BB503/BB602 - R Training - Week VIII

Ege Ulgen

Analysis of Variance (ANOVA)

We'll work on the diet data from last week. Remember there are 3 different diets:

```
diet_df <- read.csv("../data/Diet_R.csv")

head(diet_df)
```

```
##   Person gender Age Height pre.weight Diet weight6weeks
## 1     25     NA  41    171         60    2         60.0
## 2     26     NA  32    174        103    2        103.0
## 3      1      0  22    159         58    1         54.2
## 4      2      0  46    192         60    1         54.0
## 5      3      0  55    170         64    1         63.3
## 6      4      0  33    171         64    1         61.1
```

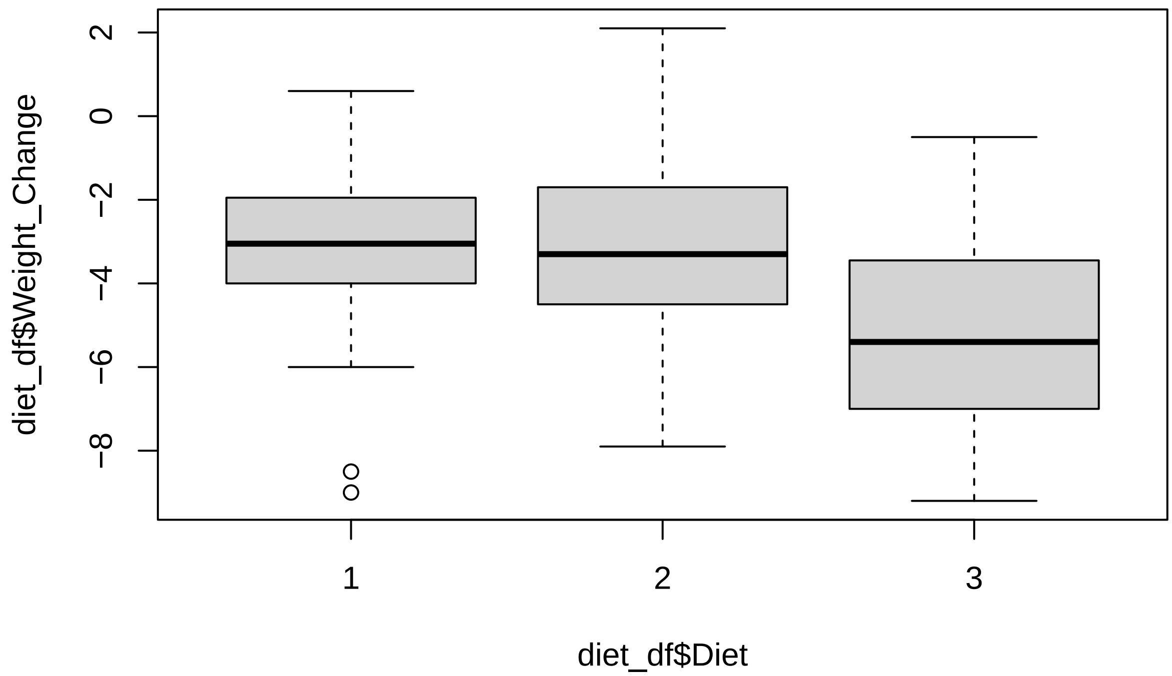
```
# turn categorical variables into factor
diet_df$Diet <- as.factor(diet_df$Diet)
diet_df$gender <- as.factor(diet_df$gender)

# create new variable
diet_df$Weight_Change <- diet_df$weight6weeks - diet_df$pre.weight

summary(diet_df)
```

```
##      Person      gender        Age           Height      pre.weight    Diet
##  Min.   : 1.0   0   :43   Min.   :16.0   Min.   :141   Min.   : 58.0   1:24
##  1st Qu.:20.2   1   :33   1st Qu.:32.2   1st Qu.:164   1st Qu.: 66.0   2:27
##  Median :39.5   NA's: 2   Median :39.0   Median :170   Median : 72.0   3:27
##  Mean   :39.5             Mean   :39.2   Mean   :171   Mean   : 72.5
##  3rd Qu.:58.8             3rd Qu.:46.8   3rd Qu.:175   3rd Qu.: 78.0
##  Max.   :78.0             Max.   :60.0   Max.   :201   Max.   :103.0
##   weight6weeks   Weight_Change
##  Min.   : 53.0   Min.   :-9.20
##  1st Qu.: 61.9   1st Qu.:-5.55
##  Median : 69.0   Median :-3.60
##  Mean   : 68.7   Mean   :-3.84
##  3rd Qu.: 73.8   3rd Qu.:-2.00
##  Max.   :103.0   Max.   : 2.10
```

```
boxplot(diet_df$Weight_Change~diet_df$Diet)
```

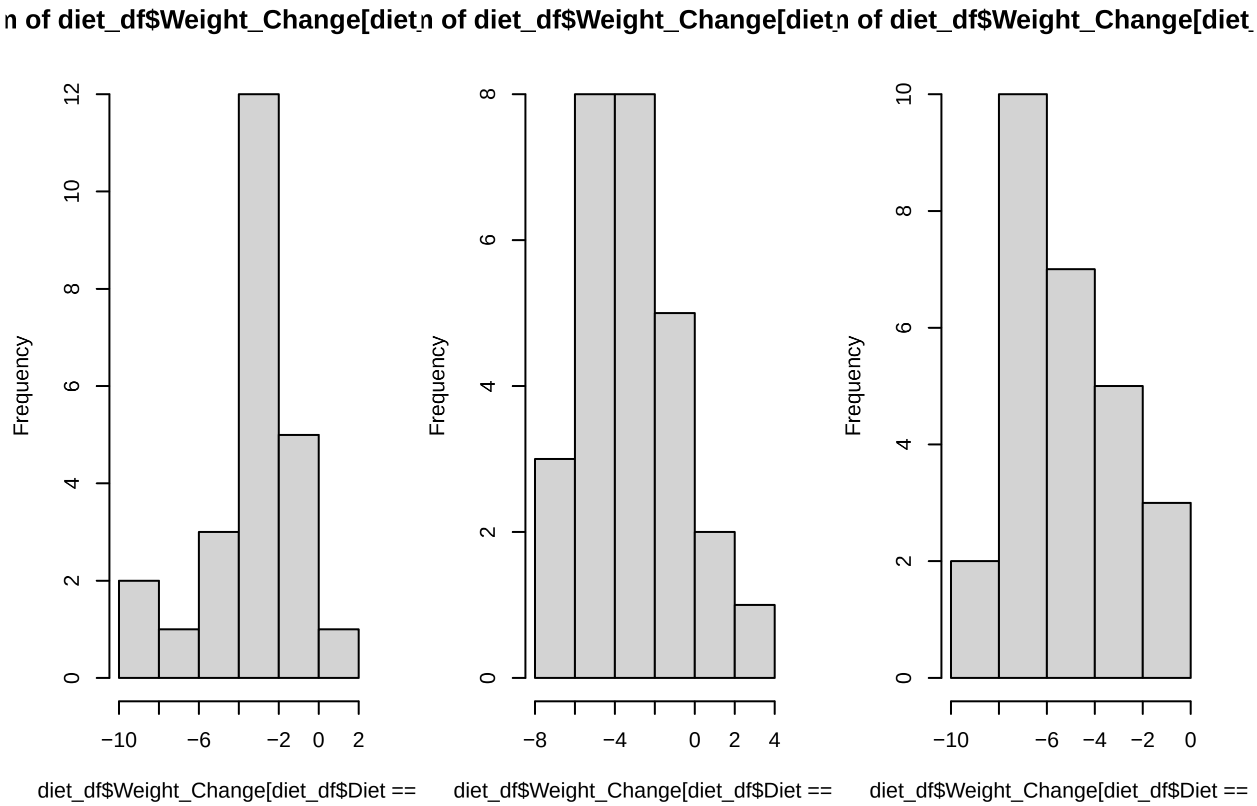


Let's test the hypothesis that at least one of the mean weight changes is different from the others between the three diets.

1. Check assumptions, determine H_0 and H_a, choose α

Inspecting the histograms of weight change by diet, we conclude that they are normally-distributed:

```
par(mfrow = c(1, 3))
hist(diet_df$Weight_Change[diet_df$Diet == 1])
hist(diet_df$Weight_Change[diet_df$Diet == 2])
hist(diet_df$Weight_Change[diet_df$Diet == 3])
```




```r
par(mfrow = c(1, 1))
```

$H_0 : \mu_1 = \mu_2 = \mu_3$ and H_a : at least one mean is different

Let's choose $\alpha = 0.05$

2. Calculate the appropriate test statistic

2.1. Calculate the grand mean and means per group

```r
grand_mean <- mean(diet_df$Weight_Change)
mean1 <- mean(diet_df$Weight_Change[diet_df$Diet == 1])
mean2 <- mean(diet_df$Weight_Change[diet_df$Diet == 2])
mean3 <- mean(diet_df$Weight_Change[diet_df$Diet == 3])
```

2.2. Calculate the (total, between group and within group) sum of squared error

Between group sum of squared error $= \sum n_i(\bar{X}_i - \bar{X})^2$

```r
SS_bw <- sum(diet_df$Diet == 1) * (mean1 - grand_mean)^2 +
    sum(diet_df$Diet == 2) * (mean2 - grand_mean)^2 +
    sum(diet_df$Diet == 3) * (mean3 - grand_mean)^2

SS_tot <- sum((diet_df$Weight_Change - grand_mean)^2)

SS_wi <- SS_tot - SS_bw
```

2.3. Calculate degrees of freedom

```
df_tot <- nrow(diet_df) - 1
df_bw <- 3 - 1
df_wi <- df_tot - df_bw
```

2.4. Calculate mean squared errors

```
MSE_bw <- SS_bw / df_bw
MSE_wi <- SS_wi / df_wi
```

2.5. Calculate F statistic

```
F_stat <- MSE_bw / MSE_wi
F_stat
```

```
## [1] 6.1974
```

```
anova_table <- data.frame(Df = c(df_bw, df_wi),
                          Sum_Sq = c(SS_bw, SS_wi),
                          Mean_Sq = c(MSE_bw, MSE_wi),
                          F_stat = c(F_stat, NA))
anova_table
```

```
##   Df  Sum_Sq Mean_Sq F_stat
## 1  2  71.094 35.5468 6.1974
## 2 75 430.179  5.7357     NA
```

3. Calculate critical values/p value

Critical values

```
F_crit <- qf(1 - 0.05, df1 = df_bw, df2 = df_wi)

F_stat > F_crit
```

```
## [1] TRUE
```

p value

```
1 - pf(F_stat, df1 = df_bw, df2 = df_wi)
```

```
## [1] 0.003229
```

4. Decide whether to reject/fail to reject H_0

- The calculated test statistic falls within the rejection region
- p value $< \alpha$

We reject the null hypothesis.

"With 95% confidence, there is enough evidence to say that at least one of the mean weight changes is significantly different than the others."

"The overall mean weight change was found to be significantly different between diets (ANOVA, p = 0.003)"

Using aov()

```
fit <- aov(Weight_Change~Diet, data = diet_df)
summary(fit)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## Diet         2     71    35.5     6.2 0.0032 **
## Residuals   75    430     5.7
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We can further investigate pairwise differences between mean weight change using the Tukey Honest Significant Differences post hoc test:

```
res <- TukeyHSD(fit)
res
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = Weight_Change ~ Diet, data = diet_df)
##
## $Diet
##         diff     lwr      upr   p adj
## 2-1  0.27407 -1.3325  1.88062 0.91247
## 3-1 -1.84815 -3.4547 -0.24161 0.02014
## 3-2 -2.12222 -3.6808 -0.56365 0.00478
```

Chi-squared Test

Is there an association between gender and diet group? In other words, do gender frequencies differ between diets?

```
table(diet_df$gender, exclude = FALSE)
```

```
##
##    0    1 <NA>
##   43   33    2
```

```
# replace missing gender values with most frequent
diet_df$gender[is.na(diet_df$gender)] <- 0

# contigency table
tbl <- table(diet_df$Diet, diet_df$gender)
tbl
```

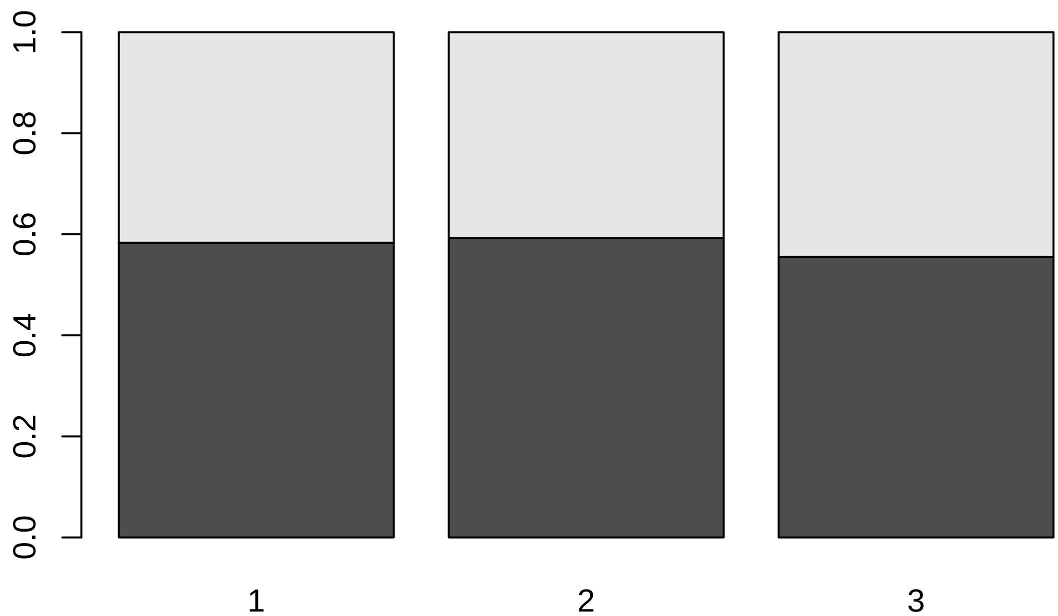
```
##
##      0  1
##   1 14 10
##   2 16 11
##   3 15 12
```

```
# relative frequencies
tbl / rowSums(tbl)
```

```
##
##           0       1
##   1 0.58333 0.41667
```

```
##   2 0.59259 0.40741
##   3 0.55556 0.44444
```

```
barplot(t(tbl / rowSums(tbl)))
```




```
chisq.test(tbl)
```

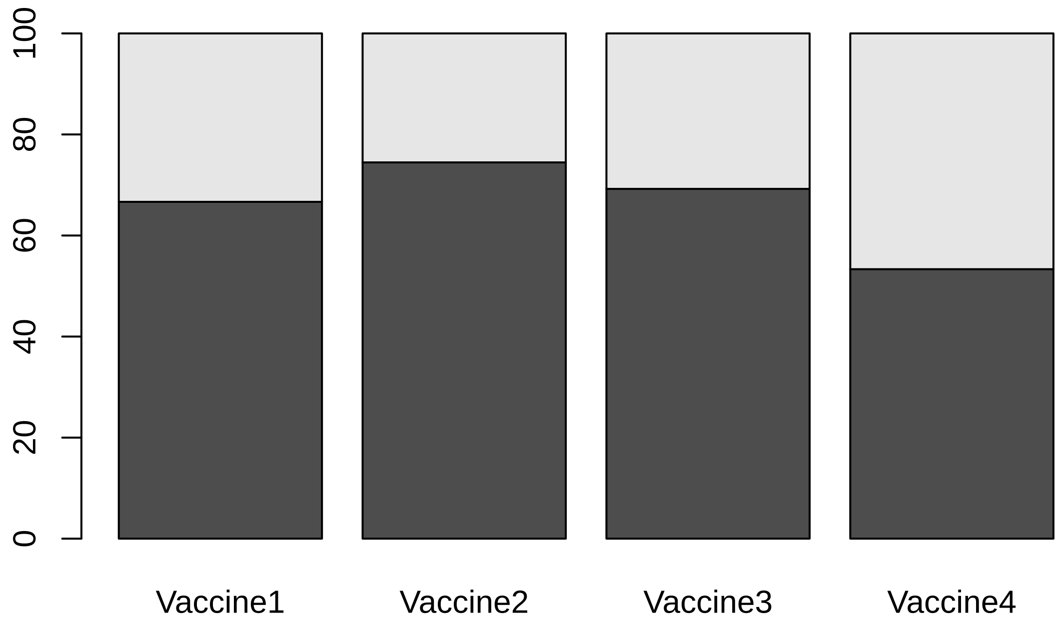
```
##
##  Pearson's Chi-squared test
##
## data:  tbl
## X-squared = 0.0817, df = 2, p-value = 0.96
```

Let's also repeat the example from the slides:

```
vac_tbl <- matrix(c(82, 70, 45, 48, 41, 24, 20, 42), ncol = 2)
colnames(vac_tbl) <- c("Protected", "Not")
rownames(vac_tbl) <- paste0("Vaccine", 1:4)
vac_tbl
```

```
##          Protected Not
## Vaccine1        82  41
## Vaccine2        70  24
## Vaccine3        45  20
## Vaccine4        48  42
```

```
# percentages
perc_tbl <- vac_tbl / rowSums(vac_tbl) * 100
barplot(t(perc_tbl))
```




```
chisq.test(vac_tbl)
```

```
##
##  Pearson's Chi-squared test
##
## data:  vac_tbl
## X-squared = 9.74, df = 3, p-value = 0.021
```

```
### Post hoc analysis
post_hoc <- c()
for (i in 1:3) {
    for (j in (i + 1):4) {
        v1 <- rownames(vac_tbl)[i]
        v2 <- rownames(vac_tbl)[j]

        res <- chisq.test(vac_tbl[c(v1, v2), ])
        post_hoc <- rbind(post_hoc,
                          data.frame(v1 = v1, v2 = v2, p = res$p.value))
    }
}
post_hoc$adj_p <- p.adjust(post_hoc$p, method = "fdr")
post_hoc
```

```
##         v1       v2         p    adj_p
## 1 Vaccine1 Vaccine2 0.2741047 0.411157
## 2 Vaccine1 Vaccine3 0.8466564 0.846656
## 3 Vaccine1 Vaccine4 0.0674289 0.135265
```

```
## 4 Vaccine2 Vaccine3 0.5854762 0.702571
## 5 Vaccine2 Vaccine4 0.0045935 0.027561
## 6 Vaccine3 Vaccine4 0.0676325 0.135265
```