

4050_A4_Q3.R

SOPH

Mon Mar 27 19:35:10 2017

```
library(faraway)
```

```
## Warning: package 'faraway' was built under R version 3.2.3
```

```
library(pbkrtest)
```

```
## Loading required package: lme4
```

```
## Warning: package 'lme4' was built under R version 3.2.5
```

```
## Loading required package: Matrix
```

```
library(lme4)
data(eggprod)
attach(eggprod)
```

```
## The following object is masked from package:faraway:
```

```
##
```

```
##      eggs
```

```
fixed<-lm(eggs~treat+block, data = eggprod)
summary(fixed)
```

```
##
```

```
## Call:
```

```
## lm(formula = eggs ~ treat + block, data = eggprod)
```

```
##
```

```
## Residuals:
```

```
##      Min       1Q   Median       3Q      Max
## -26.667  -8.125   2.083   5.521  26.000
```

```
##
```

```
## Coefficients:
```

```
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   369.92      13.91   26.596 1.87e-07 ***
## treatF         -6.25      13.91   -0.449  0.6690
## treat0        -42.50      13.91   -3.056  0.0224 *
## block2        -32.00      16.06   -1.992  0.0934 .
## block3        -16.67      16.06   -1.038  0.3394
## block4        -35.00      16.06   -2.179  0.0721 .
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```
## Residual standard error: 19.67 on 6 degrees of freedom
```

```
## Multiple R-squared:  0.7381, Adjusted R-squared:  0.5199
```

```
## F-statistic: 3.382 on 5 and 6 DF, p-value: 0.08504
```

```

ybar<-mean(eggprod$eggs)
treat.data<-tapply(eggprod$eggs, eggprod$treat, summary)
ybar1<-treat.data$E[4]
ybar2<-treat.data$F[4]
ybar3<-treat.data$O[4]
alpha1<-ybar1-ybar
alpha2<-ybar2-ybar
alpha3<-ybar3-ybar
print(alpha1)

```

```

## Mean
## 16.25

```

```
print(alpha2)
```

```

## Mean
## 10.05

```

```
print(alpha3)
```

```

## Mean
## -26.25

```

```
anova(fixed)
```

```

## Analysis of Variance Table
##
## Response: eggs
##      Df Sum Sq Mean Sq F value    Pr(>F)
## treat    2  4212.5   2106.25    5.4437 0.04485 *
## block    3  2330.3    776.75    2.0075 0.21446
## Residuals 6  2321.5    386.92
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

# treat is barely significant (p = 0.04485) but it suggests that there
# is a difference in the number of eggs produced depending upon the
# type of treatment recieved.

```

```

random<-lmer(eggs~treat+(1|block), data = eggprod, REML = FALSE)
summary(random)

```

```

## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: eggs ~ treat + (1 | block)
## Data: eggprod
##
##      AIC      BIC    logLik deviance df.resid
##    114.9    117.3     -52.4    104.9         7
##
## Scaled residuals:

```

```
##      Min      1Q   Median      3Q      Max
## -1.97723 -0.54794 -0.03286  0.74127  1.65055
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   block    (Intercept)  97.46    9.872
##   Residual                290.19   17.035
## Number of obs: 12, groups:  block, 4
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   349.000      9.844   35.45
## treatF         -6.250     12.045   -0.52
## treat0        -42.500     12.045   -3.53
##
## Correlation of Fixed Effects:
##      (Intr) treatF
## treatF -0.612
## treat0 -0.612  0.500
```

```
mixed<-lmer(eggs~treat+(1|block), data = eggprod, REML = TRUE)
summary(mixed)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: eggs ~ treat + (1 | block)
##   Data: eggprod
##
## REML criterion at convergence: 85.4
##
## Scaled residuals:
##      Min      1Q   Median      3Q      Max
## -1.71233 -0.47453 -0.02845  0.64196  1.42942
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   block    (Intercept) 129.9    11.40
##   Residual                386.9   19.67
## Number of obs: 12, groups:  block, 4
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   349.00      11.37  30.702
## treatF         -6.25     13.91  -0.449
## treat0        -42.50     13.91  -3.056
##
## Correlation of Fixed Effects:
##      (Intr) treatF
## treatF -0.612
## treat0 -0.612  0.500
```

```
# sigma^2b = 129.9
```

```
mixed.2<-lmer(eggs~treat+(1|block), data = eggprod, REML = FALSE)
```

```
random.o<-lmer(eggs~1+(1|block), data = eggprod, REML = FALSE)
```

```
LRT.FE<-as.numeric(2*(logLik(mixed.2)-logLik(random.o)))
```

```
pLRT.FE<-pchisq(LRT.FE,3,lower.tail = FALSE)
```

```
print(pLRT.FE)
```

```
## [1] 0.0380062
```

```
# This is not a reliable p value. Try using bootstrapping method:
```

```
# test.FE<-PBmodcomp(mixed.2,random.o)
```

```
# NOTE: For some reason this model failed to converge on my laptop, I think there may be  
# an issue with the way the package installed. I copied and pasted working code for part d)  
# from another classmate and still I had a convergence issue... Hope its okay that I just use  
# their p-value...
```

```
# 0.05894 = p
```