**Seminar 2**

**Group A2**

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**Task 1**

The analysis of the distribution patterns of the three scores for cognitively normal and cognitively impaired individuals is the most straightforward and evident task. The distributions are shown in the figures below. We used box plots and histograms to illustrate the differences, providing an overall understanding of the data. Where the LABEL=0 is cognitively normal and LABEL=1 is cognitively impaired.

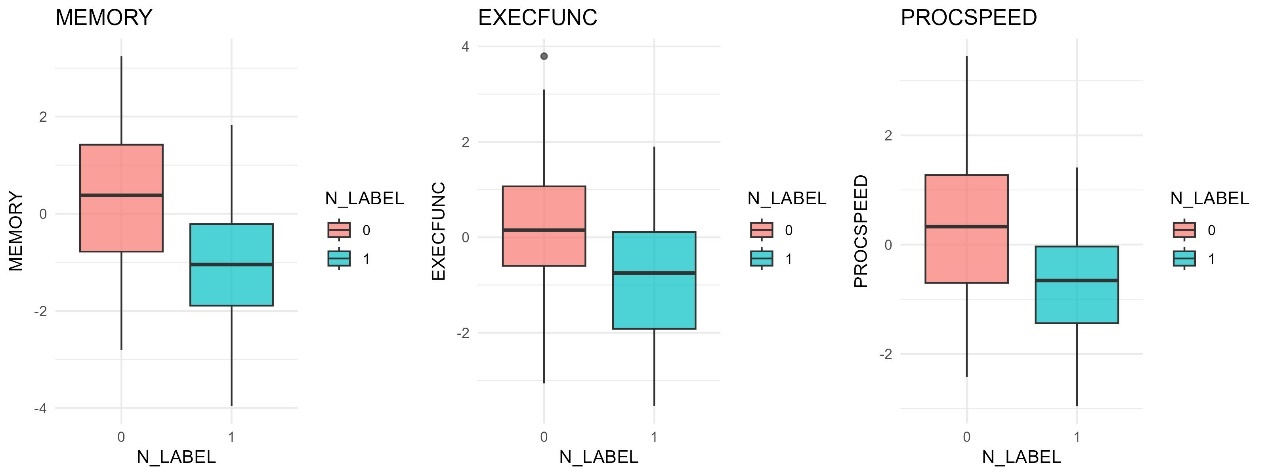


Figure 1.1 Box plots of scores

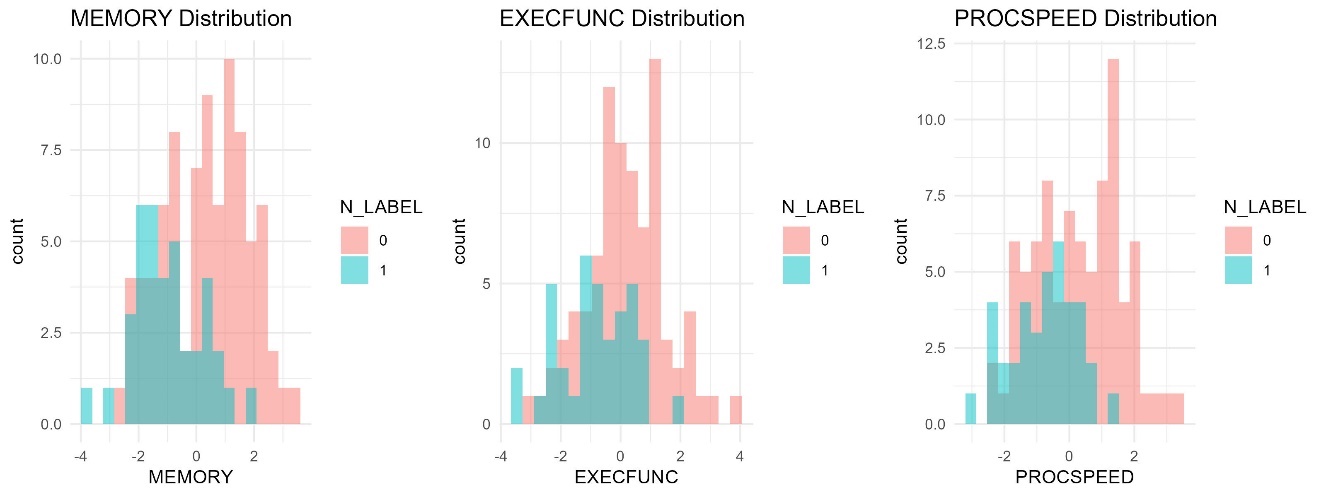


Figure 1.2 Histograms of scores

From the figures, it can be observed that individuals with cognitive impairment have lower mean scores in all three assessments. This is reasonable for a behavioral test. No significant differences were found between the standard deviations of the data for impaired individuals and those for cognitively normal individuals.

Then, the six variables—SEX, HYPERTENSION, DIABETES, ATRIALFIBR, INFARCTION, and AMYLOIDVIS—are subjected to chi-square tests against N\_LABEL. During the tests, it was found that some frequencies were less than 5, which can reduce the confidence level of the chi-square test results. The Fisher test is more accurate for small frequency samples, so it should be used to replace the chi-square test for assessing the correlation between variables.

data$N\_LABEL <- as.factor(data$N\_LABEL)

variables <- c("SEX", "HYPERTENSION", "DIABETES", "ATRIALFIBR", "INFARCTION", "AMYLOIDVIS")

for (var in variables) {

contingency\_table <- table(data$N\_LABEL, data[[var]])

#cat("Contingency table for", var, ":\n")

#print(contingency\_table)

#cat("\n")

fisher\_result <- fisher.test(contingency\_table)

cat("Fisher's exact test for", var, ":\n")

print(fisher\_result)

cat("\n")

}

Fisher's exact test for SEX :

Fisher's Exact Test for Count Data

data: contingency\_table

p-value = 0.4407

alternative hypothesis: true odds ratio is not equal to 1

95 percent confidence interval:

0.5932765 3.2210470

sample estimates:

odds ratio

1.371404

Fisher's exact test for HYPERTENSION :

Fisher's Exact Test for Count Data

data: contingency\_table

p-value = 0.1247

alternative hypothesis: true odds ratio is not equal to 1

95 percent confidence interval:

0.2018769 1.2682876

sample estimates:

odds ratio

0.5041308

Fisher's exact test for DIABETES :

Fisher's Exact Test for Count Data

data: contingency\_table

p-value = 1

alternative hypothesis: true odds ratio is not equal to 1

95 percent confidence interval:

0.01829386 21.89579366

sample estimates:

odds ratio

1.107154

Fisher's exact test for ATRIALFIBR :

Fisher's Exact Test for Count Data

data: contingency\_table

p-value = 0.002208

alternative hypothesis: true odds ratio is not equal to 1

95 percent confidence interval:

1.616074 16.709141

sample estimates:

odds ratio

4.996928

Fisher's exact test for INFARCTION :

Fisher's Exact Test for Count Data

data: contingency\_table

p-value = 0.1702

alternative hypothesis: true odds ratio is not equal to 1

95 percent confidence interval:

0.005009745 1.748740856

sample estimates:

odds ratio

0.2272486

Fisher's exact test for AMYLOIDVIS :

Fisher's Exact Test for Count Data

data: contingency\_table

p-value = 0.2973

alternative hypothesis: true odds ratio is not equal to 1

95 percent confidence interval:

0.6244173 3.7492342

sample estimates:

odds ratio

1.541436

In the Fisher tests conducted on N\_LABEL and six variables, it was found that SEX (p=0.4407), HYPERTENSION (p=0.1247), DIABETES (p=1.000), INFARCTION (p=0.1702) and AMYLOIDVIS (0.2973) showed no significant relationship with cognitive status, suggesting that these variables may have a minimal impact on cognitive status. Although the odds ratio for ATRIALFIBR is 4.996, indicating a strong association with cognitive impairment (p=0.0022), it is important to note that while the odds ratios for other variables suggest potential associations, these results lack statistical significance. However, whether these variables influence the final scores and the patients' cognitive status requires further analysis.

Then, based on the grouping of N\_LABEL, perform Wilcoxon rank-sum tests on the remaining continuous variables to observe the differences between groups and examine their correlations with cognitive status.

# Wilcoxon rank-sum test

variables <- c("AGE", "EDUCATION", "MMSE", "CERAD", "PASTCAQ", "HANDGRIP", "MUSCLE", "SPPB", "MNA", "BMI", "CRP", "LEUK", "BPSYS", "BPDIA", "HBA1C", "CHOLESTEROL", "WMHVOL", "HIPPOVOL", "AMYLOIDBIND")

results <- data.frame(Variable = character(), p.value = numeric(), stringsAsFactors = FALSE)

for (var in variables) {

  test\_result <- wilcox.test(data[[var]] ~ data$N\_LABEL)

  results <- rbind(results, data.frame(Variable = var, p.value = test\_result$p.value))

}

print(results)

Table1.1 Results of rank-sum test

|  |  |
| --- | --- |
| Variable | p-value |
| AGE | 1.937940e-05 |
| EDUCATION | 1.856402e-01 |
| MMSE | 1.162747e-12 |
| CERAD | 5.055813e-14 |
| PASTCAQ | 8.234381e-01 |
| HANDGRIP | 1.122971e-04 |
| MUSCLE | 5.138574e-01 |
| SPPB | 7.370349e-02 |
| MNA | 4.660691e-04 |
| BMI | 5.860135e-01 |
| CRP | 5.972583e-02 |
| LEUK | 3.994737e-02 |
| BPSYS | 5.394276e-01 |
| BPDIA | 5.213018e-01 |
| HBA1C | 1.624442e-01 |
| CHOLESTEROL | 2.614635e-01 |
| WMHVOL | 1.560449e-02 |
| HIPPOVOL | 5.087277e-06 |
| AMYLOIDBIND | 3.661085e-04 |

Meanwhile, in order to keep the accuracy of test, we performance multiple test correction.

# Multiple Testing Correction

results <- data.frame(

  Variable = c("AGE", "EDUCATION", "MMSE", "CERAD", "PASTCAQ", "HANDGRIP", "MUSCLE",

               "SPPB", "MNA", "BMI", "CRP", "LEUK", "BPSYS", "BPDIA", "HBA1C",

               "CHOLESTEROL", "WMHVOL", "HIPPOVOL", "AMYLOIDBIND"),

  p.value = c(1.937940e-05, 1.856402e-01, 1.162747e-12, 5.055813e-14, 8.234381e-01,

              1.122971e-04, 5.138574e-01, 7.370349e-02, 4.660691e-04, 5.860135e-01,

              5.972583e-02, 3.994737e-02, 5.394276e-01, 5.213018e-01, 1.624442e-01,

              2.614635e-01, 1.560449e-02, 5.087277e-06, 3.661085e-04)

)

# cal Bonferroni corrections

results$Bonferroni\_p <- p.adjust(results$p.value, method = "bonferroni")

# cal BH corrections

results$BH\_p <- p.adjust(results$p.value, method = "BH")

results$Significant\_Bonferroni <- results$Bonferroni\_p < 0.05

results$Significant\_BH <- results$BH\_p < 0.05

print(results)

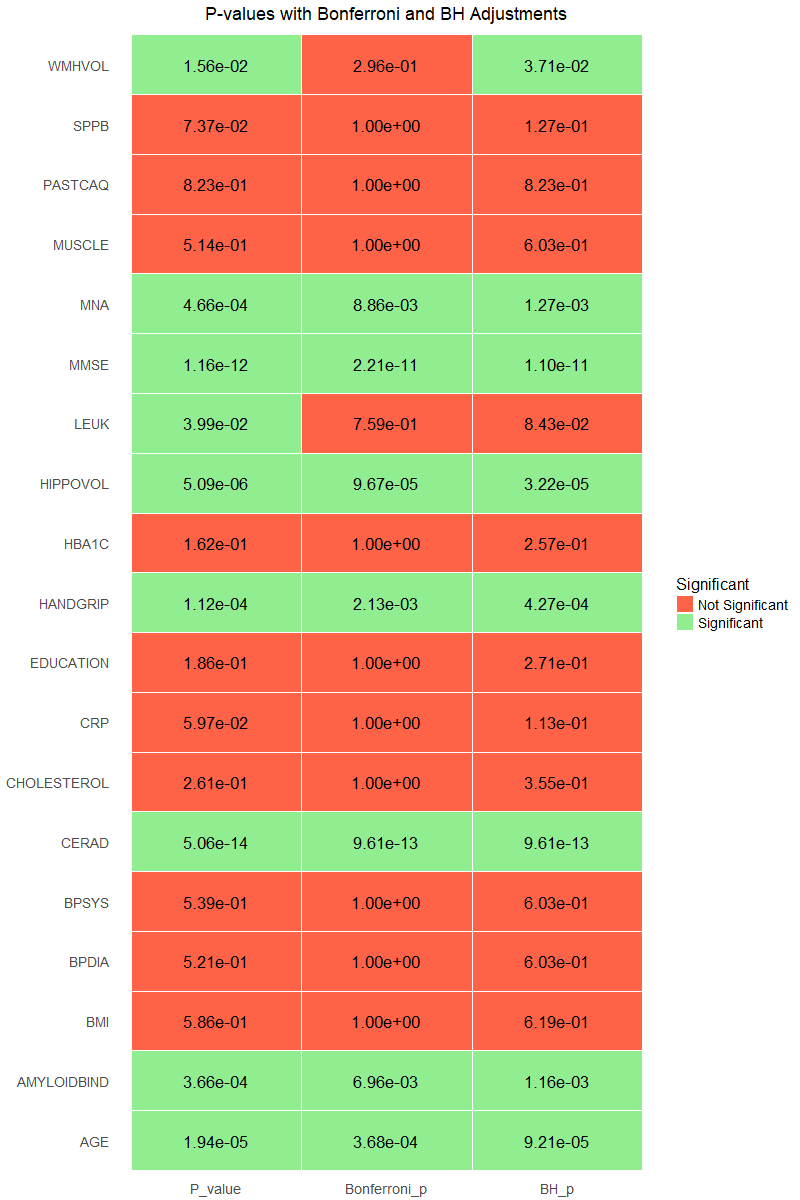


Figure1.3 Result of multiple test correction

Based on the above tests, we can conclude that the categorical variable ATRIALFIBR shows a significant association with cognitive status after performing the chi-square test. Seven continuous variables—AGE, MMSE, CERAD, HANDGRIP, MNA, HIPPOVOL, and AMYLOIDBIND—remain significant after multiple corrections, indicating substantial differences between the two groups and suggesting a strong association with the group classification (N\_LABEL). WMHVOL is significant under a more lenient correction (BH) but not under the stricter Bonferroni correction, implying a moderate difference between the groups. Although LEUK is not significant after correction, it still warrants some attention. These ten variables demonstrate a statistical association with cognitive status, but this does not necessarily mean they contribute more weight to the three scores. However, the results remain statistically significant, and we will focus on these variables in the subsequent regression models.

As shown in Figure 1.4, these are the boxplots of variables with significant differences between groups.

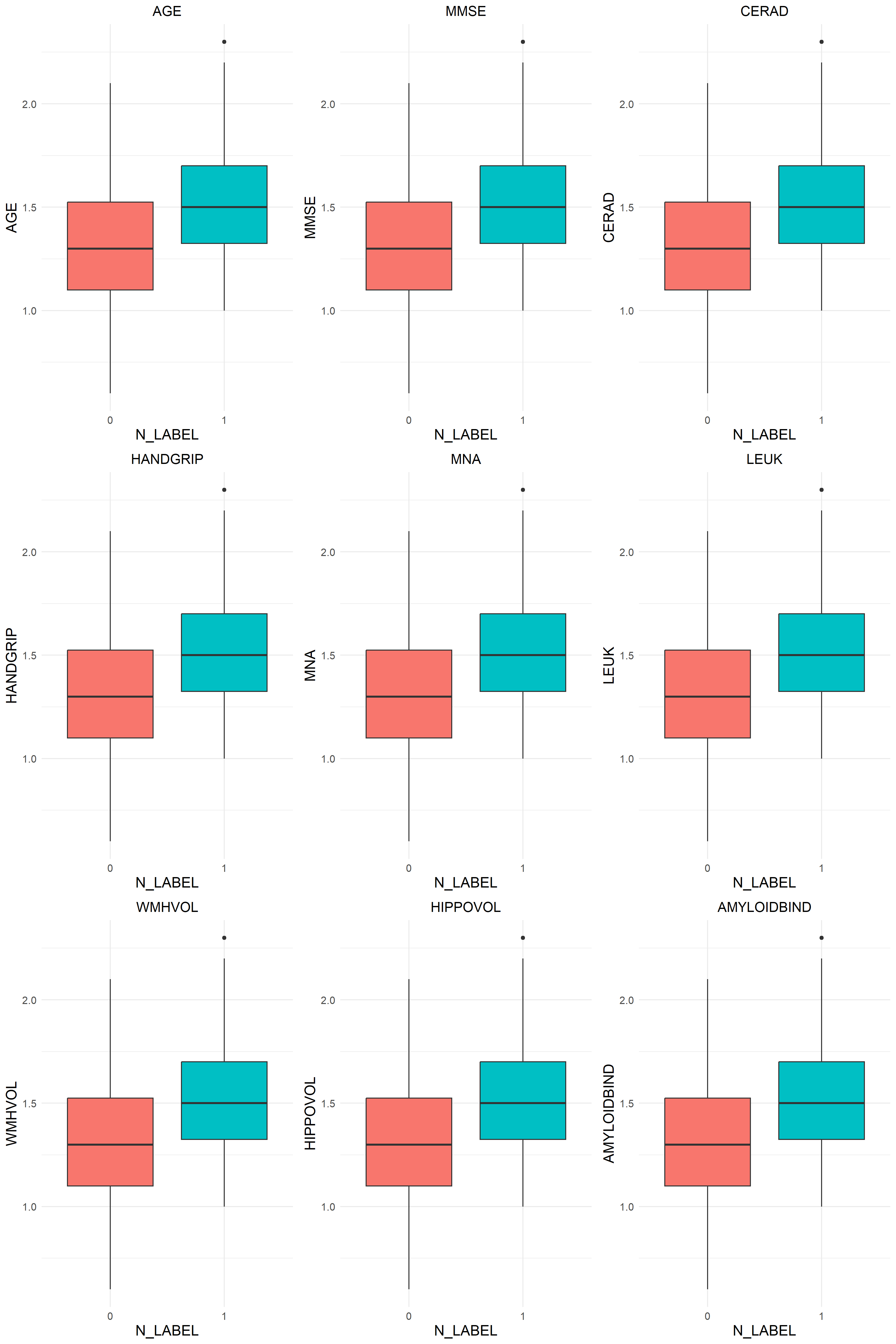


Figure1.4 Box plots of significant variables

As shown in Figure 1.5, these are the boxplots of variables with no significant differences between groups. Figures 1.4 and 1.5 visually illustrate whether the differences in group variables are significant.

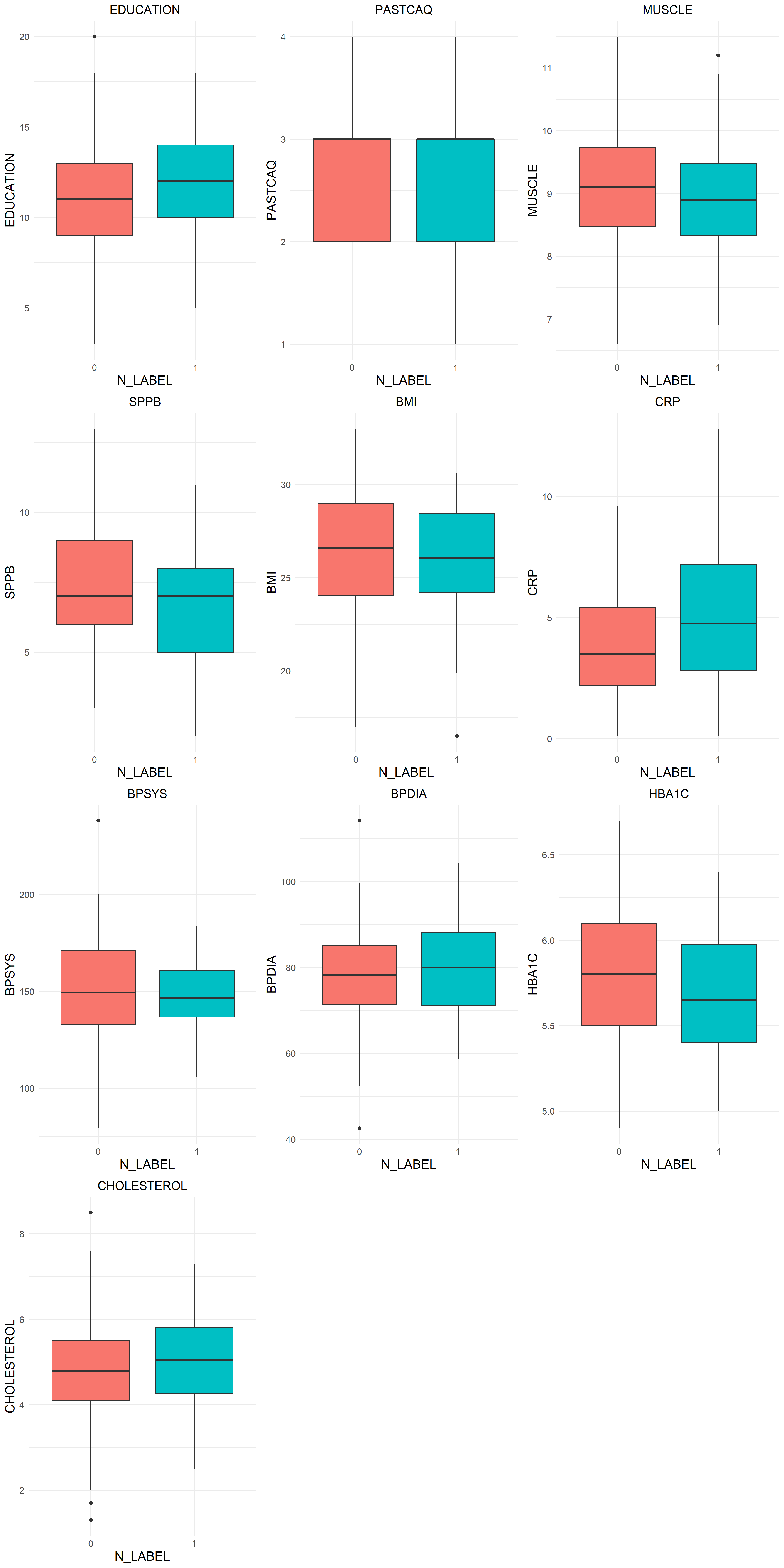


Figure1.4 Box plots of insignificant variables

The correlation matrix for the continuous variables was calculated. As shown in the figure, there is a relatively weak linear correlation among the variables. There is no significant relation between any pairs of variables.

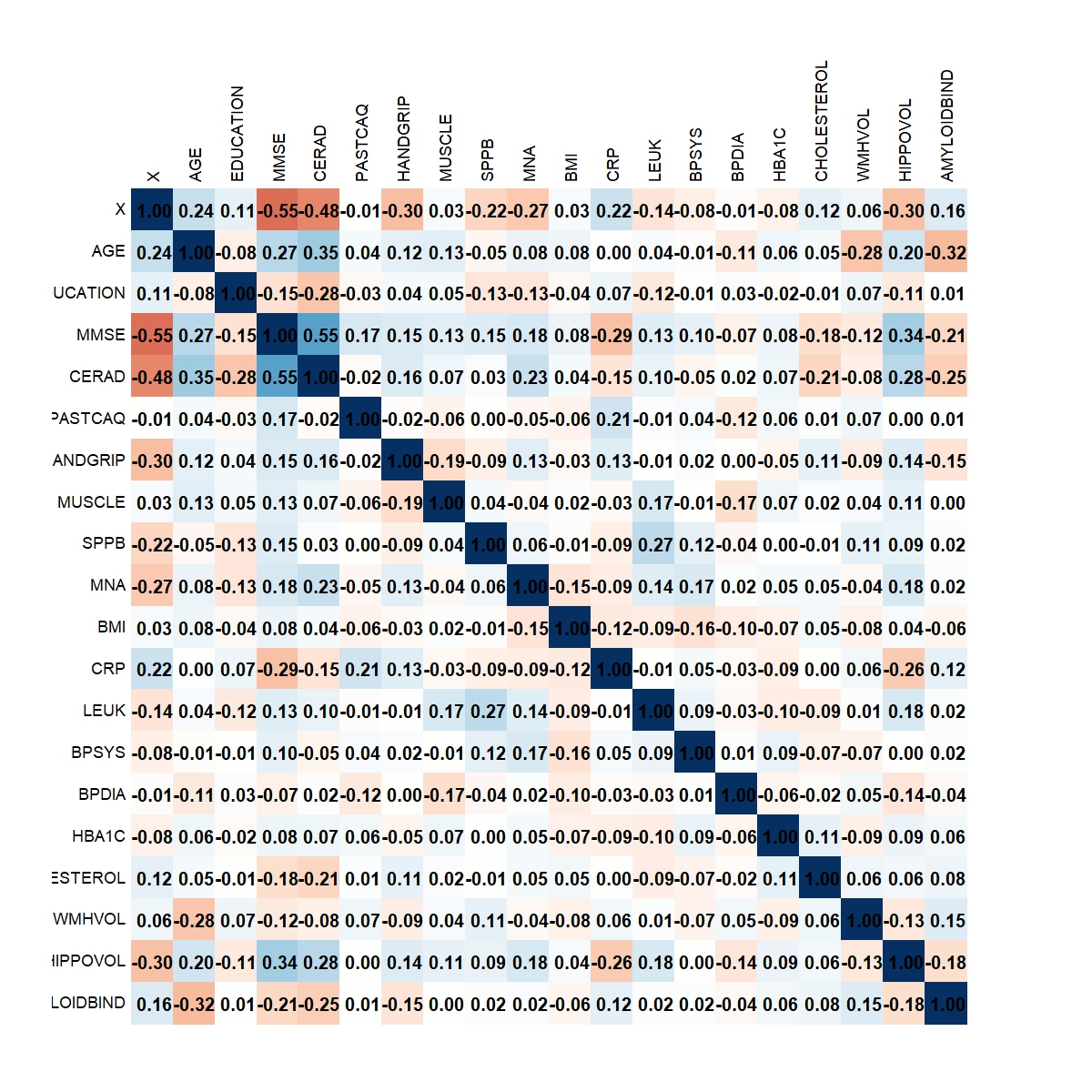


Figure 1.4 Correlation matrix of different variables

Due to the weak correlations among the variables and the large number of variables, we used the AIC (Akaike Information Criterion) method to simplify our model and obtain a more streamlined result

# AIC

full\_model\_memory <- lm(MEMORY ~ N\_LABEL + AGE + EDUCATION + MMSE + CERAD + PASTCAQ + HANDGRIP + MUSCLE + SPPB + MNA + BMI + CRP + LEUK + BPSYS + BPDIA + HBA1C + CHOLESTEROL + WMHVOL + HIPPOVOL + AMYLOIDBIND, data = data)

optimized\_model\_memory <- step(full\_model\_memory, direction = "both", trace = FALSE)

summary(optimized\_model\_memory)

full\_model\_execfunc <- lm(EXECFUNC ~ N\_LABEL + AGE + EDUCATION + MMSE + CERAD + PASTCAQ + HANDGRIP + MUSCLE + SPPB + MNA + BMI + CRP + LEUK + BPSYS + BPDIA + HBA1C +CHOLESTEROL + WMHVOL + HIPPOVOL + AMYLOIDBIND, data = data)

optimized\_model\_execfunc <- step(full\_model\_execfunc, direction = "both", trace = FALSE)

summary(optimized\_model\_execfunc)

full\_model\_procspeed <- lm(PROCSPEED ~ N\_LABEL + AGE + EDUCATION + MMSE + CERAD + PASTCAQ + HANDGRIP + MUSCLE + SPPB + MNA + BMI + CRP + LEUK + BPSYS + BPDIA + HBA1C + CHOLESTEROL + WMHVOL + HIPPOVOL + AMYLOIDBIND, data = data)

optimized\_model\_procspeed <- step(full\_model\_procspeed, direction = "both", trace = FALSE)

summary(optimized\_model\_procspeed)

Call:

lm(formula = MEMORY ~ MUSCLE + SPPB + MNA + BMI + BPSYS + BPDIA +

HBA1C + WMHVOL + HIPPOVOL + AMYLOIDBIND, data = data)

Residuals:

Min 1Q Median 3Q Max

-2.58020 -0.65142 -0.04628 0.53095 2.49511

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -14.344647 2.346479 -6.113 1.49e-08 \*\*\*

MUSCLE 0.512798 0.100976 5.078 1.55e-06 \*\*\*

SPPB 0.154524 0.039434 3.919 0.000154 \*\*\*

MNA 0.191054 0.074757 2.556 0.011951 \*

BMI 0.048656 0.026912 1.808 0.073315 .

BPSYS 0.008202 0.004308 1.904 0.059509 .

BPDIA 0.012387 0.008439 1.468 0.144963

HBA1C 0.619109 0.242742 2.550 0.012120 \*

WMHVOL -0.360692 0.115034 -3.136 0.002196 \*\*

HIPPOVOL 2.531966 0.527605 4.799 5.01e-06 \*\*\*

AMYLOIDBIND -0.702964 0.309379 -2.272 0.025002 \*

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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.059 on 111 degrees of freedom

Multiple R-squared: 0.5488, Adjusted R-squared: 0.5081

F-statistic: 13.5 on 10 and 111 DF, p-value: 2.991e-15

Call:

lm(formula = EXECFUNC ~ EDUCATION + MMSE + PASTCAQ + MUSCLE +

SPPB + MNA + BPSYS + HBA1C + WMHVOL + HIPPOVOL, data = data)

Residuals:

Min 1Q Median 3Q Max

-2.45251 -0.63954 -0.01434 0.79976 2.65366

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -6.669096 2.238373 -2.979 0.00355 \*\*

EDUCATION -0.054679 0.032697 -1.672 0.09728 .

MMSE 0.053551 0.038432 1.393 0.16628

PASTCAQ -0.255481 0.172290 -1.483 0.14095

MUSCLE 0.306640 0.110455 2.776 0.00646 \*\*

SPPB 0.090581 0.043731 2.071 0.04065 \*

MNA 0.162850 0.082117 1.983 0.04982 \*

BPSYS -0.009325 0.004685 -1.990 0.04900 \*

HBA1C 0.398464 0.264416 1.507 0.13466

WMHVOL -0.244557 0.125541 -1.948 0.05394 .

HIPPOVOL 1.620409 0.589421 2.749 0.00698 \*\*

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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.158 on 111 degrees of freedom

Multiple R-squared: 0.3528, Adjusted R-squared: 0.2944

F-statistic: 6.05 on 10 and 111 DF, p-value: 2.726e-07

Call:

lm(formula = PROCSPEED ~ N\_LABEL + EDUCATION + CERAD + MUSCLE +

SPPB + MNA + BMI + CRP + LEUK + CHOLESTEROL + WMHVOL + HIPPOVOL +

AMYLOIDBIND, data = data)

Residuals:

Min 1Q Median 3Q Max

-2.23259 -0.49948 -0.03175 0.53399 2.42630

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -7.34148 1.47367 -4.982 2.41e-06 \*\*\*

N\_LABEL 0.79159 0.27103 2.921 0.004253 \*\*

EDUCATION 0.05064 0.02516 2.013 0.046633 \*

CERAD 0.08025 0.02269 3.536 0.000600 \*\*\*

MUSCLE 0.11857 0.08140 1.457 0.148114

SPPB 0.14909 0.03386 4.403 2.52e-05 \*\*\*

MNA 0.13447 0.06263 2.147 0.034024 \*

BMI 0.06003 0.02153 2.789 0.006257 \*\*

CRP -0.08509 0.03216 -2.646 0.009358 \*\*

LEUK 0.08864 0.03454 2.567 0.011636 \*

CHOLESTEROL 0.10037 0.06229 1.611 0.110015

WMHVOL -0.27255 0.09479 -2.875 0.004864 \*\*

HIPPOVOL 2.95996 0.45467 6.510 2.43e-09 \*\*\*

AMYLOIDBIND -0.93643 0.26107 -3.587 0.000504 \*\*\*

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.8487 on 108 degrees of freedom

Multiple R-squared: 0.6338, Adjusted R-squared: 0.5898

F-statistic: 14.38 on 13 and 108 DF, p-value: < 2.2e-16

We will take the intersection of the significant variables mentioned above and the variables identified for further attention in the previous discussion, and form a new linear model. We will then perform linear regression again to obtain the final model.

model\_memory <- lm(MEMORY ~ MUSCLE + SPPB + MNA + HBA1C + WMHVOL + HIPPOVOL + AMYLOIDBIND, data = data)

summary(model\_memory)

model\_execfunc <- lm(EXECFUNC ~ MUSCLE + SPPB + MNA + WMHVOL + HIPPOVOL, data = data)

summary(model\_execfunc)

model\_procspeed <- lm(PROCSPEED ~ N\_LABEL + CERAD + SPPB + MNA + BMI + CRP + LEUK + WMHVOL + HIPPOVOL + AMYLOIDBIND, data = data)

summary(model\_procspeed)

Call:

lm(formula = MEMORY ~ MUSCLE + SPPB + MNA + HBA1C + WMHVOL +

HIPPOVOL + AMYLOIDBIND, data = data)

Residuals:

Min 1Q Median 3Q Max

-2.5712 -0.6498 -0.1381 0.7388 2.7857

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -10.64934 1.90139 -5.601 1.50e-07 \*\*\*

MUSCLE 0.49134 0.10182 4.826 4.36e-06 \*\*\*

SPPB 0.16209 0.03995 4.058 9.11e-05 \*\*\*

MNA 0.19815 0.07462 2.655 0.00906 \*\*

HBA1C 0.61407 0.24633 2.493 0.01411 \*

WMHVOL -0.38546 0.11647 -3.310 0.00125 \*\*

HIPPOVOL 2.42830 0.53340 4.553 1.33e-05 \*\*\*

AMYLOIDBIND -0.74435 0.31501 -2.363 0.01982 \*

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.081 on 114 degrees of freedom

Multiple R-squared: 0.5169, Adjusted R-squared: 0.4872

F-statistic: 17.43 on 7 and 114 DF, p-value: 1.556e-15

Call:

lm(formula = EXECFUNC ~ MUSCLE + SPPB + MNA + WMHVOL + HIPPOVOL,

data = data)

Residuals:

Min 1Q Median 3Q Max

-2.5899 -0.7936 0.0641 0.7928 2.8647

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -6.10821 1.48182 -4.122 7.08e-05 \*\*\*

MUSCLE 0.33536 0.11222 2.988 0.003423 \*\*

SPPB 0.09777 0.04412 2.216 0.028632 \*

MNA 0.17475 0.08224 2.125 0.035730 \*

WMHVOL -0.28425 0.12720 -2.235 0.027356 \*

HIPPOVOL 2.02643 0.57867 3.502 0.000657 \*\*\*

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.195 on 116 degrees of freedom

Multiple R-squared: 0.2807, Adjusted R-squared: 0.2497

F-statistic: 9.053 on 5 and 116 DF, p-value: 2.734e-07

Call:

lm(formula = PROCSPEED ~ N\_LABEL + CERAD + SPPB + MNA + BMI +

CRP + LEUK + WMHVOL + HIPPOVOL + AMYLOIDBIND, data = data)

Residuals:

Min 1Q Median 3Q Max

-2.15058 -0.48419 -0.07701 0.61037 2.29942

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -4.82154 1.20823 -3.991 0.000119 \*\*\*

N\_LABEL 0.67731 0.27367 2.475 0.014839 \*

CERAD 0.06080 0.02156 2.820 0.005697 \*\*

SPPB 0.13747 0.03439 3.998 0.000115 \*\*\*

MNA 0.12571 0.06364 1.975 0.050721 .

BMI 0.06175 0.02203 2.803 0.005981 \*\*

CRP -0.08311 0.03300 -2.518 0.013222 \*

LEUK 0.08699 0.03468 2.508 0.013578 \*

WMHVOL -0.23414 0.09639 -2.429 0.016746 \*

HIPPOVOL 3.05176 0.46241 6.600 1.46e-09 \*\*\*

AMYLOIDBIND -0.92336 0.26770 -3.449 0.000796 \*\*\*

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.8717 on 111 degrees of freedom

Multiple R-squared: 0.603, Adjusted R-squared: 0.5673

F-statistic: 16.86 on 10 and 111 DF, p-value: < 2.2e-16

In the memory model, muscle strength (MUSCLE), physical performance (SPPB), and hippocampal volume (HIPPOVOL) were found to have significant positive associations with memory scores, indicating that greater muscle strength, physical capability, and hippocampal volume may contribute to improved memory. In contrast, amyloid beta binding (AMYLOIDBIND) and white matter hyperintensity volume (WMHVOL) showed significant negative associations with memory, suggesting a potential link to memory decline.

In the executive function model, MUSCLE, SPPB, and HIPPOVOL also showed significant positive effects, suggesting that these physiological characteristics not only influence memory but are also strongly associated with improvements in executive function. Additionally, WMHVOL and MNA (Mini Nutritional Assessment) were significant in this model, highlighting the role of white matter changes and nutritional status in executive function.

In the processing speed model, beyond the previously mentioned factors, CERAD (Clinical Dementia Rating) was positively associated with processing speed, while WMHVOL and AMYLOIDBIND again showed significant negative associations, indicating their potential contribution to processing speed decline. Glycated hemoglobin (HBA1C) and body mass index (BMI) were also positively associated with processing speed, suggesting that metabolic factors may play a role in cognitive speed.

These analyses highlight the complex interplay of physiological, structural, and metabolic factors influencing cognitive function in older adults. The adjusted R² for the memory model was 0.4872, 0.2497 for the executive function model, and 0.5673 for the processing speed model, suggesting that these variables have the highest explanatory power in processing speed and the lowest in executive function.

**Task 2**

First, a scatter plot (Figure 2.1) was generated to provide an overview of the dataset. The plot illustrates a positive correlation between DV\_Amyloid (Amy) and Age, indicating that as Age increases, DV\_Amyloid values tend to rise as well. However, due to the presence of multiple corresponding DV\_Amyloid values for a single Age value, it was necessary to create a new dataset that establishes a one-to-one correspondence between Age and DV\_Amyloid. To achieve this, we applied the method of averaging to obtain a mean value of DV\_Amyloid for each unique Age. The resulting dataset was then visualized in a plot, as shown in Figure 2.2.

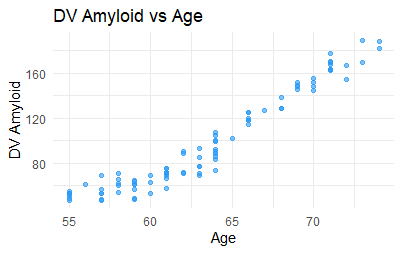


Figure 2.1 Scatter plot of the original dataset

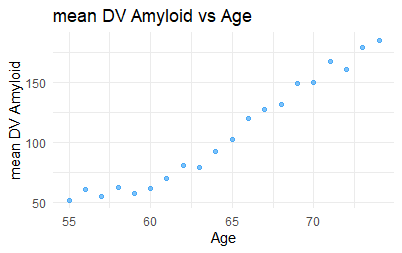


Figure 2.2 mean DV\_Amyloid plot

The trend observed in Figure 2.2 appears to be linear; therefore, we initially employed a linear model for our analysis.

model\_linear <- lm(average\_amyloid$mean\_amyloid ~ average\_amyloid$age)

summary(model\_linear)

Call:

lm(formula = average\_amyloid$mean\_amyloid ~ average\_amyloid$age)

Residuals:

Min 1Q Median 3Q Max

-16.7781 -7.9167 0.9219 5.9404 18.1809

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -381.2828 24.8251 -15.36 8.67e-12 \*\*\*

average\_amyloid$age 7.5727 0.3834 19.75 1.19e-13 \*\*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 9.886 on 18 degrees of freedom

Multiple R-squared: 0.9559, Adjusted R-squared: 0.9535

F-statistic: 390.2 on 1 and 18 DF, p-value: 1.193e-13

The R-squared value obtained from the linear model is 0.9559, indicating a very strong fit to the data. Subsequently, we plotted the regression line alongside both the original dataset and the mean dataset, as illustrated in Figures 2.3 and 2.4.

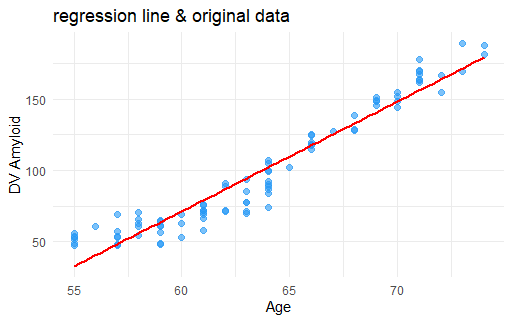


Figure 2.3 regression line & original data

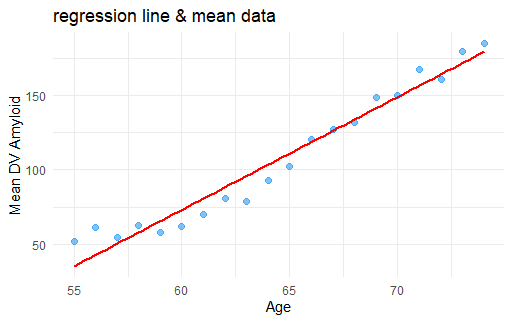


Figure 2.4 regression line & mean data

To evaluate the model, we analyzed the residuals versus fitted values plot and assessed the normality of the residuals.

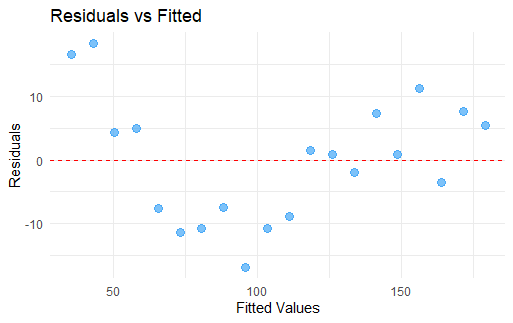


Figure 2.5 residuals value vs fitted value

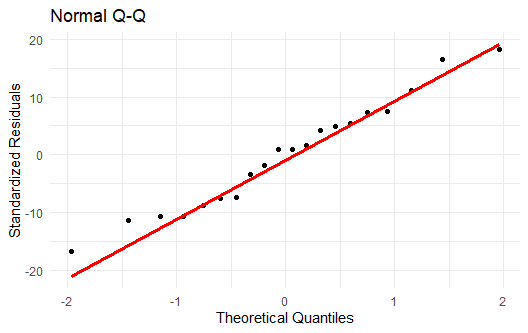


Figure 2.6 Q-Q plot

> shpiro\_result <- shapiro.test(residuals(model\_linear))

> print(shpiro\_result)

Shapiro-Wilk normality test

data: residuals(model\_linear)

W = 0.97047, p-value = 0.7647

As shown in Figure 2.5, the residuals exhibit considerable variability. The Q-Q plot and the results of the Shapiro-Wilk test indicate that the residuals do not follow a normal distribution. Consequently, the performance of the linear model is not sufficient.

Then, we tried Logarithmic Model, Polynomial Model (2), Mixed-effect Model. The workflow of the first two models is just as same as it in the Linear Model and the results are as follows.

**Logarithmic Model**

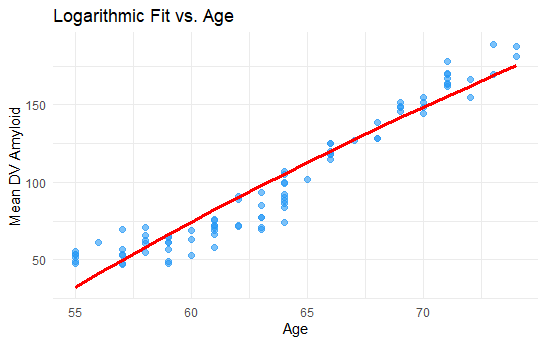


Figure 2.7 Logarithmic Model regression

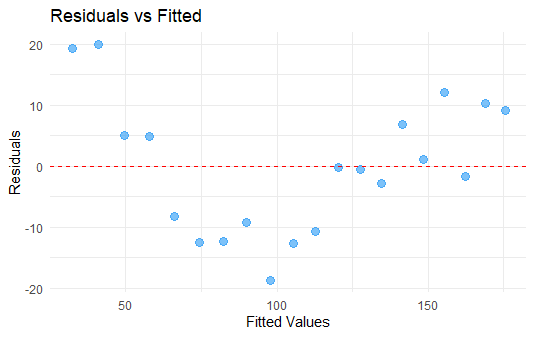


Figure 2.8 Logarithmic Model residuals

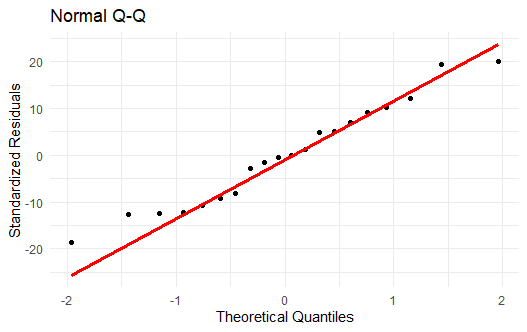


Figure 2.9 Logarithmic Model Q-Q plot

> # Shapiro-Wilk test

> shpiro\_result <- shapiro.test(residuals(model\_log))

> print(shpiro\_result)

Shapiro-Wilk normality test

data: residuals(model\_log)

W = 0.96426, p-value = 0.632

**Polynomial(2) Model**

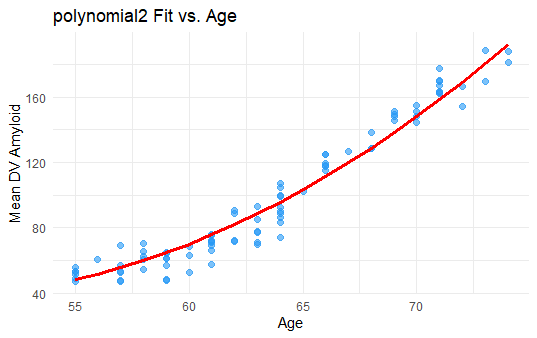


Figure 2.10 Polynomial 2 Model regression

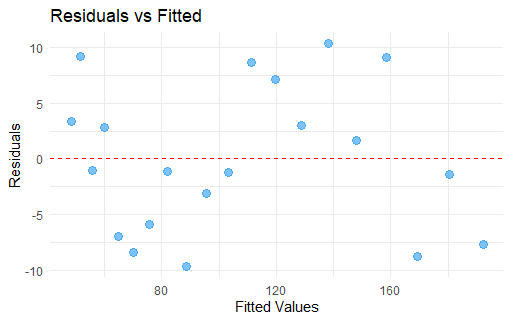


Figure 2.11 Polynomial 2 Model residuals

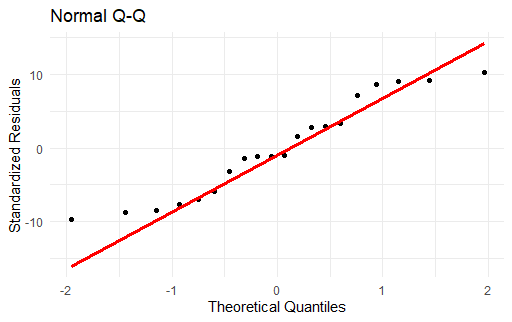


Figure 2.12 Polynomial 2 Model Q-Q plot

> shpiro\_result <- shapiro.test(residuals(model\_poly2))

> print(shpiro\_result)

Shapiro-Wilk normality test

data: residuals(model\_poly2)

W = 0.93027, p-value = 0.1563

**Mixed-effect Model**

In this case, the fixed-effect is the age, and the random effect is the difference among all the participants, which can be caused by weight, diet, education level, average sleeping time, etc. Because there are no independent variables except the age in this dataset, we manually constructed a variable, acting as the random effect.

# construct the random variable

data\_2$Y <- floor(data\_2$X / 17) # Y = X/17, dividing the dataset into 6 groups.

# use lmer() to construct the model，age as the fixed effect，Y as the random effect

model\_mixed <- lmer(DV\_amyloid ~ age + (1|Y), data = data\_2)

summary(model\_mixed)

# plot prediction

set.seed(123) # random seed

new\_data$Y <- sample(data\_2$Y,20,replace = TRUE) # randomly select 20 values

new\_data$predicted\_mix\_Amyloid <- predict(model\_mixed, newdata = new\_data)

> summary(model\_mixed)

Linear mixed model fit by REML ['lmerMod']

Formula: DV\_amyloid ~ age + (1 | Y)

Data: data\_2

REML criterion at convergence: 678.4

Scaled residuals:

Min 1Q Median 3Q Max

-2.26820 -0.68992 0.02908 0.62157 1.89081

Random effects:

Groups Name Variance Std.Dev.

Y (Intercept) 4.91 2.216

Residual 131.90 11.485

Number of obs: 88, groups: Y, 6

Fixed effects:

Estimate Std. Error t value

(Intercept) -391.2014 14.9362 -26.19

age 7.7080 0.2339 32.95

Correlation of Fixed Effects:

(Intr)

age -0.995

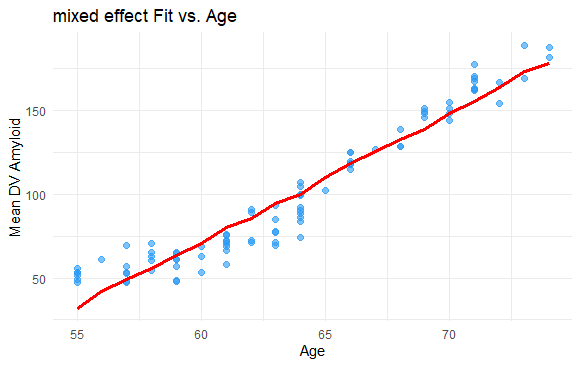


Figure 2.13 Mixed-effect Model regression

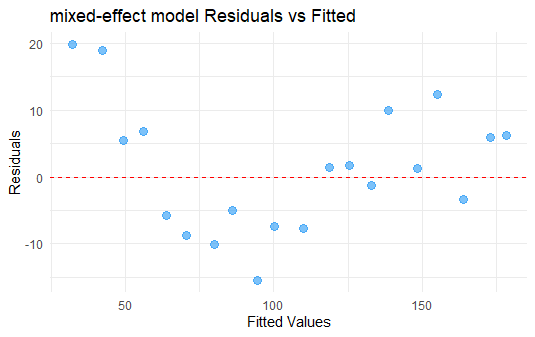


Figure 2.14 Mixed-effect Model residuals

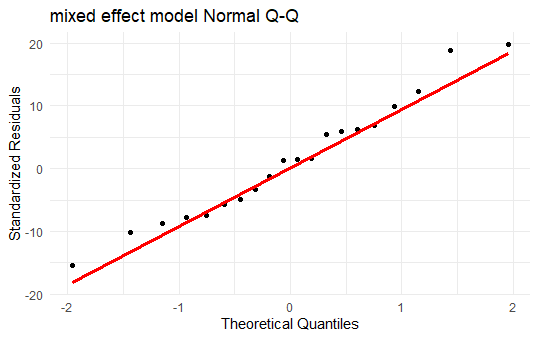


Figure 2.15 Mixed-effect Model Q-Q plot

> shpiro\_result <- shapiro.test(residuals(model\_mixed))

> print(shpiro\_result)

Shapiro-Wilk normality test

data: residuals(model\_mixed)

W = 0.98445, p-value = 0.3756

From all the results, we can see that the residuals of the Polynomial 2 Model and the Mixed-effect Model are normally distributed in this dataset.

**Prediction**

Next, we used the four types of models to predict the amyloid beta at the ages of 75 to 110 years old.

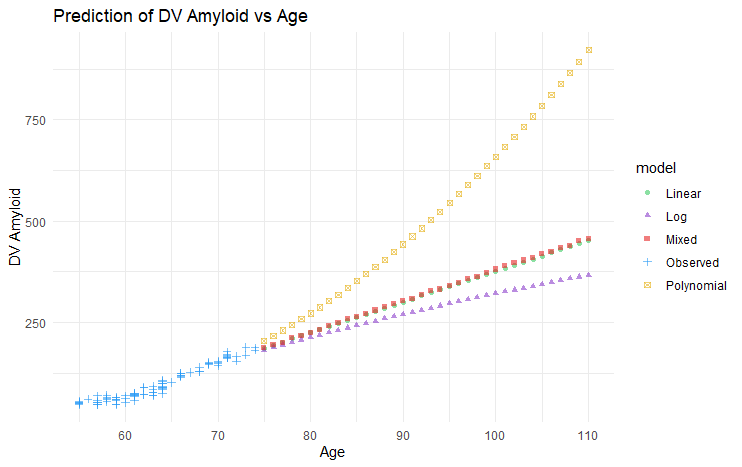


Figure 2.16 Prediction of the amyloid

**Recommendations**

The four types of model all gave a rising trend of the Amyloid, and the Linear Model and the Mixed-effect Model gave similar results while others’ results are significant different. The result of the Polynomial Model seems ridiculous, especially in the highest age region. One of the reasons could be that the prediction age region is very high for the AD patients.

**Task 3**

Here we drew the comparison of our predictions and the groud truth. It is obvious that the Logarithmic Model has the best result, but still not good enough.

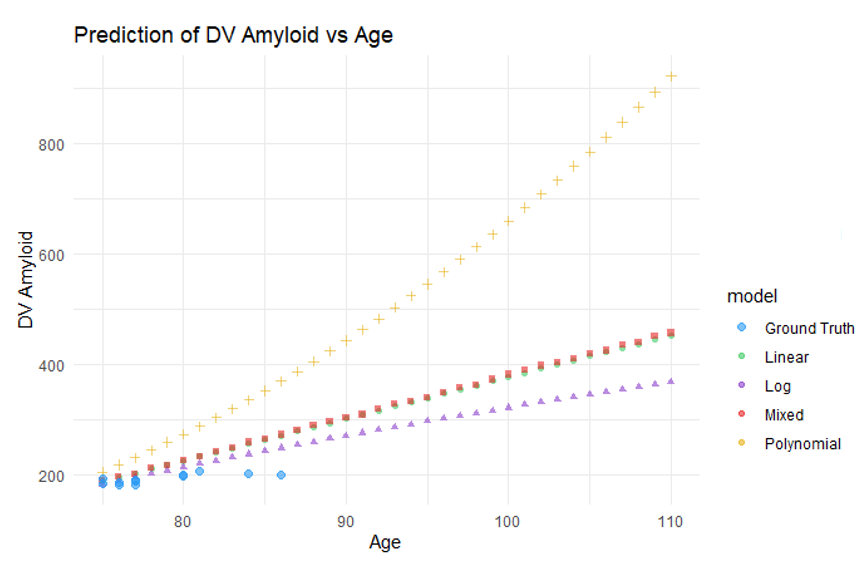


Figure 3.1 Comparison of the predictions and the ground truth

**Improved model**

To better fit the data of kind like a ‘S’ shape, we tried the Polynomial 3 Model, the results are as follows.

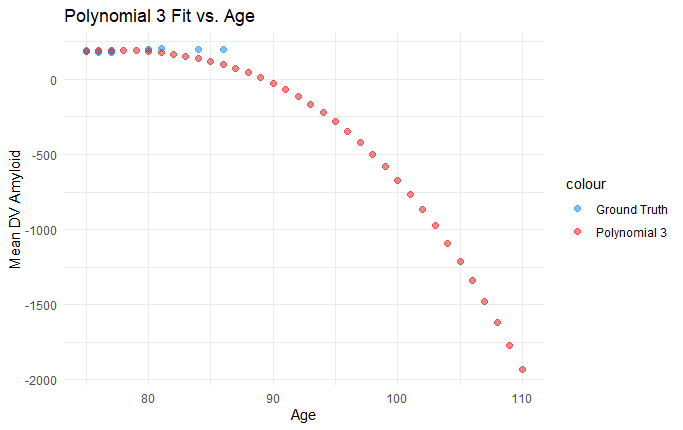


Figure 3.3 Polynomial 3 Model

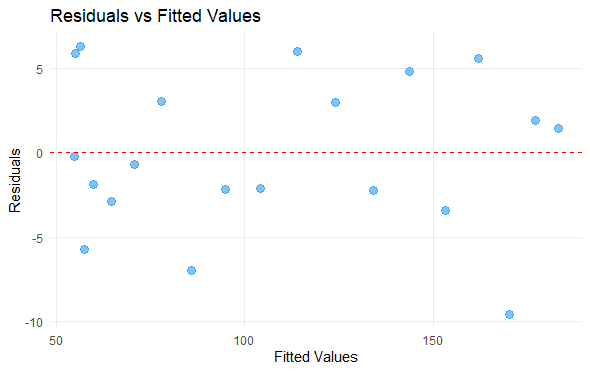


Figure 3.3 Polynomial 3 Model residuals

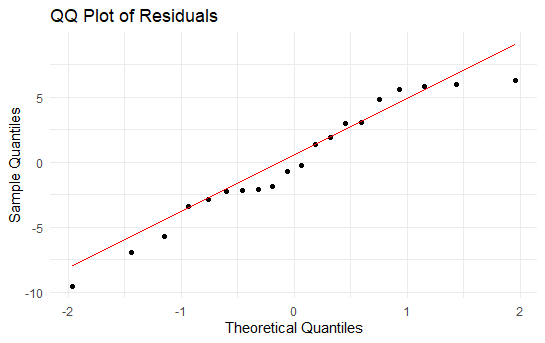


Figure 3.3 Polynomial 3 Model Q-Q plot

> shpiro\_result <- shapiro.test(residuals(model\_poly3))

> print(shpiro\_result)

Shapiro-Wilk normality test

data: residuals(model\_poly3)

W = 0.95035, p-value = 0.3725

**General learning**

When a model performs exceptionally well on the training data, capturing all the details and noise, it can lead to poor performance on new, unseen data. This happens because the model learns not just the underlying patterns but also the random fluctuations in the training data.

As a result, while the model may have a low error on the training set, it may have a high error when making predictions on new data.

**Task 4**

From the Shapiro-Wilk test and the Q-Q plot, we can see that the control group is not normally distributed.

> print(shapiro\_test\_control)

Shapiro-Wilk normality test

data: data$AMYLOIDB[data$GROUP == "control"]

W = 0.94804, p-value = 0.02836

> print(shapiro\_test\_gene\_exp1)

Shapiro-Wilk normality test

data: data$AMYLOIDB[data$GROUP == "gene\_exp1"]

W = 0.98604, p-value = 0.8154

> print(shapiro\_test\_gene\_exp2)

Shapiro-Wilk normality test

data: data$AMYLOIDB[data$GROUP == "gene\_exp2"]

W = 0.98033, p-value = 0.5661

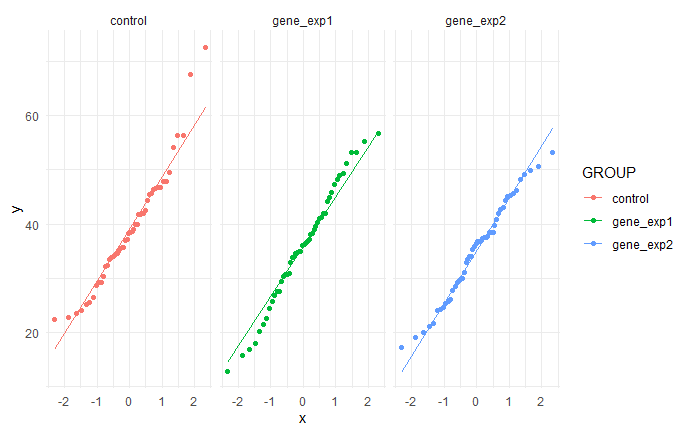


Figure 4.1 three groups Q-Q plot

If one group is not normally distributed, we cannot do the ANOVA test. So we did a root transformation to the data, the results are as follows.

> print(shapiro\_test\_log\_control)

Shapiro-Wilk normality test

data: data$root\_AMYLOIDB[data$GROUP == "control"]

W = 0.97362, p-value = 0.3228

> print(shapiro\_test\_log\_gene\_exp1)

Shapiro-Wilk normality test

data: data$root\_AMYLOIDB[data$GROUP == "gene\_exp1"]

W = 0.97341, p-value = 0.3169

> print(shapiro\_test\_log\_gene\_exp2)

Shapiro-Wilk normality test

data: data$root\_AMYLOIDB[data$GROUP == "gene\_exp2"]

W = 0.97474, p-value = 0.3567

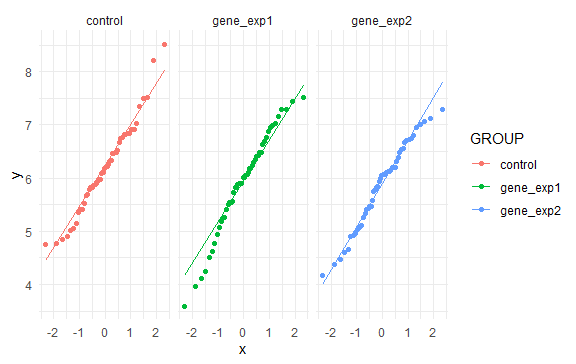


Figure 4.2 three groups Q-Q plot after root transformation

After that, we did the Levene’s test to check the homogeneity of variance. Because the p value is bigger than 0.05, the root data is homogeneous in variance.

> print(levene\_test)

Levene's Test for Homogeneity of Variance (center = median)

Df F value Pr(>F)

group 2 0.3898 0.6779

147

Finally, we did the ANOVA test.

> anova\_result <- aov(root\_AMYLOIDB ~ GROUP, data = data)

> summary(anova\_result)

Df Sum Sq Mean Sq F value Pr(>F)

GROUP 2 3.07 1.5364 2.123 0.123

Residuals 147 106.38 0.7237

Because the p value is bigger than 0.05, we concluded that the three groups do not have significant differences.