

ANCOVA_fitness.R

John

Tue Nov 27 09:58:40 2018

```
# ANCOVA_fitness.R
# ANCOVA for T. dubius fitness

# Load necessary libraries
library(car)

## Loading required package: carData
library(ggplot2)

## Warning: package 'ggplot2' was built under R version 3.5.1
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
library(emmeans)

# Read in data set
fitdata <- read.table(header=T,colClasses=c(rep("numeric",2),"factor"),text="
eggs length treat
290 5.7 DietIG
99 5.2 DietIG
340 5.5 DietIG
271 4.8 DietIG
200 5.2 DietIG
405 5.2 DietIG
178 5.1 DietIG
48 5.0 DietIG
146 4.8 DietIG
184 4.9 DietIG
66 4.6 DietCPW
93 5.0 DietCPW
9 5.4 DietCPW
404 5.4 DietCPW
244 5.1 DietCPW
195 4.9 DietCPW
343 5.2 DietCPW
516 5.0 DietCPW
```

```

215 4.6 DietCPW
412 5.6 DietCPW
167 4.8 DietCPW
316 5.2 DietCPW
334 5.3 DietCPW
 62 4.7 WildCPW
290 5.0 WildCPW
488 5.8 WildCPW
336 5.2 WildCPW
337 5.8 WildCPW
230 5.0 WildCPW
381 5.3 WildCPW
192 5.5 WildCPW
186 5.3 WildCPW
467 5.2 WildCPW
 59 4.9 WildCPW
323 5.7 WildCPW
291 4.9 WildCPW
164 5.3 WildCPW
142 5.3 WildCPW
269 5.0 WildCPW
329 5.4 WildCPW
235 5.0 WildCPW
")

# Choose y and x variables
fitdata <- transform(fitdata,y=eggs)
fitdata <- transform(fitdata,x=length)

# Print data set
print(fitdata)

```

```

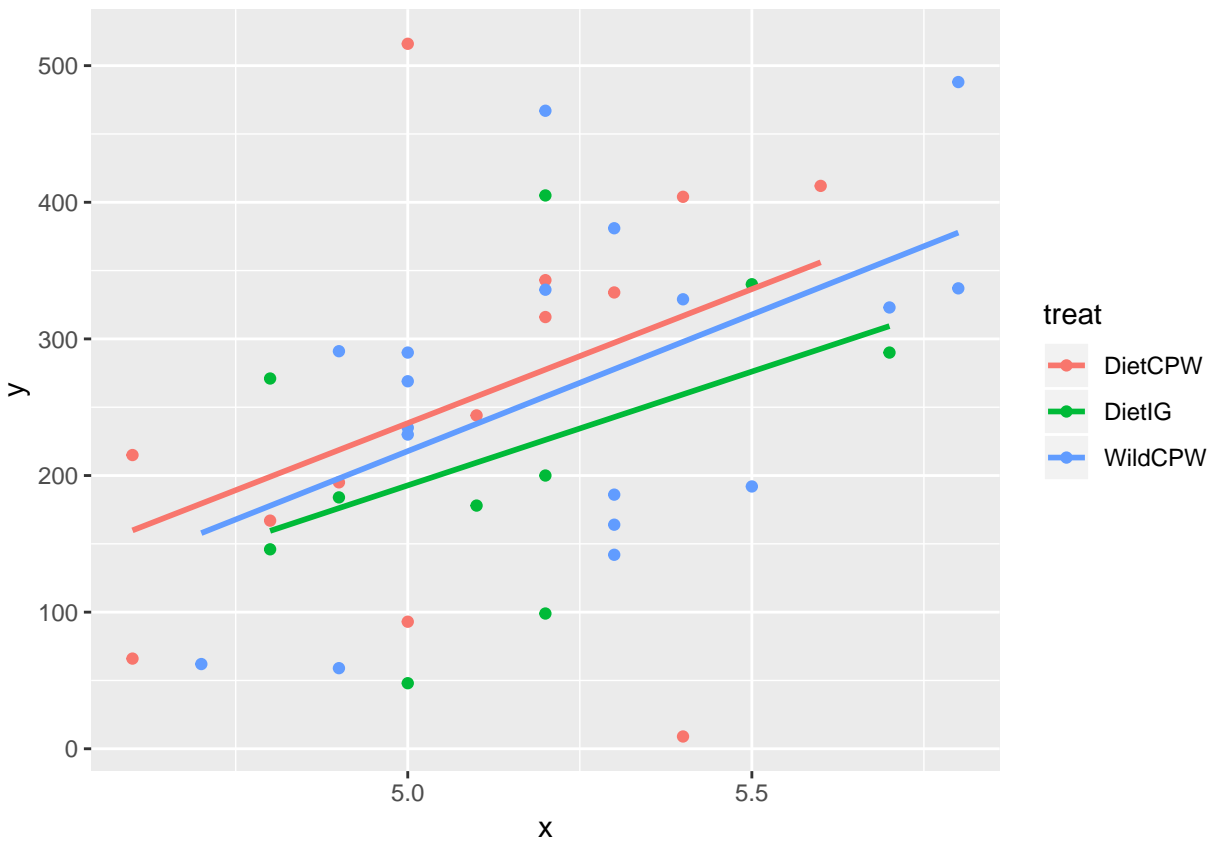
##      eggs length  treat   y   x
## 1    290    5.7 DietIG 290 5.7
## 2     99    5.2 DietIG  99 5.2
## 3    340    5.5 DietIG 340 5.5
## 4    271    4.8 DietIG 271 4.8
## 5    200    5.2 DietIG 200 5.2
## 6    405    5.2 DietIG 405 5.2
## 7    178    5.1 DietIG 178 5.1
## 8     48    5.0 DietIG  48 5.0
## 9    146    4.8 DietIG 146 4.8
## 10   184    4.9 DietIG 184 4.9
## 11    66    4.6 DietCPW  66 4.6
## 12    93    5.0 DietCPW  93 5.0
## 13     9    5.4 DietCPW   9 5.4
## 14   404    5.4 DietCPW 404 5.4
## 15   244    5.1 DietCPW 244 5.1
## 16   195    4.9 DietCPW 195 4.9
## 17   343    5.2 DietCPW 343 5.2
## 18   516    5.0 DietCPW 516 5.0
## 19   215    4.6 DietCPW 215 4.6
## 20   412    5.6 DietCPW 412 5.6
## 21   167    4.8 DietCPW 167 4.8

```

```
## 22 316 5.2 DietCPW 316 5.2
## 23 334 5.3 DietCPW 334 5.3
## 24 62 4.7 WildCPW 62 4.7
## 25 290 5.0 WildCPW 290 5.0
## 26 488 5.8 WildCPW 488 5.8
## 27 336 5.2 WildCPW 336 5.2
## 28 337 5.8 WildCPW 337 5.8
## 29 230 5.0 WildCPW 230 5.0
## 30 381 5.3 WildCPW 381 5.3
## 31 192 5.5 WildCPW 192 5.5
## 32 186 5.3 WildCPW 186 5.3
## 33 467 5.2 WildCPW 467 5.2
## 34 59 4.9 WildCPW 59 4.9
## 35 323 5.7 WildCPW 323 5.7
## 36 291 4.9 WildCPW 291 4.9
## 37 164 5.3 WildCPW 164 5.3
## 38 142 5.3 WildCPW 142 5.3
## 39 269 5.0 WildCPW 269 5.0
## 40 329 5.4 WildCPW 329 5.4
## 41 235 5.0 WildCPW 235 5.0
```

```
# Graphics using ggplot2
```

```
print(ggplot(fitdata,aes(x,y,group=treat,color=treat))+
geom_point()+
stat_smooth(method="lm",se=FALSE))
```



```

# ANCOVA
# Model with interaction
ancout <- lm(y~treat+x+treat:x,data=fitdata)
summary(ancout)

##
## Call:
## lm(formula = y ~ treat + x + treat:x, data = fitdata)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -307.807  -91.830    7.877   65.436  277.680
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -742.769     565.163  -1.314   0.1973
## treatDietIG     102.696     897.163   0.114   0.9095
## treatWildCPW   -39.141     738.801  -0.053   0.9580
## x              196.218     110.964   1.768   0.0857 .
## treatDietIG:x  -29.647     175.032  -0.169   0.8665
## treatWildCPW:x   3.733     143.298   0.026   0.9794
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 118.3 on 35 degrees of freedom
## Multiple R-squared:  0.2335, Adjusted R-squared:  0.124
## F-statistic: 2.132 on 5 and 35 DF,  p-value: 0.08451

confint(ancout)

##              2.5 %    97.5 %
## (Intercept)  -1890.1110  404.5724
## treatDietIG   -1718.6419 1924.0339
## treatWildCPW  -1538.9866 1460.7046
## x             -29.0511  421.4868
## treatDietIG:x -384.9813  325.6870
## treatWildCPW:x -287.1768  294.6432

# ANOVA using Type II SS
Anova(ancout)

## Anova Table (Type II tests)
##
## Response: y
##           Sum Sq Df F value  Pr(>F)
## treat      13846   2  0.4945 0.61404
## x          132427   1  9.4598 0.00406 **
## treat:x       622   2  0.0222 0.97806
## Residuals 489963 35
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Model without interaction
ancout_noint <- lm(y~treat+x,data=fitdata)
summary(ancout_noint)

```

```
##
## Call:
## lm(formula = y ~ treat + x, data = fitdata)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -306.38  -91.33   10.18   65.96  277.30
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -719.78     310.07  -2.321  0.02588 *
## treatDietIG    -49.44      48.55  -1.018  0.31513
## treatWildCPW   -18.89      42.94  -0.440  0.66265
## x              191.70      60.66   3.160  0.00314 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 115.1 on 37 degrees of freedom
## Multiple R-squared:  0.2325, Adjusted R-squared:  0.1703
## F-statistic: 3.736 on 3 and 37 DF,  p-value: 0.01927
```

```
confint(ancout_noint)
```

```
##              2.5 %    97.5 %
## (Intercept) -1348.03584 -91.52395
## treatDietIG  -147.81209  48.93186
## treatWildCPW -105.89663  68.12532
## x              68.79347 314.59952
```

```
# ANOVA using Type II SS
```

```
Anova(ancout_noint)
```

```
## Anova Table (Type II tests)
```

```
##
```

```
## Response: y
```

```
##           Sum Sq Df F value    Pr(>F)
## treat      13846  2  0.5221 0.597553
## x          132427  1  9.9877 0.003138 **
## Residuals 490585 37
```

```
## ---
```

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

```
# Calculate least squares means
```

```
emmeans(ancout_noint,~treat)
```

```
##      treat      emmean      SE df lower.CL upper.CL
## DietCPW  270.4962  32.31422  37 205.0213 335.9710
## DietIG    221.0561  36.44674  37 147.2080 294.9042
## WildCPW   251.6105  27.49982  37 195.8906 307.3304
##
```

```
## Confidence level used: 0.95
```

```
# Obtain multiple comparison object
```

```
compout <- glht(ancout_noint,linfct=mcp(treat="Tukey"))
```

```
# Tukey method - controls the EER
```

```
summary(compout)
```

```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = y ~ treat + x, data = fitdata)
##
## Linear Hypotheses:
##           Estimate Std. Error t value Pr(>|t|)
## DietIG - DietCPW == 0    -49.44     48.55  -1.018   0.569
## WildCPW - DietCPW == 0    -18.89     42.94  -0.440   0.899
## WildCPW - DietIG == 0     30.55     45.81   0.667   0.783
## (Adjusted p values reported -- single-step method)
```

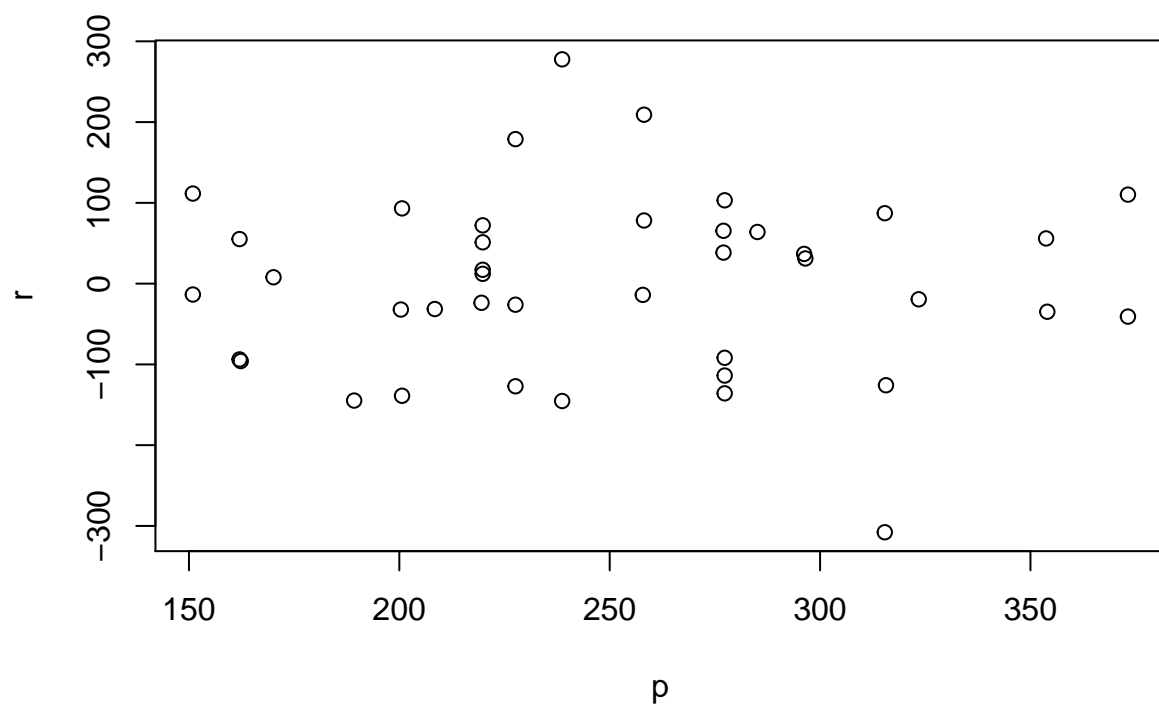
```
confint(compout)
```

```
##
## Simultaneous Confidence Intervals
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = y ~ treat + x, data = fitdata)
##
## Quantile = 2.4395
## 95% family-wise confidence level
##
##
## Linear Hypotheses:
##           Estimate   lwr      upr
## DietIG - DietCPW == 0  -49.4401 -167.8795  68.9993
## WildCPW - DietCPW == 0  -18.8857 -123.6465  85.8752
## WildCPW - DietIG == 0   30.5545  -81.1987 142.3076
```

```
cld(compout)
```

```
## DietCPW DietIG WildCPW
##      "a"      "a"      "a"
```

```
# Diagnostic plots to check ANCOVA assumptions
p <- predict(ancout_noint)
r <- resid(ancout)
plot(p,r)
```



`qqnorm(r)`

