

# Maestre\_biomass\_new.R

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```
# Maestre_biomass_new.R
# Two-way ANOVA for biomass (Maestre and Reynolds 2007)

# Load necessary libraries
library(car)

## Loading required package: carData
library(ggplot2)

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

# Read in data set
biomdata <- read.table(header=T,colClasses=c("factor","factor","numeric"),text="
nitrogen water biomass
040 125 4.372
040 125 4.482
040 125 4.221
040 125 3.977
040 250 7.400
040 250 8.027
040 250 7.883
040 250 7.769
040 375 7.226
040 375 8.126
040 375 6.840
040 375 7.901
080 125 5.140
080 125 3.913
080 125 4.669
080 125 4.306
080 250 9.099
```

```

080 250 9.711
080 250 9.123
080 250 9.709
080 375 10.701
080 375 11.552
080 375 11.356
080 375 9.759
120 125 5.021
120 125 4.970
120 125 5.055
120 125 4.862
120 250 9.029
120 250 10.791
120 250 9.115
120 250 10.319
120 375 12.189
120 375 14.381
120 375 13.153
120 375 14.066
")

# Apply transformations here
biomdata <- transform(biomdata,y=log10(biomass))

# Print data set
biomdata

```

```

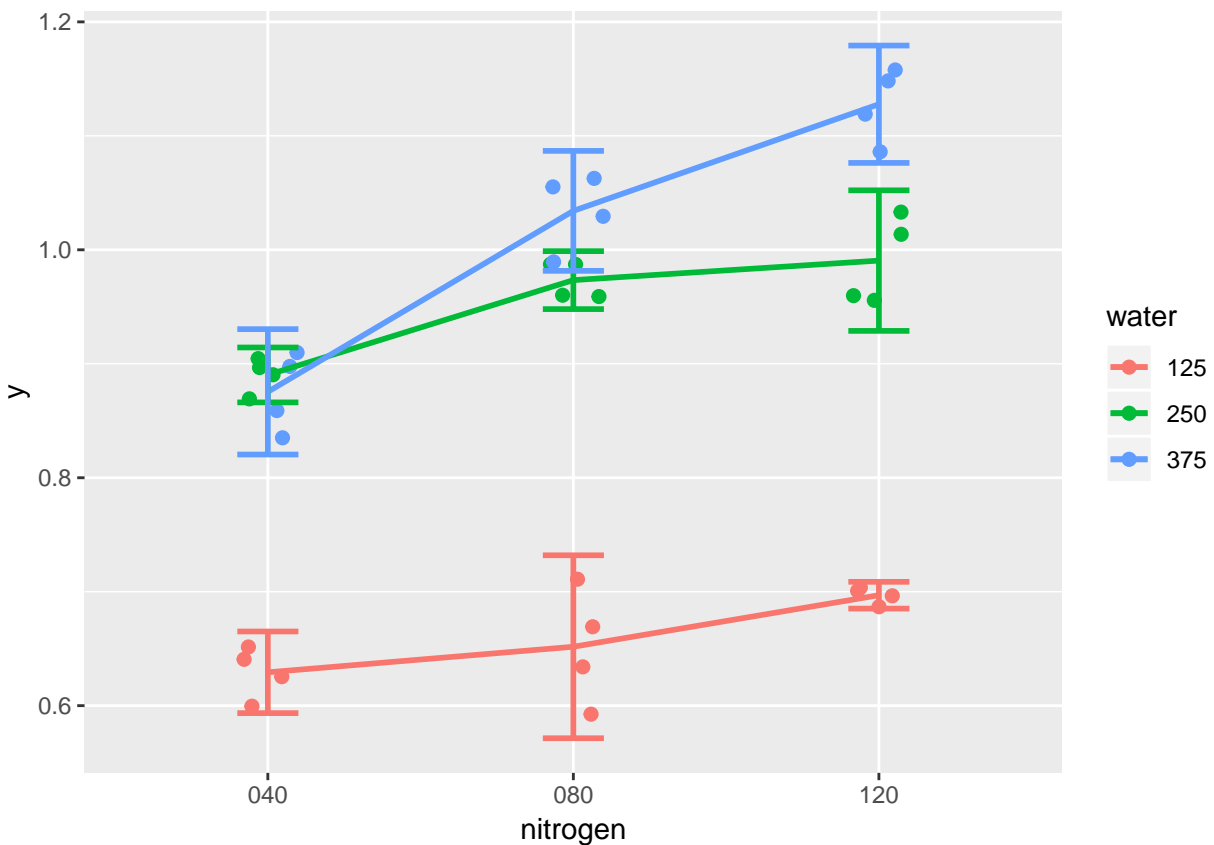
##      nitrogen water biomass      y
## 1         040    125   4.372 0.6406802
## 2         040    125   4.482 0.6514719
## 3         040    125   4.221 0.6254154
## 4         040    125   3.977 0.5995556
## 5         040    250   7.400 0.8692317
## 6         040    250   8.027 0.9045533
## 7         040    250   7.883 0.8966915
## 8         040    250   7.769 0.8903651
## 9         040    375   7.226 0.8588980
## 10        040    375   8.126 0.9098768
## 11        040    375   6.840 0.8350561
## 12        040    375   7.901 0.8976821
## 13        080    125   5.140 0.7109631
## 14        080    125   3.913 0.5925098
## 15        080    125   4.669 0.6692239
## 16        080    125   4.306 0.6340740
## 17        080    250   9.099 0.9589937
## 18        080    250   9.711 0.9872640
## 19        080    250   9.123 0.9601377
## 20        080    250   9.709 0.9871745
## 21        080    375  10.701 1.0294244
## 22        080    375  11.552 1.0626572
## 23        080    375  11.356 1.0552254
## 24        080    375   9.759 0.9894053
## 25        120    125   5.021 0.7007902
## 26        120    125   4.970 0.6963564

```

```
## 27      120    125    5.055 0.7037212
## 28      120    125    4.862 0.6868150
## 29      120    250    9.029 0.9556397
## 30      120    250   10.791 1.0330617
## 31      120    250    9.115 0.9597567
## 32      120    250   10.319 1.0136376
## 33      120    375   12.189 1.0859681
## 34      120    375   14.381 1.1577891
## 35      120    375   13.153 1.1190248
## 36      120    375   14.066 1.1481706
```

```
# Graphics using ggplot2
```

```
ggplot(biomdata,aes(nitrogen,y,group=water,color=water))+
  geom_jitter(size=2,position=position_jitter(width=0.1))+
  stat_summary(fun.y="mean",geom="line",size=1)+
  stat_summary(fun.data="mean_cl_normal",geom="errorbar",width=0.2,size=1)
```



```
# MODEL WITH INTERACTION - USE THIS OUTPUT IF INTERACTION SIGNIFICANT
```

```
aovout <- aov(y~nitrogen+water+nitrogen:water,data=biomdata)
```

```
# ANOVA using Type I SS
```

```
anova(aovout)
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: y
```

```
##          Df Sum Sq Mean Sq F value    Pr(>F)
```

```
## nitrogen      2 0.12039 0.06020 64.276 5.409e-11 ***
## water         2 0.85496 0.42748 456.458 < 2.2e-16 ***
## nitrogen:water 4 0.04235 0.01059 11.305 1.611e-05 ***
## Residuals     27 0.02529 0.00094
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# ANOVA using Type II SS
Anova(aovout)
```

```
## Anova Table (Type II tests)
##
## Response: y
##           Sum Sq Df F value    Pr(>F)
## nitrogen      0.12039  2  64.276 5.409e-11 ***
## water         0.85496  2 456.458 < 2.2e-16 ***
## nitrogen:water 0.04235  4  11.305 1.611e-05 ***
## Residuals     0.02529 27
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Calculate least squares means
emmeans(aovout,~nitrogen:water)
```

```
##  nitrogen water    emmean      SE df  lower.CL  upper.CL
##  040      125    0.6292807 0.01530128 27 0.5978851 0.6606764
##  080      125    0.6516927 0.01530128 27 0.6202971 0.6830883
##  120      125    0.6969207 0.01530128 27 0.6655251 0.7283163
##  040      250    0.8902104 0.01530128 27 0.8588148 0.9216060
##  080      250    0.9733924 0.01530128 27 0.9419968 1.0047881
##  120      250    0.9905239 0.01530128 27 0.9591283 1.0219195
##  040      375    0.8753782 0.01530128 27 0.8439826 0.9067739
##  080      375    1.0341781 0.01530128 27 1.0027824 1.0655737
##  120      375    1.1277381 0.01530128 27 1.0963425 1.1591338
##
```

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

```
# Tests for simple effects
testInteractions(aovout,fixed="water",across="nitrogen",adjustment="none")
```

```
## F Test:
## P-value adjustment method: none
##           nitrogen1 nitrogen2 Df Sum of Sq      F    Pr(>F)
## 125          -0.06764 -0.045228  2  0.009497  5.0706 0.0135008 *
## 250          -0.10031 -0.017131  2  0.023034 12.2977 0.0001596 ***
## 375          -0.25236 -0.093560  2  0.130209 69.5175 2.242e-11 ***
## Residuals                                27  0.025286
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
testInteractions(aovout,fixed="nitrogen",across="water",adjustment="none")
```

```
## F Test:
## P-value adjustment method: none
##           water1    water2 Df Sum of Sq      F    Pr(>F)
## 040          -0.24610  0.014832  2  0.17182  91.736 9.126e-13 ***
## 080          -0.38249 -0.060786  2  0.33797 180.442 2.376e-16 ***
```

```

## 120      -0.43082 -0.137214  2    0.38751 206.890 < 2.2e-16 ***
## Residuals                27    0.02529
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# MODEL WITHOUT INTERACTION - USE THIS OUTPUT IF INTERACTION NS
aovout_noint <- aov(y~nitrogen+water,data=biomdata) # Model without interaction

# Type I SS
anova(aovout_noint)

## Analysis of Variance Table
##
## Response: y
##          Df Sum Sq Mean Sq F value    Pr(>F)
## nitrogen   2  0.12039  0.06020    27.59  1.31e-07 ***
## water       2  0.85496  0.42748   195.93 < 2.2e-16 ***
## Residuals  31  0.06764  0.00218
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Type II SS
Anova(aovout_noint)

## Anova Table (Type II tests)
##
## Response: y
##          Sum Sq Df F value    Pr(>F)
## nitrogen  0.12039  2    27.59  1.31e-07 ***
## water     0.85496  2   195.93 < 2.2e-16 ***
## Residuals 0.06764 31
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Calculate least squares means
emmeans(aovout_noint,~nitrogen)

##   nitrogen    emmean      SE df lower.CL upper.CL
##   040        0.7982898 0.01348391 31  0.7707892 0.8257904
##   080        0.8864211 0.01348391 31  0.8589205 0.9139217
##   120        0.9383942 0.01348391 31  0.9108936 0.9658949
##
## Results are averaged over the levels of: water
## Confidence level used: 0.95

emmeans(aovout_noint,~water)

##   water    emmean      SE df lower.CL upper.CL
##   125    0.6592980 0.01348391 31  0.6317974 0.6867987
##   250    0.9513756 0.01348391 31  0.9238750 0.9788762
##   375    1.0124315 0.01348391 31  0.9849309 1.0399321
##
## Results are averaged over the levels of: nitrogen
## Confidence level used: 0.95

# All pairwise comparisons - Tukey method
compout <- glht(aovout_noint,linfct=mcp(nitrogen="Tukey"))
summary(compout)

```

```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: aov(formula = y ~ nitrogen + water, data = biomdata)
##
## Linear Hypotheses:
##           Estimate Std. Error t value Pr(>|t|)
## 080 - 040 == 0  0.08813    0.01907   4.622  <0.001 ***
## 120 - 040 == 0  0.14010    0.01907   7.347  <0.001 ***
## 120 - 080 == 0  0.05197    0.01907   2.726   0.0275 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
confint(compout)
```

```
##
## Simultaneous Confidence Intervals
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: aov(formula = y ~ nitrogen + water, data = biomdata)
##
## Quantile = 2.4611
## 95% family-wise confidence level
##
##
## Linear Hypotheses:
##           Estimate lwr      upr
## 080 - 040 == 0 0.088131 0.041199 0.135063
## 120 - 040 == 0 0.140104 0.093173 0.187036
## 120 - 080 == 0 0.051973 0.005041 0.098905
```

```
cld(compout)
```

```
## 040 080 120
## "a" "b" "c"
```

```
# All pairwise comparisons - Tukey method
compout <- glht(aovout_noint, linfct=mcp(water="Tukey"))
summary(compout)
```

```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: aov(formula = y ~ nitrogen + water, data = biomdata)
##
## Linear Hypotheses:
##           Estimate Std. Error t value Pr(>|t|)
```

```
## 250 - 125 == 0 0.29208 0.01907 15.317 < 0.001 ***
## 375 - 125 == 0 0.35313 0.01907 18.519 < 0.001 ***
## 375 - 250 == 0 0.06106 0.01907 3.202 0.00859 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

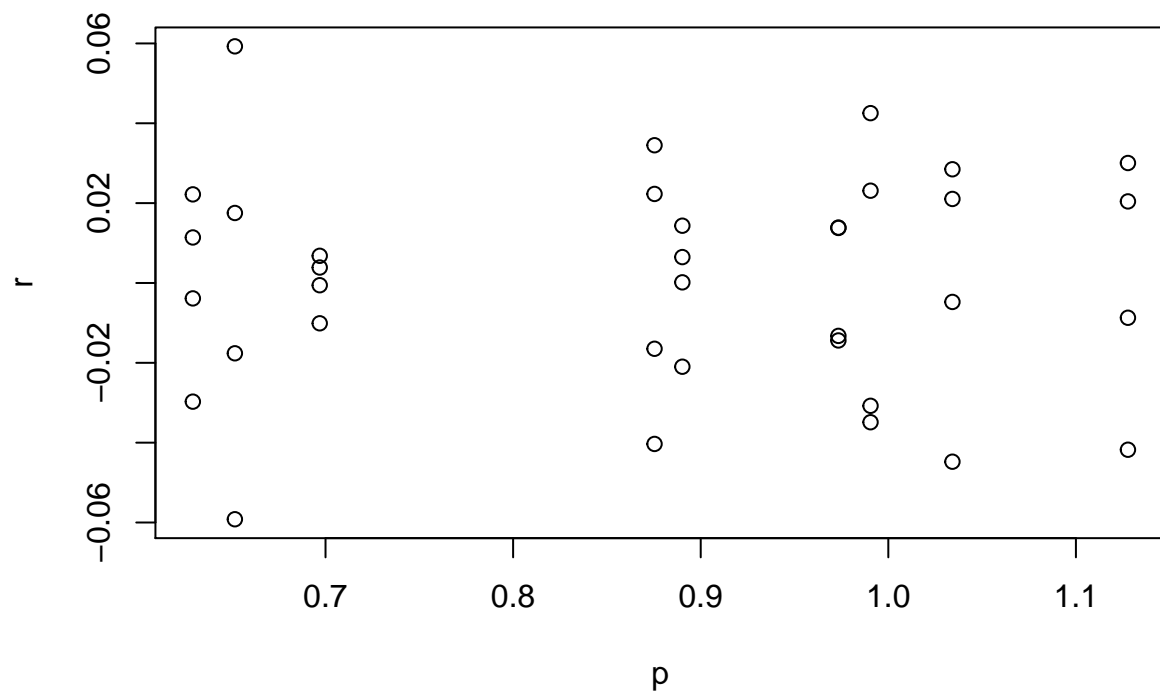
```
confint(compout)
```

```
##
## Simultaneous Confidence Intervals
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: aov(formula = y ~ nitrogen + water, data = biomdata)
##
## Quantile = 2.4625
## 95% family-wise confidence level
##
##
## Linear Hypotheses:
##           Estimate lwr      upr
## 250 - 125 == 0 0.29208 0.24512 0.33904
## 375 - 125 == 0 0.35313 0.30618 0.40009
## 375 - 250 == 0 0.06106 0.01410 0.10801
```

```
cld(compout)
```

```
## 125 250 375
## "a" "b" "c"
```

```
# Diagnostic plots to check ANOVA assumptions
p <- predict(aovout)
r <- resid(aovout)
plot(p,r)
```



`qqnorm(r)`



