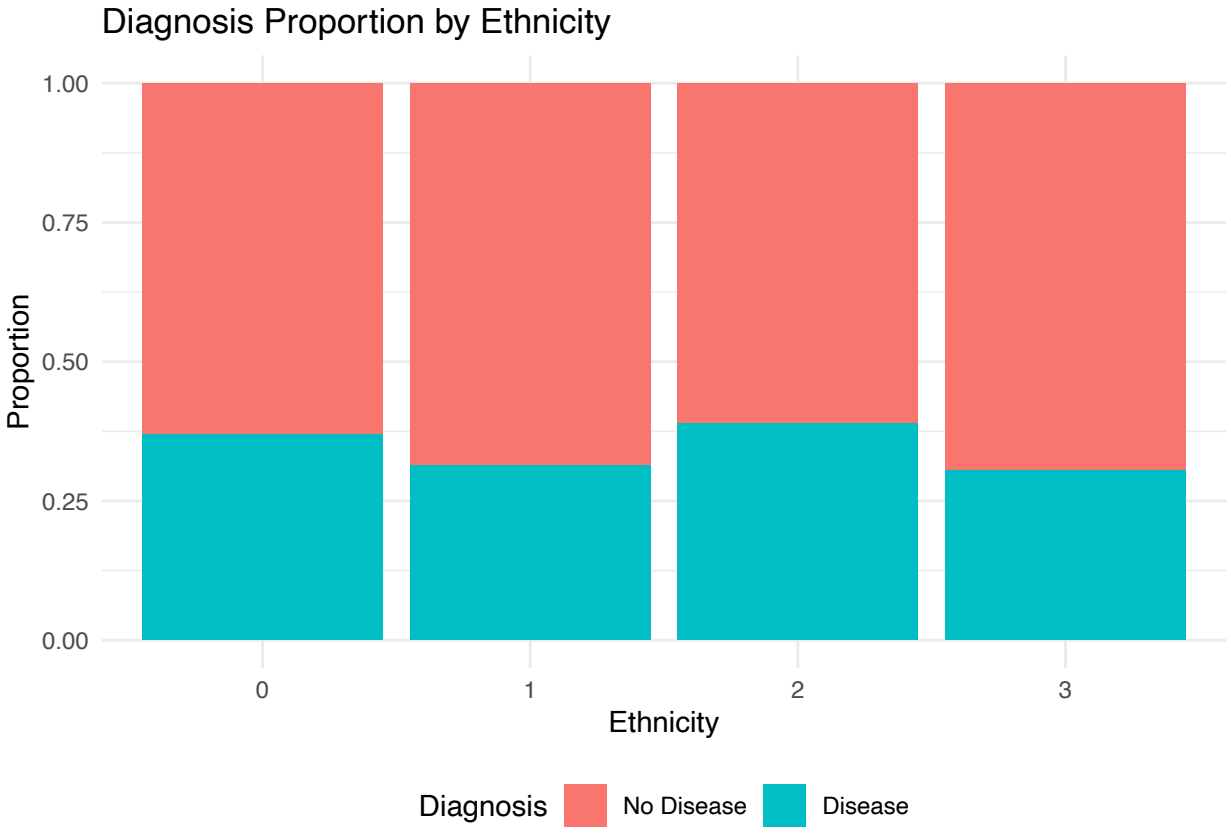



```r
# Load necessary libraries
library(ggplot2)

# Bar charts for categorical variables vs Diagnosis
for (var in setdiff(categorical_vars, 'Diagnosis')) {
  # Create ggplot object
  p <- ggplot(train, aes(x = .data[[var]], fill = Diagnosis)) +
    geom_bar(position = 'fill') +
    labs(y = 'Proportion') +
    theme_minimal() +
    ggtitle(paste('Diagnosis Proportion by', var)) +
    theme(legend.position = 'bottom') +
    scale_fill_brewer(palette = 'Set1')+
    scale_fill_discrete(labels = c('0' = 'No Disease', '1' = 'Disease'))

  # Print the plot
  print(p)
}
```

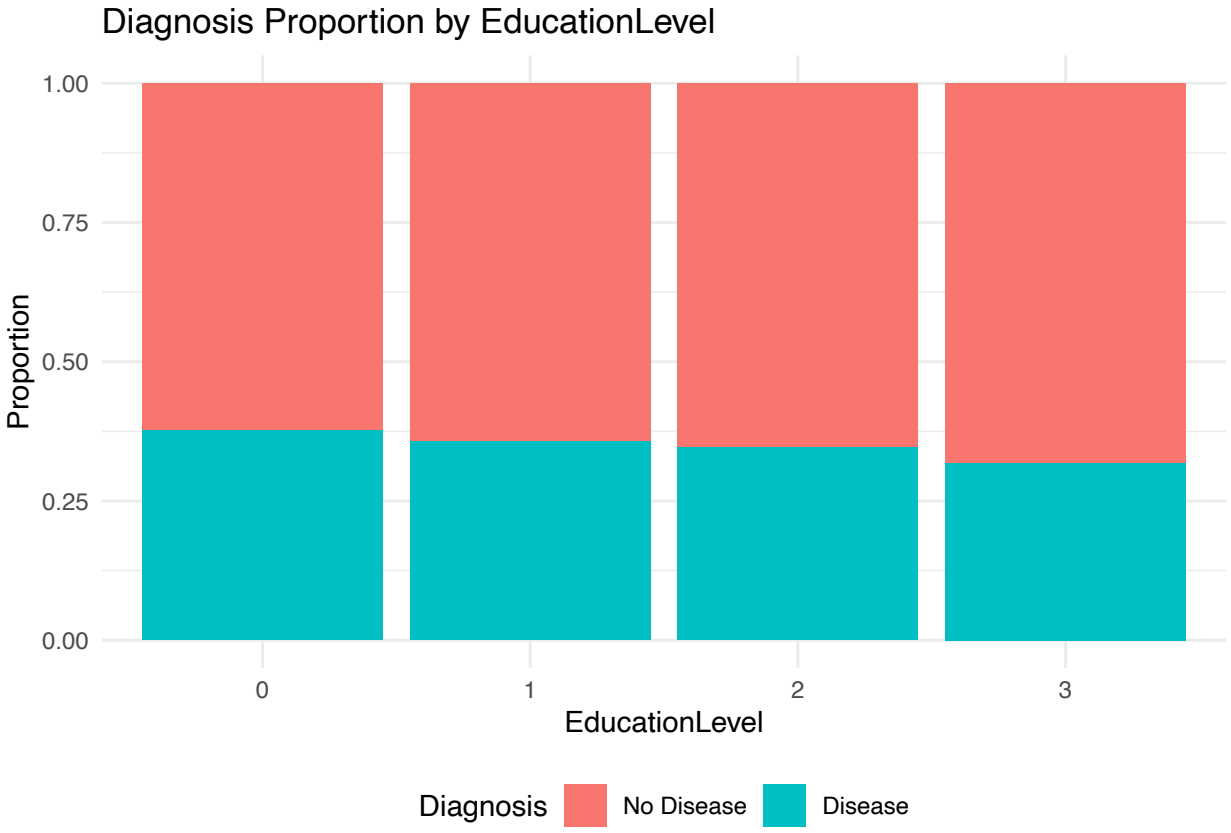
```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```



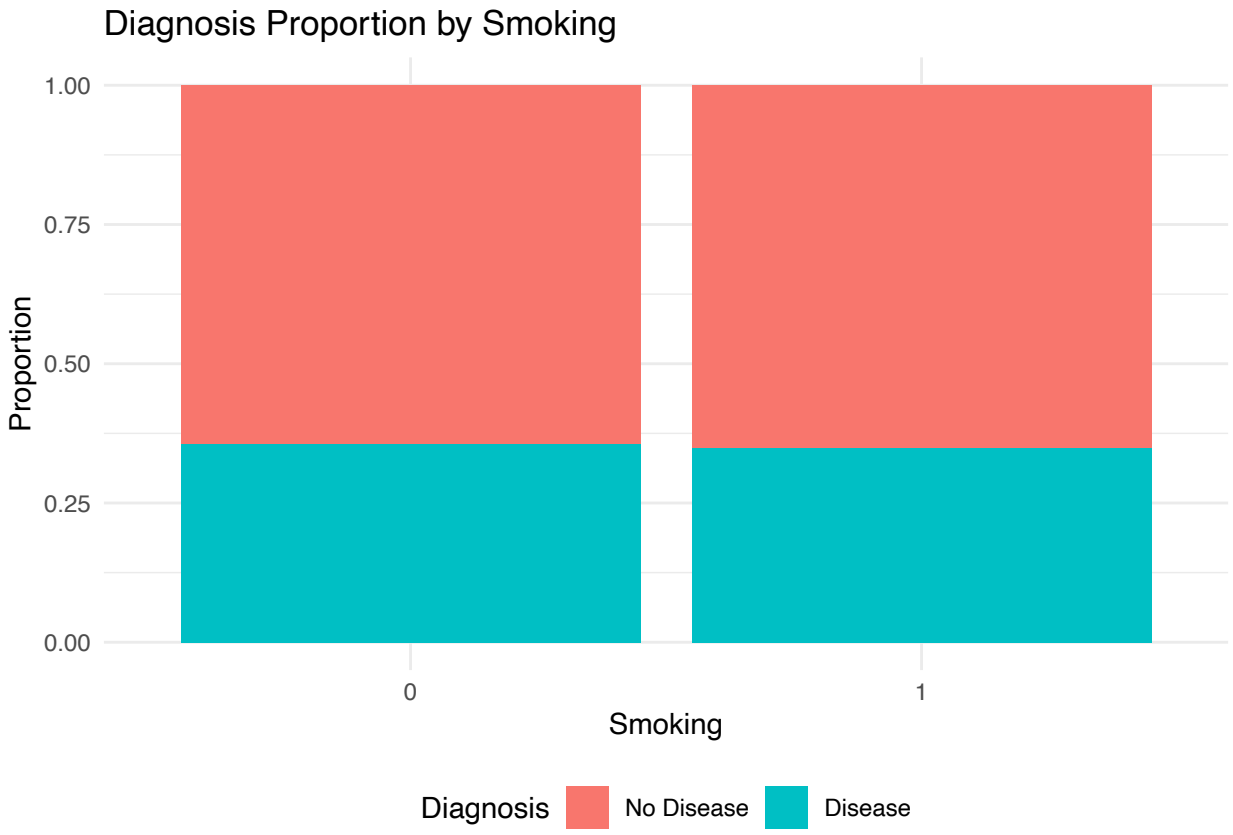

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```




```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```

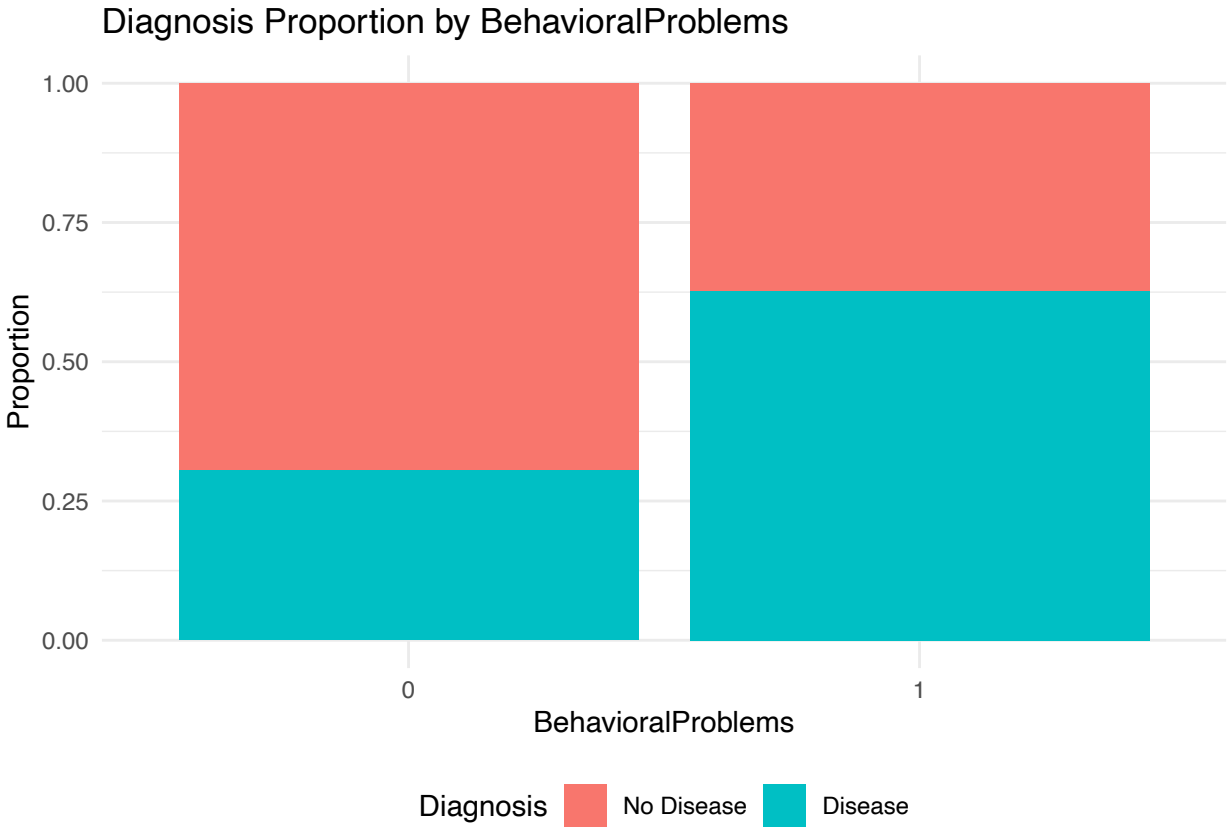



```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```

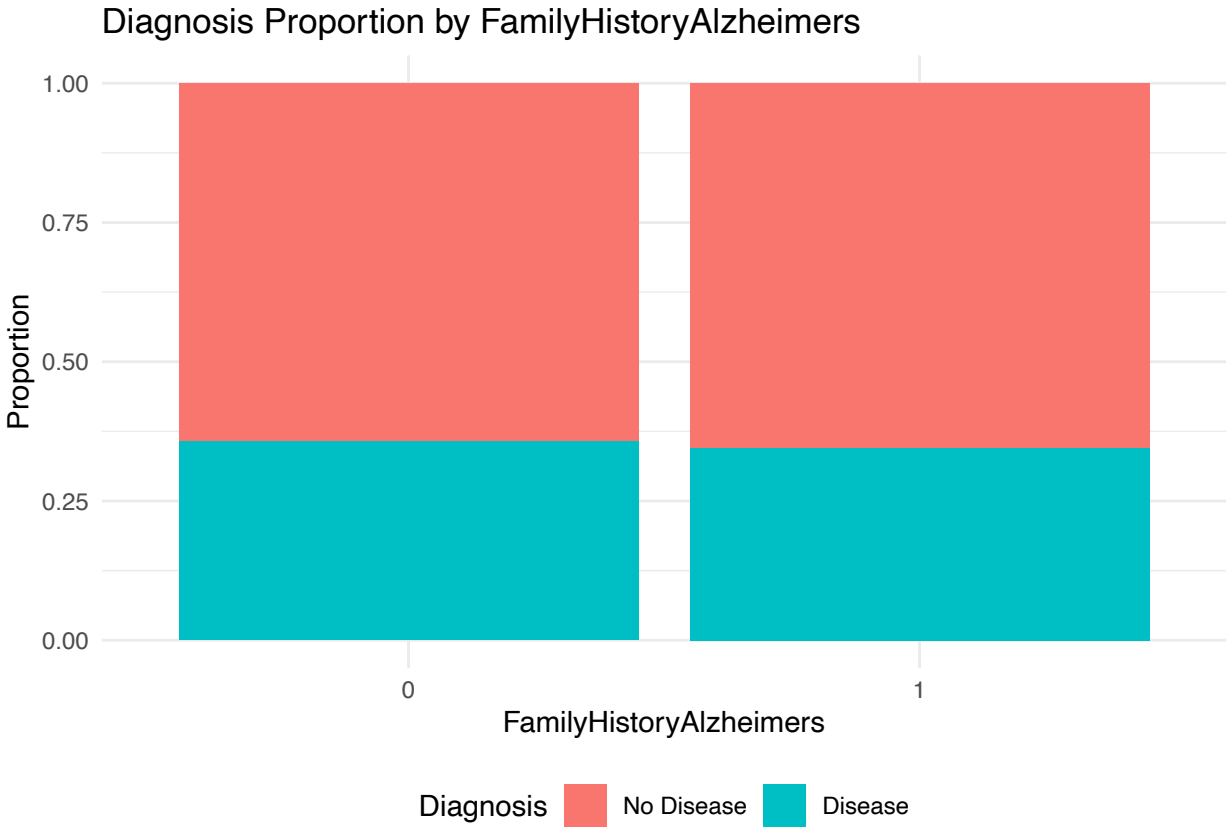



```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```

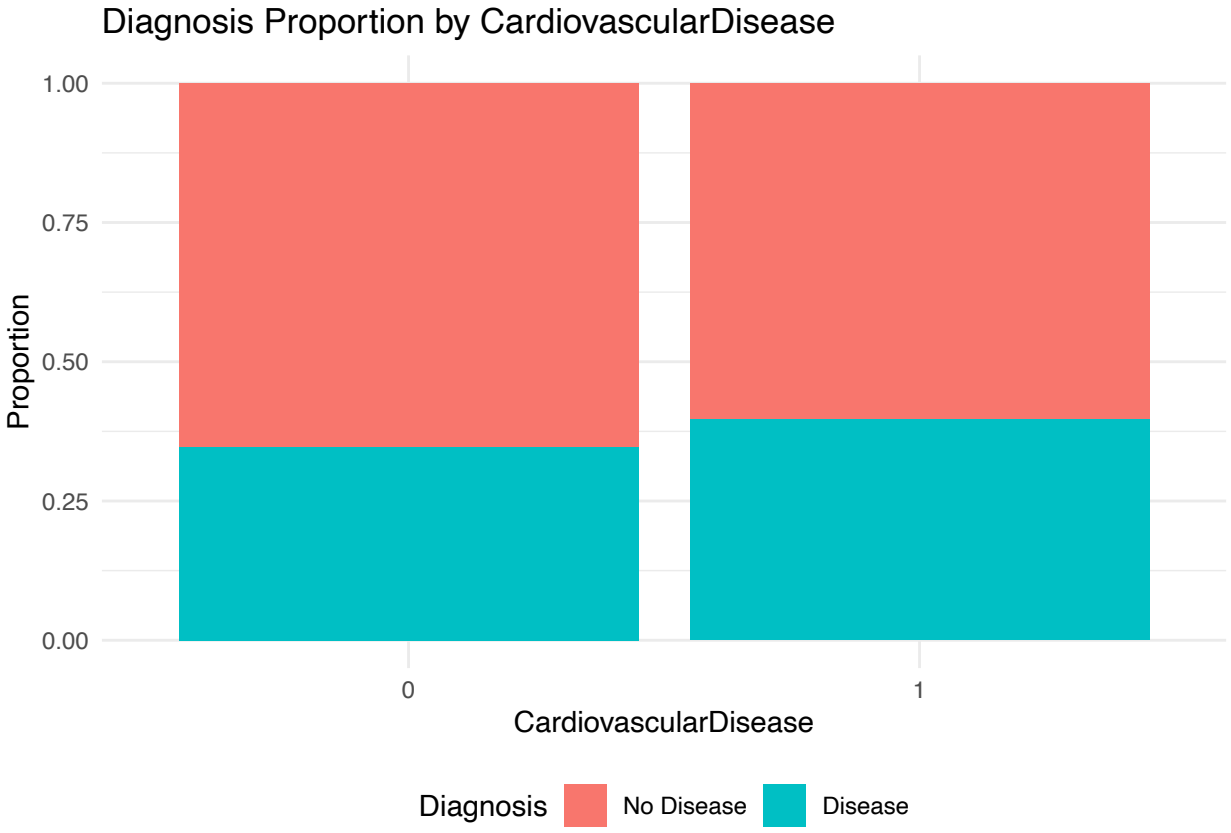

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```



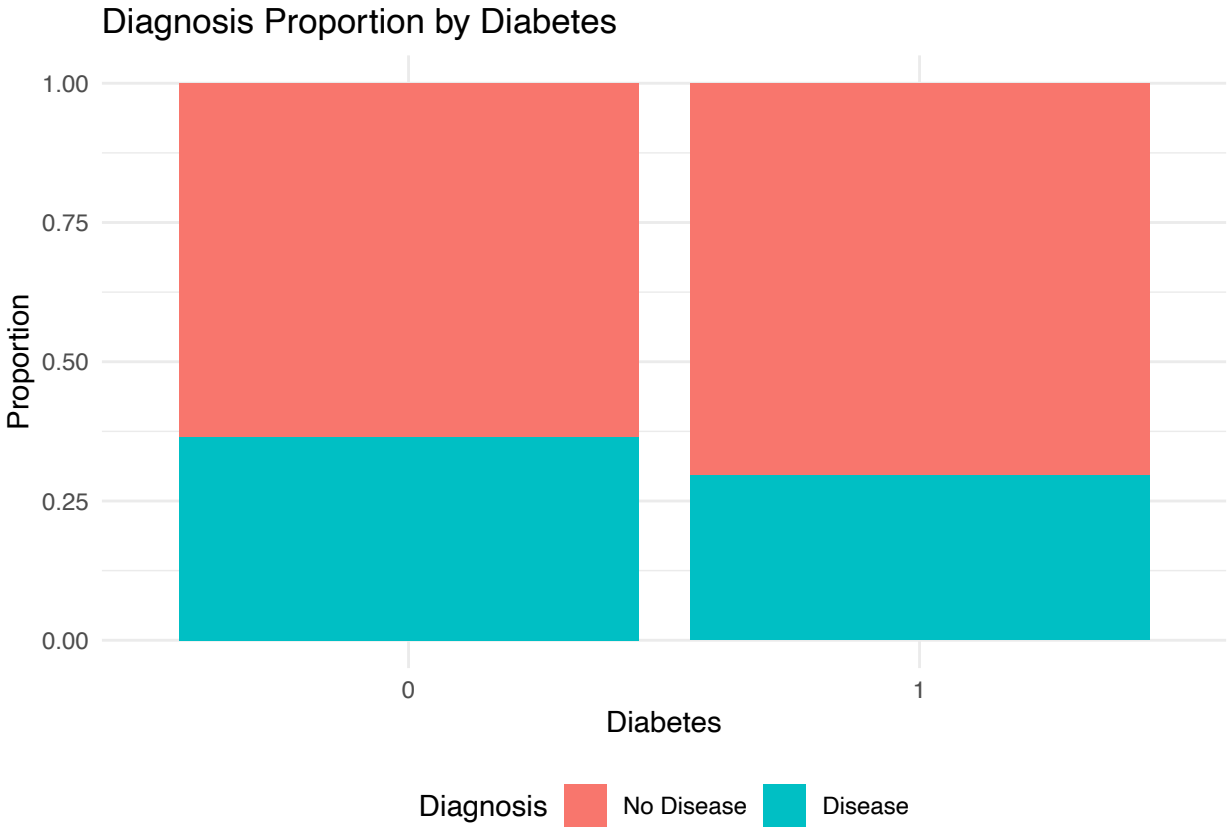

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```



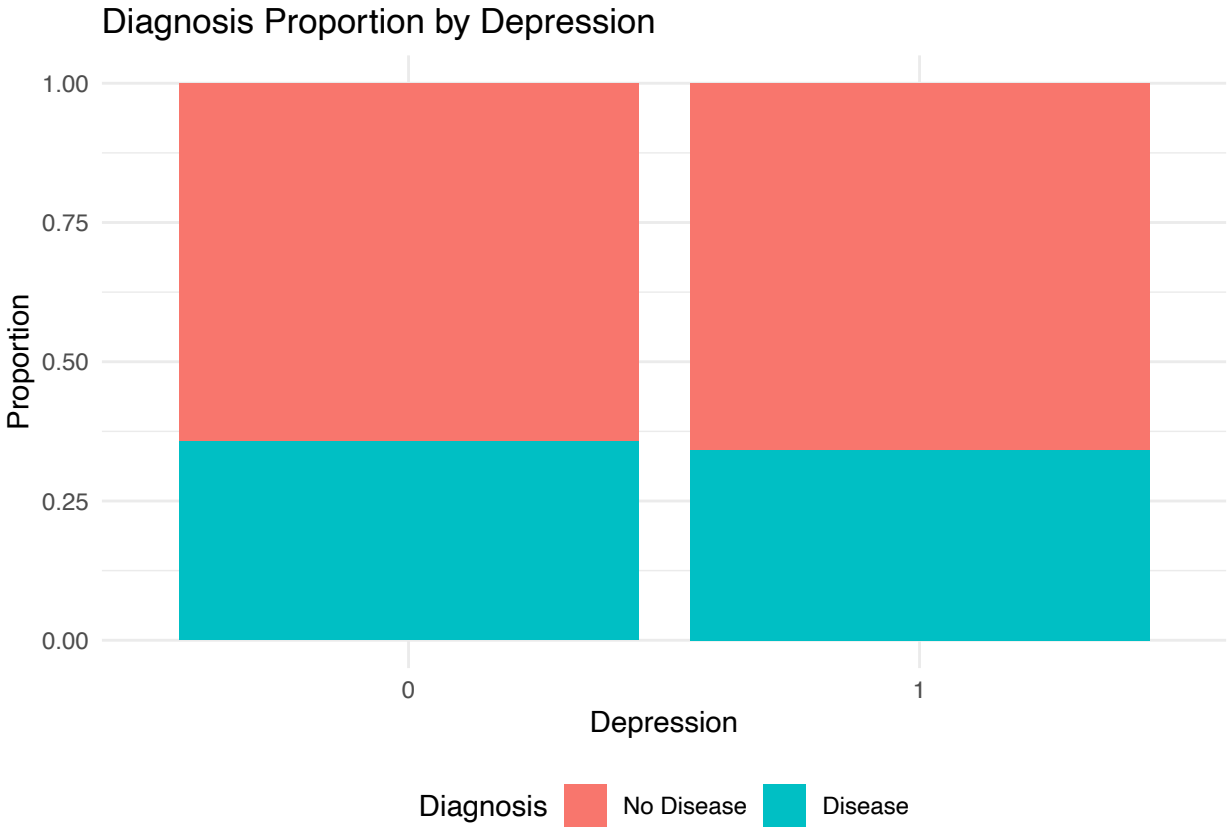

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```



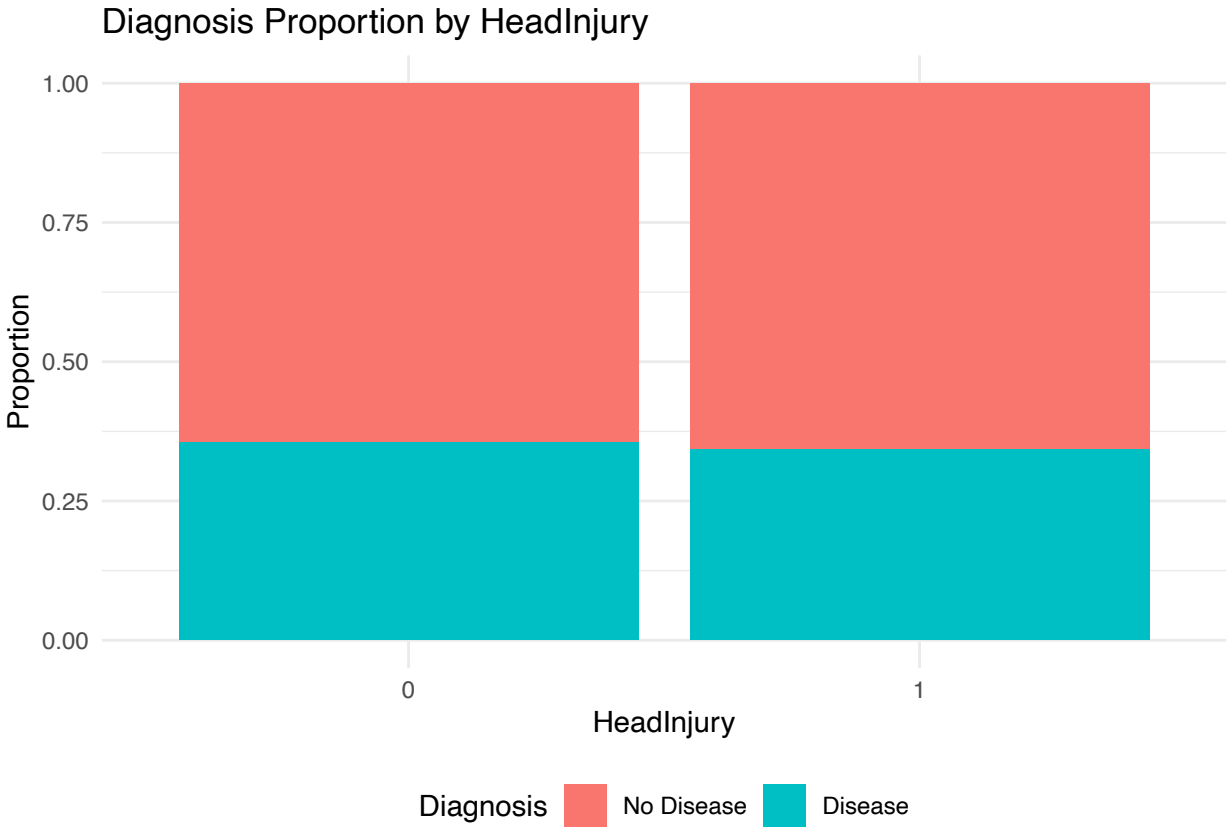

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```



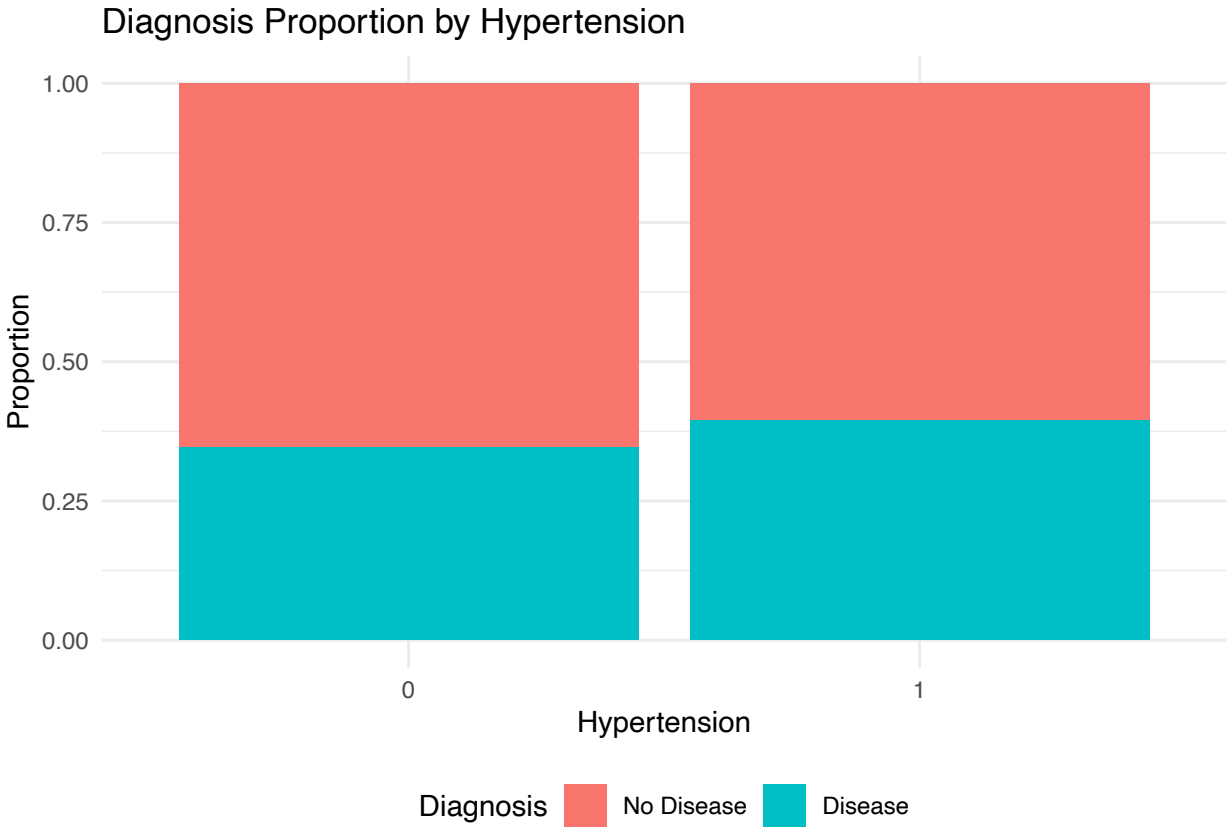

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```



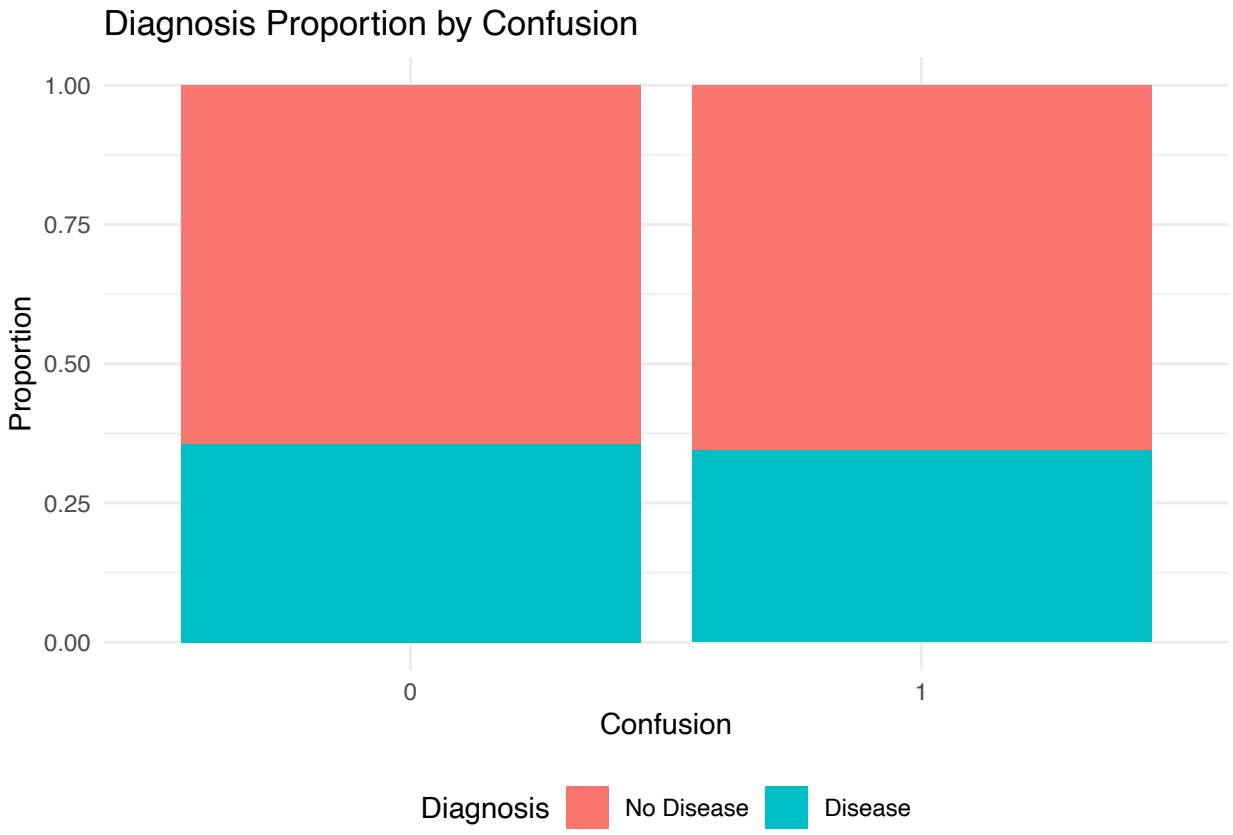

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```



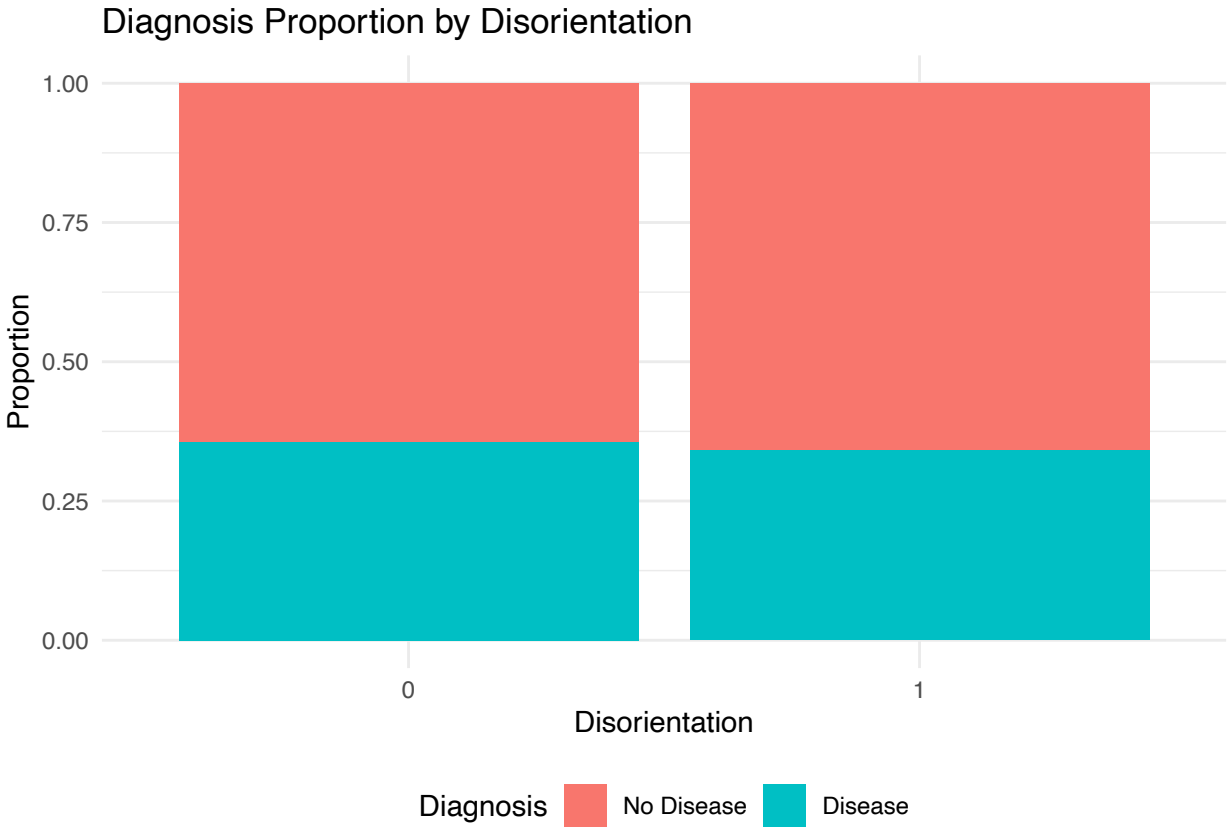

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```



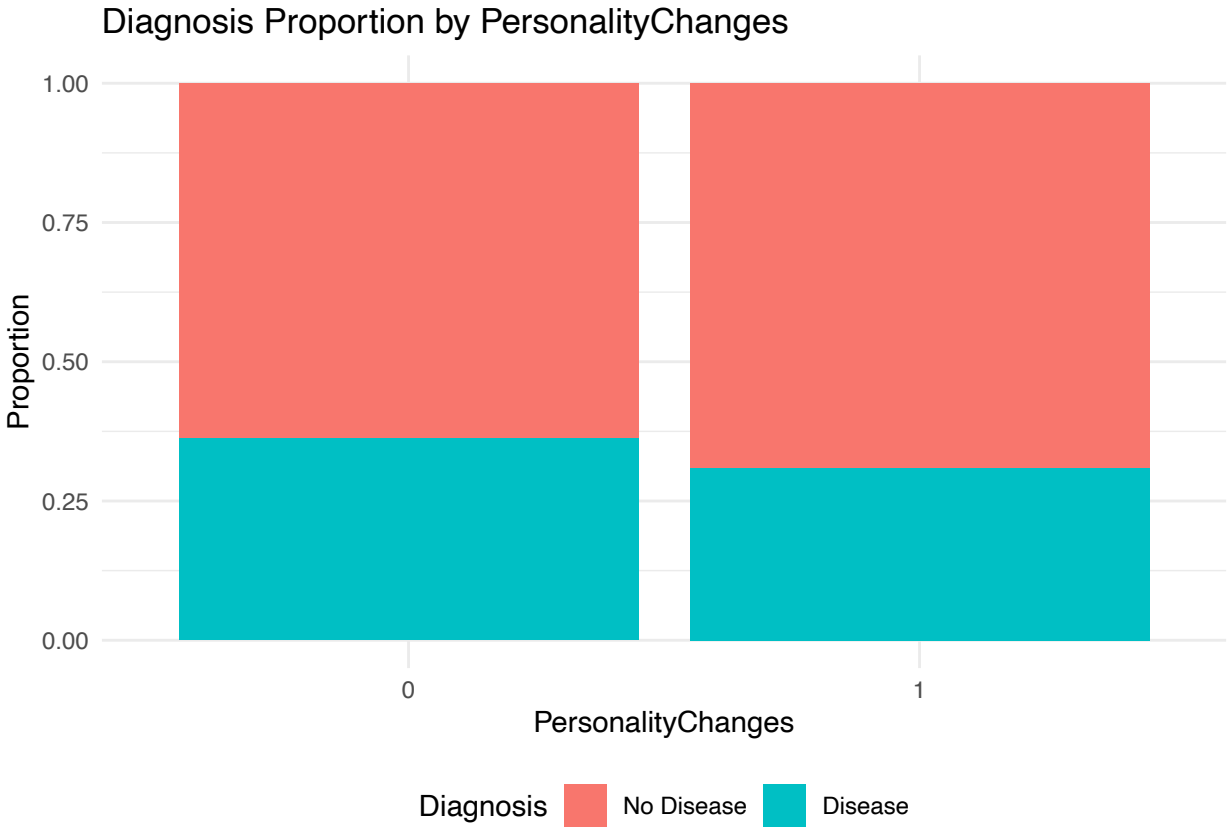

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```



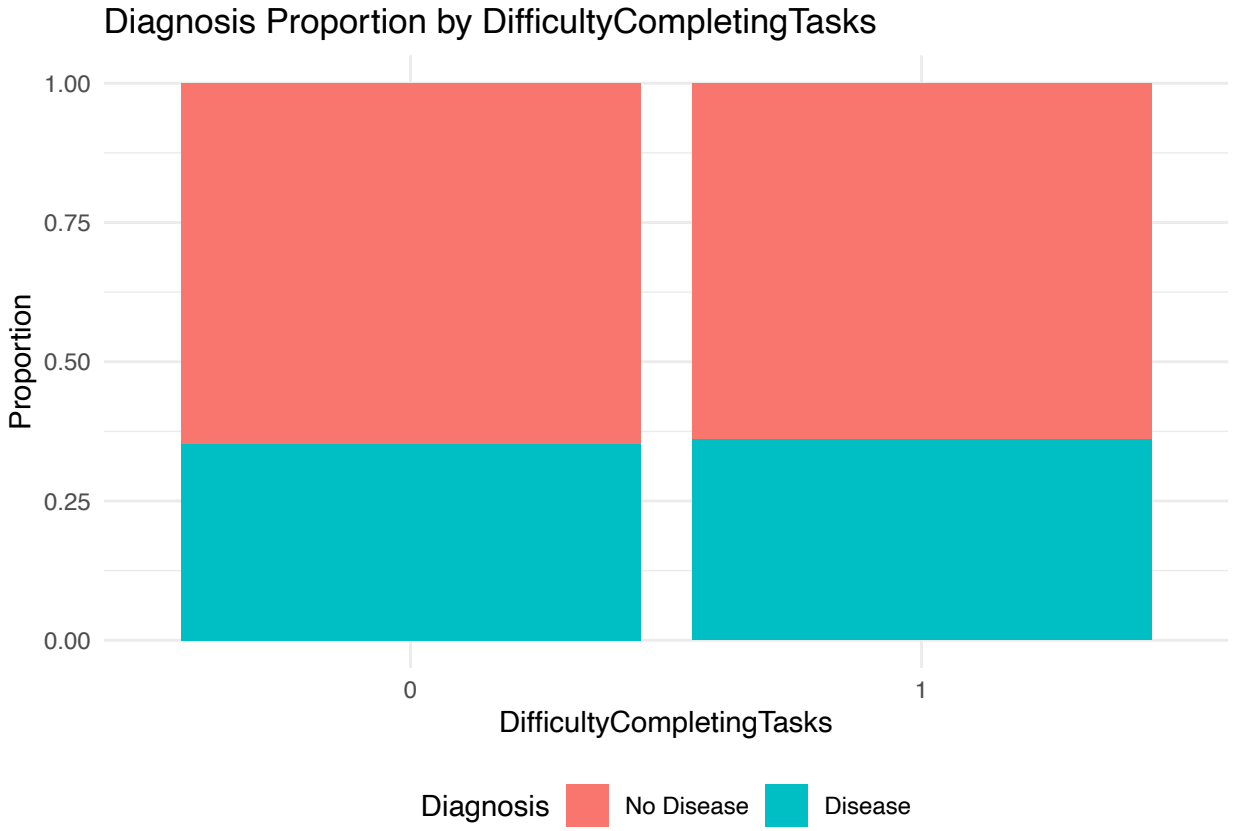

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```

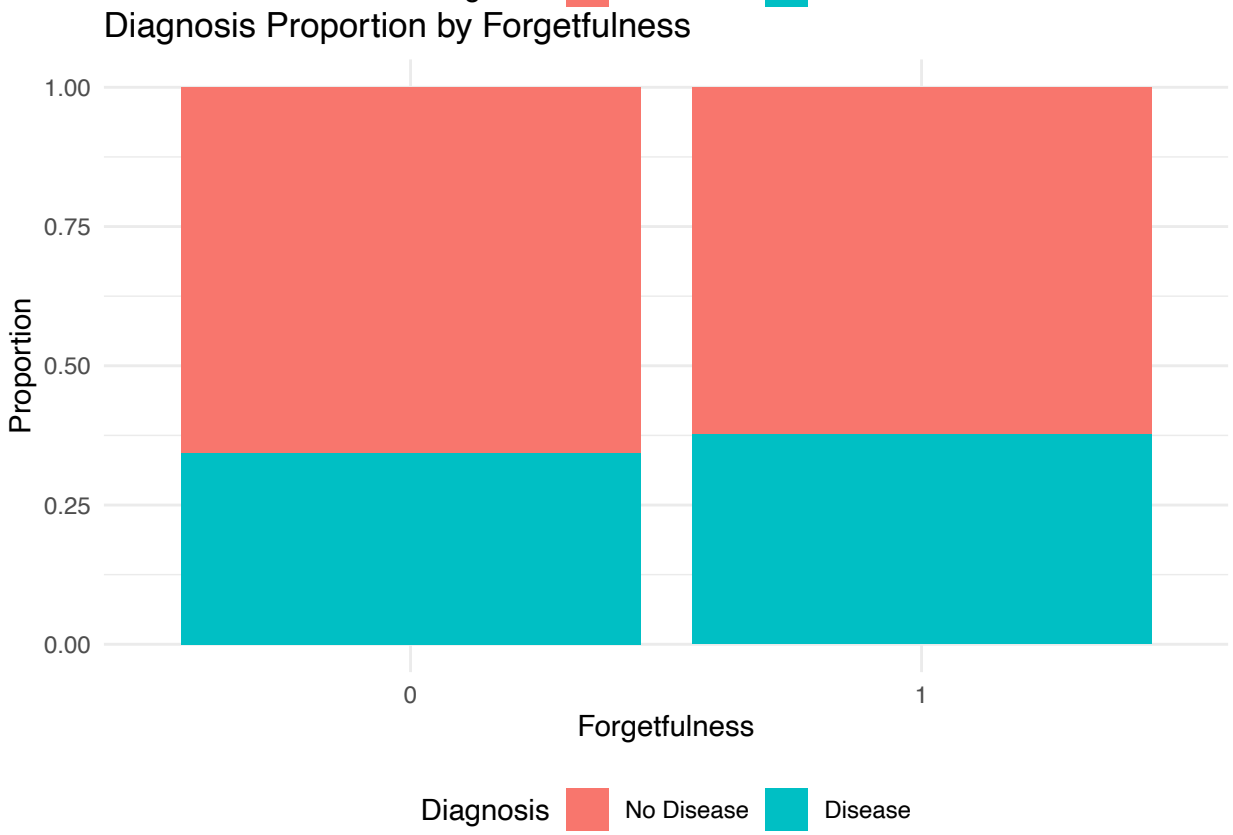



```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```




```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```





2. Prediction of the Target Variable (Diagnosis)

2.1. Data Preparation

```r
library(caret)
set.seed(123)
train_index <- createDataPartition(train$Diagnosis, p = 0.8, list = FALSE)
train_data <- train[train_index, ]
valid_data <- train[-train_index, ]
```

2.2. Logistic Regression

```r
# Build logistic regression model
glm_model <- glm(Diagnosis ~ ., data = train_data, family = binomial)

# Summary of the model
summary(glm_model)
```

```
##
## Call:
## glm(formula = Diagnosis ~ ., family = binomial, data = train_data)
##
## Coefficients:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 3.8921148  1.2854894   3.028  0.00246 **
## Age                        -0.0063797  0.0095330  -0.669  0.50335
## Gender1                    -0.2703788  0.1712112  -1.579  0.11429
## Ethnicity1                 -0.3707940  0.2246670  -1.650  0.09886 .
## Ethnicity2                  0.0396992  0.3019202   0.131  0.89539
## Ethnicity3                 -0.2845124  0.3094524  -0.919  0.35788
## EducationLevel1            -0.1315280  0.2313651  -0.568  0.56970
## EducationLevel2             0.0732989  0.2426823   0.302  0.76262
## EducationLevel3            -0.2520521  0.3291101  -0.766  0.44376
## BMI                         0.0057538  0.0118589   0.485  0.62754
## Smoking1                   -0.1789221  0.1943481  -0.921  0.35725
## AlcoholConsumption         -0.0064046  0.0148680  -0.431  0.66664
## PhysicalActivity           -0.0137382  0.0292531  -0.470  0.63862
## DietQuality                 0.0332433  0.0298383   1.114  0.26523
## SleepQuality               -0.0619417  0.0491758  -1.260  0.20781
## FamilyHistoryAlzheimers1    0.1512638  0.2002817   0.755  0.45010
## CardiovascularDisease1      0.2548065  0.2339869   1.089  0.27616
## Diabetes1                  -0.0271540  0.2364758  -0.115  0.90858
## Depression1                 0.2251362  0.2064860   1.090  0.27557
## HeadInjury1                -0.1827456  0.2878455  -0.635  0.52551
## Hypertension1               0.1965996  0.2373693   0.828  0.40753
## SystolicBP                  0.0021187  0.0033137   0.639  0.52258
## DiastolicBP                 0.0038221  0.0047613   0.803  0.42212
## CholesterolTotal           -0.0001103  0.0019985  -0.055  0.95598
## CholesterolLDL             -0.0002450  0.0020092  -0.122  0.90294
## CholesterolHDL              0.0039594  0.0037458   1.057  0.29050
## CholesterolTriglycerides    0.0006160  0.0008376   0.735  0.46208
## MMSE                       -0.1085405  0.0110849  -9.792  < 2e-16 ***
## FunctionalAssessment       -0.4329772  0.0351008 -12.335  < 2e-16 ***
## MemoryComplaints1           2.4297325  0.2228794  10.902  < 2e-16 ***
## BehavioralProblems1         2.5422929  0.2553676   9.955  < 2e-16 ***
## ADL                        -0.4089033  0.0349830 -11.689  < 2e-16 ***
## Confusion1                 -0.2629195  0.2107773  -1.247  0.21226
```

```
## Disorientation1            -0.0173571  0.2367329  -0.073  0.94155
## PersonalityChanges1        -0.0547501  0.2423071  -0.226  0.82124
## DifficultyCompletingTasks1  0.1356912  0.2346503   0.578  0.56308
## Forgetfulness1             -0.0455041  0.1890322  -0.241  0.80977
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1564.67  on 1203  degrees of freedom
## Residual deviance:  895.94  on 1167  degrees of freedom
## AIC: 969.94
##
## Number of Fisher Scoring iterations: 6
```

```r
# Predictions on validation set
glm_probs <- predict(glm_model, valid_data, type = 'response')
glm_preds <- ifelse(glm_probs > 0.5, 1, 0)

# Confusion matrix
glm_cm <- confusionMatrix(as.factor(glm_preds), valid_data$Diagnosis)
print(glm_cm)
```

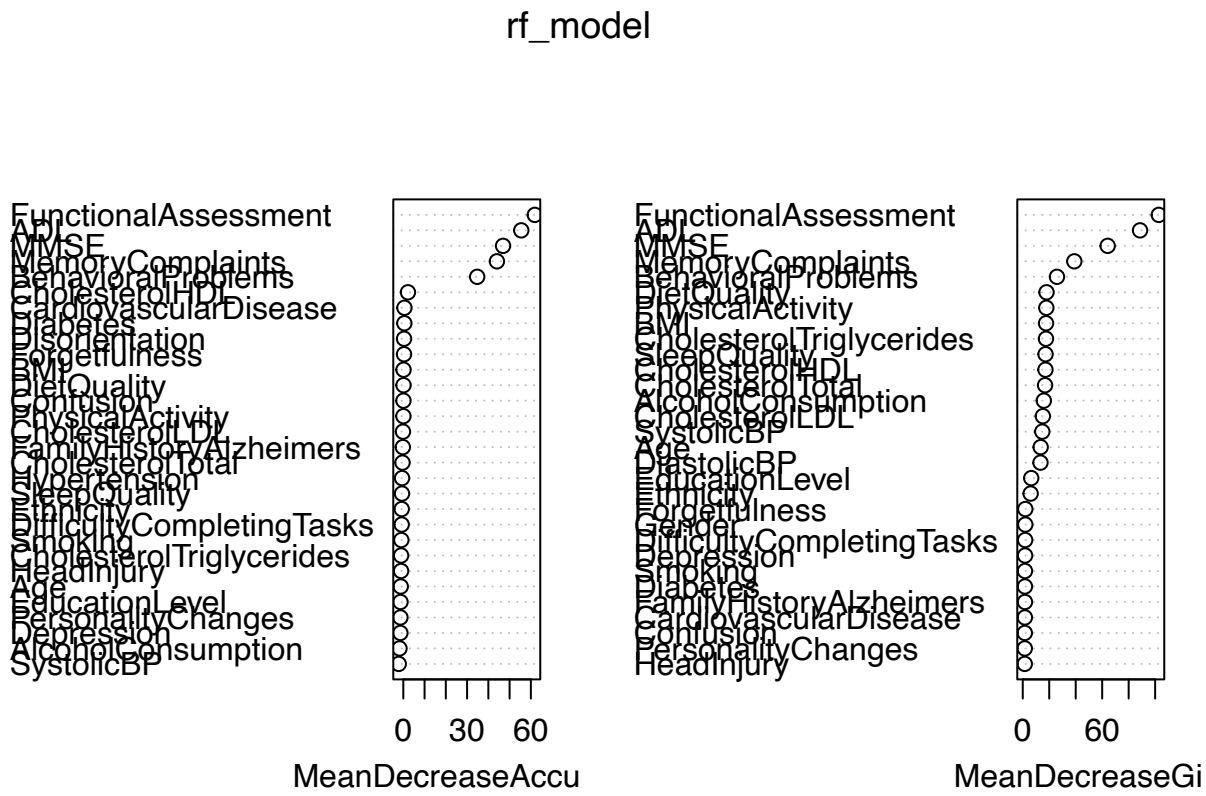
```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 175  22
##          1  19  84
##
##                Accuracy : 0.8633
##                  95% CI : (0.8192, 0.9001)
##     No Information Rate : 0.6467
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.699
##
##  Mcnemar's Test P-Value : 0.7548
##
##             Sensitivity : 0.9021
##             Specificity : 0.7925
##          Pos Pred Value : 0.8883
##          Neg Pred Value : 0.8155
##              Prevalence : 0.6467
##          Detection Rate : 0.5833
##    Detection Prevalence : 0.6567
##       Balanced Accuracy : 0.8473
##
##        'Positive' Class : 0
##
```

```r
# Calculate accuracy
glm_accuracy <- mean(glm_preds == valid_data$Diagnosis)
print(paste("Logistic Regression Accuracy:", round(glm_accuracy * 100, 2), "%"))
```

```
## [1] "Logistic Regression Accuracy: 86.33 %"
```

2.3. Random Forest

```
# Build random forest model
library(randomForest)
set.seed(123)
rf_model <- randomForest(Diagnosis ~ ., data = train_data, ntree = 500, importance = TRUE)

# Variable importance plot
varImpPlot(rf_model)
```




```
# Predictions on validation set
rf_preds <- predict(rf_model, valid_data)

# Confusion matrix
rf_cm <- confusionMatrix(rf_preds, valid_data$Diagnosis)
print(rf_cm)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 191  14
##          1   3  92
##
##                Accuracy : 0.9433
##                  95% CI : (0.9108, 0.9666)
##     No Information Rate : 0.6467
##     P-Value [Acc > NIR] : < 2e-16
##
##                   Kappa : 0.873
```

```
##
##  Mcnemar's Test P-Value : 0.01529
##
##             Sensitivity : 0.9845
##             Specificity : 0.8679
##          Pos Pred Value : 0.9317
##          Neg Pred Value : 0.9684
##              Prevalence : 0.6467
##          Detection Rate : 0.6367
##    Detection Prevalence : 0.6833
##       Balanced Accuracy : 0.9262
##
##        'Positive' Class : 0
##
```

```
# Calculate accuracy
rf_accuracy <- mean(rf_preds == valid_data$Diagnosis)
print(paste("Random Forest Accuracy:", round(rf_accuracy * 100, 2), "%"))
```

```
## [1] "Random Forest Accuracy: 94.33 %"
```

2.4. Linear Discriminant Analysis (LDA)

```
# Load dplyr and MASS

library(dplyr)
library(MASS)
```

```
##
## Attaching package: 'MASS'
```

```
## The following object is masked from 'package:dplyr':
##
##     select
```

```
library(caret)

# Fit LDA model
lda_model <- lda(Diagnosis ~ ., data = train_data)

# Print model summary
print(lda_model)
```

```
## Call:
## lda(Diagnosis ~ ., data = train_data)
##
## Prior probabilities of groups:
##         0         1
## 0.6461794 0.3538206
##
## Group means:
##        Age   Gender1 Ethnicity1 Ethnicity2 Ethnicity3 EducationLevel1
## 0 74.88046 0.5334190  0.2133676 0.09511568 0.10539846       0.3920308
## 1 74.80986 0.4741784  0.1830986 0.10798122 0.08685446       0.3873239
##   EducationLevel2 EducationLevel3      BMI  Smoking1 AlcoholConsumption
## 0       0.3071979      0.09897172 27.32396 0.2802057          10.130905
## 1       0.3075117      0.08920188 27.96298 0.2746479           9.948297
```

```
##   PhysicalActivity DietQuality SleepQuality FamilyHistoryAlzheimers1
## 0         4.944288    4.835363     7.160377                0.2455013
## 1         4.917248    4.999600     6.958219                0.2535211
##   CardiovascularDisease1 Diabetes1 Depression1 HeadInjury1 Hypertension1
## 0              0.1311054 0.1645244   0.2082262  0.09640103     0.1478149
## 1              0.1619718 0.1455399   0.1948357  0.09154930     0.1760563
##   SystolicBP DiastolicBP CholesterolTotal CholesterolLDL CholesterolHDL
## 0   134.6311    89.98972         225.2968       125.2710       58.86803
## 1   134.8192    90.08685         225.0832       124.7023       61.23251
##   CholesterolTriglycerides     MMSE FunctionalAssessment MemoryComplaints1
## 0                 227.1754 16.04460             5.977068         0.1092545
## 1                 232.6116 11.80636             3.762495         0.3544601
##   BehavioralProblems1      ADL Confusion1 Disorientation1 PersonalityChanges1
## 0          0.07969152 5.632153  0.2082262       0.1619537           0.1696658
## 1          0.25821596 3.540788  0.1995305       0.1455399           0.1361502
##   DifficultyCompletingTasks1 Forgetfulness1
## 0                  0.1516710      0.2827763
## 1                  0.1643192      0.2957746
##
## Coefficients of linear discriminants:
##                                       LD1
## Age                         -0.0031298602
## Gender1                     -0.1048469013
## Ethnicity1                  -0.1851671870
## Ethnicity2                   0.0369142134
## Ethnicity3                  -0.1241550146
## EducationLevel1             -0.0863701595
## EducationLevel2              0.0302193105
## EducationLevel3             -0.0965470095
## BMI                          0.0044450949
## Smoking1                    -0.0871835147
## AlcoholConsumption          -0.0014390817
## PhysicalActivity            -0.0082078076
## DietQuality                  0.0123216784
## SleepQuality                -0.0431747893
## FamilyHistoryAlzheimers1     0.0791679580
## CardiovascularDisease1       0.1613434490
## Diabetes1                    0.0020964082
## Depression1                  0.1241455056
## HeadInjury1                 -0.0949781102
## Hypertension1                0.1298414929
## SystolicBP                   0.0013070684
## DiastolicBP                  0.0012543748
## CholesterolTotal             0.0001494060
## CholesterolLDL              -0.0002221857
## CholesterolHDL               0.0019657492
## CholesterolTriglycerides     0.0003558030
## MMSE                        -0.0548221303
## FunctionalAssessment        -0.2287531941
## MemoryComplaints1            1.4209330852
## BehavioralProblems1          1.3786160168
## ADL                         -0.2102776442
## Confusion1                  -0.1331946883
## Disorientation1             -0.0315523419
```

```
## PersonalityChanges1          0.0002448730
## DifficultyCompletingTasks1   0.0407550635
## Forgetfulness1              -0.0090783603
```

```
# Predict on validation set
lda_preds <- predict(lda_model, valid_data)$class

# Confusion matrix
lda_cm <- confusionMatrix(lda_preds, valid_data$Diagnosis)
print(lda_cm)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 173  22
##          1  21  84
##
##                Accuracy : 0.8567
##                  95% CI : (0.8118, 0.8943)
##     No Information Rate : 0.6467
##     P-Value [Acc > NIR] : 2.716e-16
##
##                   Kappa : 0.6857
##
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.8918
##             Specificity : 0.7925
##          Pos Pred Value : 0.8872
##          Neg Pred Value : 0.8000
##              Prevalence : 0.6467
##          Detection Rate : 0.5767
##    Detection Prevalence : 0.6500
##       Balanced Accuracy : 0.8421
##
##        'Positive' Class : 0
##
```

```
# Calculate accuracy
lda_accuracy <- mean(lda_preds == valid_data$Diagnosis)
print(paste("LDA Accuracy:", round(lda_accuracy * 100, 2), "%"))
```

```
## [1] "LDA Accuracy: 85.67 %"
```

2.5. Naive Bayes

```
# Fit Naive Bayes model
library(e1071)
nb_model <- naiveBayes(Diagnosis ~ ., data = train_data)

# Print model summary
print(nb_model)
```

```
##
## Naive Bayes Classifier for Discrete Predictors
##
```

```
## Call:
## naiveBayes.default(x = X, y = Y, laplace = laplace)
##
## A-priori probabilities:
## Y
##         0         1
## 0.6461794 0.3538206
##
## Conditional probabilities:
##    Age
## Y       [,1]     [,2]
##   0 74.88046 8.866077
##   1 74.80986 9.180491
##
##    Gender
## Y           0         1
##   0 0.4665810 0.5334190
##   1 0.5258216 0.4741784
##
##    Ethnicity
## Y            0          1          2          3
##   0 0.58611825 0.21336761 0.09511568 0.10539846
##   1 0.62206573 0.18309859 0.10798122 0.08685446
##
##    EducationLevel
## Y            0          1          2          3
##   0 0.20179949 0.39203085 0.30719794 0.09897172
##   1 0.21596244 0.38732394 0.30751174 0.08920188
##
##    BMI
## Y       [,1]     [,2]
##   0 27.32396 7.185095
##   1 27.96298 7.231224
##
##    Smoking
## Y           0         1
##   0 0.7197943 0.2802057
##   1 0.7253521 0.2746479
##
##    AlcoholConsumption
## Y        [,1]     [,2]
##   0 10.130905 5.687622
##   1  9.948297 5.716819
##
##    PhysicalActivity
## Y       [,1]     [,2]
##   0 4.944288 2.884589
##   1 4.917248 2.879578
##
##    DietQuality
## Y       [,1]     [,2]
##   0 4.835363 2.918154
##   1 4.999600 2.971120
##
```

```
##    SleepQuality
## Y       [,1]     [,2]
##   0 7.160377 1.739710
##   1 6.958219 1.744981
##
##    FamilyHistoryAlzheimers
## Y           0         1
##   0 0.7544987 0.2455013
##   1 0.7464789 0.2535211
##
##    CardiovascularDisease
## Y           0         1
##   0 0.8688946 0.1311054
##   1 0.8380282 0.1619718
##
##    Diabetes
## Y           0         1
##   0 0.8354756 0.1645244
##   1 0.8544601 0.1455399
##
##    Depression
## Y           0         1
##   0 0.7917738 0.2082262
##   1 0.8051643 0.1948357
##
##    HeadInjury
## Y            0          1
##   0 0.90359897 0.09640103
##   1 0.90845070 0.09154930
##
##    Hypertension
## Y           0         1
##   0 0.8521851 0.1478149
##   1 0.8239437 0.1760563
##
##    SystolicBP
## Y       [,1]     [,2]
##   0 134.6311 25.41813
##   1 134.8192 25.98502
##
##    DiastolicBP
## Y       [,1]     [,2]
##   0 89.98972 17.75378
##   1 90.08685 17.49513
##
##    CholesterolTotal
## Y       [,1]     [,2]
##   0 225.2968 41.82247
##   1 225.0832 43.65304
##
##    CholesterolLDL
## Y       [,1]     [,2]
##   0 125.2710 43.07952
##   1 124.7023 43.25795
```

```
##
##    CholesterolHDL
## Y       [,1]     [,2]
##   0 58.86803 22.90476
##   1 61.23251 23.02539
##
##    CholesterolTriglycerides
## Y       [,1]     [,2]
##   0 227.1754 102.4079
##   1 232.6116 101.9677
##
##    MMSE
## Y       [,1]     [,2]
##   0 16.04460 8.966840
##   1 11.80636 7.119611
##
##    FunctionalAssessment
## Y       [,1]     [,2]
##   0 5.977068 2.759017
##   1 3.762495 2.600731
##
##    MemoryComplaints
## Y           0         1
##   0 0.8907455 0.1092545
##   1 0.6455399 0.3544601
##
##    BehavioralProblems
## Y           0          1
##   0 0.92030848 0.07969152
##   1 0.74178404 0.25821596
##
##    ADL
## Y       [,1]     [,2]
##   0 5.632153 2.830142
##   1 3.540788 2.577678
##
##    Confusion
## Y           0         1
##   0 0.7917738 0.2082262
##   1 0.8004695 0.1995305
##
##    Disorientation
## Y           0         1
##   0 0.8380463 0.1619537
##   1 0.8544601 0.1455399
##
##    PersonalityChanges
## Y           0         1
##   0 0.8303342 0.1696658
##   1 0.8638498 0.1361502
##
##    DifficultyCompletingTasks
## Y           0         1
##   0 0.8483290 0.1516710
```

```
##   1 0.8356808 0.1643192
##
##    Forgetfulness
## Y           0         1
##   0 0.7172237 0.2827763
##   1 0.7042254 0.2957746
```

```r
# Predict on validation set
nb_preds <- predict(nb_model, valid_data)

# Confusion matrix
nb_cm <- confusionMatrix(nb_preds, valid_data$Diagnosis)
print(nb_cm)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 182  28
##          1  12  78
##
##                Accuracy : 0.8667
##                  95% CI : (0.8229, 0.903)
##     No Information Rate : 0.6467
##     P-Value [Acc > NIR] : < 2e-16
##
##                   Kappa : 0.6979
##
##  Mcnemar's Test P-Value : 0.01771
##
##             Sensitivity : 0.9381
##             Specificity : 0.7358
##          Pos Pred Value : 0.8667
##          Neg Pred Value : 0.8667
##              Prevalence : 0.6467
##          Detection Rate : 0.6067
##    Detection Prevalence : 0.7000
##       Balanced Accuracy : 0.8370
##
##        'Positive' Class : 0
##
```

```r
# Calculate accuracy
nb_accuracy <- mean(nb_preds == valid_data$Diagnosis)
print(paste("Naive Bayes Accuracy:", round(nb_accuracy * 100, 2), "%"))
```

```
## [1] "Naive Bayes Accuracy: 86.67 %"
```

2.6. Hyperparameter

```r
#Define Hyperparameter Grid
# Define a grid for the 'mtry' parameter in Random Forest
tuneGrid <- expand.grid(mtry = c(10:25))
#Cross-Validation Setup (using stratified sampling)
library(caret)
control <- trainControl(method = "cv",
                        number = 5,
```

```
                        summaryFunction = defaultSummary,
                        savePredictions = TRUE,
                        classProbs = FALSE,
                        sampling = "smote")  # Handle class imbalance in small datasets
# Model Training with Hyperparameter Tuning
# Train the Random Forest model using the 'caret' package and grid search
library(themis)
model <- train(Diagnosis ~ .,
               data = train_data,
               method = "rf",
               metric = "Accuracy",   # Set the metric explicitly for classification
               trControl = control,
               tuneGrid = tuneGrid,
               allowParallel = TRUE)
```

```
# Print the Best Tuned Model
print(model$bestTune)   # Output the best 'mtry' value
```

```
##   mtry
## 6   15
```

```
print(model)
```

```
## Random Forest
##
## 1204 samples
##   32 predictor
##    2 classes: '0', '1'
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 963, 964, 963, 963, 963
## Addtional sampling using SMOTE
##
## Resampling results across tuning parameters:
##
##   mtry  Accuracy   Kappa
##   10    0.9385477  0.8653593
##   11    0.9443534  0.8780547
##   12    0.9443534  0.8782919
##   13    0.9443499  0.8782092
##   14    0.9443465  0.8783467
##   15    0.9493326  0.8889993
##   16    0.9451833  0.8800479
##   17    0.9451833  0.8802500
##   18    0.9443465  0.8784436
##   19    0.9435166  0.8770358
##   20    0.9443430  0.8785835
##   21    0.9476694  0.8853683
##   22    0.9460097  0.8819662
##   23    0.9476763  0.8854381
##   24    0.9435097  0.8766191
##   25    0.9443465  0.8784236
##
## Accuracy was used to select the optimal model using the largest value.
```

```
## The final value used for the model was mtry = 15.
```

```
library(randomForest)
# choose best mtry
best_mtry <- model$bestTune$mtry

# use best mtry fit final model
final_model <- randomForest(
  Diagnosis ~ .,
  data = train_data,
  mtry = best_mtry
)

print(model$results)
```

```
##    mtry  Accuracy     Kappa  AccuracySD    KappaSD
## 1    10 0.9385477 0.8653593 0.012876783 0.02785057
## 2    11 0.9443534 0.8780547 0.009543346 0.02117667
## 3    12 0.9443534 0.8782919 0.013629776 0.02935481
## 4    13 0.9443499 0.8782092 0.013959545 0.02982843
## 5    14 0.9443465 0.8783467 0.013349639 0.02901719
## 6    15 0.9493326 0.8889993 0.012937979 0.02825621
## 7    16 0.9451833 0.8800479 0.015072679 0.03253412
## 8    17 0.9451833 0.8802500 0.011510444 0.02495441
## 9    18 0.9443465 0.8784436 0.018252914 0.03926280
## 10   19 0.9435166 0.8770358 0.019393416 0.04137937
## 11   20 0.9443430 0.8785835 0.014306363 0.03062035
## 12   21 0.9476694 0.8853683 0.012338043 0.02687689
## 13   22 0.9460097 0.8819662 0.015542090 0.03334288
## 14   23 0.9476763 0.8854381 0.014836854 0.03252920
## 15   24 0.9435097 0.8766191 0.013712685 0.02956718
## 16   25 0.9443465 0.8784236 0.015718849 0.03382019
```

```
print(model$bestTune)
```

```
##   mtry
## 6   15
```

```
# final parameter
model$finalModel
```

```
##
## Call:
##  randomForest(x = x, y = y, mtry = param$mtry, allowParallel = TRUE)
##                Type of random forest: classification
##                      Number of trees: 500
## No. of variables tried at each split: 15
##
##         OOB estimate of  error rate: 4.43%
## Confusion matrix:
##     0   1 class.error
## 0 752  26  0.03341902
## 1  43 735  0.05526992
```

```
print(model$finalModel)
```

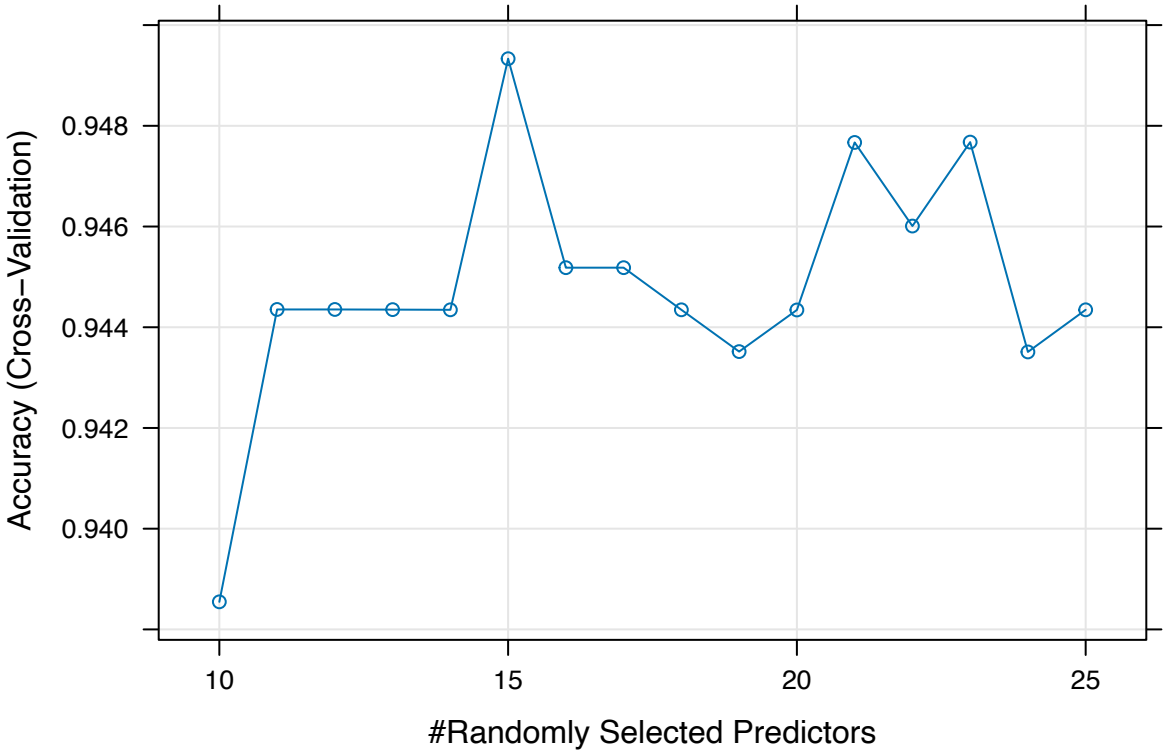
```
##
```

```
## Call:
##  randomForest(x = x, y = y, mtry = param$mtry, allowParallel = TRUE)
##                Type of random forest: classification
##                      Number of trees: 500
## No. of variables tried at each split: 15
##
##         OOB estimate of  error rate: 4.43%
## Confusion matrix:
##     0   1 class.error
## 0 752  26  0.03341902
## 1  43 735  0.05526992
```

```
summary(model$finalModel)
```

```
##                 Length Class      Mode
## call               5   -none-     call
## type               1   -none-     character
## predicted       1556   factor     numeric
## err.rate        1500   -none-     numeric
## confusion          6   -none-     numeric
## votes           3112   matrix     numeric
## oob.times       1556   -none-     numeric
## classes            2   -none-     character
## importance        36   -none-     numeric
## importanceSD       0   -none-     NULL
## localImportance    0   -none-     NULL
## proximity          0   -none-     NULL
## ntree              1   -none-     numeric
## mtry               1   -none-     numeric
## forest            14   -none-     list
## y               1556   factor     numeric
## test               0   -none-     NULL
## inbag              0   -none-     NULL
## xNames            36   -none-     character
## problemType        1   -none-     character
## tuneValue          1   data.frame list
## obsLevels          2   -none-     character
## param              1   -none-     list
```

```
# Visualize the Tuning Results
# Plot the performance of different hyperparameter values
plot(model)
```



2.7. ROC Curves

```
# ROC for logistic regression
library(pROC)
glm_roc <- roc(valid_data$Diagnosis, glm_probs)
```

```
## Setting levels: control = 0, case = 1
```

```
## Setting direction: controls < cases
```

```
plot(glm_roc, col = 'blue', main = 'ROC Curves')
auc(glm_roc)
```

```
## Area under the curve: 0.9149
```

```
# ROC for random forest
rf_probs <- predict(rf_model, valid_data, type = 'prob')[,2]
rf_roc <- roc(valid_data$Diagnosis, rf_probs)
```

```
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases
```

```
plot(rf_roc, col = 'red', add = TRUE)
auc(rf_roc)
```

```
## Area under the curve: 0.9616
```

```
# ROC for lda
lda_probs <- predict(lda_model, valid_data)$posterior[, 2]
lda_roc <- roc(valid_data$Diagnosis, lda_probs)
```

```
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases
```

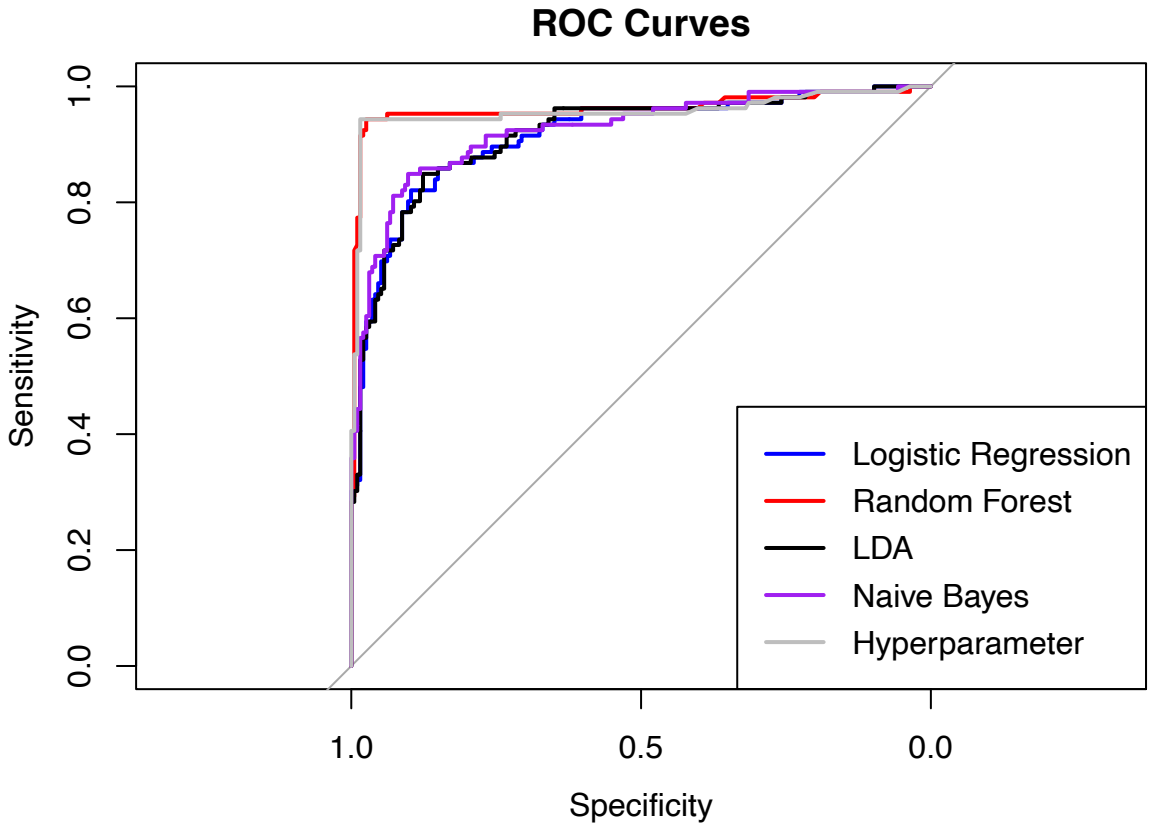
```r
plot(lda_roc, col = 'black', add = TRUE)
auc_value <- auc(lda_roc)

#ROC for Naive Bayes
nb_probs <- predict(nb_model, valid_data, type = 'raw')[, 2]
nb_roc <- roc(valid_data$Diagnosis, nb_probs)
```

```
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases
```

```r
plot(nb_roc, col = 'purple', add = TRUE)
auc_value <- auc(nb_roc)

# ROC of Hyperparameter
rf_probs <- predict(final_model, valid_data, type = "prob")[, 2]
rf_roc <- roc(valid_data$Diagnosis, rf_probs)
```

```
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases
```

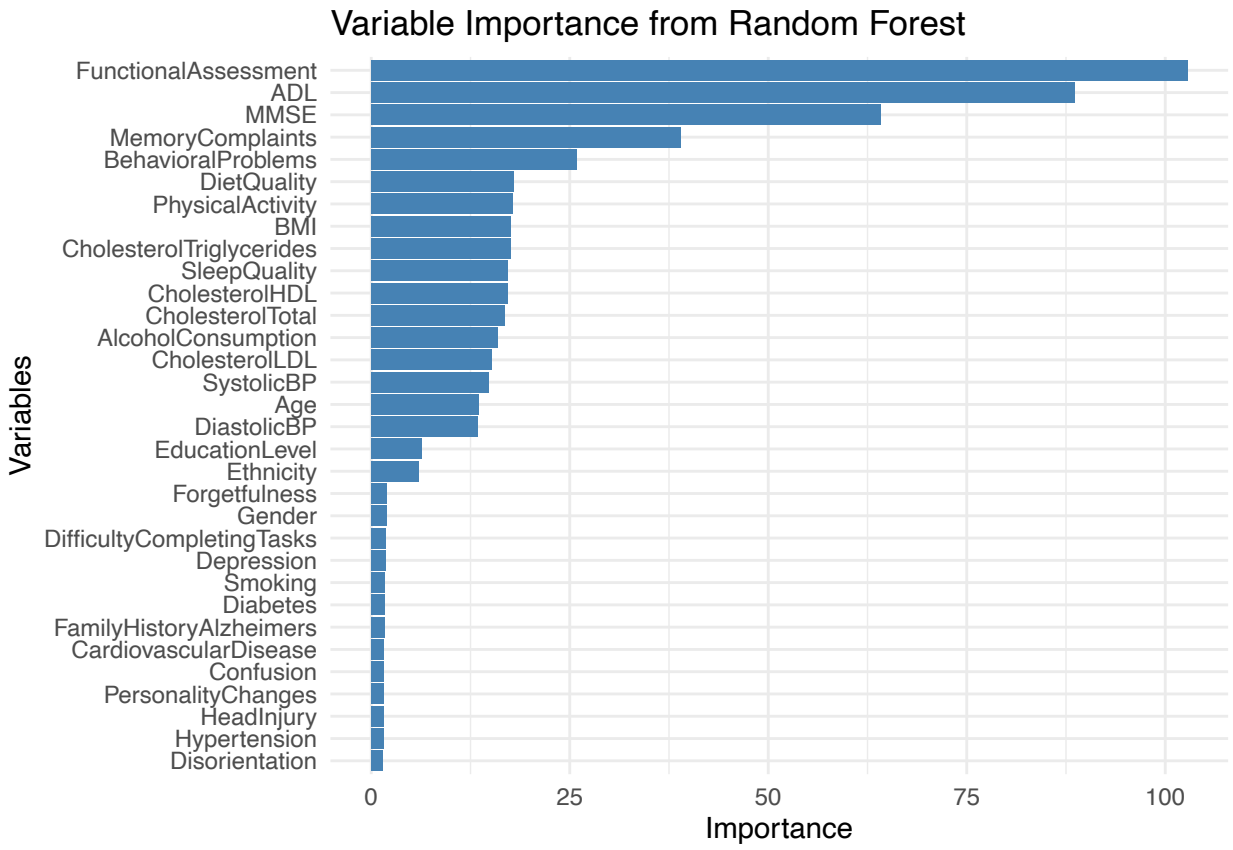
```r
plot(rf_roc, col = 'grey', add = TRUE)
auc_value <- auc(rf_roc)

legend('bottomright',
       legend = c('Logistic Regression', 'Random Forest', 'LDA', 'Naive Bayes','Hyperparameter'),
       col = c('blue', 'red','black','purple','grey'), lwd = 2)
```



3. Feature Selection

3.1. Variable Importance from Random Forest

```
# Get variable importance from random forest
library(randomForest)
importance <- importance(rf_model)
var_importance <- data.frame(Variables = row.names(importance), Importance = importance[, 'MeanDecrease

library(ggplot2)
# Plot variable importance
ggplot(var_importance, aes(x = reorder(Variables, Importance), y = Importance)) +
  geom_bar(stat = 'identity', fill = 'steelblue') +
  coord_flip() +
  theme_minimal() +
  labs(title = 'Variable Importance from Random Forest', x = 'Variables', y = 'Importance')
```



3.2. Recursive Feature Elimination (RFE)

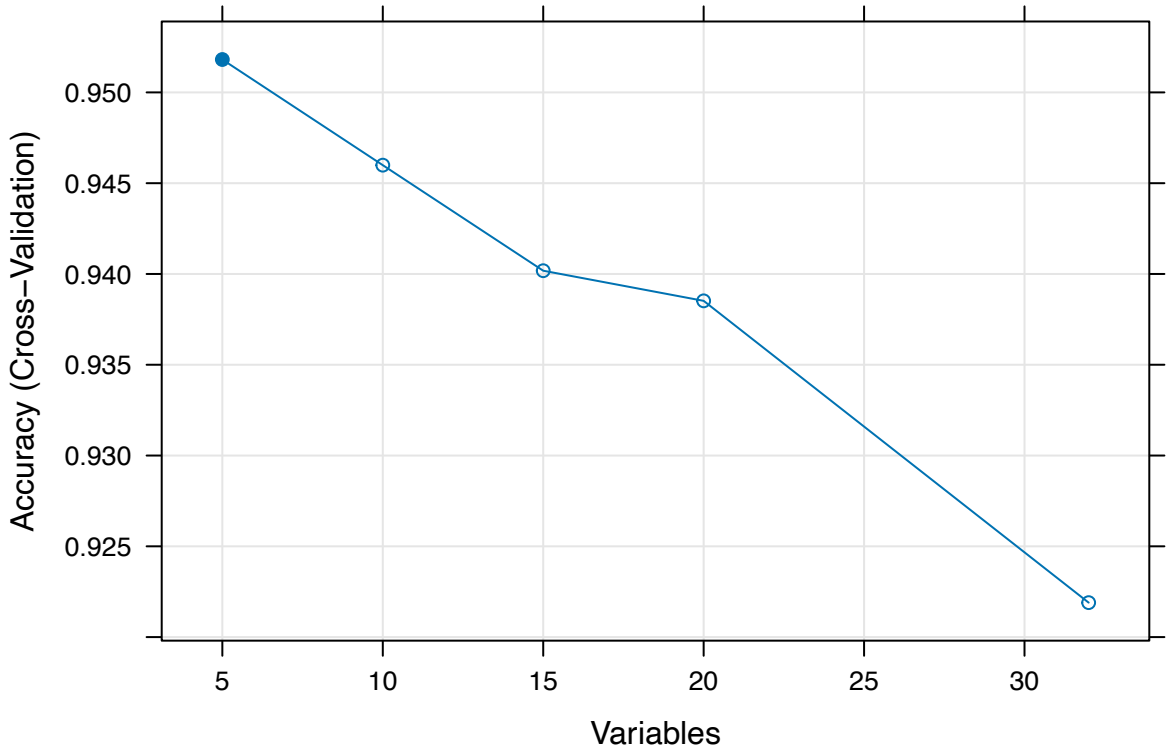
```
# Use caret's RFE with random forest
library(caret)
control <- rfeControl(functions = rfFuncs, method = 'cv', number = 5)
set.seed(123)
rfe_model <- rfe(train_data[, -which(names(train_data) == 'Diagnosis')], train_data$Diagnosis, sizes = 

# Optimal variables
optimal_vars <- rfe_model$optVariables
print("Optimal Variables Selected:")
```

```
## [1] "Optimal Variables Selected:"
```

```r
print(optimal_vars)
```

```
## [1] "FunctionalAssessment" "ADL"                  "MMSE"
## [4] "MemoryComplaints"     "BehavioralProblems"
```

```r
# Plot RFE results
plot(rfe_model, type = c('g', 'o'))
```



4. Statistical Inference

4.1. Hypothesis Testing

```r
#4.1.1. Comparing Means
# T-test for 'Age' variable
t_test_age <- t.test(Age ~ Diagnosis, data = train)
print(t_test_age)
```

```
##
##  Welch Two Sample t-test
##
## data:  Age by Diagnosis
## t = 0.38758, df = 1071.3, p-value = 0.6984
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
## 95 percent confidence interval:
##  -0.7653557  1.1421310
## sample estimates:
## mean in group 0 mean in group 1
##        74.97222        74.78383
```

```r
# Wilcoxon test for 'MMSE' if not normally distributed
wilcox_test_mmse <- wilcox.test(MMSE ~ Diagnosis, data = train)
print(wilcox_test_mmse)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  MMSE by Diagnosis
## W = 333042, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

```
#4.1.2. Chi-Squared Test for Categorical Variables
# Chi-squared test for 'Gender'
table_gender <- table(train$Gender, train$Diagnosis)
chi_test_gender <- chisq.test(table_gender)
print(chi_test_gender)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  table_gender
## X-squared = 2.3131, df = 1, p-value = 0.1283
```

4.2. Confidence Intervals and Odds Ratios

```
# Confidence intervals for logistic regression coefficients
confint_glm <- confint(glm_model)
```

```
## Waiting for profiling to be done...
```

```
print(confint_glm)
```

```
##                                 2.5 %       97.5 %
## (Intercept)                1.388765824  6.433636386
## Age                       -0.025119736  0.012290173
## Gender1                   -0.607313884  0.064517849
## Ethnicity1                -0.815834214  0.065970342
## Ethnicity2                -0.556288291  0.628940577
## Ethnicity3                -0.898958503  0.315977015
## EducationLevel1           -0.585156091  0.322851072
## EducationLevel2           -0.401787218  0.550630522
## EducationLevel3           -0.901892433  0.390177949
## BMI                       -0.017504461  0.029032371
## Smoking1                  -0.562244867  0.200455498
## AlcoholConsumption        -0.035602421  0.022742193
## PhysicalActivity          -0.071210824  0.043583663
## DietQuality               -0.025126150  0.091977048
## SleepQuality              -0.158515658  0.034463882
## FamilyHistoryAlzheimers1  -0.242475479  0.543547233
## CardiovascularDisease1    -0.205347481  0.713224950
## Diabetes1                 -0.494457851  0.433816004
## Depression1               -0.180840132  0.629589491
## HeadInjury1               -0.754217243  0.376207163
## Hypertension1             -0.270579756  0.661179069
## SystolicBP                -0.004373535  0.008630021
## DiastolicBP               -0.005499528  0.013184058
## CholesterolTotal          -0.004031215  0.003811052
## CholesterolLDL            -0.004187059  0.003697898
## CholesterolHDL            -0.003378804  0.011320514
## CholesterolTriglycerides  -0.001024752  0.002262310
## MMSE                      -0.130757272 -0.087258212
```

```
## FunctionalAssessment       -0.503698523 -0.365949004
## MemoryComplaints1           2.002028391  2.876764308
## BehavioralProblems1         2.051924648  3.054235053
## ADL                        -0.479378649 -0.342087607
## Confusion1                 -0.679496213  0.147712813
## Disorientation1            -0.485358449  0.443968762
## PersonalityChanges1        -0.534040036  0.417311094
## DifficultyCompletingTasks1 -0.327100101  0.593997380
## Forgetfulness1             -0.417800109  0.324032250
```

```
# Odds ratios and confidence intervals
odds_ratios <- exp(cbind(OR = coef(glm_model), confint(glm_model)))
```

```
## Waiting for profiling to be done...
```

```
print(odds_ratios)
```

```
##                                   OR     2.5 %      97.5 %
## (Intercept)                49.0144311 4.0098981 622.4332452
## Age                         0.9936406 0.9751931   1.0123660
## Gender1                     0.7630903 0.5448123   1.0666446
## Ethnicity1                  0.6901861 0.4422702   1.0681950
## Ethnicity2                  1.0404978 0.5733332   1.8756224
## Ethnicity3                  0.7523810 0.4069933   1.3715987
## EducationLevel1             0.8767548 0.5570189   1.3810597
## EducationLevel2             1.0760522 0.6691231   1.7343462
## EducationLevel3             0.7772042 0.4058010   1.4772436
## BMI                         1.0057704 0.9826479   1.0294579
## Smoking1                    0.8361710 0.5699282   1.2219592
## AlcoholConsumption          0.9936159 0.9650239   1.0230028
## PhysicalActivity            0.9863557 0.9312655   1.0445474
## DietQuality                 1.0338020 0.9751869   1.0963397
## SleepQuality                0.9399377 0.8534096   1.0350646
## FamilyHistoryAlzheimers1    1.1633035 0.7846830   1.7221047
## CardiovascularDisease1      1.2902119 0.8143643   2.0405614
## Diabetes1                   0.9732114 0.6099015   1.5431349
## Depression1                 1.2524933 0.8345688   1.8768400
## HeadInjury1                 0.8329800 0.4703787   1.4567489
## Hypertension1               1.2172566 0.7629370   1.9370749
## SystolicBP                  1.0021209 0.9956360   1.0086674
## DiastolicBP                 1.0038294 0.9945156   1.0132714
## CholesterolTotal            0.9998897 0.9959769   1.0038183
## CholesterolLDL              0.9997550 0.9958217   1.0037047
## CholesterolHDL              1.0039672 0.9966269   1.0113848
## CholesterolTriglycerides    1.0006162 0.9989758   1.0022649
## MMSE                        0.8971425 0.8774307   0.9164404
## FunctionalAssessment        0.6485752 0.6042915   0.6935382
## MemoryComplaints1          11.3558443 7.4040592  17.7567248
## BehavioralProblems1        12.7087770 7.7828660  21.2049586
## ADL                         0.6643785 0.6191680   0.7102860
## Confusion1                  0.7688038 0.5068723   1.1591799
## Disorientation1             0.9827926 0.6154765   1.5588818
## PersonalityChanges1         0.9467217 0.5862318   1.5178746
## DifficultyCompletingTasks1  1.1453282 0.7210116   1.8112141
## Forgetfulness1              0.9555157 0.6584938   1.3826919
```

5. Model Selection Techniques

5.1. Model Selection with AIC and BIC

5.1.1. AIC-based Selection

```
# Full model
full_model <- glm(Diagnosis ~ ., data = train_data, family = binomial)

# Null model
null_model <- glm(Diagnosis ~ 1, data = train_data, family = binomial)

# reduction of the model
reduced_formula <- as.formula(paste("Diagnosis ~", paste(optimal_vars, collapse = "+")))
reduced_model <- glm(reduced_formula, data = train_data, family = binomial)

# Stepwise selection based on AIC
step_model_aic <- stepAIC(reduced_model, direction = "both", trace = FALSE)
summary(step_model_aic)
```

```
##
## Call:
## glm(formula = Diagnosis ~ FunctionalAssessment + ADL + MMSE +
##     MemoryComplaints + BehavioralProblems, family = binomial,
##     data = train_data)
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)            3.74991    0.30057  12.476   <2e-16 ***
## FunctionalAssessment -0.42257    0.03395 -12.447   <2e-16 ***
## ADL                  -0.40222    0.03393 -11.854   <2e-16 ***
## MMSE                 -0.10584    0.01072  -9.872   <2e-16 ***
## MemoryComplaints1     2.45117    0.21848  11.219   <2e-16 ***
## BehavioralProblems1   2.53497    0.24783  10.229   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1564.67  on 1203  degrees of freedom
## Residual deviance:  915.26  on 1198  degrees of freedom
## AIC: 927.26
##
## Number of Fisher Scoring iterations: 6
```

```
# AIC value
aic_value <- AIC(step_model_aic)
print(paste("AIC of selected model:", aic_value))
```

```
## [1] "AIC of selected model: 927.257577904444"
```

```
# Stepwise selection based on BIC
n <- nrow(train_data)
step_model_bic <- stepAIC(reduced_model, direction = "both", k = log(n), trace = FALSE)

# Summary of the model
summary(step_model_bic)
```

```
##
## Call:
## glm(formula = Diagnosis ~ FunctionalAssessment + ADL + MMSE +
##     MemoryComplaints + BehavioralProblems, family = binomial,
##     data = train_data)
##
## Coefficients:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)           3.74991    0.30057  12.476   <2e-16 ***
## FunctionalAssessment -0.42257    0.03395 -12.447   <2e-16 ***
## ADL                  -0.40222    0.03393 -11.854   <2e-16 ***
## MMSE                 -0.10584    0.01072  -9.872   <2e-16 ***
## MemoryComplaints1     2.45117    0.21848  11.219   <2e-16 ***
## BehavioralProblems1   2.53497    0.24783  10.229   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1564.67  on 1203  degrees of freedom
## Residual deviance:  915.26  on 1198  degrees of freedom
## AIC: 927.26
##
## Number of Fisher Scoring iterations: 6
```

```
# BIC value
bic_value <- BIC(step_model_bic)
print(paste("BIC of selected model:", bic_value))
```

```
## [1] "BIC of selected model: 957.818005659656"
```

```
# AIC model predictions
aic_preds_prob <- predict(step_model_aic, valid_data, type = 'response')
aic_preds <- ifelse(aic_preds_prob > 0.5, 1, 0)

# Confusion matrix
aic_cm <- confusionMatrix(as.factor(aic_preds), valid_data$Diagnosis)
print(aic_cm)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 173  20
##          1  21  86
##
##                Accuracy : 0.8633
##                  95% CI : (0.8192, 0.9001)
##     No Information Rate : 0.6467
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.7016
##
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.8918
```

```
##             Specificity : 0.8113
##          Pos Pred Value : 0.8964
##          Neg Pred Value : 0.8037
##              Prevalence : 0.6467
##          Detection Rate : 0.5767
##    Detection Prevalence : 0.6433
##       Balanced Accuracy : 0.8515
##
##        'Positive' Class : 0
##
```

```
# BIC model predictions
bic_preds_prob <- predict(step_model_bic, valid_data, type = 'response')
bic_preds <- ifelse(bic_preds_prob > 0.5, 1, 0)

# Confusion matrix
bic_cm <- confusionMatrix(as.factor(bic_preds), valid_data$Diagnosis)
print(bic_cm)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 173  20
##          1  21  86
##
##                Accuracy : 0.8633
##                  95% CI : (0.8192, 0.9001)
##     No Information Rate : 0.6467
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.7016
##
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.8918
##             Specificity : 0.8113
##          Pos Pred Value : 0.8964
##          Neg Pred Value : 0.8037
##              Prevalence : 0.6467
##          Detection Rate : 0.5767
##    Detection Prevalence : 0.6433
##       Balanced Accuracy : 0.8515
##
##        'Positive' Class : 0
##
```

6. Comparing All Models

6.1. Summary of Model Performances

```
model_performance <- data.frame(
  Model = c('Logistic Regression', 'Random Forest', 'LDA', 'Naive Bayes', 'AIC Logistic', 'BIC Logistic
  Accuracy = c(
    glm_accuracy * 100,
    rf_accuracy * 100,
```

```
    lda_accuracy * 100,
    nb_accuracy * 100,
    mean(aic_preds == valid_data$Diagnosis) * 100,
    mean(bic_preds == valid_data$Diagnosis) * 100
  )
)
```

7. Final Prediction on Test Data

7.1. Data Preparation

```
# Load necessary library
library(dplyr)

# Remove 'PatientID' and 'DoctorInCharge' from test data
test_ids <- test$PatientID
test_data <- test %>% dplyr::select(-PatientID, -DoctorInCharge)

# Convert categorical variables to factors
test_data[categorical_vars[-length(categorical_vars)]] <- lapply(test_data[categorical_vars[-length(cat

# Ensure levels match between train and test
for (var in categorical_vars[-length(categorical_vars)]) {
  levels(test_data[[var]]) <- levels(train_data[[var]])
}

# Handle missing values if any
test_data[numerical_vars] <- lapply(test_data[numerical_vars], function(x) ifelse(is.na(x), median(x, na
# Predict on test data
test_preds <- predict(model, test_data)

# Prepare submission file
submission <- data.frame(PatientID = test_ids, Diagnosis = test_preds)

# Convert 'Diagnosis' to integer
submission$Diagnosis <- as.integer(as.character(submission$Diagnosis))

# Save submission file
write.csv(submission, 'submission.csv', row.names = FALSE)
```