TDS10 Final Project

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Abstract

IF you wish, you may add here a short abstract of 100 words max.

Introduction

Dataset Description

For the project, we will be using a heart-disease dataset that contains health data for different patients.The dataset mixes numeric and categorical values such as age, sex, chest-pain type, resting blood pressure etc. The target variable of is hdc which indicates the category of heart disease each patient has (0-4). The dataset contains 920 rows with 15 variables in total. Out of these 15 variables, 14 are predictors and 1 is the target - hdc.

Multinomial Logistic Regression — Theory

We are using multinomial Logistic Regression because the response variable can take more than 2 categories. For these categories there is a separate set of coefficients and we choose one as the baseline. The coefficients describe how the predictors(age, sex, chol etc.) affect the probability of belonging to each outcome category.

In this regression the response variable Y can take K-number of different categories. We have to pick one of the categories to be the baseline - category 0, for every other category - k = 1,2. . . ,K-1.

The model shows the probability of an observation belonging to category K using the multinomial logistic regression function:

$$P(Y = k \mid X) = \frac{\exp(\beta_{0k} + \beta_k^T X)}{1 + \sum_{j=1}^{K-1} \exp(\beta_{0j} + \beta_j^T X)}$$

The probability of the baseline category is:

$$P(Y = 0 \mid X) = \frac{1}{1 + \sum_{j=1}^{K-1} \exp(\beta_{0j} + \beta_j^T X)}$$

Data Preparation

There are several variables in the dataset containing missing values.In order to prepare the data for the multinomial logistic model,we observed how many missing values each variable had and saw that the variables ca, thal, and slope had extremely high numbers of missing values. Because these variables are categorical, and because imputing such a large amount of missing data would introduce strong bias, we decided to remove them from the dataset. For the remaining numeric variables with less missing values- (trestbps, chol, thalach, oldpeak) we applied median imputation.

We chose this method because replacing each missing value with the median of the corresponding variable is a robust measure that is not affected by extreme values.

For the categorial variables with very few missing values, we replaced missing entries with the most frequent category (the mode).

This approach ensures that there are no missing values before using the multinomial logistic regression model.

```
##      age      sex    place       cp trestbps     chol      fbs  restecg 
##        0        0        0        0        0        0        0        0 
##   thalch    exang  oldpeak      hdc 
##        0        0        0        0 
```

```
##   age sex     place              cp trestbps chol fbs        restecg thalch
## 1  63   1 Cleveland  typical angina      145  233   1 lv hypertrophy    150
## 2  67   1 Cleveland    asymptomatic      160  286   0 lv hypertrophy    108
## 3  67   1 Cleveland    asymptomatic      120  229   0 lv hypertrophy    129
## 4  37   1 Cleveland     non-anginal      130  250   0         normal    187
## 5  41   0 Cleveland atypical angina      130  204   0 lv hypertrophy    172
## 6  56   1 Cleveland atypical angina      120  236   0         normal    178
##   exang oldpeak hdc
## 1     0     2.3   0
## 2     1     1.5   2
## 3     1     2.6   1
## 4     0     3.5   0
## 5     0     1.4   0
## 6     0     0.8   0
```

Exploratory Data Analysis

Before establishing the multinomial logistic regression model, we looked at some of the predictors' visual variations over the response variable hdc's various levels. This enables us to recognise potential patterns and comprehend which factors might be helpful in predicting the seriousness of heart disease.

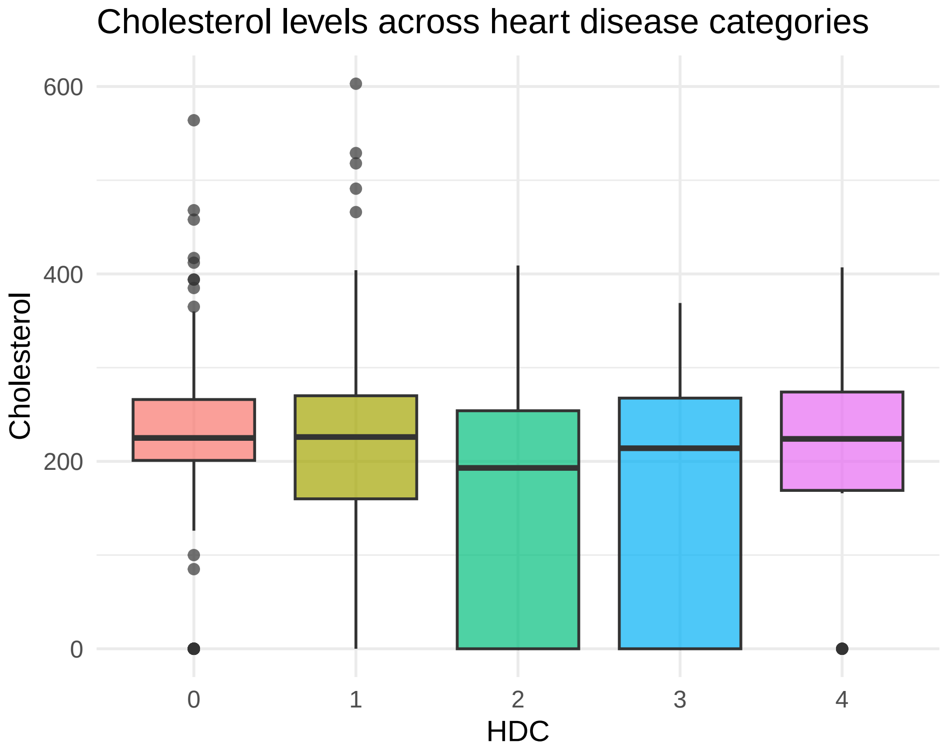
To investigate numerical factors like cholesterol, resting blood pressure, maximal heart rate, and ST depression, we employed boxplots. These charts illustrate the variations in these variables' distributions among the various categories of heart disease.

To determine how the frequency of each category varies throughout the hdc levels, we made barplots for categorical variables including the type of chest discomfort and the resting ECG result.

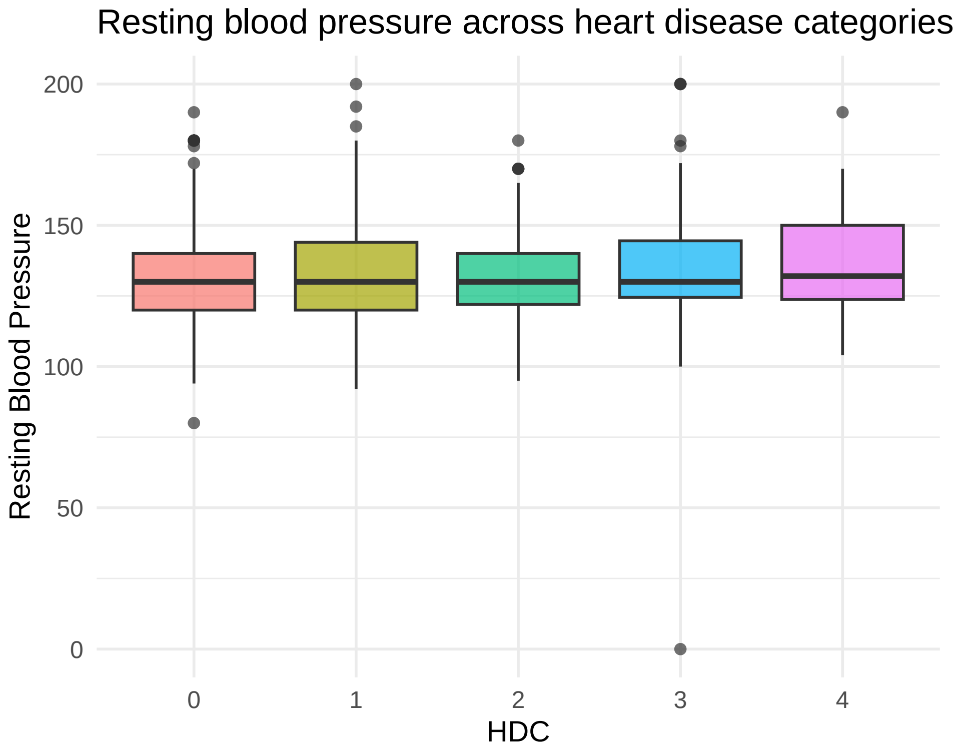
An introductory comprehension of the connections between predictors and the response variable is provided by this visual investigation.

Cholesterol levels across heart disease categories Cholesterol levels appear broadly similar across categories, though higher HDC groups show slightly more variability.

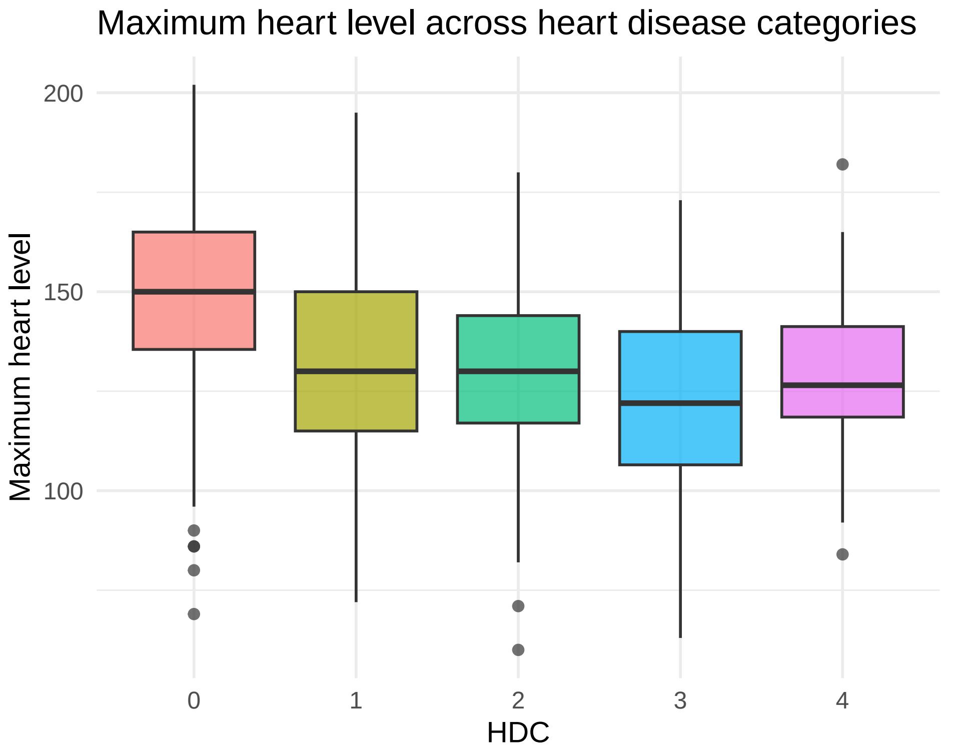
```
## Warning: package 'ggplot2' was built under R version 4.5.2
```



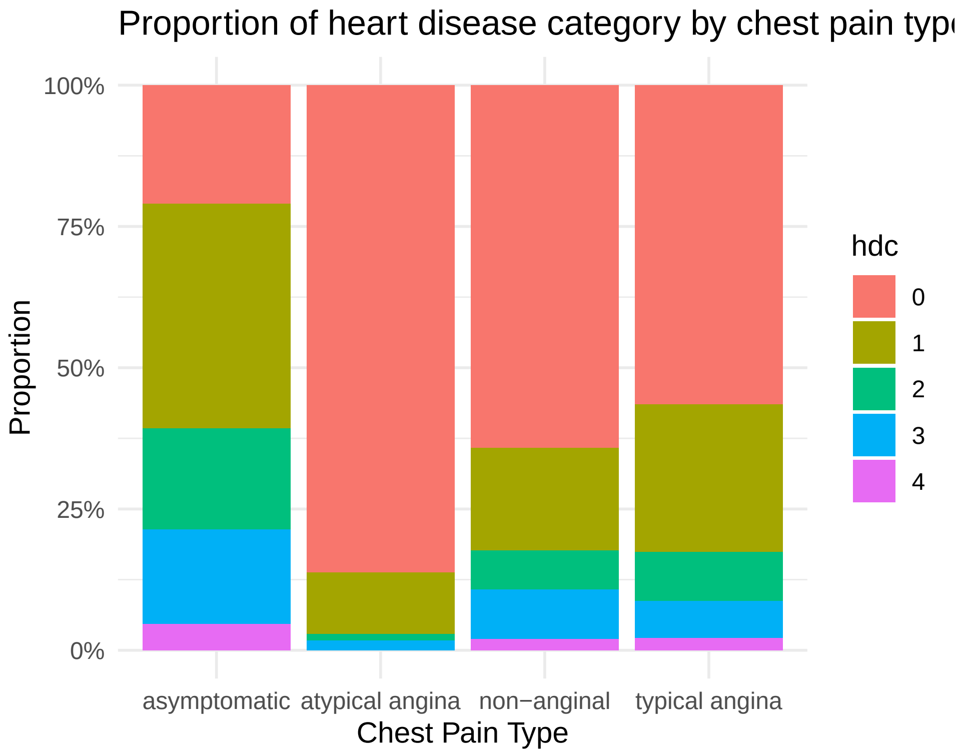
Resting blood pressure across heart disease categories Resting blood pressure shows a mild increasing trend with higher HDC, but overall differences between groups are modest.



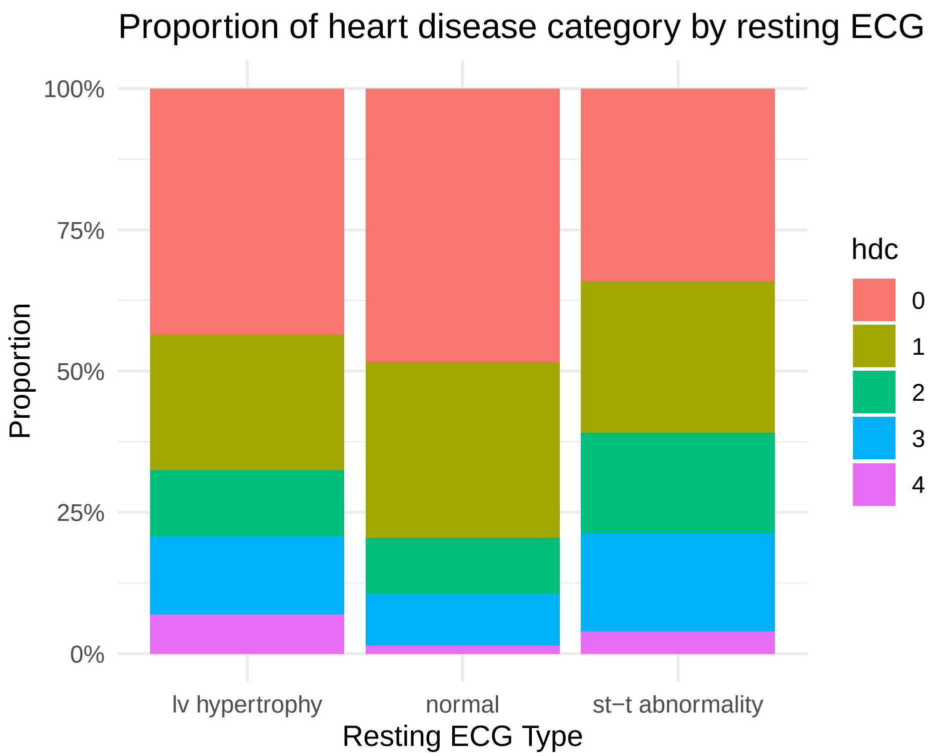
Maximum heart rate across heart disease categories Patients with higher HDC values generally demonstrate lower maximum heart rates compared to those without heart disease.



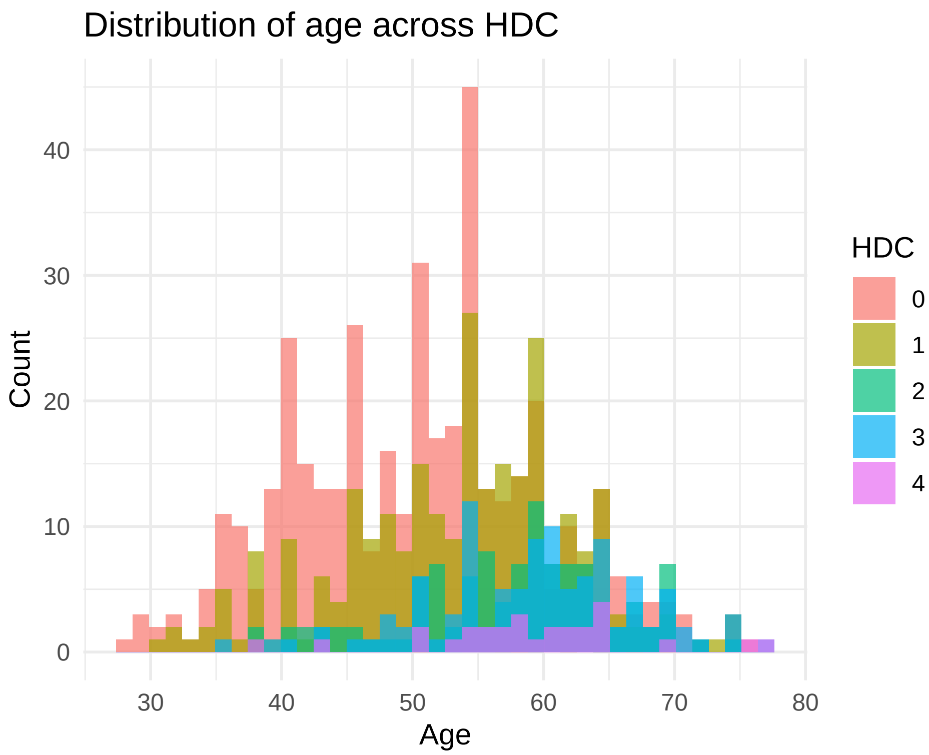
Proportion of heart disease category by chest pain type Atypical and non-anginal chest pain types contain a higher proportion of severe heart disease cases compared to typical angina.



Proportion of heart disease category by resting ECG type ST-T abnormalities and LV hypertrophy are associated with a greater share of higher heart disease categories compared to normal ECG results.



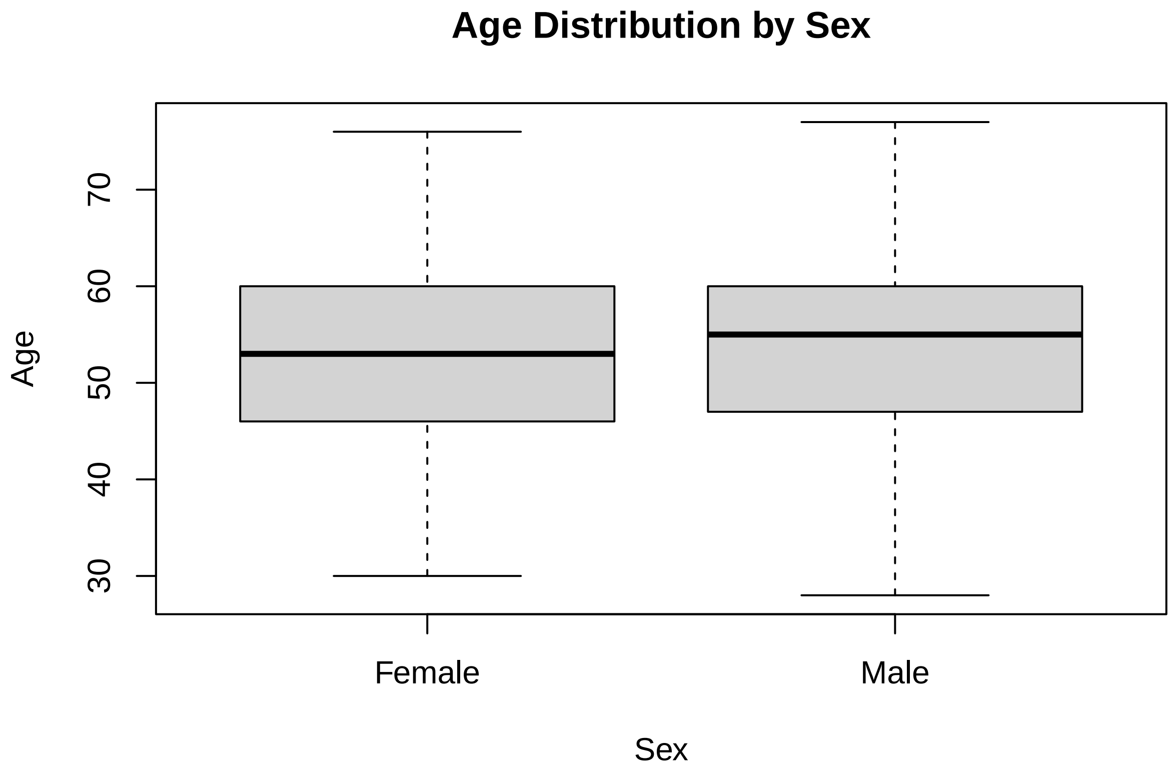
Distribution of age across HDC Patients with higher heart disease categories tend to be older, with the age distribution shifting toward later decades as HDC increases.



By looking at the box plot and p-test results we can conclude that we do not have statistically significant evidence that males and females have different mean ages.

With the p-value being above 0.05, we get the confirmation that the difference is not strong enough to be called significant.

```
boxplot(age ~ sex, data = heartData,
        names = c("Female", "Male"),
        main = "Age Distribution by Sex",
        xlab = "Sex",
        ylab = "Age")
```



```
t.test(age ~ sex, data = heartData)
```

```
##
##  Welch Two Sample t-test
##
## data:  age by sex
## t = -1.7155, df = 301.61, p-value = 0.08727
## alternative hypothesis: true difference in means between group 0 and group 1 is not e
## 95 percent confidence interval:
##  -2.8205168  0.1932128
## sample estimates:
## mean in group 0 mean in group 1
##        52.47423        53.78788
```

Multinomial Logistic Regression

We decided to fit the regression model using multinom() from the nnet, with hdc as the target variable and we included all of the predictors.

The baseline category is choosen to be hdc = 0 and for each other category hdc = 1-4 the model estimates how much each predictor affects the odds of belonging to a category 1-4 versus the baseline.

Multiple predictors appear as strong. Sex has a positive coefficient, indicating that males have higher chance of heart disease compared to females. Another one is exang. It increases the odds of being in any of the disease categories 1-4. In addition cp has a large negative indicating that certain chest pains reduces the risk of higher disease categories.

Overall the model selects oldpeak, exang, cp and maximum heart rate as key predictors

```r
library(nnet)
multinomial_regression <- multinom(
  hdc ~ age + sex + place +chol + cp + trestbps
  +fbs + restecg + thalch + exang + oldpeak,
  data = heartData
)

summary(multinomial_regression)
```

Model Evaluation

We tested our model using 4 different validation methods- Vanilla validation set, stratified validation,K-Fold Cross-Validation (K = 5) and K-Fold Cross Validation (K = 10), each giving different results.

Here are the said results:

The vanila validation gave us accuracy of around 0.565 and error rate of around 0.435. This is deffinetly the simplest approach we used which just splits data 70/30 allocating 70% for training and 30% of the data for testing. The problem with this is that is the split is unlucky the accuracy can change a lot.

The stratified validation (70/30 split) gave us accuracy of around 0.604 and an error rate of around 0.396. This result is expected since hdc is imbalanced, for example category 4 is very rare, the validation avoids creating a training set that lacks classes.

The k-fold cross validation for k = 5 gave us accuracy of around 0.170 and error rate of around 0.830.

This happens because some folds may not contain some hdc categories, whenever this is the case the model cannot estimate the coefficients correctly and ends up predicting almost the same class for most observations.

The k-fold cross validation for k = 10 gave us accuracy of around 0.175 and error rate of around 0.825, from which we conclude the same inefficiency as the model with the fewer folds because the problem is still the same - may not contain certain categories.

```
## Selected: John Doe
```

```
## Seed is: 9072005
```

```
## CV Method: K-Fold (K = 10)
```

```
## Accuracy: 0.173  Error: 0.827
```

Model Improvement

(Stepwise model / alternative model)

Binary Logistic Regression

(Create hdc01 + logistic model)

Model Comparison

(Compare multinomial vs binary)

Conclusion

(Brief summary)