STAT 512 Homework 7

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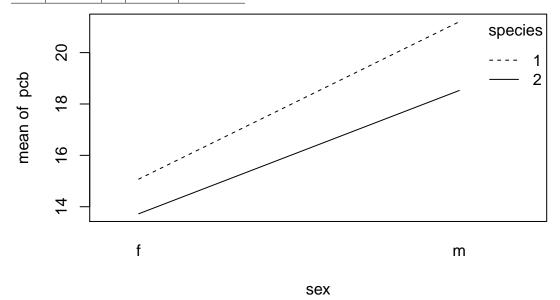
Part 1: PCB data

In this group of questions we use the "PCB.csv" data available from Canvas. A researcher is interested in comparing PCB concentrations by sex (m, f) and species (1, 2). This corresponds to four groups (sp1f, sp1m, sp2f, sp2m). Note that depending on the analysis you will use group OR sex and species in the analysis but not all three!

Question A: Table and plot

Create a table of summary statistics including sample size, mean and standard deviation for each sex, species combination. Then construct an interaction plot. For consistency, please put sex on the X axis. Include both the summary table and interaction plot in your assignment. (4 pts)

sex	species	n	mean	sd
f	1	4	15.075	1.236595
f	2	4	13.725	1.209339
m	1	4	21.200	1.329160
m	2	4	18.525	1.837344



Question B: One-way ANOVA

Fit a one-way ANOVA model to the data using group as the predictor. Construct the Type 3 ANOVA table.

```
##
        [,1] [,2] [,3]
## sp1f
                0
           1
## sp1m
           0
## sp2f
           0
                0
                     1
## sp2m
         -1
               -1
## Anova Table (Type III tests)
##
## Response: pcb
##
               Sum Sq Df F value
                                     Pr(>F)
## (Intercept) 4695.7 1 2309.112 4.317e-15 ***
                137.3 3
                           22.508 3.230e-05 ***
## group
## Residuals
                 24.4 12
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

Question C: Estimated marginal means

With model from 2B, use emmeans to calculate (Tukey adjusted) pairwise comparisons for all four groups.

```
## $emmeans
##
   group emmean
                    SE df lower.CL upper.CL
   sp1f
            15.1 0.713 12
                              13.5
                              19.6
                                       22.8
##
   sp1m
            21.2 0.713 12
##
   sp2f
            13.7 0.713 12
                              12.2
                                       15.3
##
            18.5 0.713 12
                              17.0
                                       20.1
   sp2m
##
## Confidence level used: 0.95
##
## $contrasts
  contrast
                           SE df t.ratio p.value
                estimate
   sp1f - sp1m
##
                   -6.12 1.01 12 -6.074 0.0003
##
   sp1f - sp2f
                   1.35 1.01 12 1.339
                                        0.5576
##
   sp1f - sp2m
                   -3.45 1.01 12 -3.421
                                        0.0227
  sp1m - sp2f
                   7.47 1.01 12 7.413 <.0001
## sp1m - sp2m
                    2.67 1.01 12 2.653 0.0857
## sp2f - sp2m
                   -4.80 1.01 12 -4.760 0.0023
##
## P value adjustment: tukey method for comparing a family of 4 estimates
```

Question D: Two-way ANOVA

Fit a two-way ANOVA model to the data using sex and species as predictors. Be sure to include the interaction. Construct the Type 3 ANOVA table.

```
## Anova Table (Type II tests)
##
## Response: pcb
##
             Sum Sq Df F value
                               Pr(>F)
             16.201 1 7.9667
                              0.01539 *
## species
## sex:species
              1.756 1
                      0.8633
                              0.37112
## Residuals
             24.403 12
## ---
```

```
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

Question E: Sex/species emmeans

Use emmeans (, pairwise ~ sex:species) to calculate (Tukey adjusted) pairwise comparisons for all four groups.

```
## $emmeans
##
   sex species emmean
                          SE df lower.CL upper.CL
##
   f
        1
                  15.1 0.713 12
                                    13.5
                                              16.6
##
                  21.2 0.713 12
                                     19.6
                                             22.8
        2
                  13.7 0.713 12
                                    12.2
                                              15.3
##
   f
##
                  18.5 0.713 12
                                    17.0
                                              20.1
##
## Confidence level used: 0.95
##
## $contrasts
##
  contrast estimate
                         SE df t.ratio p.value
                 -6.12 1.01 12 -6.074 0.0003
  f, 1 - m, 1
## f,1 - f,2
                  1.35 1.01 12 1.339
                                       0.5576
## f,1 - m,2
                 -3.45 1.01 12 -3.421
                                       0.0227
## m, 1 - f, 2
                  7.47 1.01 12 7.413
                                       <.0001
## m, 1 - m, 2
                  2.67 1.01 12 2.653 0.0857
                 -4.80 1.01 12 -4.760 0.0023
## f,2 - m,2
##
## P value adjustment: tukey method for comparing a family of 4 estimates
```

Question F: Species emmeans

Use emmeans (, pairwise ~ species) to calculate the pairwise comparison corresponding to the main effect of species. Note that the p-value from this comparison should match the F-test corresponding to species from the ANOVA table from question 4.

```
## $emmeans
   species emmean
                      SE df lower.CL upper.CL
                                          19.2
##
   1
              18.1 0.504 12
                                   17
##
              16.1 0.504 12
                                   15
                                          17.2
##
## Results are averaged over the levels of: sex
## Confidence level used: 0.95
##
## $contrasts
  contrast estimate
                         SE df t.ratio p.value
                 2.01 0.713 12 2.823
##
## Results are averaged over the levels of: sex
```

Question G: Reflection

Consider the output from the two previous questions. From question 5, for the "m,1 - m,2" comparison you should have found an estimate = 2.67, p-value = 0.0857. From question 6, for the "1 - 2" comparison you

should have found an estimate = 2.01, p-value = 0.0154. Briefly explain why we find a smaller p-value for the "1 - 2" comparison even though the estimated difference is smaller.

When more tests are conducted (6 vs. 1), there is a Tukey correction ("penalty") to minimize the family-wise error rate.

Note: The two models from above are equivalent. This can be seen by comparing the ANOVA tables (questions 2 and 4) and the pairwise comparisons (questions 3, 5). Either analysis approach is acceptable. However, one benefit of the two-way analysis is that since the interaction is not significant, we can easily discuss main effects.

Part 2: Roadways

Questions 8 through 13 (Roadways): For this group of questions use the data described in Ott & Longnecker problem 15.14 (p 907 in the 7th Edition). 8. Create a table of summary statistics including sample size, mean and standard deviation for each Treatment*Concentration combination. Then construct an interaction plot. For consistency, please put Treatment on the X axis. Include both the summary table and interaction plot in your assignment. (4 pts) 9. Describe the blocking and treatment structure. 10. Considering your answer to the previous question, fit an appropriate model and include the Type 3 ANOVA table in your assignment. (4 pts) 11. Discuss the value of the blocking for this data. Justify your response with appropriate test-statistic(s) and p-value(s). 12. Compare mean response for High vs Low Concentration separately for each Treatment. This can be done using emmeans. Include the emmeans "contrasts" output in your assignment, but also (briefly) summarize your findings. (4 pts) 13. Compare mean responses between the 3 Treatments separately for each Concentration. This can be done using emmeans (default Tukey adjustment is fine). Include the emmeans "contrasts" output in your assignment, but also (briefly) summarize your findings for Concentration = Low. (4 pts)

Appendix

```
# load packages
library(tidyverse)
library(janitor)
library(kableExtra)
library(car)
library(emmeans)
# set global options
knitr::opts_chunk$set(fig.width = 6,
                      fig.height = 4,
                      fig.path = "figs/",
                      echo = FALSE,
                      warning = FALSE,
                      message = FALSE)
# 1. load pcb data
pcb_data <- readr::read_csv("data/PCB.csv") %>%
  dplyr::mutate(sex = as.factor(sex),
                species = as.factor(species),
                group = as.factor(group))
# 1a. create summary statistics table for pcb data
pcb_table <- pcb_data %>%
  dplyr::group_by(sex, species) %>%
  dplyr::summarize(
    n = n(),
    mean = mean(pcb),
    sd = sd(pcb))
# 1a. kable pcb sum stat table
kableExtra::kable(pcb_table)
# 1a. create interaction plot
with(interaction.plot(x.factor = sex,
                      trace.factor = species,
                      response = pcb),
     data = pcb_data)
# 1b. change contrast defaults
options(contrasts = c("contr.sum", "contra.poly"))
contrasts(pcb_data$group)
# 1b. construct one-way anova model with group as predictor
pcb_1anova <- lm(pcb ~ group, data = pcb_data)</pre>
car::Anova(pcb lanova, type = 3)
# 1c. extract emmeans for group
emmeans::emmeans(pcb_1anova, pairwise ~ group)
# 1d. change contrast defaults
options(contrasts = c("contr.sum", "contra.poly"))
# 1d. build two-way anova model
pcb_2anova <- lm(pcb ~ sex*species, data = pcb_data)</pre>
car::Anova(pcb_2anova)
# 1e. extract emmeans for group by sex*species
emmeans::emmeans(pcb_2anova, pairwise ~ sex:species)
# 1f. extract emmeans for group by species
emmeans::emmeans(pcb_2anova, pairwise ~ species)
```