STAT631 Mini Project Report

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Data Description

This analysis uses the Right Heart Catheterization (RHC) dataset, which includes 5,735 critically ill adult patients from the SUPPORT study (Study to Understand Prognoses and Preferences for Outcomes and Risks of Treatments), conducted from 1989 to 1994 across five U.S. teaching hospitals. The dataset is publicly available through the Vanderbilt University Department of Biostatistics. For the purpose of this study, the outcome of interest is hospital length of stay, defined as the number of days from admission to discharge. The independent variables examined are sex (male or female), age group (categorized as <50, 50–65, 65–80, and 80+), and history of cardiovascular disease (yes or no).

Right Heart Catheterization (RHC) Dataset Overview

Source: Vanderbilt University Department of Biostatistics

Direct Download: https://hbiostat.org/data/repo/rhc.csv

Dataset Documentation: https://search.r-project.org/CRAN/refmans/ATbounds/html/RHC.html

Study Reference: Connors, A.F., et al. (1996). "The effectiveness of right heart catheterization in the initial care of critically ill patients." JAMA, 276(11), 889–897. DOI: 10.1001/jama.1996.03540110043030

Research Question

This study examines whether sex, age group, and history of cardiovascular disease (cardiohx) individually or interactively influence hospital length of stay among critically ill patients.

Load Libraries and Data

```
library(ggplot2)
library(dplyr)
```

```
Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

    filter, lag

The following objects are masked from 'package:base':

    intersect, setdiff, setequal, union
```

```
library(multcomp)
```

```
Loading required package: mvtnorm

Loading required package: survival

Loading required package: TH.data

Loading required package: MASS

Attaching package: 'MASS'

The following object is masked from 'package:dplyr':

    select

Attaching package: 'TH.data'

The following object is masked from 'package:MASS':

    geyser
```

```
library(stats)
library(car)
```

```
Loading required package: carData
```

```
Attaching package: 'car'
```

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

    recode
```

```
df <- read.csv("rhc.csv")
summary(df)
```

```
       X            cat1               cat2                ca           
 Min.   :   1   Length:5735        Length:5735        Length:5735       
 1st Qu.:1434   Class :character   Class :character   Class :character  
 Median :2868   Mode  :character   Mode  :character   Mode  :character  
 Mean   :2868                                                           
 3rd Qu.:4302                                                           
 Max.   :5735                                                           

    sadmdte         dschdte          dthdte         lstctdte    
 Min.   :10754   Min.   :10757   Min.   :10757   Min.   :10756  
 1st Qu.:11164   1st Qu.:11184   1st Qu.:11267   1st Qu.:11316  
 Median :11759   Median :11777   Median :11832   Median :11868  
 Mean   :11639   Mean   :11660   Mean   :11754   Mean   :11781  
 3rd Qu.:12097   3rd Qu.:12120   3rd Qu.:12208   3rd Qu.:12244  
 Max.   :12441   Max.   :12560   Max.   :12783   Max.   :12644  
                 NA's   :1       NA's   :2013                   
    death              cardiohx          chfhx          dementhx      
 Length:5735        Min.   :0.0000   Min.   :0.000   Min.   :0.00000  
 Class :character   1st Qu.:0.0000   1st Qu.:0.000   1st Qu.:0.00000  
 Mode  :character   Median :0.0000   Median :0.000   Median :0.00000  
                    Mean   :0.1766   Mean   :0.178   Mean   :0.09834  
                    3rd Qu.:0.0000   3rd Qu.:0.000   3rd Qu.:0.00000  
                    Max.   :1.0000   Max.   :1.000   Max.   :1.00000  

    psychhx           chrpulhx         renalhx           liverhx      
```

```
Min.   :0.00000   Min.   :0.0000   Min.   :0.00000   Min.   :0.00000
1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:0.00000   1st Qu.:0.00000
Median :0.00000   Median :0.0000   Median :0.00000   Median :0.00000
Mean   :0.06731   Mean   :0.1899   Mean   :0.04446   Mean   :0.06992
3rd Qu.:0.00000   3rd Qu.:0.0000   3rd Qu.:0.00000   3rd Qu.:0.00000
Max.   :1.00000   Max.   :1.0000   Max.   :1.00000   Max.   :1.00000

   gibledhx          malighx          immunhx         transhx
Min.   :0.00000   Min.   :0.0000   Min.   :0.000   Min.   :0.0000
1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:0.000   1st Qu.:0.0000
Median :0.00000   Median :0.0000   Median :0.000   Median :0.0000
Mean   :0.03226   Mean   :0.2295   Mean   :0.269   Mean   :0.1154
3rd Qu.:0.00000   3rd Qu.:0.0000   3rd Qu.:1.000   3rd Qu.:0.0000
Max.   :1.00000   Max.   :1.0000   Max.   :1.000   Max.   :1.0000

    amihx              age             sex                 edu
Min.   :0.00000   Min.   : 18.04   Length:5735        Min.   : 0.00
1st Qu.:0.00000   1st Qu.: 50.15   Class :character   1st Qu.:10.00
Median :0.00000   Median : 64.05   Mode  :character   Median :12.00
Mean   :0.03487   Mean   : 61.38                      Mean   :11.68
3rd Qu.:0.00000   3rd Qu.: 73.93                      3rd Qu.:13.00
Max.   :1.00000   Max.   :101.85                      Max.   :30.00

   surv2md1         das2d3pc         t3d30          dth30
Min.   :0.0000   Min.   :11.00   Min.   : 2.00   Length:5735
1st Qu.:0.4709   1st Qu.:16.06   1st Qu.:16.00   Class :character
Median :0.6280   Median :19.75   Median :30.00   Mode  :character
Mean   :0.5925   Mean   :20.50   Mean   :23.61
3rd Qu.:0.7430   3rd Qu.:23.43   3rd Qu.:30.00
Max.   :0.9620   Max.   :33.00   Max.   :30.00

     aps1            scoma1        meanbp1           wblc1
Min.   :  3.00   Min.   :  0   Min.   :  0.00   Min.   :  0.000
1st Qu.: 41.00   1st Qu.:  0   1st Qu.: 50.00   1st Qu.:  8.398
Median : 54.00   Median :  0   Median : 63.00   Median : 14.100
Mean   : 54.67   Mean   : 21   Mean   : 78.52   Mean   : 15.645
3rd Qu.: 67.00   3rd Qu.: 41   3rd Qu.:115.00   3rd Qu.: 20.049
Max.   :147.00   Max.   :100   Max.   :259.00   Max.   :192.000

     hrt1            resp1            temp1           pafi1
Min.   :  0.0   Min.   :  0.00   Min.   :27.00   Min.   : 11.6
1st Qu.: 97.0   1st Qu.: 14.00   1st Qu.:36.09   1st Qu.:133.3
Median :124.0   Median : 30.00   Median :38.09   Median :202.5
```

```
Mean   :115.2   Mean   : 28.09   Mean   :37.62   Mean   :222.3
3rd Qu.:141.0   3rd Qu.: 38.00   3rd Qu.:39.00   3rd Qu.:316.6
Max.   :250.0   Max.   :100.00   Max.   :43.00   Max.   :937.5

     alb1            hema1           bili1              crea1
Min.   : 0.300   Min.   : 2.00   Min.   : 0.09999   Min.   : 0.09999
1st Qu.: 2.600   1st Qu.:26.10   1st Qu.: 0.79993   1st Qu.: 1.00000
Median : 3.500   Median :30.00   Median : 1.00977   Median : 1.50000
Mean   : 3.093   Mean   :31.87   Mean   : 2.26707   Mean   : 2.13302
3rd Qu.: 3.500   3rd Qu.:36.30   3rd Qu.: 1.39990   3rd Qu.: 2.39990
Max.   :29.000   Max.   :66.19   Max.   :58.19531   Max.   :25.09766

     sod1            pot1            paco21            ph1
Min.   :101.0   Min.   : 1.100   Min.   :  1.00   Min.   :6.579
1st Qu.:132.0   1st Qu.: 3.400   1st Qu.: 31.00   1st Qu.:7.340
Median :136.0   Median : 3.800   Median : 37.00   Median :7.400
Mean   :136.8   Mean   : 4.067   Mean   : 38.75   Mean   :7.388
3rd Qu.:142.0   3rd Qu.: 4.600   3rd Qu.: 42.00   3rd Qu.:7.460
Max.   :178.0   Max.   :11.898   Max.   :156.00   Max.   :7.770

   swang1             wtkilo1          dnr1             ninsclas
Length:5735        Min.   :  0.00   Length:5735        Length:5735
Class :character   1st Qu.: 56.30   Class :character   Class :character
Mode  :character   Median : 70.00   Mode  :character   Mode  :character
                   Mean   : 67.83
                   3rd Qu.: 83.70
                   Max.   :244.00

    resp               card              neuro              gastr
Length:5735        Length:5735        Length:5735        Length:5735
Class :character   Class :character   Class :character   Class :character
Mode  :character   Mode  :character   Mode  :character   Mode  :character

   renal              meta              hema               seps
Length:5735        Length:5735        Length:5735        Length:5735
Class :character   Class :character   Class :character   Class :character
Mode  :character   Mode  :character   Mode  :character   Mode  :character
```

```
   trauma             ortho              adld3p          urin1
Length:5735        Length:5735        Min.   :0.000   Min.   :   0
Class :character   Class :character   1st Qu.:0.000   1st Qu.:1110
Mode  :character   Mode  :character   Median :0.000   Median :1927
                                      Mean   :1.182   Mean   :2192
                                      3rd Qu.:2.000   3rd Qu.:2955
                                      Max.   :7.000   Max.   :9000
                                      NA's   :4296    NA's   :3028
    race               income              ptid
Length:5735        Length:5735        Min.   :    5
Class :character   Class :character   1st Qu.: 2562
Mode  :character   Mode  :character   Median : 5131
                                      Mean   : 5134
                                      3rd Qu.: 7689
                                      Max.   :10278
```

Data Preparation

```r
# Create age group categories from continuous age variable
df$age_group <- cut(df$age,
                    breaks = c(0, 50, 65, 80, 100),
                    labels = c("<50", "50-65", "65-80", "80+"),
                    right = FALSE)

# Convert categorical variables to factors
df$sex <- as.factor(df$sex)
df$cardiohx <- as.factor(df$cardiohx)

# Ensure death is a factor and create numeric binary version (if not already)
df$death <- as.factor(df$death)
df$death_num <- ifelse(df$death == "Yes", 1, 0)

# Select variables and drop rows with any missing values in selected columns
df_clean <- na.omit(df[, c("death", "sex", "age", "age_group", "cardiohx",
                           "death_num", "race", "income", "adld3p",
                           "urin1", "dschdte", "sadmdte")])

# Ensure date columns are in Date or DateTime format
df_clean$dschdte <- as.Date(df_clean$dschdte)
```

```r
df_clean$sadmdte <- as.Date(df_clean$sadmdte)

# Calculate length of stay in days
df_clean$length_of_stay <- as.numeric(df_clean$dschdte - df_clean$sadmdte)

summary(df_clean)
```

```
 death          sex           age         age_group   cardiohx   death_num
 No :365   Female:275   Min.   :18.75   <50  :184   0:471    Min.   :0.0000
 Yes:269   Male  :359   1st Qu.:47.79   50-65:174   1:163    1st Qu.:0.0000
                        Median :63.17   65-80:206            Median :0.0000
                        Mean   :60.03   80+  : 70            Mean   :0.4243
                        3rd Qu.:72.59                        3rd Qu.:1.0000
                        Max.   :95.40                        Max.   :1.0000
    race              income              adld3p          urin1
 Length:634         Length:634         Min.   :0.000   Min.   :   0
 Class :character   Class :character   1st Qu.:0.000   1st Qu.:1335
 Mode  :character   Mode  :character   Median :0.000   Median :2228
                                       Mean   :1.058   Mean   :2451
                                       3rd Qu.:1.000   3rd Qu.:3278
                                       Max.   :7.000   Max.   :9000
   dschdte              sadmdte           length_of_stay
 Min.   :2002-01-10   Min.   :2002-01-07   Min.   :  2.00
 1st Qu.:2002-07-31   1st Qu.:2002-07-15   1st Qu.:  7.00
 Median :2003-01-01   Median :2002-12-14   Median : 11.00
 Mean   :2003-01-13   Mean   :2002-12-30   Mean   : 14.89
 3rd Qu.:2003-07-06   3rd Qu.:2003-06-13   3rd Qu.: 17.00
 Max.   :2004-03-05   Max.   :2004-01-24   Max.   :107.00
```

Assumption Checking Before ANOVA

1. **Independence**

Assumed by study design (random sampling or independent subjects).
No formal test—assume valid if no clustering/repeated measures.

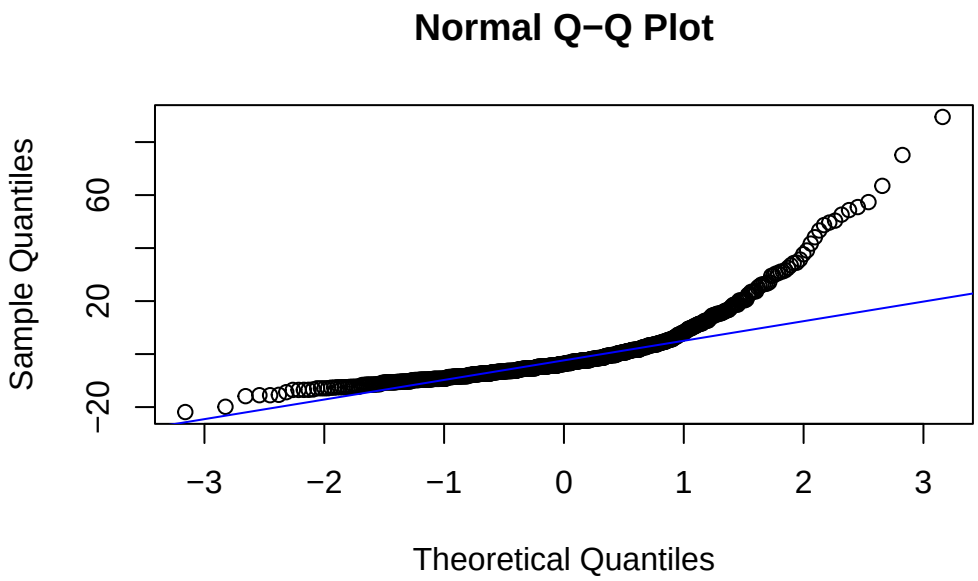
2. **Normality of Residuals**

```r
# Fit the model:
anova_model <- aov(length_of_stay ~ sex * age_group * cardiohx, data = df_clean)
# Check residual normality:
```

```r
resid_anova <- residuals(anova_model)
shapiro.test(resid_anova)
```

```
    Shapiro-Wilk normality test

data:  resid_anova
W = 0.76042, p-value < 2.2e-16
```

```r
qqnorm(resid_anova)
qqline(resid_anova, col = "blue")
```



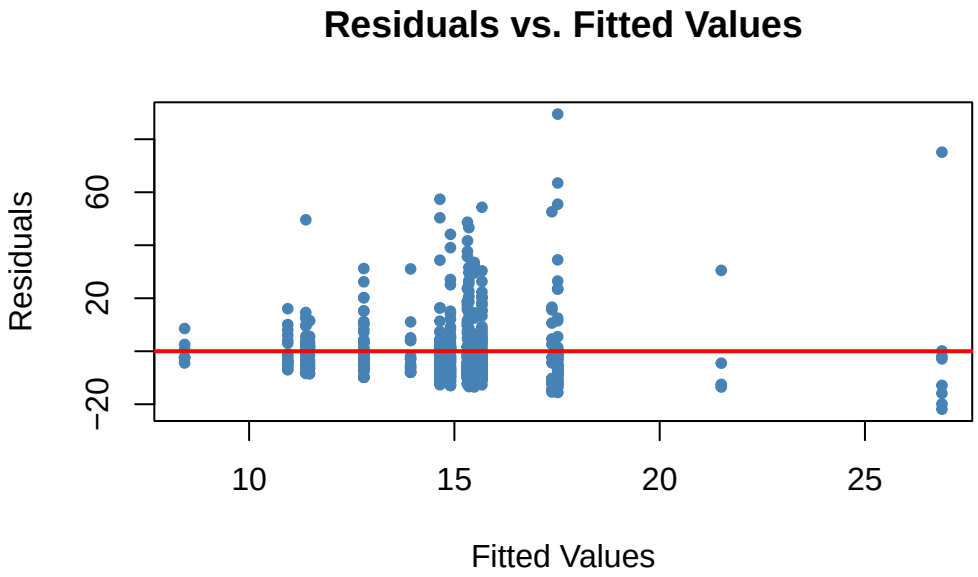
Since $p < 0.05$ **Normality of Residuals** is violated → Consider **transformation (e.g., log, sqrt) or** Logistic Regression

3. **Equal Variance**

```r
# Levene's Test
library(car)
leveneTest(resid_anova ~ interaction(sex, age_group, cardiohx), data = df_clean)
```

```
Levene's Test for Homogeneity of Variance (center = median)
       Df F value Pr(>F)
group  15  1.3023 0.1948
      618
```

```r
# Fit the ANOVA model
anova_model <- aov(length_of_stay ~ sex * age_group * cardiohx, data = df_clean)

# Extract residuals and fitted values
resid_anova <- residuals(anova_model)
fitted_anova <- fitted(anova_model)

# Plot: Residuals vs. Fitted Values
plot(fitted_anova, resid_anova,
     xlab = "Fitted Values",
     ylab = "Residuals",
     main = "Residuals vs. Fitted Values",
     pch = 20,
     col = "steelblue")
abline(h = 0, col = "red", lwd = 2)
```



Interpretation:

Levene p $> 0.05 \rightarrow$ Variances are **equal**

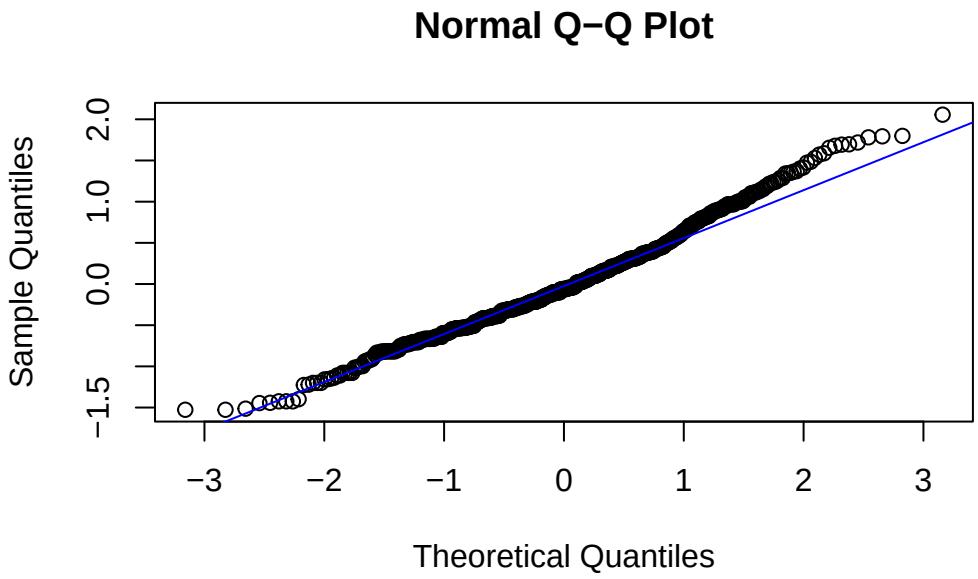
Plot: Look for random scatter around 0 (no funnel pattern)

Option 1: Log Transformation

```r
# Add a small constant to avoid log(0), if needed
df_clean$log_los <- log(df_clean$length_of_stay + 1)

# Fit the model using log-transformed outcome
anova_model_log <- aov(log_los ~ sex * age_group * cardiohx, data = df_clean)

# Check residuals again
resid_log <- residuals(anova_model_log)
shapiro.test(resid_log)
```

```
    Shapiro-Wilk normality test

data:  resid_log
W = 0.98635, p-value = 1.199e-05
```

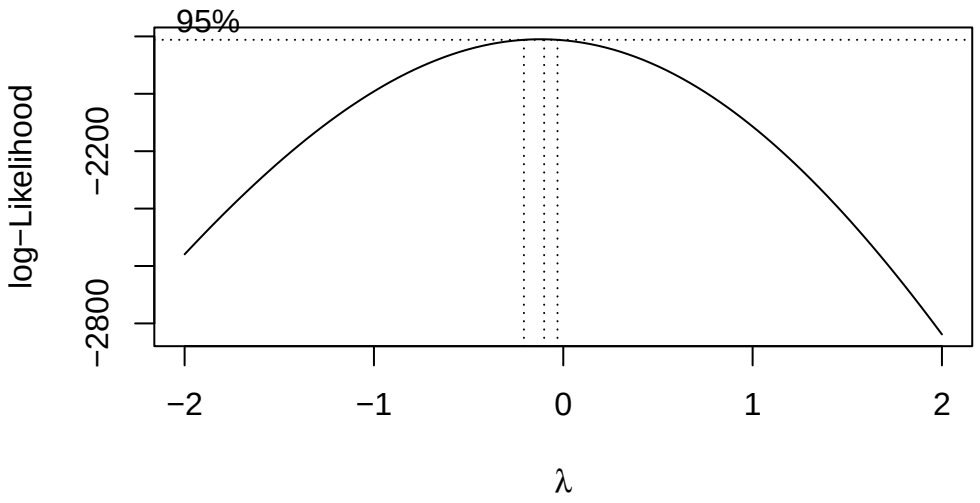
```r
qqnorm(resid_log)
qqline(resid_log, col = "blue")
```



Option 2: Box-Cox Transformation

```r
# Use lm instead of aov for Box-Cox compatibility
library(MASS)
lm_model <- lm(length_of_stay ~  sex * age_group * cardiohx, data = df_clean)

# Apply Box-Cox transformation
boxcox_result <- boxcox(lm_model, lambda = seq(-2, 2, 0.1),
                        main = "Box-Cox Transformation")
```

```
Warning: In lm.fit(x, y, offset = offset, singular.ok = singular.ok, ...) :
 extra argument 'main' will be disregarded
```




```r
# Find optimal lambda
best_lambda <- boxcox_result$x[which.max(boxcox_result$y)]
best_lambda
```

```
[1] -0.1010101
```

Since `lambda` 0, then **log transformation** is best.

check if the design is balanced

```r
table(df_clean$sex, df_clean$age_group, df_clean$cardiohx)
```

```
, ,  = 0


        <50 50-65 65-80 80+
  Female  73    63    62  31
  Male    91    51    85  15

, ,  = 1


        <50 50-65 65-80 80+
  Female   4     8    17  17
  Male    16    52    42   7
```

Since this variability clearly indicates an **unbalanced design**, type II ANOVA is better suited.

1. Three-Way Type II ANOVA: Effects of Sex, Age Group, and Cardiac History on Hospital Length of Stay (Full Model)

```r
library(car)

# Log-transform length_of_stay (add 1 to avoid log(0))
df_clean$log_los <- log(df_clean$length_of_stay + 1)

# Fit the Type II ANOVA model (three-way design) using log-transformed length of stay
lm_full <- lm(log_los ~ sex * age_group * cardiohx, data = df_clean)
Anova(lm_full, type = 2)
```

```
Anova Table (Type II tests)

Response: log_los
                       Sum Sq  Df F value  Pr(>F)
sex                     0.216   1  0.5269 0.46817
age_group               0.767   3  0.6224 0.60073
cardiohx                1.120   1  2.7271 0.09916 .
sex:age_group           0.102   3  0.0827 0.96945
sex:cardiohx            0.786   1  1.9129 0.16714
age_group:cardiohx      4.064   3  3.2988 0.02011 *
sex:age_group:cardiohx  0.716   3  0.5813 0.62747
```

```
Residuals              253.799 618
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Key Findings (Full Model, Type II ANOVA):

The Type II ANOVA model, fitted using the log-transformed hospital length of stay, revealed that most main effects and two-way interactions were not statistically significant. Specifically, sex ($p = 0.468$), age group ($p = 0.601$), and cardiac history ($p = 0.099$) did not individually predict length of stay, nor did their respective two-way interactions involving sex.

The only statistically significant effect was the interaction between age group and cardiac history ($F(3, 618) = 3.30$, $p = 0.020$), indicating that the influence of cardiac history on hospital length of stay differs depending on the patient's age group. The three-way interaction among sex, age group, and cardiac history was not significant ($p = 0.627$), suggesting no combined effect across all three variables.

These results validate the choice to proceed with a reduced model focusing on age group and cardiac history, as sex and higher-order interactions did not contribute meaningfully to the explanation of variation in hospital length of stay.

2. Two-Way Type II ANOVA for Age Group × Cardiac History (Reduced Model)

Since the **three-way type II ANOVA** showed that only the **interaction between age group and cardiac history** is significant, it's appropriate to fit a **reduced Two-Way Type II ANOVA model** including just those two variables and their interaction.

```r
# Fit the Type II ANOVA model (two-way design) using log-transformed length of stay
lm_reduced <- lm(log_los ~ age_group * cardiohx, data = df_clean)
Anova(lm_reduced, type = 2)
```

```
Anova Table (Type II tests)

Response: log_los
                    Sum Sq  Df F value  Pr(>F)
age_group            0.667   3  0.5447 0.65189
cardiohx             1.152   1  2.8206 0.09356 .
age_group:cardiohx   3.441   3  2.8097 0.03879 *
Residuals          255.576 626
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Key Findings (Reduced Model, Type II ANOVA):

In the reduced two-way ANOVA model using log-transformed hospital length of stay as the response variable, neither age group ($p = 0.652$) nor cardiac history ($p = 0.094$) demonstrated a significant main effect. However, the interaction between age group and cardiac history was statistically significant ($F(3, 626) = 2.81$, $p = 0.0388$).

This result indicates that the impact of cardiac history on hospital length of stay differs across age groups, or conversely, that the effect of age group on length of stay varies depending on whether or not the patient has a history of cardiovascular disease. The lack of main effects alongside a significant interaction suggests that the two variables do not independently influence length of stay but instead **interact** to shape outcomes in a joint and context-dependent manner.

ANOVA model comparison

```
anova(lm_reduced, lm_full)
```

```
Analysis of Variance Table

Model 1: log_los ~ age_group * cardiohx
Model 2: log_los ~ sex * age_group * cardiohx
  Res.Df    RSS Df Sum of Sq     F Pr(>F)
1    626 255.58
2    618 253.80  8    1.7773 0.541 0.8258
```

This test if the reduced model provides a **significantly better fit** than the full odel. Since the p-value is **not significant** and Residual Sum of Squares (RSS) barely changed, then the **reduced model is sufficient**.

AIC/ BIC Comparison

```
# Compare AIC values
AIC(lm_reduced, lm_full)
```

```
           df      AIC
lm_reduced  9 1241.207
lm_full    17 1252.783
```

```r
# Compare BIC values
BIC(lm_reduced, lm_full)
```

```
           df      BIC
lm_reduced  9 1281.276
lm_full    17 1328.468
```

Interpretation of AIC/ BIC comparisons:

The reduced model (which includes only age group, cardiac history, and their interaction) has a lower AIC than the full model by **11.57 points**. A difference in AIC greater than 10 is considered **strong evidence** in favor of the simpler model. Based on this AIC comparison, the reduced model is **strongly preferred** over the full model. Removing the non-significant terms involving sex improves **model parsimony** without sacrificing model performance.

Similarly, the **Bayesian Information Criterion (BIC)** further supports this conclusion. The reduced model has a BIC of **1281.28**, while the full model's BIC is **1328.47**, yielding a difference of over **47 points**. Since BIC penalizes model complexity more heavily than AIC, this substantial gap provides **very strong evidence** that the reduced model offers a more efficient and generalizable fit.

Model Comparison Table

(these are linear models with a log-transformed response)

Model	Residual DF	Residual SS	AIC	BIC	Nested ANOVA p-value
Full Model	618	253.80	1252.78	1328.47	0.8258
Reduced Model	626	255.58	1241.21	1281.28	—

Model Decision:

The **reduced model** (including only age group, cardiac history, and their interaction) is preferred. It has **lower AIC and BIC values**, and the **ANOVA comparison** shows no significant loss of fit when the non-significant sex-related terms are removed (nested ANOVA

p-value = 0.8258).

Tukey HSD Post-Hoc Analysis of Age Groups on Hospital Length of Stay

based on reduced model:

```
# Fit one-way ANOVA on log-transformed outcome by age_group
anova_age <- aov(log_los ~ age_group, data = df_clean)

# Tukey HSD post-hoc test
TukeyHSD(anova_age)
```

```
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = log_los ~ age_group, data = df_clean)

$age_group
                    diff        lwr        upr     p adj
50-65-<50    -0.08350586 -0.2585489 0.09153719 0.6087007
65-80-<50    -0.06099560 -0.2289056 0.10691444 0.7856357
80+-<50      -0.13245221 -0.3649109 0.10000649 0.4577271
65-80-50-65   0.02251026 -0.1479293 0.19294983 0.9864422
80+-50-65    -0.04894635 -0.2832387 0.18534602 0.9496878
80+-65-80    -0.07145661 -0.3004689 0.15755568 0.8526800
```

Conclusion:

There is **no evidence** that hospital length of stay differs significantly by age group based on Tukey's multiple comparisons. All group differences were small and not statistically meaningful.

We run **separate ANOVAs within levels** of `cardiohx` or `age_group` and then do Tukey on `age_group` inside each subgroup.

Tukey HSD Post-Hoc Analysis: Age Group Differences in Length of Stay Among Patients With Cardiac History

based on reduced model:

```r
library(emmeans)
```

```
Welcome to emmeans.
Caution: You lose important information if you filter this package's results.
See '? untidy'
```

```r
# Post-hoc comparisons of age_group within each level of cardiac history
emmeans(lm_reduced, pairwise ~ age_group | cardiohx, adjust = "tukey")
```

```
$emmeans
cardiohx = 0:
 age_group emmean     SE  df lower.CL upper.CL
 <50         2.60 0.0499 626     2.50     2.69
 50-65       2.48 0.0598 626     2.36     2.60
 65-80       2.62 0.0527 626     2.51     2.72
 80+         2.54 0.0942 626     2.36     2.73

cardiohx = 1:
 age_group emmean     SE  df lower.CL upper.CL
 <50         2.60 0.1430 626     2.32     2.88
 50-65       2.58 0.0825 626     2.42     2.74
 65-80       2.33 0.0832 626     2.17     2.50
 80+         2.32 0.1300 626     2.06     2.57

Confidence level used: 0.95

$contrasts
cardiohx = 0:
 contrast          estimate     SE  df t.ratio p.value
 <50 - (50-65)       0.1168 0.0779 626   1.499  0.4385
 <50 - (65-80)      -0.0215 0.0726 626  -0.296  0.9910
 <50 - (80+)         0.0552 0.1070 626   0.518  0.9547
 (50-65) - (65-80)  -0.1383 0.0797 626  -1.734  0.3069
 (50-65) - (80+)    -0.0616 0.1120 626  -0.552  0.9461
 (65-80) - (80+)     0.0767 0.1080 626   0.710  0.8929

cardiohx = 1:
 contrast          estimate     SE  df t.ratio p.value
 <50 - (50-65)       0.0251 0.1650 626   0.152  0.9987
 <50 - (65-80)       0.2709 0.1650 626   1.639  0.3577
 <50 - (80+)         0.2854 0.1930 626   1.475  0.4532
```

```
 (50-65) - (65-80)   0.2458 0.1170 626   2.098  0.1549
 (50-65) - (80+)     0.2602 0.1540 626   1.686  0.3318
 (65-80) - (80+)     0.0145 0.1550 626   0.093  0.9997

P value adjustment: tukey method for comparing a family of 4 estimates
```

Post-Hoc Comparison Conclusion (Based on Reduced Model)

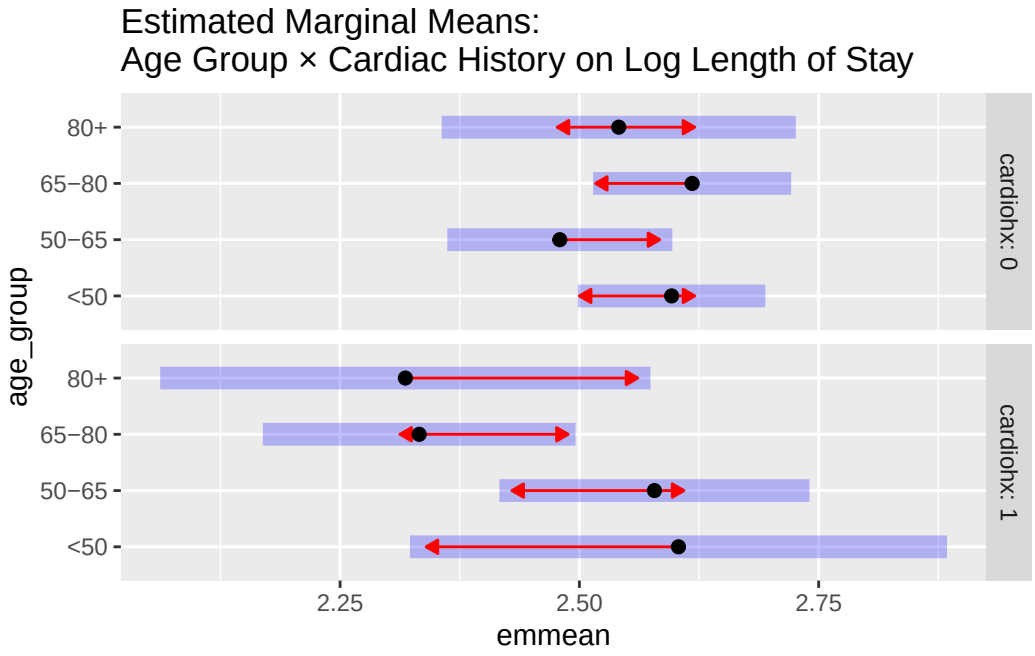
Post-hoc comparisons of age group within each level of cardiac history were conducted using estimated marginal means with Tukey adjustment. In both subgroups—patients with and without a history of cardiovascular disease—no statistically significant pairwise differences were observed between age groups at the 0.05 significance level.

Among patients without cardiac history, mean log-transformed length of stay values ranged from 2.48 to 2.62 across age groups, with all pairwise comparisons yielding adjusted p-values above 0.30. Similarly, in patients with cardiac history, estimated means ranged from 2.32 to 2.60, and none of the age group contrasts reached statistical significance. Although patients aged 65–80 and 80+ with cardiac history exhibited lower average hospitalization durations, these differences were not statistically significant after multiple comparison adjustment.

These results suggest that **age group alone did not significantly influence hospital length of stay** within either cardiac history stratum, despite the overall interaction between age group and cardiac history being statistically significant in the main model.

Plot of model-adjusted means and confidence intervals

```r
library(emmeans)
library(ggplot2)

# Generate estimated marginal means
emm <- emmeans(lm_reduced, ~ age_group * cardiohx)

# Create ggplot object
emm_plot <- plot(emm, comparisons = TRUE, by = "cardiohx")

# Add a custom title
emm_plot + ggtitle("Estimated Marginal Means:\nAge Group × Cardiac History on Log Length of S
```



Interpretation:

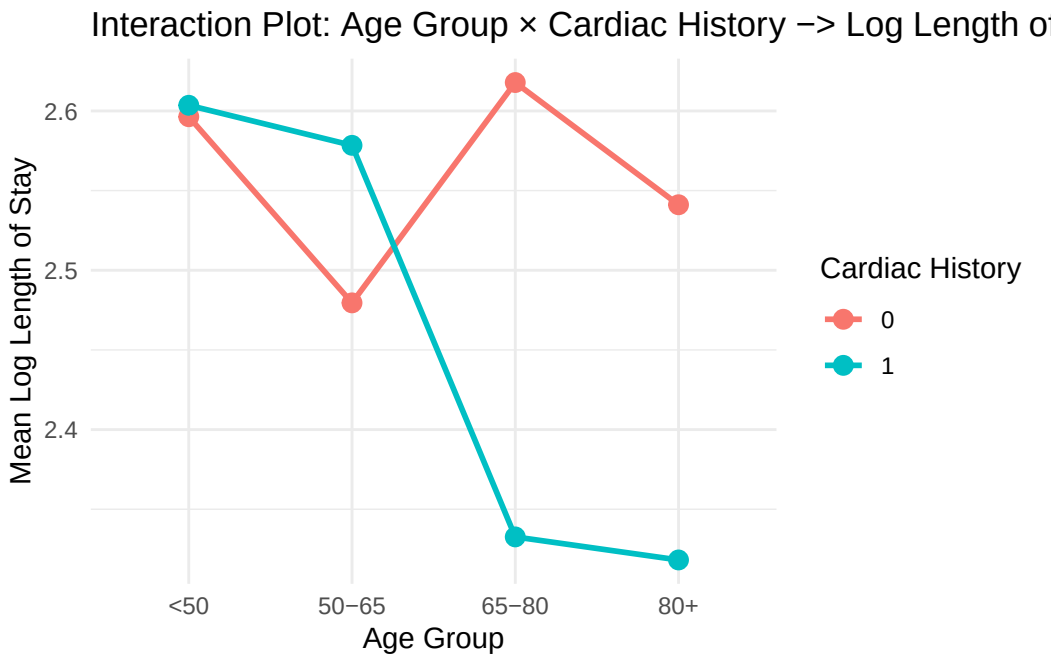
This plot displays the estimated marginal means of log-transformed hospital length of stay across age groups, stratified by cardiac history. While the differences between age groups are not statistically significant after Tukey adjustment (as shown by overlapping confidence intervals), the pattern varies by cardiac history status:

- **For patients without cardiac history (cardiohx = 0):** Mean log length of stay is relatively stable across age groups, with minor fluctuations.
- **For patients with cardiac history (cardiohx = 1):** There is a visible decrease in mean log length of stay from younger to older age groups, suggesting a potential trend where older patients with cardiac history are discharged sooner.

These trends visually support the **significant interaction** found in the ANOVA, indicating that the effect of age group on length of stay depends on cardiac history status—even if no specific age group pair reaches significance in post-hoc comparisons.

Interaction Plot for Age Group × Cardiac History → Length of Stay

```r
library(dplyr)
library(ggplot2)

# Summarize log-transformed mean length of stay by age group and cardiac history
plot_data <- df_clean %>%
  group_by(age_group, cardiohx) %>%
  summarise(mean_log_los = mean(log_los, na.rm = TRUE), .groups = "drop")

# Plot interaction
ggplot(plot_data, aes(x = age_group, y = mean_log_los, color = cardiohx, group = cardiohx)) +
  geom_point(size = 3) +
  geom_line(linewidth = 1) +
  labs(
    title = "Interaction Plot: Age Group × Cardiac History → Log Length of Stay",
    x = "Age Group",
    y = "Mean Log Length of Stay",
    color = "Cardiac History"
  ) +
  theme_minimal()
```



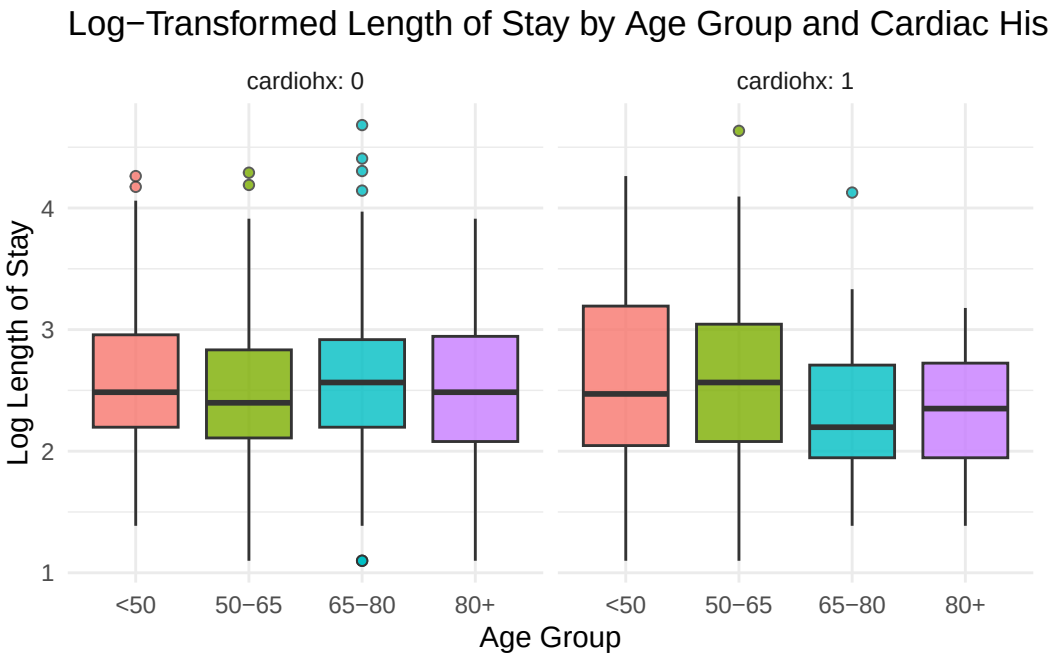
Interpretation of Interaction Plot:

The plot illustrates a **statistically significant interaction** between **age group** and **cardiac history** ($p = 0.0388$), indicating that the effect of age on hospital length of stay depends on whether the patient has a history of cardiovascular disease.

- For patients **without cardiac history** (red line), length of stay is relatively stable but peaks in the **65–80** age group.
- For patients **with cardiac history** (blue line), length of stay **decreases sharply with age**, especially after 50–65.
- This crossover pattern supports a meaningful interaction: the direction and strength of the age effect **differs by cardiac history group**.

Boxplot for Age Group × Cardiac History

```
library(ggplot2)

ggplot(df_clean, aes(x = age_group, y = log_los, fill = age_group)) +
  geom_boxplot(outlier.shape = 21, outlier.size = 1.5, alpha = 0.8) +
  facet_wrap(~ cardiohx, labeller = label_both) +
  labs(
    title = "Log-Transformed Length of Stay by Age Group and Cardiac History",
    x = "Age Group",
    y = "Log Length of Stay"
  ) +
  theme_minimal() +
  theme(legend.position = "none")
```



Log Length of Stay by Age Group and Cardiac History:

This plot reveals that patients with a history of cardiovascular disease (right panel) generally show a **steeper decline** in length of stay with increasing age, particularly in the 65–80 group. In contrast, patients **without cardiac history** (left panel) exhibit **more stable median lengths of stay** across age groups, with slightly elevated values in the <50 and 65–80 categories. The variability (IQR and outliers) appears wider in some younger groups, especially for those without cardiac history.

Final Conclusion

This study utilized the Right Heart Catheterization (RHC) dataset from the SUPPORT study to investigate how age group and cardiac history influence hospital length of stay among critically ill patients. After verifying ANOVA assumptions and applying a log transformation to correct for skewness, a three-way ANOVA model was initially fitted including sex, age group, and cardiac history. However, model comparison via Type II ANOVA and information criteria (AIC and BIC) revealed that a reduced two-way ANOVA model — including only age group, cardiac history, and their interaction — offered equivalent or better model fit with greater parsimony.

Type II ANOVA was chosen instead of the traditional (Type I) approach because the study design is unbalanced, meaning that group sizes vary across the combinations of sex, age group, and cardiac history. Type II ANOVA provides more accurate tests of main effects and interactions in such settings by accounting for the unequal distribution of observations.

The reduced Type II ANOVA model identified a statistically significant interaction between age group and cardiac history ($p = 0.0388$), indicating that the effect of age on length of stay depends on cardiac history status. Specifically, length of stay decreased with age among patients with cardiac history, while those without cardiac history showed relatively stable or increasing patterns in older age groups. These trends were confirmed through interaction plots and supported by Tukey HSD post-hoc comparisons, although no pairwise differences were statistically significant.

To better visualize these results, a plot of model-adjusted means and confidence intervals was generated using the estimated marginal means from the reduced model. This visualization clearly displayed the pattern of log-transformed length of stay across age groups and cardiac history strata, aligning with the statistical findings and highlighting the nature of the interaction effect.

Visualizations, including boxplots and interaction plots, further illustrated this interaction. While sex did not contribute significantly to explaining variation in length of stay, the age group $\times$ cardiac history interaction emerged as a meaningful and interpretable driver of variation in hospital resource use.

In summary, this study concludes that the interaction between age group and cardiac history significantly affects hospital length of stay. A reduced two-way Type II ANOVA model provides a more efficient and statistically supported explanation than a full model including sex. These findings highlight the importance of considering both age and comorbid conditions when analyzing healthcare utilization in critical care populations.
