BMEG 802 – Advanced Biomedical Experimental Design and Analysis

Assignment 5

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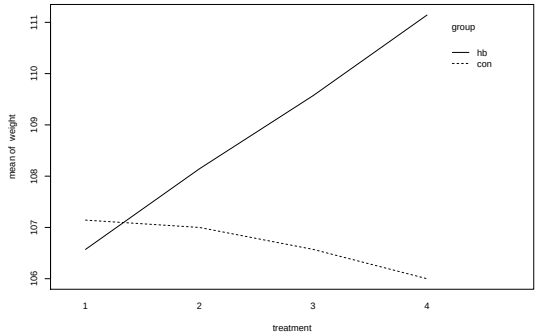
Question 1

```
weight <- c(96,98,103,104,116,116,118,119,102,102,101,101,112,115,116,118,
treatment <- factor(rep(c(1,2,3,4),14))
group <- factor(c(rep('hb',28),rep('con',28)))
subject <- factor(c(rep(1,4),rep(2,4),rep(3,4),
                    rep(4,4),rep(5,4), rep(6,4),rep(7,4),rep(8,4),rep(9,4)
mydata <- data.frame(subject, weight, treatment, group)
```

Question 1 Cont'd

```
interaction.plot(treatment, group, weight)
```



Question 1 Cont'd

```
library(rstatix)
```

```
##
## Attaching package: 'rstatix'
```

```
## The following object is masked from 'package:stats':
##
##     filter
```

Question 1 Cont'd

```r
library(rstatix)
res.aov <- anova_test(weight ~ group * treatment + Error(subject/(treatment)), data = mydata, type = 3, effect.size = "pes")
res.aov # note subject divided by within factor # pes is partial eta squared
```

```
## ANOVA Table (type III tests)
##
## $ANOVA
##            Effect DFn DFd     F        p p<.05   pes
## 1           group   1  12 0.162 0.694000       0.013
## 2       treatment   3  36 2.812 0.053000       0.190
## 3 group:treatment   3  36 7.923 0.000348     * 0.398
##
## $`Mauchly's Test for Sphericity`
##            Effect     W       p p<.05
## 1       treatment 0.048 5.4e-06     *
## 2 group:treatment 0.048 5.4e-06     *
##
## $`Sphericity Corrections`
##            Effect   GGe      DF[GG] p[GG] p[GG]<.05   HFe      DF[HF] p[HF]
## 1       treatment 0.403 1.21, 14.53  0.11           0.424 1.27, 15.28 0.107
## 2 group:treatment 0.403 1.21, 14.53  0.01         * 0.424 1.27, 15.28 0.009
##   p[HF]<.05
## 1
## 2         *
```

Question 1 Cont'd

Greenhouse-Geisser Corrections

```
# Main effect of Treatment
pval = 0.11
df1_adj = 1.21
df2_adj = 14.53
Fscore = qf(1 - pval, df1=df1_adj, df2=df2_adj) # chi-square function
Fscore
```

```
## [1] 2.814809
```

```
# Interaction of Group and Treatment
pval = 0.01
df1_adj = 1.21
df2_adj = 14.53
Fscore = qf(1 - pval, df1=df1_adj, df2=df2_adj) # chi-square function
Fscore
```

```
## [1] 8.016918
```

Sphericity was violated

Question 1 Cont'd

```
HB1 = c(weight[1],weight[5],weight[9],weight[13], weight[17], weight[21], weight[25])
HB2 = c(weight[2],weight[6],weight[10],weight[14], weight[18], weight[22], weight[26])
HB3 = c(weight[3],weight[7],weight[11],weight[15], weight[19], weight[23], weight[27])
HB4 = c(weight[4],weight[8],weight[12],weight[16], weight[20], weight[24], weight[28])
C1 = c(weight[29],weight[33],weight[37],weight[41], weight[45], weight[49], weight[53])
C2 = c(weight[30],weight[34],weight[38],weight[42], weight[46], weight[50], weight[54])
C3 = c(weight[31],weight[35],weight[39],weight[43], weight[47], weight[51], weight[55])
C4 = c(weight[32],weight[36],weight[40],weight[44], weight[48], weight[52], weight[56])
```

Question 1 Cont'd

```
shapiro.test(HB1)$p.value
```

```
## [1] 0.8326176
```

```
shapiro.test(HB2)$p.value
```

```
## [1] 0.5840771
```

```
shapiro.test(HB3)$p.value
```

```
## [1] 0.5186714
```

```
shapiro.test(HB4)$p.value
```

```
## [1] 0.3069774
```

Question 1 Cont'd

```
shapiro.test(C1)$p.value
```

```
## [1] 0.7459329
```

```
shapiro.test(C2)$p.value
```

```
## [1] 0.5056195
```

```
shapiro.test(C3)$p.value
```

```
## [1] 0.3699244
```

```
shapiro.test(C4)$p.value
```

```
## [1] 0.3390716
```

Since $p > 0.05$ for all, no violations of normality

Question 1 Cont'd

```
pH1vC1 = t.test(HB1, C1, paired = FALSE, alternative = "two.sided")$p.value #
pH2vC2 = t.test(HB2, C2, paired = FALSE, alternative = "two.sided")$p.value #
pH3vC3 = t.test(HB3, C3, paired = FALSE, alternative = "two.sided")$p.value #
pH4vC4 = t.test(HB4, C4, paired = FALSE, alternative = "two.sided")$p.value #
pvals = c(pH1vC1, pH2vC2, pH3vC3,pH4vC4)
pvals
```

```
## [1] 0.9188436 0.8347511 0.5945855 0.3676081
```

```
pvals_holm = p.adjust(pvals, method = "holm", n = length(pvals))
sprintf("%.5f", pvals_holm) #outputs in decimal (not scientific notation)
```

```
## [1] "1.00000" "1.00000" "1.00000" "1.00000"
```

Since $p > 0.05$, there are no significant differences between the heartbeat and control group

Question 1 Cont'd

```
library(effsize)
abs(cohen.d(HB1, C1, paired = FALSE)$estimate) #
```

```
## [1] 0.05562086
```

```
abs(cohen.d(HB2, C2, paired = FALSE)$estimate) #
```

```
## [1] 0.1139606
```

```
abs(cohen.d(HB3, C3, paired = FALSE)$estimate) #
```

```
## [1] 0.2923725
```

```
abs(cohen.d(HB4, C4, paired = FALSE)$estimate) #
```

```
## [1] 0.5005313
```

Question 1 Cont'd

- We found a significant interaction of group and treatment [F(1.2,14.5) = 8.017, p = 0.01 (GG corrected), $\eta_p^2 = 0.725$]. Note: not necessary to summarize main effect.
- There were no significant differences between the heartbeat and control groups (p > 0.05 for all comparisons, d range [0.06, 0.50]).

Question 1 Cont'd

install.packages("WebPower")

```
library(WebPower)
```

```
## Loading required package: MASS
##
## Attaching package: 'MASS'
## The following object is masked from 'package:rstatix':
##
##     select
## Loading required package: lme4
## Loading required package: Matrix
## Registered S3 methods overwritten by 'lme4':
##   method                          from
##   cooks.distance.influence.merMod car
```

Question 1 Cont'd

install.packages("WebPower")

```
library(WebPower)
# n=sub, ng=#ofgroups, nm=#ofmeasurements, nscor=sphericity(1=perfect)
#type "0" between-effect; "1" within-effect; and "2" interaction effect
wp.rmanova(n = NULL, ng = 2, nm = 4, f = .4, nscor = 1,
           alpha = 0.05, power = 0.8, type = 2)
```

```
## Repeated-measures ANOVA analysis
##
##             n   f ng nm nscor alpha power
##      69.47025 0.4  2  4     1  0.05   0.8
##
## NOTE: Power analysis for interaction-effect test
## URL: http://psychstat.org/rmanova
```

We need 70 participants per group for a sufficiently powered.

Question 2

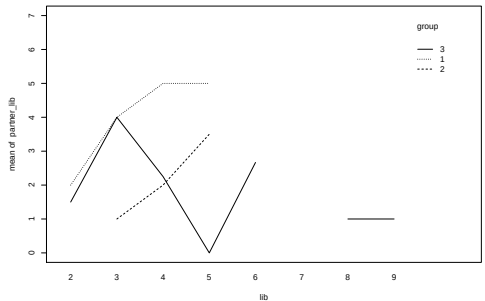
Setting up the Data

```
lib <- c(3,2,5,2,2,2,7,2,4,7,5,3,4,4,7,5,4,
              9,2,6,3,4,4,4,6,4,6,2,8,5)
partner_lib <- c(4,1,5,1,2,2,7,4,5,5,3,1,2,2,6,4,
                 2,1,3,5,4,3,3,2,0,1,3,0,1,0)
group <- factor(c(rep('1',9),rep('2',8),rep('3',13)))
subject <- factor(c(1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,
                    16,17,18,19,20,21,22,23,24,25,26,27,28,29,30))
mydata <- data.frame(subject, group, lib, partner_lib)
```

Question 2 Cond't

Plot Data

```
interaction.plot(lib, group, partner_lib)
```



Question 2 Cond't

install.package("rstatix")

```
library(rstatix)
```

Question 2 Cond't

```r
# note, we are controlling for high school marks
res.aov <- anova_test(lib ~ group + partner_lib, data = mydata,
                      type = 3, effect.size = "pes")
```

```
## Coefficient covariances computed by hccm()
```

```r
res.aov
```

```
## ANOVA Table (type III tests)
##
##        Effect DFn DFd     F     p p<.05   pes
## 1       group   2  26 4.142 0.027     * 0.242
## 2 partner_lib   1  26 4.959 0.035     * 0.160
```

When controlling for partner's libido, these results suggest that there is a significant main effect of group (Viagra dosage) on libido [F(2,26) = 4.142, p = 0.027, $\eta_p^2 = 0.242$]

Question 2 Cond't

There is a significant linear relationship between the covariate (partner's libido) and DV (libido) [F(1,26) $= 4.959$, p $= 0.035$, $\eta_p^2 = 0.160$]

Question 2 Cond't

```
anova_test(lib ~ group*partner_lib, data = mydata)
```

```
## Coefficient covariances computed by hccm()
```

```
## ANOVA Table (type II tests)
##
##               Effect DFn DFd     F     p p<.05   ges
## 1              group   2  24 5.156 0.014     * 0.301
## 2        partner_lib   1  24 6.172 0.020     * 0.205
## 3 group:partner_lib   2  24 4.181 0.028     * 0.258
```

There is NOT homogeneity of regression slopes since was a significant interaction between Section and high school marks [$F(2,24) = 4.181$, $p = 0.028$)]

Question 2 Cond't

```r
# fit the linear model (covariate goes first)
model <- lm(lib ~ partner_lib + group, data = mydata)
# find residuals of the linear model fit
model.metrics <- augment(model)
# test whether residulas are normally distributed
shapiro_test(model.metrics$.resid)
```

```
## # A tibble: 1 x 3
##   variable             statistic p.value
##   <chr>                    <dbl>   <dbl>
## 1 model.metrics$.resid     0.943   0.111
```

The Shapiro Wilk test was not significant ($p > 0.05$), so we can assume normality of residuals

Question 2 Cond't

```
model.metrics %>% levene_test(.resid ~ group)
```

```
## # A tibble: 1 x 4
##     df1   df2 statistic      p
##   <int> <int>     <dbl>  <dbl>
## 1     2    27      3.74 0.0368
```

The Levene's test was significant ($p < 0.05$), so we CANNOT assume homogeneity of the residual variances for all groups.

Question 2 Cond't

Let's compare the Adjusted Means

```
library(emmeans)
pwc <- emmeans_test(mydata, lib ~ group, covariate = partner_lib, p.adjust.method = "holm")
pwc
```

```
## # A tibble: 3 x 9
##   term            .y.   group1 group2    df statistic      p  p.adj p.adj.signif
## * <chr>           <chr> <chr>  <chr>  <dbl>     <dbl>  <dbl>  <dbl> <chr>
## 1 partner_lib*gr~ lib   1      2         26    -2.10  0.0454 0.0907 ns
## 2 partner_lib*gr~ lib   1      3         26    -2.77  0.0102 0.0305 *
## 3 partner_lib*gr~ lib   2      3         26    -0.541 0.593  0.593  ns
```

```
get_emmeans(pwc)
```

```
## # A tibble: 3 x 8
##   partner_lib group emmean    se    df conf.low conf.high method
##         <dbl> <fct>  <dbl> <dbl> <dbl>    <dbl>     <dbl> <chr>
## 1        2.73 1       2.93 0.596    26     1.70      4.15 Emmeans test
## 2        2.73 2       4.71 0.621    26     3.44      5.99 Emmeans test
## 3        2.73 3       5.15 0.503    26     4.12      6.18 Emmeans test
```

Adjusted means are significantly different between the Placebo and High Dose group ($p = 0.030$)

Question 2 Cond't

```
em_section <- emmeans(model, ~group)
em_section
```

```
##  group emmean    SE df lower.CL upper.CL
##  1       2.93 0.596 26     1.70     4.15
##  2       4.71 0.621 26     3.44     5.99
##  3       5.15 0.503 26     4.12     6.18
##
## Confidence level used: 0.95
```

Question 2 Cond't

```
d = eff_size(em_section, sigma = sigma(model), edf = df.residual(model))
d
```

```
##  contrast effect.size    SE df lower.CL upper.CL
##  1 - 2         -1.024 0.507 26    -2.07   0.0189
##  1 - 3         -1.276 0.493 26    -2.29  -0.2621
##  2 - 3         -0.252 0.467 26    -1.21   0.7071
##
## sigma used for effect sizes: 1.744
## Confidence level used: 0.95
```

Question 2 Cond't

- There was a significant main effect of Viagra on libido [F(2,26) = 4.142, p = 0.027, $\eta_p^2 = 0.242$], as well as a significant relationship between participant libido and partner libido [F(1,26) = 4.959, p = 0.035, $\eta_p^2 = 0.160$]. Mean comparison's showed there was a significant difference between the Placebo and High Dose Groups (p = 0.035, d = 1.276).
  - Caveats: interpretation should be taken cautiously, as we violated homogeneity of regression slopes and homegeneity of residual variances.

Question 2 Cond't

install.packages("pwr2ppl")

```
library(pwr2ppl)
# m1.1, s1.1 = mean and stdev for group 1.
# r = correlation between dv and covariate
anc(m1.1=.85,m2.1=2.5, m3.1 = 1.25, s1.1 = 1.7, s2.1=1, s3.1 = 1.2, alpha = 0.05,
    r= 0.4, n=9, factors = 1,levelsA = 3)
```

```
## Sample size per cell = 9
```

```
## Power IV1 = 0.8105 for partial eta-squared = 0.329
```

We need 9 participants per group for a sufficiently powered.