

Lab 10

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Section: 91973 Friday 9am

Question 1

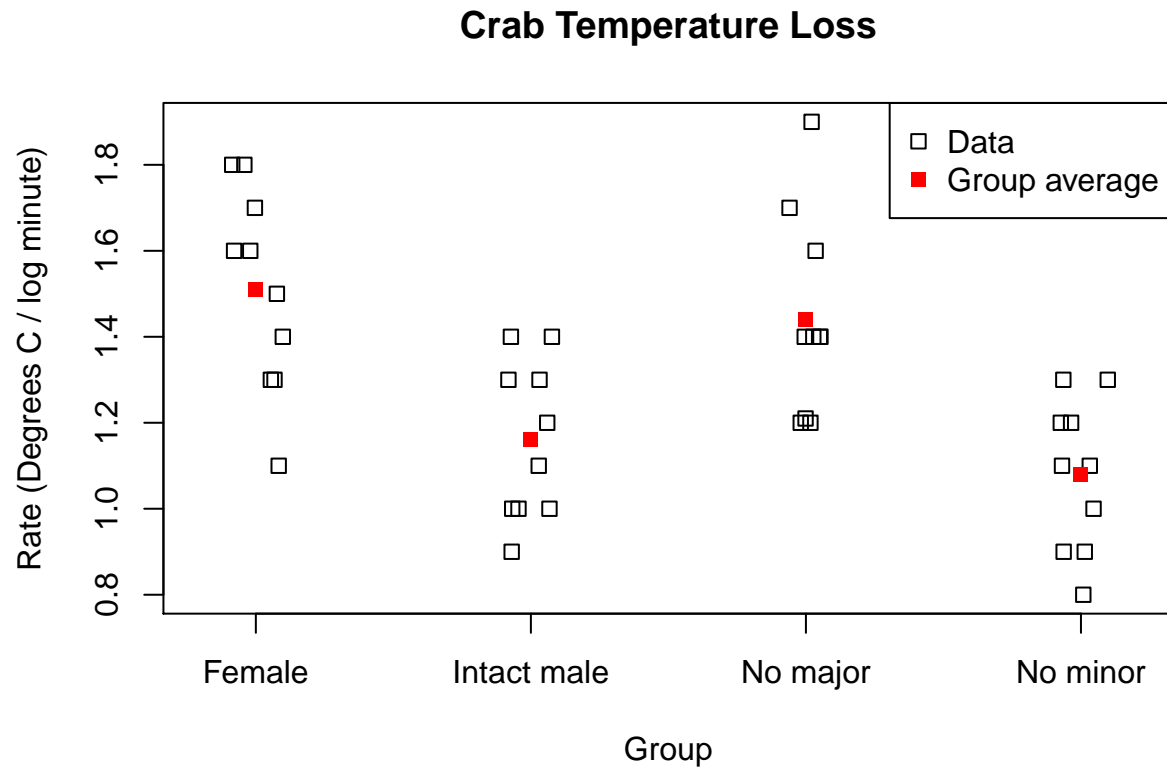
Script

```
suppressPackageStartupMessages(library(gplots))

setwd("~/code/biometry-lab/lab10/")
crab <- read.csv("crabs.csv")
means <- tapply(crab$rate, crab$group, mean)

# Make a strip chart of the data.
stripchart(rate~group,
            data = crab,
            method = "jitter",
            vertical = T,
            main = "Crab Temperature Loss",
            xlab = "Group",
            ylab = "Rate (Degrees C / log minute)")
points(means, pch=15, col = 'red') #add average points to plot
legend('topright', legend = c("Data", "Group average"), col= c('black', 'red'), pch=c(0,15))
```

Output



Answers

Question 2

Script

```
# Do an ANOVA to test for any differences in mean rate of
# heat gain among the groups.
df_treatment <- length(means) - 1
df_error <- length(crab$rate) - length(means)
total_mean <- mean(crab$rate)
SS_treatment <- sum(tapply(crab$rate, crab$group, FUN=function(x){sum(length(x)*(mean(x) - total_mean)^2)}))
SS_error <- sum(tapply(crab$rate, crab$group, FUN=function(x){sum((x - mean(x))^2)}))
MS_treatment <- SS_treatment/df_treatment
MS_error <- SS_error / df_error
fval <- MS_treatment/MS_error
pval <- 1 - pf(fval, df_treatment, df_error)
```

Output

Answers

Use your results to fill in an ANOVA table like the one below.

Category	df	SS	MS	F	P
Treatment	3	1.3196075	0.4398692	10.2275995	5.18e-5
Error	36	1.54829	0.0430081		

In addition, make a clear statement of the null and alternative hypotheses that you tested and the results of your test.

H0: The mean of each treatment group is the same.

Ha: There is a mean group that is not the same as the others.

With a confidence level of 0.05, I reject the null hypothesis that the mean of each treatment group is identical (ANOVA, $F_{3,36} = 10.228$, $p = 5.18e-5$).

Question 3

Script

```
# 3. Re-do the ANOVA using R's aov command.
mod <- aov(rate~group, data = crab)
summary(mod)
```

Output

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## group         3   1.320   0.4399    10.23 5.18e-05 ***
## Residuals    36   1.548   0.0430
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Answers

Question 4

Script

```
# a. Estimate the group's mean rate of heat gain.
means

# b. Calculate the 95% confidence interval of the mean.
se <- sqrt(MS_error/length(crab$rate))
tcrit <- qt(c(.025,.975),df_error)
cis <- lapply(means, FUN = function(x){x + tcrit * se}) #confidence interval for each grp
cis
```

Output

```
##      Female Intact male      No major      No minor
##      1.510      1.160      1.441      1.080
```

```
## $Female
## [1] 1.443498 1.576502
##
## $`Intact male`
## [1] 1.093498 1.226502
##
## $`No major`
## [1] 1.374498 1.507502
##
## $`No minor`
## [1] 1.013498 1.146502
```

Answers

Question 5

Script

```
# Now determine perform pairwise comparisons to test which groups differ from which.
comparisons <- combn(unique(crab$group),2,simplify = F)

# Perform Tukey-Kramer tests on all possible comparisons
diffs <- sapply(comparisons, FUN=function(x){means[x[2]] - means[x[1]]})
SE_tukeys <- sapply(comparisons, FUN=function(x){sqrt(0.5 * (MS_error/sum(crab$group == x[1]))+MS_error/sum(crab$group == x[2]))})
qs <- abs(diffs)/SE_tukeys
pvals <- 1 - ptukey(qs,length(unique(crab$group)),df_error)
conclusions <- ifelse(pvals < 0.05, "Reject", "Fail to Reject")

tukeytable <- data.frame(comparison = sapply(comparisons, paste, collapse = " - "), diff = diffs, q = qs, p = pvals, conclusion = conclusions)
```

Output

Answers

Do these tests by hand and present your results in a table like this:

comparison	diff	q	p	conclusion
Female - Intact male	-0.350	5.336950	0.0031168	Reject
Female - No minor	-0.430	6.556824	0.0002558	Reject
Female - No major	-0.069	1.052142	0.8786067	Fail to Reject
Intact male - No minor	-0.080	1.219874	0.8239361	Fail to Reject
Intact male - No major	0.281	4.284808	0.0223605	Reject
No minor - No major	0.361	5.504683	0.0022342	Reject

Question 6

Script

```
# Repeat these Tukey-Kramer tests using R's TukeyHSD command.  
TukeyHSD(mod)
```

Output

```
## Tukey multiple comparisons of means  
## 95% family-wise confidence level  
##  
## Fit: aov(formula = rate ~ group, data = crab)  
##  
## $group  
##  
## diff lwr upr p adj  
## Intact male-Female -0.350 -0.59978301 -0.100217 0.0031168  
## No major-Female -0.069 -0.31878301 0.180783 0.8786067  
## No minor-Female -0.430 -0.67978301 -0.180217 0.0002558  
## No major-Intact male 0.281 0.03121699 0.530783 0.0223605  
## No minor-Intact male -0.080 -0.32978301 0.169783 0.8239361  
## No minor-No major -0.361 -0.61078301 -0.111217 0.0022342
```

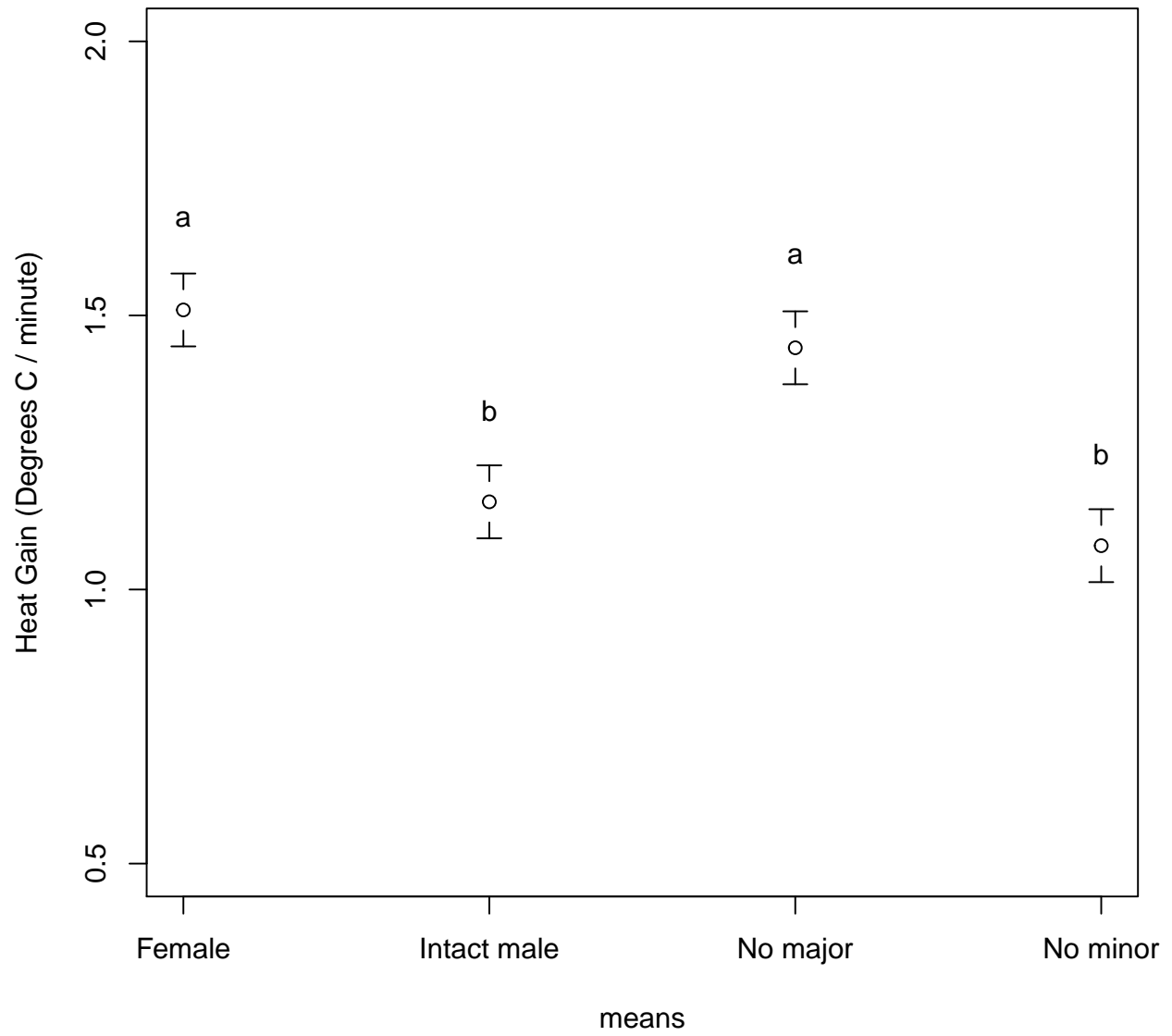
Answers

Question 7

Script

```
# Make an error bar plot, and label it to indicate the  
# Tukey-Kramer test results. For your measure of precision, use the 95%  
# confidence interval of the mean for each group.  
tcrit <- qt(.975,df_error)  
cilen <- tcrit * se #interval length  
  
#plot ci  
plotCI(means, uiw = cilen, xaxt = "n", ylim=c(0.5,2), ylab = "Heat Gain (Degrees C / minute)")  
  
#add back x axis  
axis(1, at=1:4, labels = names(means))  
  
#add group labels from Tukey test  
text(x = 1:4, y = means+cilen+.1, labels=c("a","b","a","b"))
```

Output



Answers