MA500HW8

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Question 2

```r
treatment <- factor(c(1,2,3,4))
flowers <- c("Rose", "Carnation", "Daisy", "Tulip")
temps <- c("Cold", "Medium", "Warm")

block_combinations <- expand.grid(Flower = flowers, Temp = temps)
randomized_plan <- do.call(rbind, lapply(1:nrow(block_combinations), function(i) {
  t <- sample(treatment)
  data.frame(
    Flower = block_combinations$Flower[i],
    Temp = block_combinations$Temp[i],
    FlowerNumber = 1:4,
    Treatment = t
  )
}))
write.csv(randomized_plan, "TwoBlockRCBPlan.csv", row.names = FALSE)


head(randomized_plan)
```

```
##       Flower Temp FlowerNumber Treatment
## 1       Rose Cold            1         4
## 2       Rose Cold            2         1
## 3       Rose Cold            3         3
## 4       Rose Cold            4         2
## 5  Carnation Cold            1         3
## 6  Carnation Cold            2         4
```

Question 6

```r
# Create the data
Patient <- rep(1:5, each = 5)
Week <- rep(1:5, times = 5)
Treatment <- c("B", "E", "A", "C", "D",
               "D", "A", "E", "B", "C",
               "E", "B", "C", "D", "A",
```

```r
                "A", "C", "D", "E", "B",
                "C", "D", "B", "A", "E")

Score <- c(2.92, 2.43, 2.19, 2.71, 2.71,
           2.86, 1.64, 3.02, 3.03, 3.03,
           1.97, 2.50, 2.47, 2.65, 1.89,
           1.99, 2.39, 2.37, 2.33, 2.71,
           2.64, 2.31, 2.44, 1.89, 2.78)

sleep_data <- data.frame(Patient = factor(Patient),
                         Week = factor(Week),
                         Treatment = factor(Treatment),
                         Score = Score)
```

```r
# Fit the Latin Square ANOVA model
model <- aov(Score ~ Treatment + Patient + Week, data = sleep_data)

summary(model)
```

(b)

```
##             Df Sum Sq Mean Sq F value  Pr(>F)
## Treatment    4 2.0498  0.5125  10.725 0.00062 ***
## Patient      4 0.6073  0.1518   3.178 0.05358 .
## Week         4 0.3689  0.0922   1.930 0.17000
## Residuals   12 0.5734  0.0478
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Define contrast: A vs. average of B, C, D, E
contrast_matrix <- rbind("Placebo vs Others" = c(1, -0.25, -0.25, -0.25, -0.25))
glht_test <- glht(model, linfct = mcp(Treatment = contrast_matrix))
summary(glht_test)
```

(c)

```
##
##    Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: User-defined Contrasts
##
##
## Fit: aov(formula = Score ~ Treatment + Patient + Week, data = sleep_data)
##
## Linear Hypotheses:
##                     Estimate Std. Error t value Pr(>|t|)
## Placebo vs Others == 0  -0.6935     0.1093  -6.345 3.69e-05 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```r
# Subset data to exclude placebo (A)
drug_data <- subset(sleep_data, Treatment != "A")

# Refit model
drug_model <- aov(Score ~ Treatment + Patient + Week, data = drug_data)

# Pairwise comparison among B, C, D, E
TukeyHSD(drug_model, "Treatment")
```
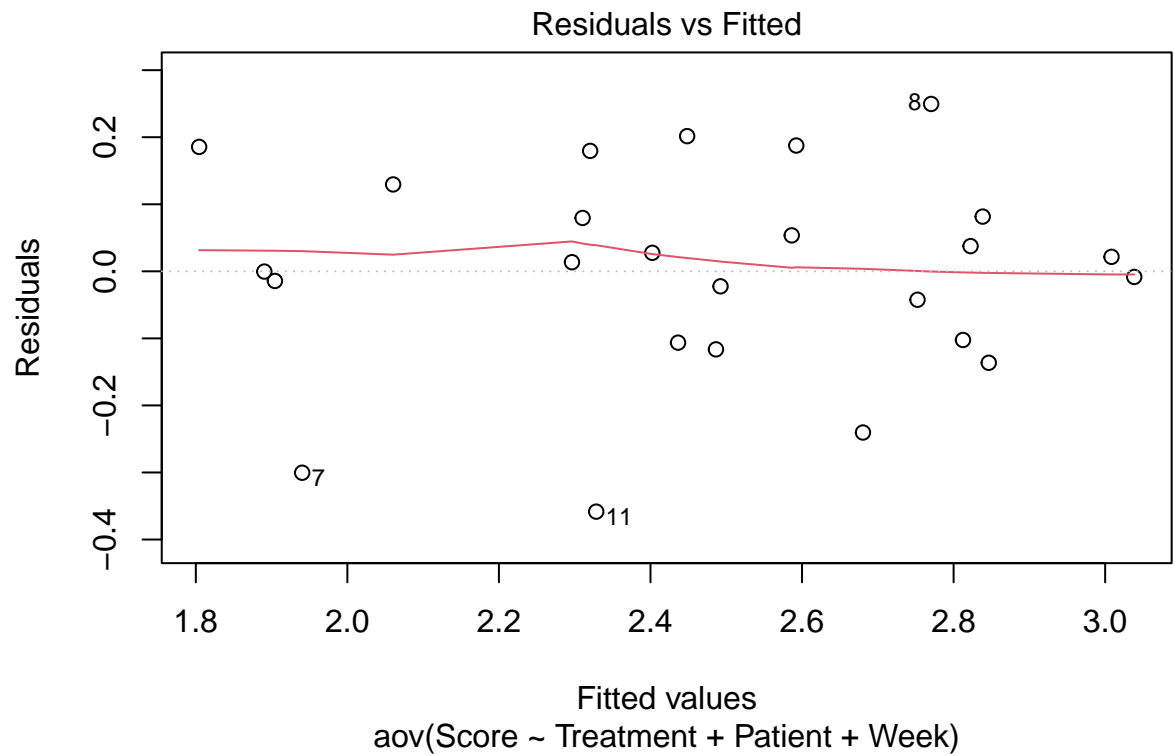
```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = Score ~ Treatment + Patient + Week, data = drug_data)
##
## $Treatment
##        diff        lwr       upr     p adj
## C-B -0.072 -0.4878128 0.3438128 0.9427121
## D-B -0.140 -0.5558128 0.2758128 0.7114739
## E-B -0.214 -0.6298128 0.2018128 0.4069492
## D-C -0.068 -0.4838128 0.3478128 0.9509577
## E-C -0.142 -0.5578128 0.2738128 0.7029836
## E-D -0.074 -0.4898128 0.3418128 0.9383205
```
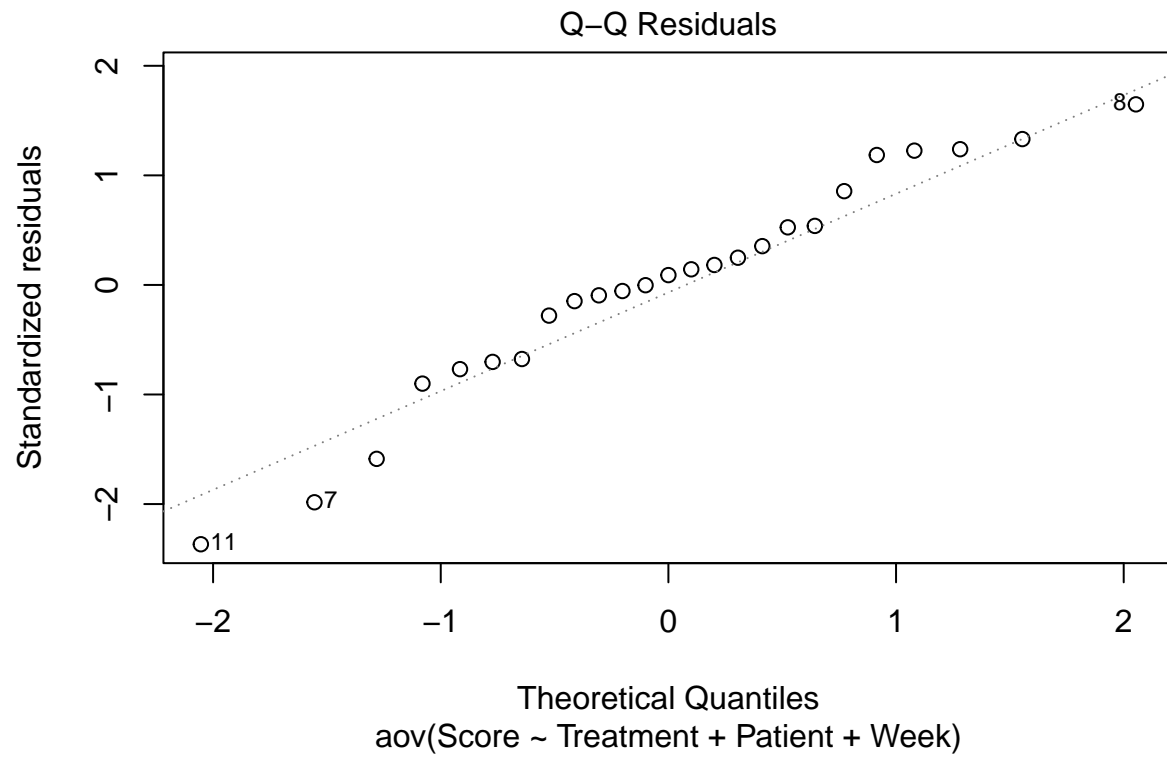
```r
model <- aov(Score ~ Treatment + Patient + Week, data = sleep_data)

# 1. Residuals vs Fitted
plot(model, which = 1)
```
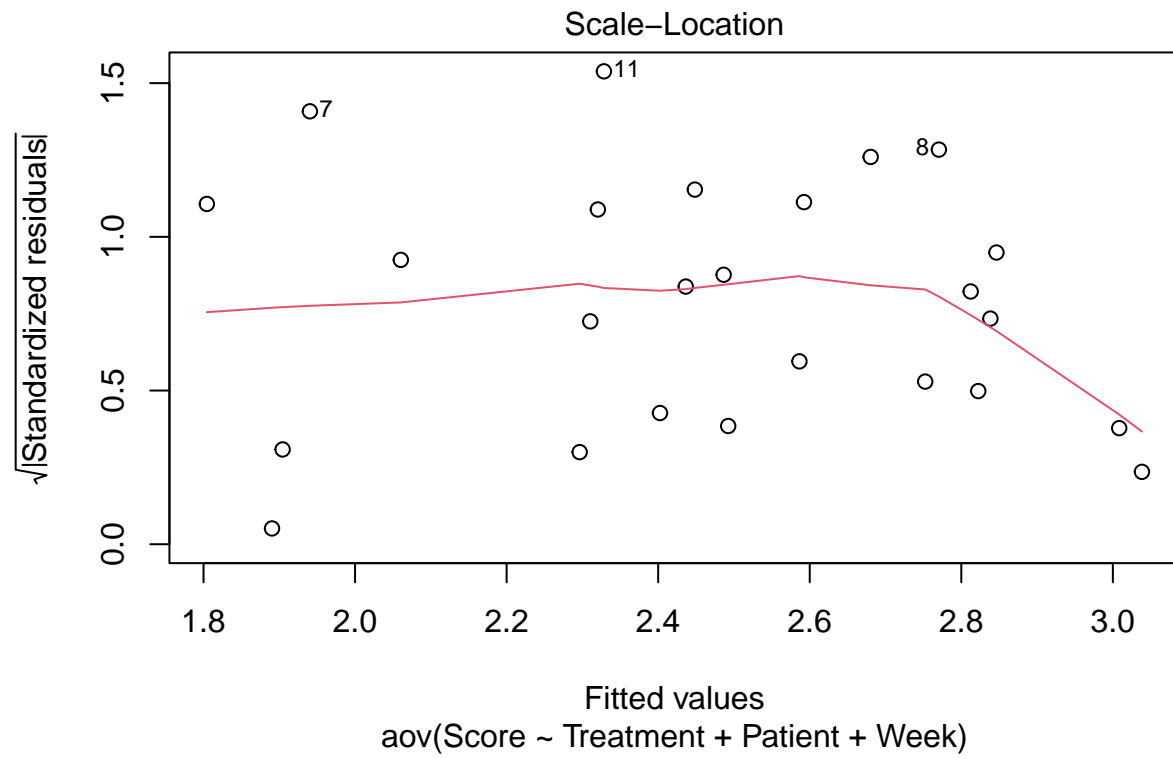
**Residuals vs Fitted**

Residuals (y-axis): 0.2, 0.0, −0.2, −0.4

Fitted values: 1.8, 2.0, 2.2, 2.4, 2.6, 2.8, 3.0

aov(Score ~ Treatment + Patient + Week)

(d)

```
# 2. Normal Q-Q plot
plot(model, which = 2)
```

Q–Q Residuals

Theoretical Quantiles
aov(Score ~ Treatment + Patient + Week)

```r
# 3. Scale-Location plot
plot(model, which = 3)
```

Scale–Location

Fitted values
aov(Score ~ Treatment + Patient + Week)

```r
# 4. Residuals vs Leverage
plot(model, which = 5)
```

Constant Leverage:
Residuals vs Factor Levels
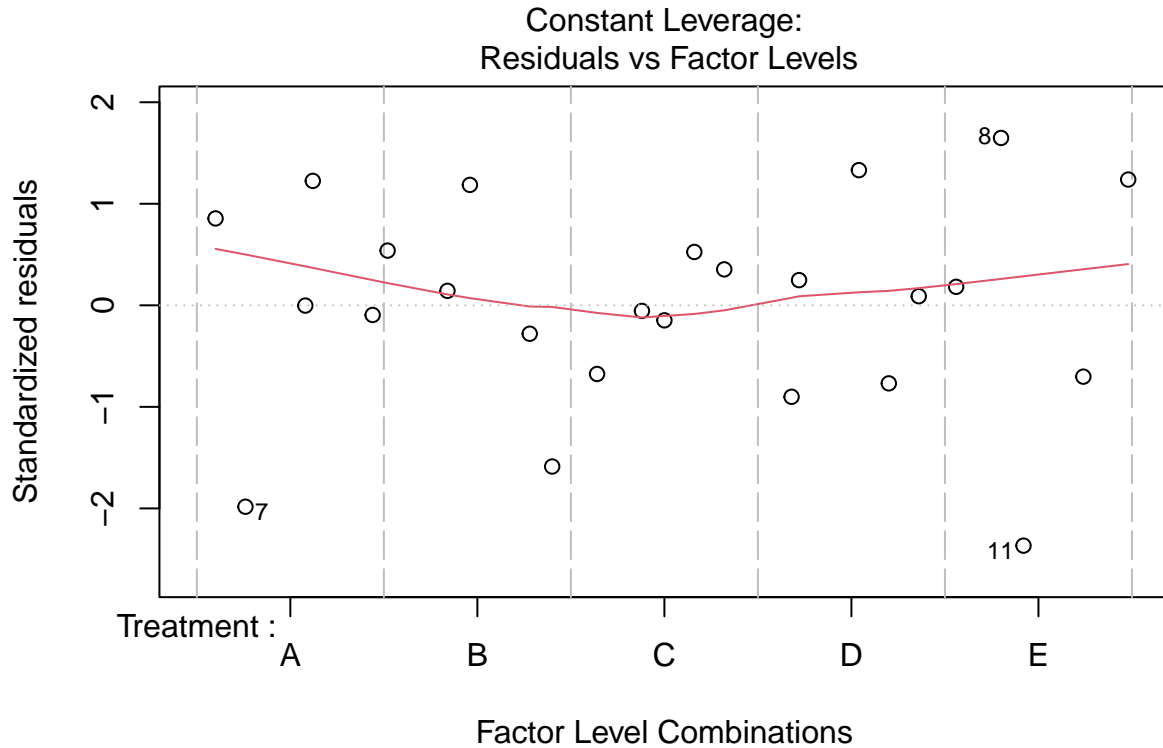
Question 8

```r
# Exercise 6 Chapter 2
rmin <- 2          # min number of replicates to try
rmax <- 10         # max number of replicates to try
alpha <- rep(0.05, rmax - rmin + 1)   # significance level
nlev <- 4          # number of treatment levels
nreps <- rmin:rmax   # replicates to consider

Delta <- 2         # Delta = 2\sigma
sigma <- 1         # Set sigma = 1 for simplicity; Delta is in units of sigma

power <- Fpower1(alpha, nlev, nreps, Delta, sigma)
power
```

```
##       alpha nlev nreps Delta sigma      power
## [1,]  0.05    4     2     2     1 0.1698028
## [2,]  0.05    4     3     2     1 0.3390584
## [3,]  0.05    4     4     2     1 0.5037050
## [4,]  0.05    4     5     2     1 0.6442332
## [5,]  0.05    4     6     2     1 0.7545861
## [6,]  0.05    4     7     2     1 0.8361289
## [7,]  0.05    4     8     2     1 0.8935978
## [8,]  0.05    4     9     2     1 0.9325774
```

```
## [9,]  0.05    4    10    2    1 0.9581855
```

```
# Question 8 (b)
sigma <- sqrt(0.4)
nlev <- 4
nreps <- 4
Delta <- 2
alpha <- 0.05
Fpower1(alpha, nlev, nreps, Delta, sigma)
```

```
##       alpha nlev nreps Delta    sigma      power
## [1,]  0.05    4    4    2 0.6324555 0.9027768
```