Fall 2022 Stat 407/507 Exam 3 solutions
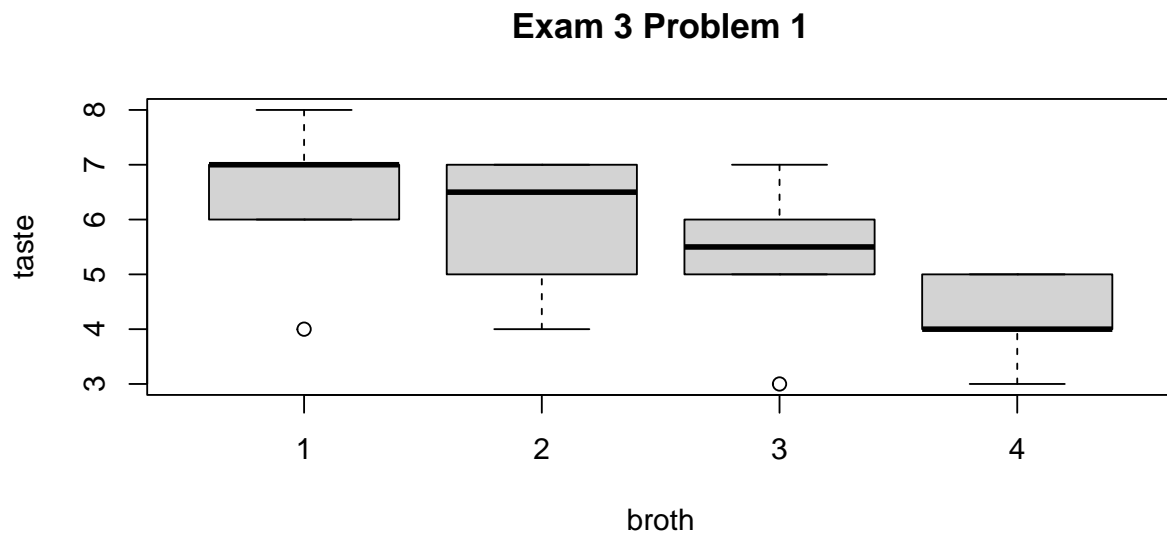
Problem 1

Problem 1a

This is a balanced incomplete block design (BIBD). The model equation is: $y_{ij} = \mu + \alpha_i + \beta_j + \epsilon_{ij}$.

Problem 1b

```
BIBD1 <- read.table("https://webpages.uidaho.edu/~chrisw/stat507live/RamenBrothEx3F22.txt",header=T)

#head(BIBD1)
BIBD1$subj <- as.factor(BIBD1$subj)
BIBD1$broth <- as.factor(BIBD1$broth)
boxplot(taste ~ broth, data=BIBD1, main="Exam 3 Problem 1")
```


There is a clear suggestion of differences in mean taste due to broth type. Possible skewness and outliers may lead to problems with model assumptions.

Problem 1c

```
BIBD1.lm1 <- lm(taste ~ subj + broth, data=BIBD1)
anova(BIBD1.lm1)
```

```
## Analysis of Variance Table
##
## Response: taste
##           Df Sum Sq Mean Sq F value    Pr(>F)
## subj       7 32.000  4.5714  10.888 0.0001523 ***
## broth      3 10.542  3.5139   8.369 0.0023474 **
## Residuals 13  5.458  0.4199
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
library(multcomp)
```

```
## Loading required package: mvtnorm
```

```
## Loading required package: survival
```

```
## Loading required package: TH.data
```

```
## Loading required package: MASS
```

```
##
## Attaching package: 'TH.data'
```

```
## The following object is masked from 'package:MASS':
##
##     geyser
```

```
trt.Tukey <- glht(BIBD1.lm1,linfct=mcp(broth="Tukey"))
summary(trt.Tukey)
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = taste ~ subj + broth, data = BIBD1)
##
## Linear Hypotheses:
##             Estimate Std. Error t value Pr(>|t|)
## 2 - 1 == 0  -0.6875     0.3968  -1.733  0.34696
## 3 - 1 == 0  -1.1250     0.3968  -2.835  0.05970 .
## 4 - 1 == 0  -1.9375     0.3968  -4.883  0.00176 **
## 3 - 2 == 0  -0.4375     0.3968  -1.103  0.69426
## 4 - 2 == 0  -1.2500     0.3968  -3.150  0.03410 *
```

```
## 4 - 3 == 0  -0.8125     0.3968  -2.048  0.22117
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```r
# with interblock recovery
library(afex)
```

```
## Loading required package: lme4

## Loading required package: Matrix

## ************
## Welcome to afex. For support visit: http://afex.singmann.science/

## - Functions for ANOVAs: aov_car(), aov_ez(), and aov_4()
## - Methods for calculating p-values with mixed(): 'S', 'KR', 'LRT', and 'PB'
## - 'afex_aov' and 'mixed' objects can be passed to emmeans() for follow-up tests
## - NEWS: emmeans() for ANOVA models now uses model = 'multivariate' as default.
## - Get and set global package options with: afex_options()
## - Set orthogonal sum-to-zero contrasts globally: set_sum_contrasts()
## - For example analyses see: browseVignettes("afex")
## ************

##
## Attaching package: 'afex'

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

```r
library(emmeans)

BIBD1.afex1  <- mixed(taste ~ (1|subj) + broth, data = BIBD1)
```

```
## Contrasts set to contr.sum for the following variables: subj, broth
```

```r
#summary(BIBD1.afex1)
nice(BIBD1.afex1)
```

```
## Mixed Model Anova Table (Type 3 tests, S-method)
##
## Model: taste ~ (1 | subj) + broth
## Data: BIBD1
##   Effect       df      F p.value
## 1  broth 3, 13.39 9.01 **    .002
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '+' 0.1 ' ' 1
```

```
emmeans(BIBD1.afex1, list(pairwise ~ broth), adjust = "tukey")
```

```
## $`emmeans of broth`
##  broth emmean    SE   df lower.CL upper.CL
##  1       6.45 0.457 12.3     5.45     7.44
##  2       5.78 0.457 12.3     4.79     6.78
##  3       5.32 0.457 12.3     4.32     6.31
##  4       4.46 0.457 12.3     3.46     5.45
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of broth`
##  1               estimate    SE   df t.ratio p.value
##  broth1 - broth2    0.663 0.396 13.4   1.673  0.3742
##  broth1 - broth3    1.130 0.396 13.4   2.852  0.0569
##  broth1 - broth4    1.989 0.396 13.4   5.018  0.0011
##  broth2 - broth3    0.467 0.396 13.4   1.179  0.6497
##  broth2 - broth4    1.326 0.396 13.4   3.344  0.0232
##  broth3 - broth4    0.858 0.396 13.4   2.166  0.1828
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 4 estimates
```

From the intra-block analysis, the treatment effect of broth is clearly significant with $F = 8.37$ on 3 and 13 degrees of freedom and $P < .01$. The subject effect also explained much of the variation in the responses. The Tukey multiple comparisons show that broth 4 has significantly lower mean taste than broths 1 and 2, and is approaching significantly lower mean taste than broth 3. The mixed model using interblock recovery of information gives similar, but slightly more significant results.

Problem 1d

```
par(mfrow=c(1,2))
plot(BIBD1.lm1,which=c(1,2))
```

4
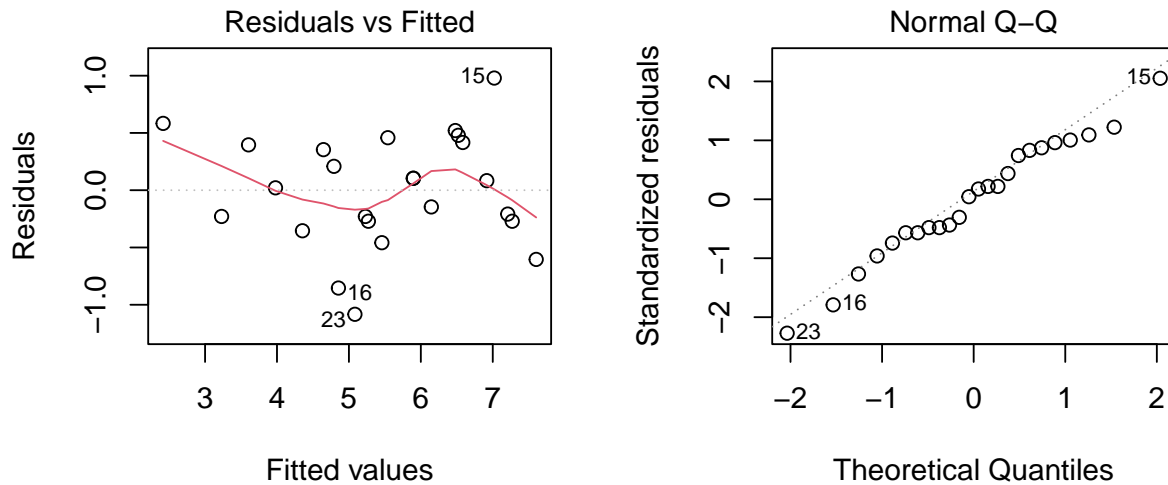
```
par(mfrow=c(1,1))
```

The S shaped line in the residual x predicted plot is mainly due to a couple of outliers, but the overall pattern does not suggest heterogeneity of variance. The normal plot is fairly good. Model assumptions seem reasonable.

Problem 1e

A balanced incomplete block design was used to compare the taste of four different broths. Eight subjects were used and each tried three broths. The intra-block analysis shows a significant effect of broths, and follow-up Tukey multiple comparisons showed that broth 4 has significantly lower mean taste than broths 1 and 2, and nearly significantly lower mean taste than broth 3.

Problem 1f

As shown above, the mixed model analysis can lead to a more efficient (powerful) test by incorporating between block variation.

Problem 2

Problem 2a

This is a repeated measures experiment, which we can express initially as a split-plot experiment with one whole-plot treatment and one split-plot treatment, with the whole plot treatment having completely randomized treatment structure. The equation for the split-plot model with completely randomized whole plot treatment structure is: $y_{ijk} = \mu + \alpha_i + \eta_{k(i)} + \beta_j + \alpha\beta_{ij} + \epsilon_{k(ij)}$.
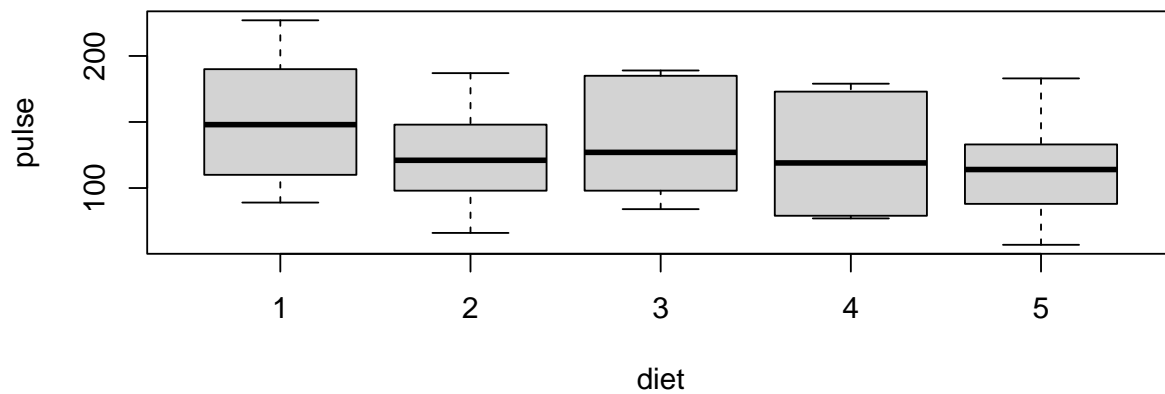
Problem 2b

```
RM0 <- read.table("https://webpages.uidaho.edu/~chrisw/stat507live/ExercisePulseEx3F22.txt",header=T)

#head(RM0)
RM0$subj <- as.factor(RM0$subj)
RM0$diet <- as.factor(RM0$diet)
RM0$time <- as.factor(RM0$time)

#par(mfrow=c(2,2))
boxplot(pulse ~ diet, data=RM0, main="Exam 3 Problem 2")
```
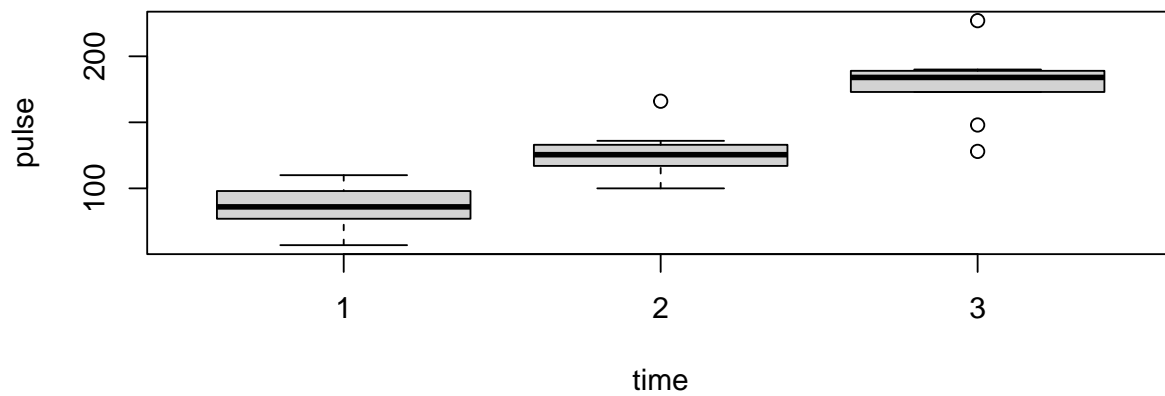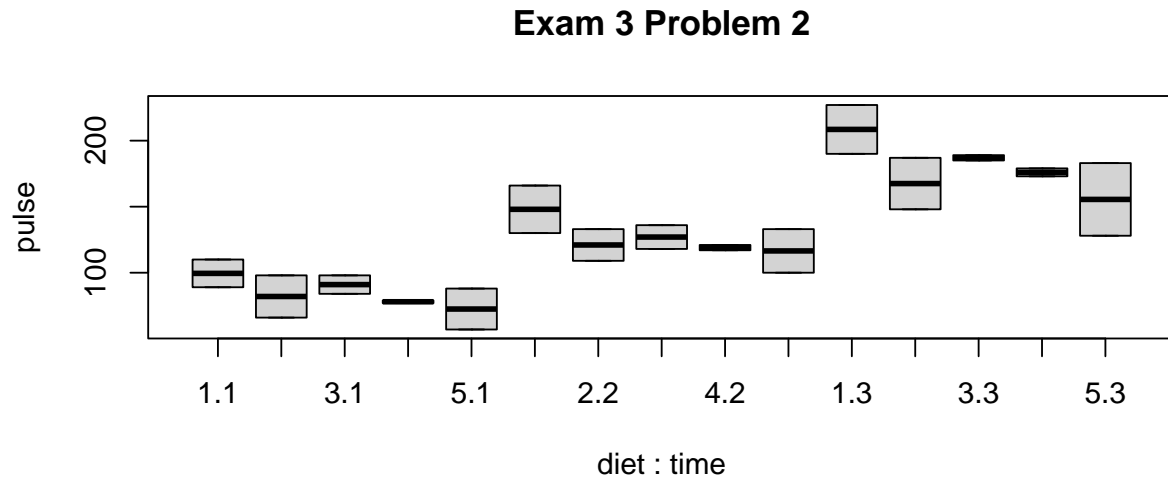
Exam 3 Problem 2


```
boxplot(pulse ~ time, data=RM0, main="Exam 3 Problem 2")
```

Exam 3 Problem 2

```r
boxplot(pulse ~ diet:time, data=RM0, main="Exam 3 Problem 2")
```

Exam 3 Problem 2


```r
#par(mfrow=c(1,1))
```

Here are three boxplots with the third one using both treatments, allowing it to give us insight into potential interactions. The first two boxplots show a clear effect of exercise type (time) but not necessarily an effect of diet type. The interaction boxplot shows similar diet patterns across the three times, not giving much evidence for an interaction. The boxplot for time shows some potential outliers, but otherwise there are not signs of serious problems with model assumptions.

Problem 2c

```r
RM0.lm1 <- lm(pulse ~ diet +subj:diet  +time +diet:time, data=RM0)
anova(RM0.lm1)
```

```
## Analysis of Variance Table
##
## Response: pulse
##           Df Sum Sq Mean Sq  F value    Pr(>F)
## diet       4   4880  1220.0  26.0324 2.872e-05 ***
## time       2  44660 22330.2 476.4630 1.208e-10 ***
## diet:subj  5   5478  1095.7  23.3784 3.220e-05 ***
## diet:time  8    592    74.0   1.5795    0.2449
## Residuals 10    469    46.9
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
library(afex)
library(emmeans)
```

```
RM0.afex0  <- mixed(pulse ~ diet + (1|diet:subj) +time +diet:time,
                             data = RM0)
```

```
## Contrasts set to contr.sum for the following variables: diet, subj, time
```

```
nice(RM0.afex0)
```

```
## Mixed Model Anova Table (Type 3 tests, S-method)
##
## Model: pulse ~ diet + (1 | diet:subj) + time + diet:time
## Data: RM0
##        Effect     df           F p.value
## 1        diet   4, 5        1.11    .443
## 2        time  2, 10  476.46 ***   <.001
## 3   diet:time  8, 10        1.58    .245
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '+' 0.1 ' ' 1
```

```
emmeans(RM0.afex0, list(pairwise ~ time), adjust = "tukey")
```

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

```
## $`emmeans of time`
##  time emmean  SE   df lower.CL upper.CL
##  1      84.6 6.3 5.87     69.1      100
##  2     126.3 6.3 5.87    110.8      142
##  3     178.9 6.3 5.87    163.4      194
##
## Results are averaged over the levels of: diet
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of time`
##  1              estimate   SE df t.ratio p.value
##  time1 - time2     -41.7 3.06 10 -13.620  <.0001
##  time1 - time3     -94.3 3.06 10 -30.801  <.0001
##  time2 - time3     -52.6 3.06 10 -17.181  <.0001
##
## Results are averaged over the levels of: diet
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 3 estimates
```

The correct mixed-model analysis shows a highly significant effect due to time (exercise type) with $F = 476.5$ on 2 and 10 degrees of freedom and $P < .001$. The effects of diet and interaction were not significant. Tukey multiple comparison tests for the time factor show that all three times (exercise types) are significantly different.

Problem 2d

```
par(mfrow=c(1,2))
plot(RM0.lm1,which=c(1,2))
```
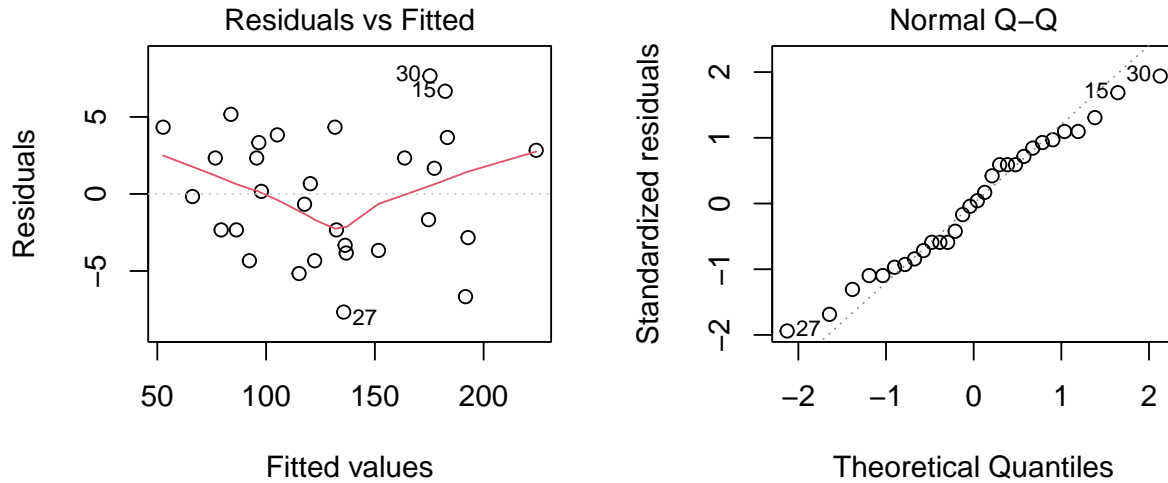


```
par(mfrow=c(1,1))
```

There are several ways to assess split-plot model assumptions. The plots above are from the fixed-effects model and so are approximate. These plots do not show any severe problems with variance heterogeneity (from the residual x predicted plot) or normality (from the qq plot). Plots from other models similarly do not show problems with model assumptions.

Problem 2e

An experiment involving five different diets and three exercise types was conducted to study if either factor effected pulse rate. Although the diets were randomized to subjects, the exercise types were administered in a fixed sequence and hence constitute a repeated-measures experiment. An initial split-plot model analysis showed only a significant effect of exercise type but not diet or the diet-exercise interaction. Tukey multiple comparison tests for exercise type showed that all three types were significantly different. Mauchley's test was used to test the sphericity assumption and failed to reject the null hypothesis of sphericity, so the initial split-plot analysis is valid.

Problem 2f

```
RM0.afex1 <- aov_ez(id="subj",dv="pulse",data=RM0, between=c("diet"),within=c("time"))
```

```
## Contrasts set to contr.sum for the following variables: diet
```

```
summary(RM0.afex1)
```

```
##
## Univariate Type III Repeated-Measures ANOVA Assuming Sphericity
##
##             Sum Sq num Df Error SS den Df  F value     Pr(>F)
## (Intercept) 506480      1   5478.3      5 462.2575 4.037e-06 ***
## diet          4880      4   5478.3      5   1.1135    0.4430
## time         44660      2    468.7     10 476.4630 1.208e-10 ***
## diet:time      592      8    468.7     10   1.5795    0.2449
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
## Mauchly Tests for Sphericity
##
##           Test statistic p-value
## time             0.59875  0.3585
## diet:time        0.59875  0.3585
##
##
## Greenhouse-Geisser and Huynh-Feldt Corrections
##  for Departure from Sphericity
##
##           GG eps Pr(>F[GG])
## time      0.71365  4.432e-08 ***
## diet:time 0.71365      0.279
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##             HF eps    Pr(>F[HF])
## time      0.9185975 6.448972e-10
## diet:time 0.9185975 2.538158e-01
```

The P value for Mauchley's test (P = .359) indicates that we do not reject the null hypothesis of sphericity. The sphericity assumption (or HF condition) is that the variance of the differences between any two repeated measures means are equal. A less general but easier to explain condition is that of compound symmetry, where the covariances between different repeated measures are equal and the variances of the repeated measures are equal.