homework4stat631

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# Problem 10.3

library(tidyverse)

## Warning: package 'tidyverse' was built under R version 4.1.3

## -- Attaching packages --------------------------------------- tidyverse 1.3.1 --

## v ggplot2 3.3.5 v purrr 0.3.4  
## v tibble 3.1.6 v dplyr 1.0.7  
## v tidyr 1.2.0 v stringr 1.4.0  
## v readr 2.1.2 v forcats 0.5.1

## Warning: package 'readr' was built under R version 4.1.3

## Warning: package 'forcats' was built under R version 4.1.3

## -- Conflicts ------------------------------------------ tidyverse\_conflicts() --  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag() masks stats::lag()

rating <- c(3.5, 3.6, 2.1, 4.0, 3.1,  
3.0, 2.9, 4.5, NA, NA,  
7.2, 6.8, 6.7, 7.5, 6.8,  
NA, NA, 4.8, 6.9, 9.3,  
4.1, 5.8, 4.5, 5.3, 4.1,  
5.6, 4.8, 4.6, 7.3, 5.3,  
5.3, 4.8, 5.0, 6.7, 5.2,  
NA, 3.2, 7.2, 6.7, 4.2,  
4.5, 5.1, 5.0, 4.9, 4.5,  
2.7, 3.7, 4.5, 4.7, NA)  
protein <- rep(1:5, 5) %>% as.factor()  
gum <- rep(1:5, each = 10) %>% as.factor()  
icecream <- data.frame(rating, protein, gum) %>% na.omit(icecream)  
head(icecream)

## rating protein gum  
## 1 3.5 1 1  
## 2 3.6 2 1  
## 3 2.1 3 1  
## 4 4.0 4 1  
## 5 3.1 5 1  
## 6 3.0 1 1

library("car")

## Loading required package: carData

##   
## Attaching package: 'car'

## The following object is masked from 'package:dplyr':  
##   
## recode

## The following object is masked from 'package:purrr':  
##   
## some

model1 <- lm(rating ~ protein\*gum, data = icecream)  
Anova(model1, type = "II")

## Anova Table (Type II tests)  
##   
## Response: rating  
## Sum Sq Df F value Pr(>F)   
## protein 7.075 4 1.7099 0.1894   
## gum 51.775 4 12.5123 3.741e-05 \*\*\*  
## protein:gum 14.053 16 0.8490 0.6261   
## Residuals 19.655 19   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Hypothesis for protein: H0: a=0 H1: a> 0

We have p-value of protein is 0.1894 > 0.05, we failto reject the null hypothesis, protein has no significant eect on the sensory rating. Hypothesis for gum: H0: b=0 H1: b> 0 We have p-value of gum is ¥ 0 < 0.05, we can reject the null hypothesis, so the data gave proficient proof that gum has significant eect on the sensory rating. Determine which, if any, proteins and/or gums dier in their sensory ratings.

library(emmeans)  
lsmGum <- lsmeans(model1, ~ gum)

## NOTE: Results may be misleading due to involvement in interactions

TkGum <- summary(contrast(lsmGum, method="pairwise", adjust="tukey"))  
TkGum

## contrast estimate SE df t.ratio p.value  
## 1 - 2 -3.62 0.538 19 -6.726 <.0001  
## 1 - 3 -1.76 0.498 19 -3.532 0.0167  
## 1 - 4 -1.98 0.519 19 -3.818 0.0090  
## 1 - 5 -1.03 0.519 19 -1.986 0.3097  
## 2 - 3 1.86 0.498 19 3.733 0.0109  
## 2 - 4 1.64 0.519 19 3.162 0.0365  
## 2 - 5 2.59 0.519 19 4.994 0.0007  
## 3 - 4 -0.22 0.477 19 -0.461 0.9899  
## 3 - 5 0.73 0.477 19 1.530 0.5566  
## 4 - 5 0.95 0.498 19 1.907 0.3474  
##   
## Results are averaged over the levels of: protein   
## P value adjustment: tukey method for comparing a family of 5 estimates

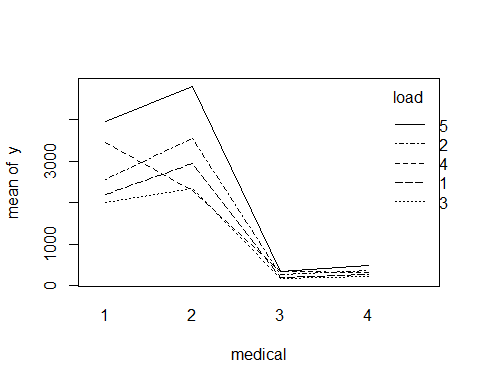
From the Tukey contrast table, we have the contrast of group 2 vs others have p-values : 1 - 2: 0.0001 2 - 3: 0.0109 2 - 4: 0.0365 2 - 5: 0.0007 The p-values are < 0.05, So we can conclude the group 2 is significantly dierent with other group in sensory ratings.

|  |
| --- |
| #Exercise 11.6 |
| r a<- 30:50 crt <- 1/(1+2)\*qf(0.99,a-1,a) power<- 1-pf(crt,a-1,a) plot(a,power) abline(h=0.9) |
|  |
| r a=45 crt <- 1/(1+2)\*qf(0.99,a-1,a) power<- 1-pf(crt,a-1,a) power |
| ## [1] 0.9017425 Summary: we need 45 individuals to achieve the 90% power given that the significance level of 0.01 and for alternative hypothesis. |

# Problem 11.2

a <- c(2200, 2200, 2600, 2500, 1900, 2100, 2600, 4300, 4000, 3900,  
3000, 2900, 3600, 3500, 2500, 2200, 2800, 1800, 4800, 4800,  
210, 200, 290, 240, 160, 200, 330, 340, 370, 340,  
270, 260, 360, 380, 230, 230, 350, 290, 500, 480)  
pull <- data.frame(y=a,medical = factor(rep(1:4,each = 10)),load=factor(rep(rep(1:5,each=2),4)))

with(pull,interaction.plot(x.factor = medical,trace.factor = load,response = y))



library(lmerTest)

## Warning: package 'lmerTest' was built under R version 4.1.3

## Loading required package: lme4

## Loading required package: Matrix

##   
## Attaching package: 'Matrix'

## The following objects are masked from 'package:tidyr':  
##   
## expand, pack, unpack

##   
## Attaching package: 'lmerTest'

## The following object is masked from 'package:lme4':  
##   
## lmer

## The following object is masked from 'package:stats':  
##   
## step

library(lme4)  
lm1 <- lmer(a~1+(1|medical)+(1|load)+(1|load:medical),data = pull)  
ranova(lm1)

## boundary (singular) fit: see ?isSingular

## ANOVA-like table for random-effects: Single term deletions  
##   
## Model:  
## a ~ (1 | medical) + (1 | load) + (1 | load:medical)  
## npar logLik AIC LRT Df Pr(>Chisq)   
## <none> 5 -306.83 623.66   
## (1 | medical) 4 -318.33 644.66 22.9947 1 1.624e-06 \*\*\*  
## (1 | load) 4 -307.64 623.27 1.6101 1 0.2044756   
## (1 | load:medical) 4 -313.22 634.45 12.7858 1 0.0003493 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

grandmean = 1 fixed effect of 1 is 5 and fixed effect of 2 is 4,degree of freedom (1) = 4;degree of freedom for (2) is 3. random effect = 20,degree of freedom for random effect is 4\*3 = 12 sample = 40,degree of freedom for total sample equal to 40-1-4-3-12=20