

ANCOVA_fitness.R

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

# Load necessary libraries
library(car)

## Loading required package: carData
library(ggplot2)
library(multcomp)

## Warning: package 'multcomp' was built under R version 4.0.4
## Loading required package: mvtnorm
## Loading required package: survival
## Loading required package: TH.data
## Warning: package 'TH.data' was built under R version 4.0.4
## Loading required package: MASS
##
## Attaching package: 'TH.data'
## The following object is masked from 'package:MASS':
##
##      geyser
library(emmeans)

## Warning: package 'emmeans' was built under R version 4.0.5
# 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
```

```
fitdata
```

```

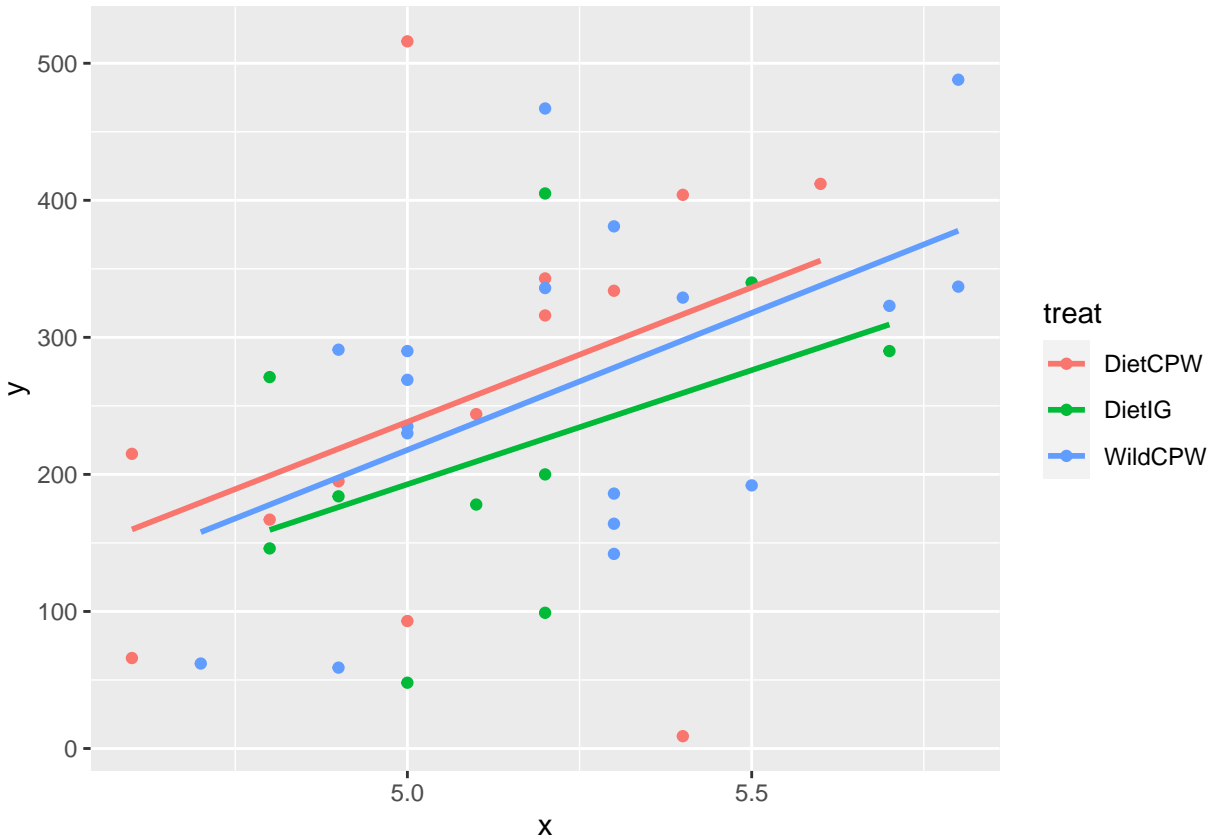
##      eggs length  treat   y   x
## 1    290    5.7 DietIG 290 5.7
## 2     99    5.2 DietIG  99 5.2
## 3    340    5.5 DietIG 340 5.5
## 4    271    4.8 DietIG 271 4.8
## 5    200    5.2 DietIG 200 5.2
## 6    405    5.2 DietIG 405 5.2
## 7    178    5.1 DietIG 178 5.1
## 8     48    5.0 DietIG  48 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
ggplot(fitdata,aes(x,y,group=treat,color=treat))+
geom_point()+
stat_smooth(method="lm",se=FALSE)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



```
# 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 32.3 37      205      336
## DietIG     221 36.4 37      147      295
## WildCPW    252 27.5 37      196      307
##
## 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 = 2.44

```

```
## 95% family-wise confidence level
##
##
## Linear Hypotheses:
##           Estimate   lwr      upr
## DietIG - DietCPW == 0  -49.4401 -167.9032   69.0230
## WildCPW - DietCPW == 0  -18.8857 -123.6674   85.8961
## WildCPW - DietIG == 0   30.5545  -81.2211  142.3300
```

```
cld(compout)
```

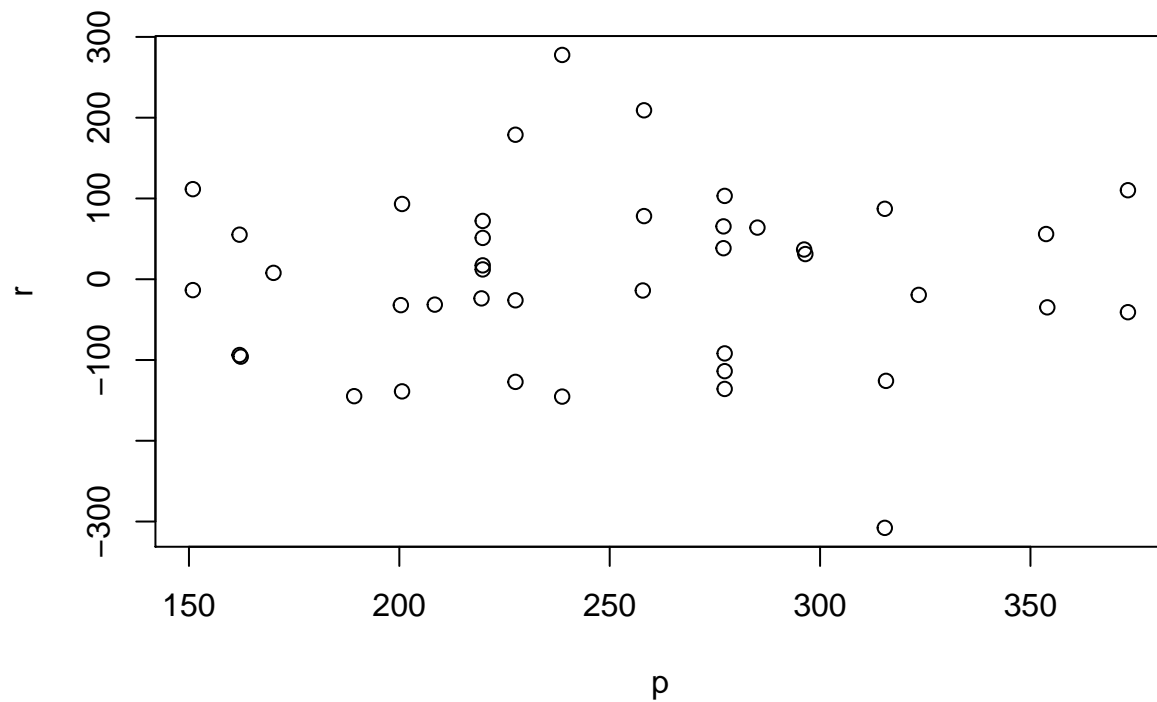
```
## DietCPW DietIG WildCPW
##      "a"      "a"      "a"
```

```
# Diagnostic plots to check ANCOVA assumptions
```

```
p <- predict(ancout_noint)
```

```
r <- resid(ancout)
```

```
plot(p,r)
```



```
qqnorm(r)
```

