stats101B_project

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libraries:

```
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(pwr)
```

```
data = read.csv("/Users/samreade/Desktop/101b Final Proj/proj.csv")

names(data)
```

```
##  [1] "Islander.Name"
##  [2] "Island.Location"
##  [3] "Island.City"
##  [4] "City.house.."
##  [5] "Gender"
##  [6] "Age"
##  [7] "Age.range..12.19....20.29....30.39....40.49....50.59....60.69....70.79....80.89....90.99."
##  [8] "Assigned.Treatment..30.min."
##  [9] "cortisol.day.0..before...µg.dL"
## [10] "NEW.cortisol.day.0..before...µg.dL"
## [11] "cortisol.day.1..µg.dL"
## [12] "NEW.cortisol.day.1..µg.dL"
## [13] "cortisol.day.2..µg.dL"
## [14] "cortisol.day.3..µg.dL"
## [15] "cortisol.day.4..µg.dL"
## [16] "cortisol.day.5..µg.dL"
## [17] "Sort.Key"
```

```
new_data <- data[, c("Islander.Name", "Island.Location", "Island.City", "City.house..", "Gender",
                     "Age", "Assigned.Treatment..30.min.", "NEW.cortisol.day.0..before...µg.dL", "NEW.c
```

```
head(new_data)
```

```
##     Islander.Name Island.Location Island.City City.house.. Gender Age
## 1 Nicolas Edwards     Bonne Sante      Riroua          166   Male  59
## 2  Kahaan Tamboli     Bonne Sante       Pauma          247   Male  74
## 3     Paresh Shah     Bonne Sante       Vaiku          373   Male  69
## 4    Beau Carlsen     Bonne Sante      Valais           76   Male  18
## 5   Chaman Kapoor     Bonne Sante      Riroua           70   Male  42
## 6    Sascha Grimm        Ironbard        Hofn          566 Female  41
##   Assigned.Treatment..30.min. NEW.cortisol.day.0..before...µg.dL
## 1         Brisk Walk Outdoors                                0.178
## 2         Brisk Walk Outdoors                                0.160
## 3         Brisk Walk Outdoors                                0.186
## 4         Brisk Walk Outdoors                                0.237
## 5         Brisk Walk Outdoors                                0.146
## 6         Brisk Walk Outdoors                                0.257
##   NEW.cortisol.day.1..µg.dL
## 1                     0.147
## 2                     0.153
## 3                     0.168
## 4                     0.196
## 5                     0.142
## 6                     0.221
##   Age.range..12.19....20.29....30.39....40.49....50.59....60.69....70.79....80.89....90.99.
## 1                                                                                       50-59
## 2                                                                                       70-79
## 3                                                                                       60-69
## 4                                                                                       12-19
## 5                                                                                       40-49
## 6                                                                                       40-49
```

```
new_data = new_data[new_data$Islander.Name != "Violaine Reynaud", ]
new_data = new_data[new_data$Islander.Name != "Jochen Voigt", ]
```

```
new_data$cortisol_diff = new_data$NEW.cortisol.day.0..before...µg.dL - new_data$NEW.cortisol.day.1..µg.d
```

Within means:

```
new_data %>%
  group_by(Assigned.Treatment..30.min.) %>%
  summarize(group_mean = mean(cortisol_diff, na.rm = TRUE))
```

```
## # A tibble: 6 x 2
##   Assigned.Treatment..30.min. group_mean
##   <chr>                             <dbl>
## 1 Brisk Walk Outdoors             0.0156
```

```
## 2 Nothing (Control)             -0.0096
## 3 Run Outdoors                   0.0121
## 4 Strength Training              0.0111
## 5 Swim Freestyle                 0.00373
## 6 Yoga                           0.00580
```

Within SD:

```
sd_within <- new_data %>%
  group_by(Assigned.Treatment..30.min.) %>%
  summarize(var = var(cortisol_diff, na.rm = TRUE)) %>%
  pull(var) %>%
  mean() %>%
  sqrt()

sd_within
```

```
## [1] 0.0254051
```

```
group_means <- c(0.015600000, -0.009600000, 0.012066667, 0.011133333, 0.003733333, 0.005800000)
sd_within <- 0.02524062

grand_mean <- mean(group_means)
k <- length(group_means)

numerator <- sum((group_means - grand_mean)^2) / k

f <- sqrt(numerator / sd_within^2)
f
```

```
## [1] 0.3245381
```

```
pwr.anova.test(k = 6, f = 0.3245381, n = NULL, sig.level = 0.05, power = 0.9)
```

```
##
##      Balanced one-way analysis of variance power calculation
##
##               k = 6
##               n = 27.00035
##               f = 0.3245381
##       sig.level = 0.05
##           power = 0.9
##
## NOTE: n is number in each group
```

```
new_data$age_range <- factor(new_data$Age.range..12.19....20.29....30.39....40.49....50.59....60.69....
```

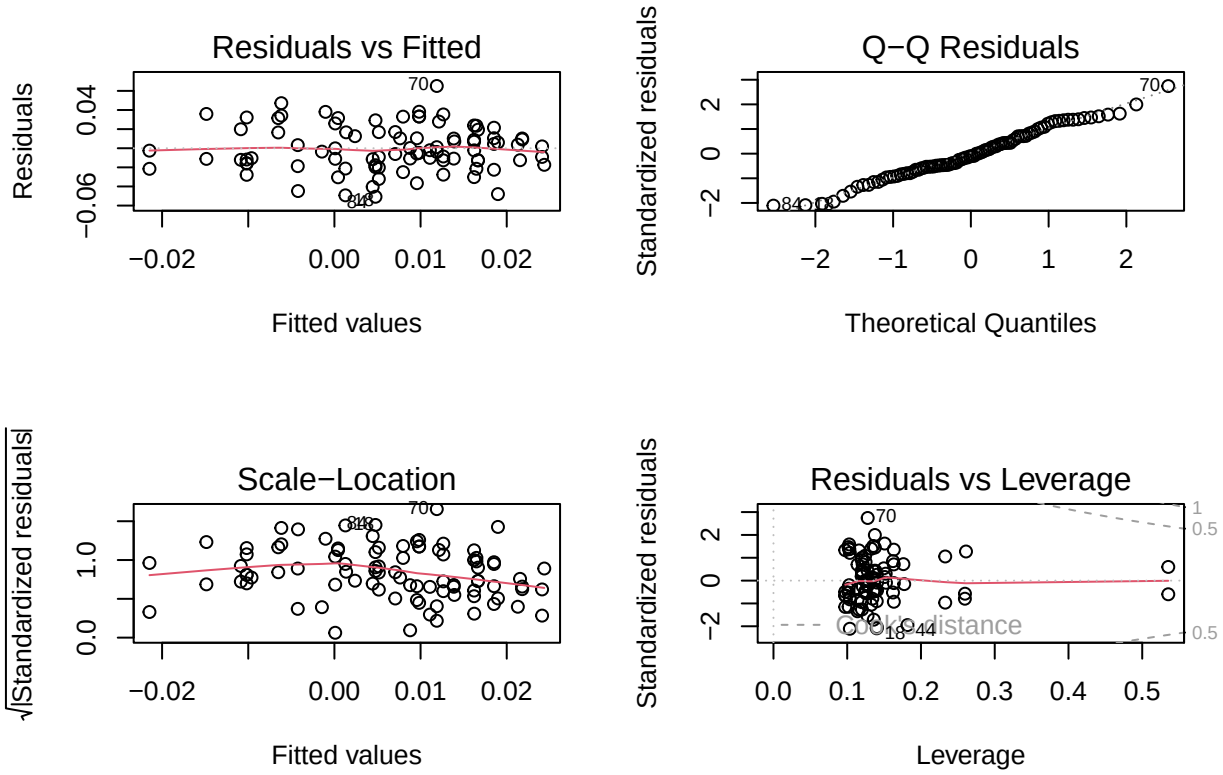
Model:

```
mod = aov(cortisol_diff ~ Assigned.Treatment..30.min. + age_range, data = new_data)

summary(mod)
```

```
##                              Df  Sum Sq   Mean Sq F value Pr(>F)
## Assigned.Treatment..30.min.   5 0.00604 0.0012078   1.868  0.110
## age_range                     7 0.00443 0.0006323   0.978  0.453
## Residuals                    77 0.04979 0.0006466
```

```
par(mfrow = c(2, 2))
plot(mod)
```




```
filtered_data <- new_data[new_data$Assigned.Treatment..30.min. == "Strength Training", ]

head(filtered_data)
```

```
##    Islander.Name Island.Location Island.City City.house.. Gender Age
## 46  Bimala Bhatt     Bonne Sante      Riroua          260 Female  14
## 47  Darcy Morris     Bonne Sante        Eden          356 Female  21
## 48  Corina Gupta     Bonne Sante      Valais          510 Female  48
## 49  Jaya Mishra      Bonne Sante      Riroua          429 Female  22
```

```
## 50 Paul Blomgren     Bonne Sante      Colmar          990   Male  50
## 51   Lea Solberg        Ironbard      Helvig           22 Female  19
##    Assigned.Treatment..30.min. NEW.cortisol.day.0..before...µg.dL
## 46           Strength Training                              0.136
## 47           Strength Training                              0.212
## 48           Strength Training                              0.185
## 49           Strength Training                              0.261
## 50           Strength Training                              0.200
## 51           Strength Training                              0.186
##    NEW.cortisol.day.1..µg.dL
## 46                     0.114
## 47                     0.207
## 48                     0.161
## 49                     0.218
## 50                     0.175
## 51                     0.213
##    Age.range..12.19....20.29....30.39....40.49....50.59....60.69....70.79....80.89....90.99.
## 46                                                                                      12-19
## 47                                                                                      20-29
## 48                                                                                      40-49
## 49                                                                                      20-29
## 50                                                                                      50-59
## 51                                                                                      12-19
##    cortisol_diff age_range
## 46         0.022     12-19
## 47         0.005     20-29
## 48         0.024     40-49
## 49         0.043     20-29
## 50         0.025     50-59
## 51        -0.027     12-19
```

```
t.test(filtered_data$NEW.cortisol.day.0..before...µg.dL, filtered_data$NEW.cortisol.day.1..µg.dL, paire
```

```
##
##  Paired t-test
##
## data:  filtered_data$NEW.cortisol.day.0..before...µg.dL and filtered_data$NEW.cortisol.day.1..µg.dL
## t = 1.7599, df = 14, p-value = 0.05012
## alternative hypothesis: true mean difference is greater than 0
## 95 percent confidence interval:
##  -8.645227e-06           Inf
## sample estimates:
## mean difference
##      0.01113333
```

```
new_data$cortisol_diff <- new_data$NEW.cortisol.day.0..before...µg.dL - new_data$NEW.cortisol.day.1..µg

mod = lm(cortisol_diff ~ Island.Location, data = new_data)

anova(mod)
```

```
## Analysis of Variance Table
##
```

```
## Response: cortisol_diff
##                  Df   Sum Sq    Mean Sq F value Pr(>F)
## Island.Location   2 0.000184 0.00009221  0.1336 0.8752
## Residuals        87 0.060070 0.00069046
```

```
model = lm(cortisol_diff ~ 1, data = new_data)
summary(model)
```

```
##
## Call:
## lm(formula = cortisol_diff ~ 1, data = new_data)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.055456 -0.021206  0.002044  0.018544  0.070544
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.006456   0.002743   2.354   0.0208 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02602 on 89 degrees of freedom
```

```
modelEZ <- lm(cortisol_diff ~ Assigned.Treatment..30.min., data = new_data)
anova(modelEZ)
```

```
## Analysis of Variance Table
##
## Response: cortisol_diff
##                              Df   Sum Sq    Mean Sq F value Pr(>F)
## Assigned.Treatment..30.min.   5 0.006039 0.00120782  1.8714  0.108
## Residuals                    84 0.054215 0.00064542
```

```
new_data$Assigned.Treatment..30.min. <- factor(new_data$Assigned.Treatment..30.min.)

modelJK <- lm(cortisol_diff ~ 0 + Assigned.Treatment..30.min., data = new_data)

summary(modelJK)
```

```
##
## Call:
## lm(formula = cortisol_diff ~ 0 + Assigned.Treatment..30.min.,
##     data = new_data)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.061067 -0.016117 -0.001367  0.016050  0.073267
##
## Coefficients:
##                                                Estimate Std. Error t value
## Assigned.Treatment..30.min.Brisk Walk Outdoors  0.015600   0.006560   2.378
```

```
## Assigned.Treatment..30.min.Nothing (Control)   -0.009600   0.006560  -1.464
## Assigned.Treatment..30.min.Run Outdoors         0.012067   0.006560   1.840
## Assigned.Treatment..30.min.Strength Training    0.011133   0.006560   1.697
## Assigned.Treatment..30.min.Swim Freestyle       0.003733   0.006560   0.569
## Assigned.Treatment..30.min.Yoga                 0.005800   0.006560   0.884
##                                                Pr(>|t|)
## Assigned.Treatment..30.min.Brisk Walk Outdoors   0.0197 *
## Assigned.Treatment..30.min.Nothing (Control)     0.1471
## Assigned.Treatment..30.min.Run Outdoors          0.0694 .
## Assigned.Treatment..30.min.Strength Training     0.0933 .
## Assigned.Treatment..30.min.Swim Freestyle        0.5708
## Assigned.Treatment..30.min.Yoga                  0.3791
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02541 on 84 degrees of freedom
## Multiple R-squared:  0.153,  Adjusted R-squared:  0.09245
## F-statistic: 2.528 on 6 and 84 DF,  p-value: 0.02677
```

```
coefs <- summary(modelJK)$coefficients

# One-sided p-value for reduction > 0:
p_one_sided <- pt(coefs[, "t value"], df = modelJK$df.residual, lower.tail = FALSE)
p_one_sided
```

```
## Assigned.Treatment..30.min.Brisk Walk Outdoors
##                                     0.009833114
##   Assigned.Treatment..30.min.Nothing (Control)
##                                     0.926470138
##       Assigned.Treatment..30.min.Run Outdoors
##                                     0.034683336
##   Assigned.Treatment..30.min.Strength Training
##                                     0.046674369
##      Assigned.Treatment..30.min.Swim Freestyle
##                                     0.285388871
##                Assigned.Treatment..30.min.Yoga
##                                     0.189554829
```