

Maestre_biomass_3way_new.R

SIU850486795

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```
# Maestre_biomass_3way_new.R
# Three-way ANOVA for biomass (Maestre and Reynolds 2007)

# Load necessary libraries
library(car)

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

## Warning: package 'emmeans' was built under R version 4.0.5
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(phia)

## Warning: package 'phia' was built under R version 4.0.5
# Read in data set
biomdata <- read.table(header=T,colClasses=c(rep("factor",3),"numeric"),text="
nitrohet nitrogen water biomass
N 040 125 4.372
N 040 125 4.482
N 040 125 4.221
N 040 125 3.977
N 040 250 7.400
N 040 250 8.027
N 040 250 7.883
N 040 250 7.769
```

N	040	375	7.226
N	040	375	8.126
N	040	375	6.840
N	040	375	7.901
N	080	125	5.140
N	080	125	3.913
N	080	125	4.669
N	080	125	4.306
N	080	250	9.099
N	080	250	9.711
N	080	250	9.123
N	080	250	9.709
N	080	375	10.701
N	080	375	11.552
N	080	375	11.356
N	080	375	9.759
N	120	125	5.021
N	120	125	4.970
N	120	125	5.055
N	120	125	4.862
N	120	250	9.029
N	120	250	10.791
N	120	250	9.115
N	120	250	10.319
N	120	375	12.189
N	120	375	14.381
N	120	375	13.153
N	120	375	14.066
Y	040	125	5.458
Y	040	125	5.017
Y	040	125	5.479
Y	040	125	5.714
Y	040	250	8.972
Y	040	250	9.234
Y	040	250	8.032
Y	040	250	8.372
Y	040	375	9.464
Y	040	375	9.563
Y	040	375	9.385
Y	040	375	8.226
Y	080	125	6.616
Y	080	125	6.909
Y	080	125	6.851
Y	080	125	6.098
Y	080	250	10.792
Y	080	250	10.164
Y	080	250	10.947
Y	080	250	9.582
Y	080	375	14.936
Y	080	375	13.607
Y	080	375	14.231
Y	080	375	12.038
Y	120	125	7.389

```

Y 120 125 6.683
Y 120 125 7.759
Y 120 125 6.752
Y 120 250 10.731
Y 120 250 12.640
Y 120 250 10.350
Y 120 250 11.550
Y 120 375 14.697
Y 120 375 17.826
Y 120 375 14.711
Y 120 375 13.614
")

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

# Print data
biomdata

```

```

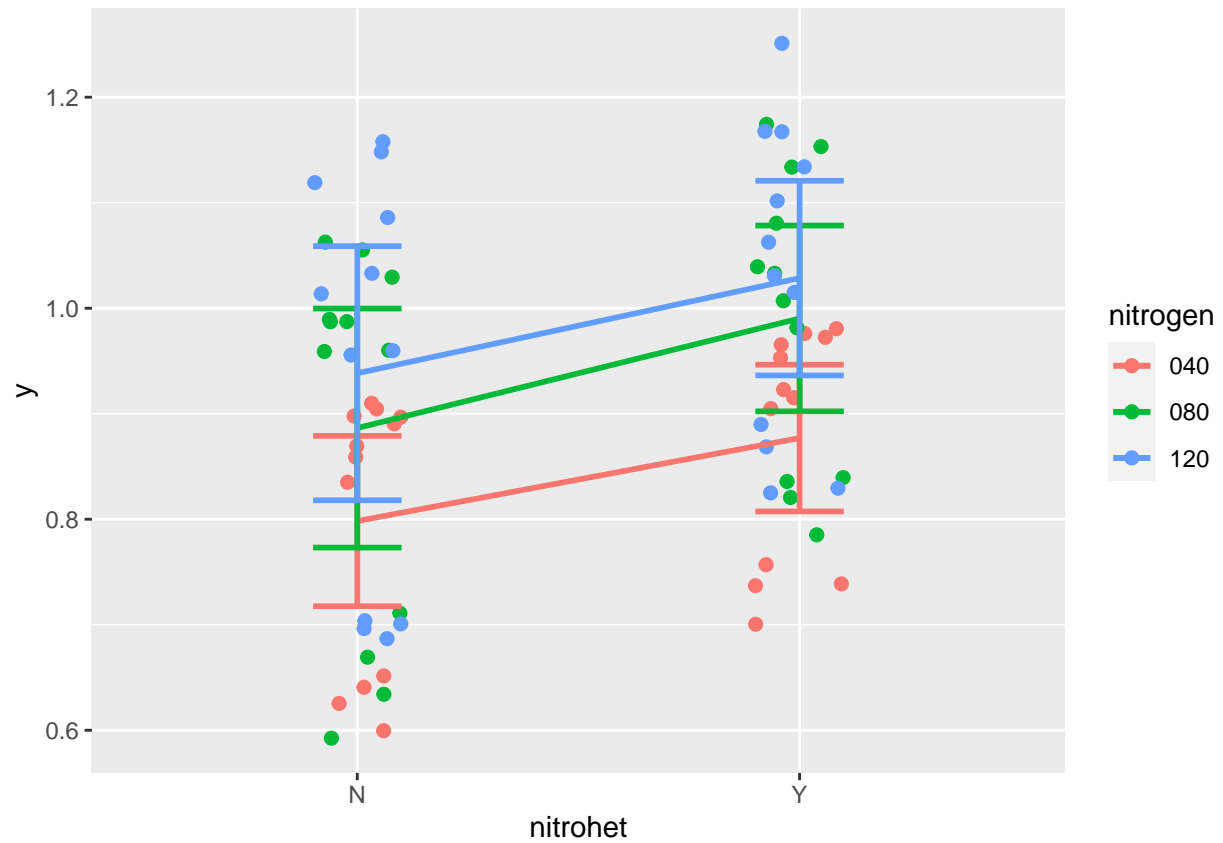
##      nitrohet nitrogen water biomass      y
## 1          N      040   125   4.372 0.6406802
## 2          N      040   125   4.482 0.6514719
## 3          N      040   125   4.221 0.6254154
## 4          N      040   125   3.977 0.5995556
## 5          N      040   250   7.400 0.8692317
## 6          N      040   250   8.027 0.9045533
## 7          N      040   250   7.883 0.8966915
## 8          N      040   250   7.769 0.8903651
## 9          N      040   375   7.226 0.8588980
## 10         N      040   375   8.126 0.9098768
## 11         N      040   375   6.840 0.8350561
## 12         N      040   375   7.901 0.8976821
## 13         N      080   125   5.140 0.7109631
## 14         N      080   125   3.913 0.5925098
## 15         N      080   125   4.669 0.6692239
## 16         N      080   125   4.306 0.6340740
## 17         N      080   250   9.099 0.9589937
## 18         N      080   250   9.711 0.9872640
## 19         N      080   250   9.123 0.9601377
## 20         N      080   250   9.709 0.9871745
## 21         N      080   375  10.701 1.0294244
## 22         N      080   375  11.552 1.0626572
## 23         N      080   375  11.356 1.0552254
## 24         N      080   375   9.759 0.9894053
## 25         N      120   125   5.021 0.7007902
## 26         N      120   125   4.970 0.6963564
## 27         N      120   125   5.055 0.7037212
## 28         N      120   125   4.862 0.6868150
## 29         N      120   250   9.029 0.9556397
## 30         N      120   250  10.791 1.0330617
## 31         N      120   250   9.115 0.9597567
## 32         N      120   250  10.319 1.0136376
## 33         N      120   375  12.189 1.0859681

```

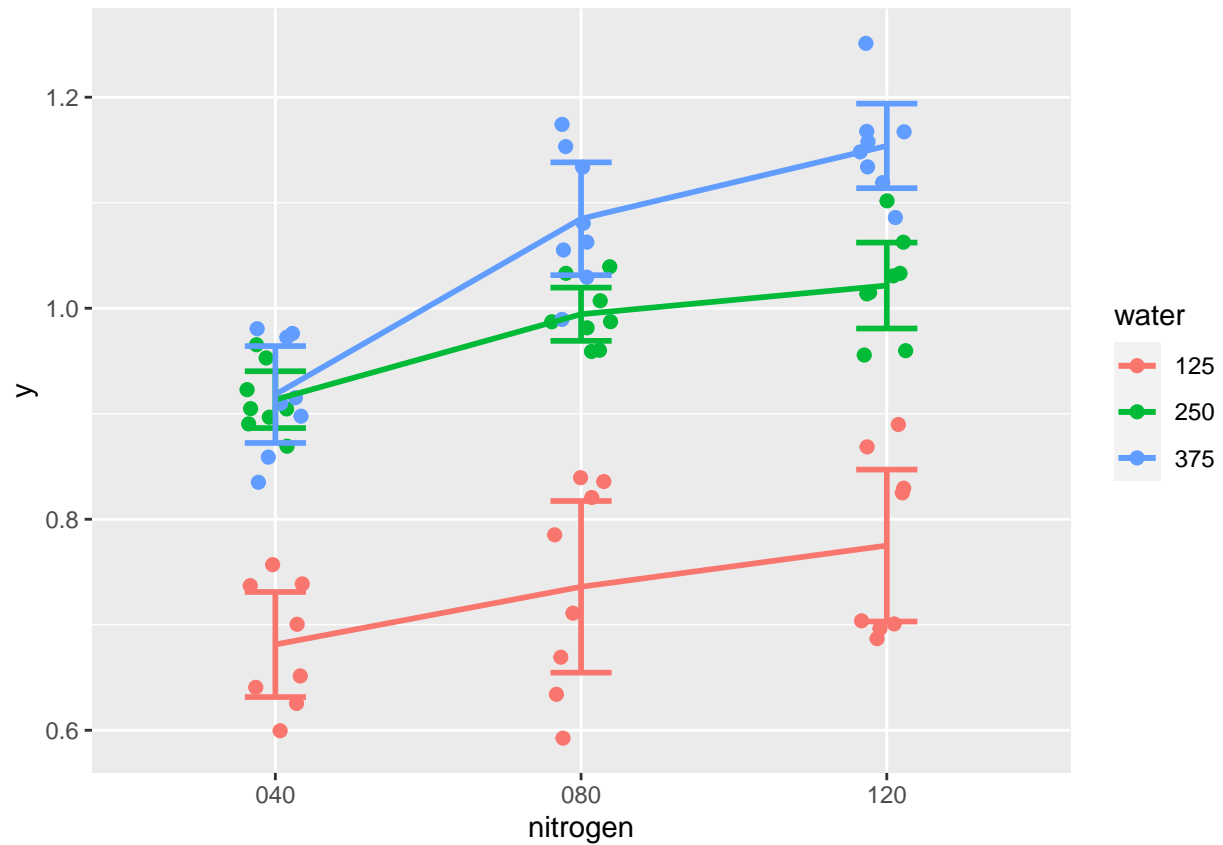
```
## 34      N      120    375  14.381  1.1577891
## 35      N      120    375  13.153  1.1190248
## 36      N      120    375  14.066  1.1481706
## 37      Y      040    125   5.458  0.7370335
## 38      Y      040    125   5.017  0.7004441
## 39      Y      040    125   5.479  0.7387013
## 40      Y      040    125   5.714  0.7569402
## 41      Y      040    250   8.972  0.9528893
## 42      Y      040    250   9.234  0.9653899
## 43      Y      040    250   8.032  0.9048237
## 44      Y      040    250   8.372  0.9228292
## 45      Y      040    375   9.464  0.9760747
## 46      Y      040    375   9.563  0.9805942
## 47      Y      040    375   9.385  0.9724343
## 48      Y      040    375   8.226  0.9151887
## 49      Y      080    125   6.616  0.8205955
## 50      Y      080    125   6.909  0.8394152
## 51      Y      080    125   6.851  0.8357540
## 52      Y      080    125   6.098  0.7851874
## 53      Y      080    250  10.792  1.0331019
## 54      Y      080    250  10.164  1.0070647
## 55      Y      080    250  10.947  1.0392951
## 56      Y      080    250   9.582  0.9814562
## 57      Y      080    375  14.936  1.1742343
## 58      Y      080    375  13.607  1.1337624
## 59      Y      080    375  14.231  1.1532354
## 60      Y      080    375  12.038  1.0805543
## 61      Y      120    125   7.389  0.8685857
## 62      Y      120    125   6.683  0.8249715
## 63      Y      120    125   7.759  0.8898058
## 64      Y      120    125   6.752  0.8294324
## 65      Y      120    250  10.731  1.0306402
## 66      Y      120    250  12.640  1.1017471
## 67      Y      120    250  10.350  1.0149403
## 68      Y      120    250  11.550  1.0625820
## 69      Y      120    375  14.697  1.1672287
## 70      Y      120    375  17.826  1.2510539
## 71      Y      120    375  14.711  1.1676422
## 72      Y      120    375  13.614  1.1339857
```

```
# Graphics using ggplot2
```

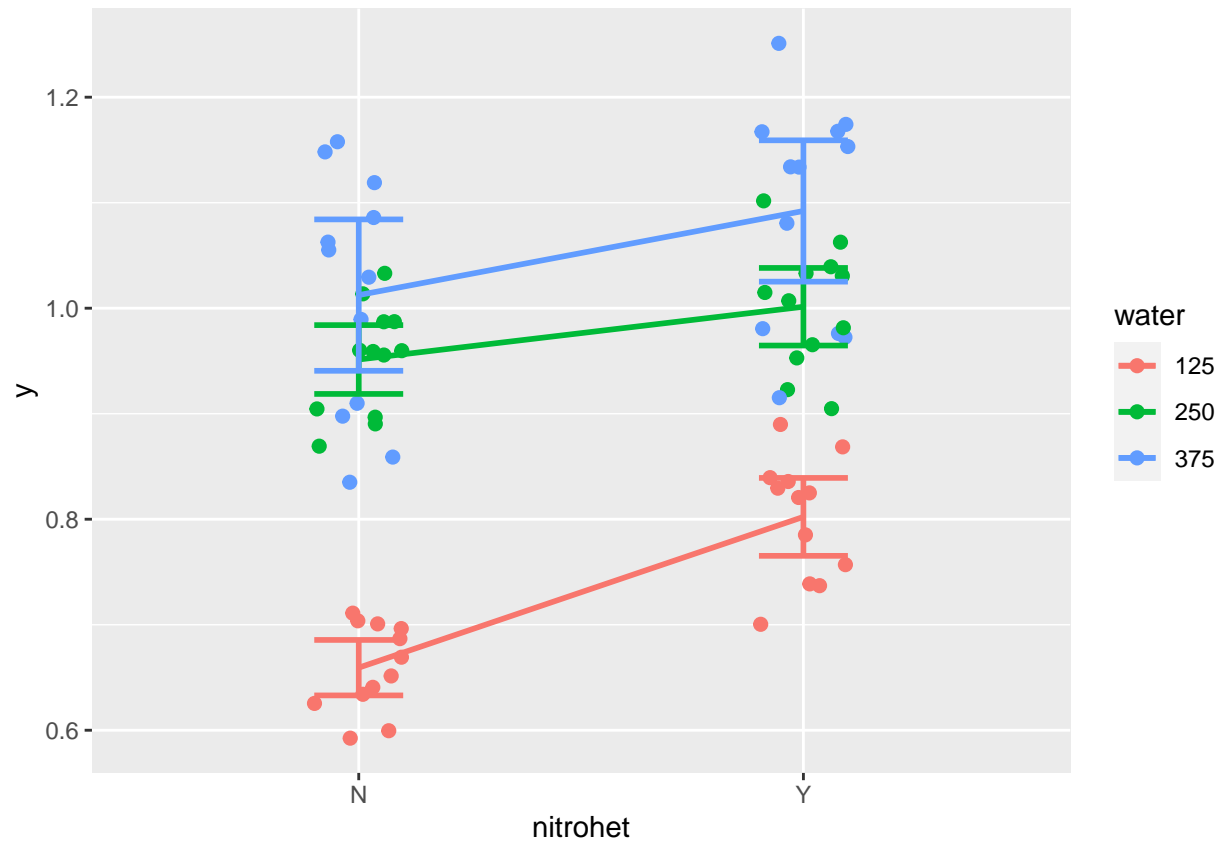
```
ggplot(biomdata,aes(nitrohet,y,group=nitrogen,color=nitrogen))+
geom_jitter(size=2,position=position_jitter(width=0.1))+
stat_summary(fun="mean",geom="line",linewidth=1)+
stat_summary(fun.data="mean_cl_normal",geom="errorbar",width=0.2,linewidth=1)
```



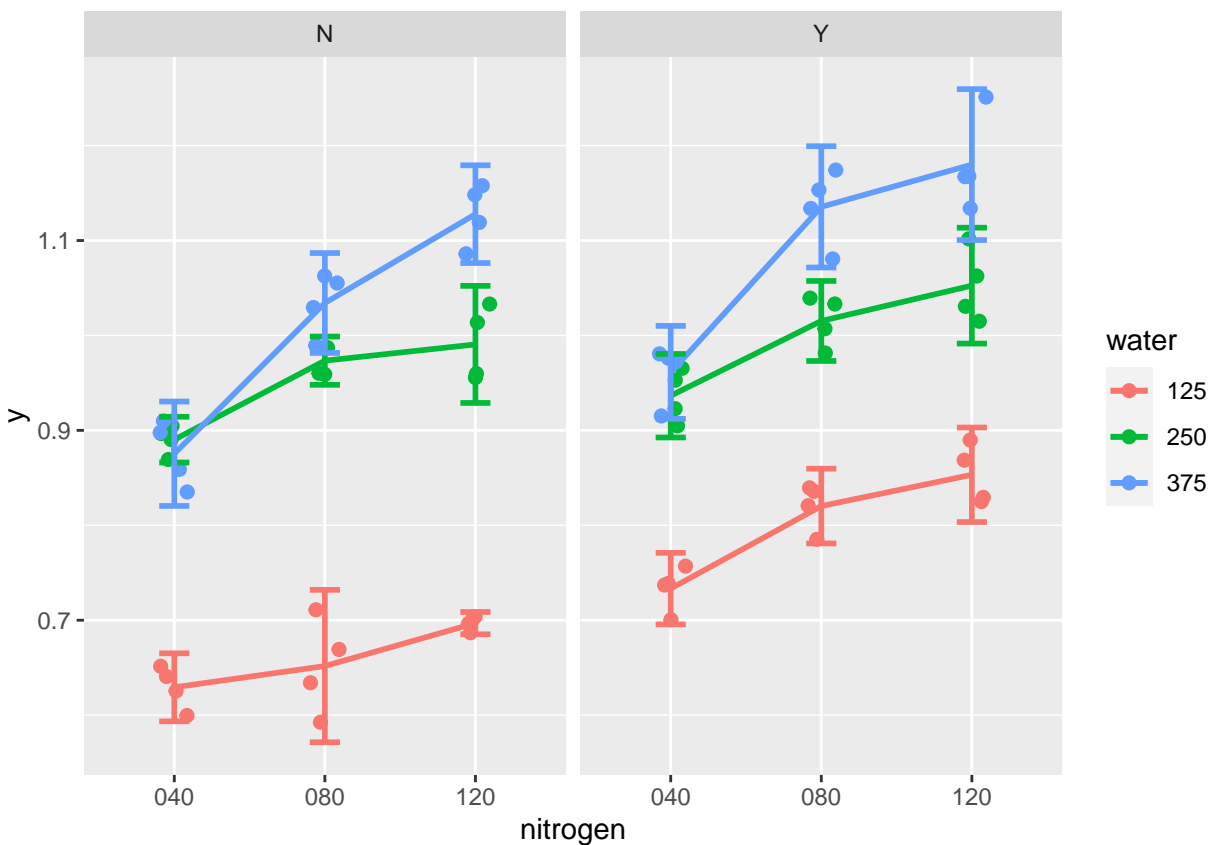
```
ggplot(biomdata,aes(nitrogen,y,group=water,color=water))+
geom_jitter(size=2,position=position_jitter(width=0.1))+
stat_summary(fun="mean",geom="line",linewidth=1)+
stat_summary(fun.data="mean_cl_normal",geom="errorbar",width=0.2,linewidth=1)
```



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



```
# Plots to show three-way interaction
ggplot(biomdata,aes(nitrogen,y,group=water,color=water))+
  geom_jitter(size=2,position=position_jitter(width=0.1))+
  stat_summary(fun="mean",geom="line",linewidth=1)+
  stat_summary(fun.data="mean_cl_normal",geom="errorbar",width=0.2,linewidth=1)+
  facet_grid(.~nitrohet)
```



```
# MODEL WITH ALL FOUR INTERACTIONS
```

```
aovout <- aov(y~nitrohet*nitrogen*water,data=biomdata)
```

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

```
Anova(aovout)
```

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

```
##
```

```
## Response: y
```

	Sum Sq	Df	F value	Pr(>F)
## nitrohet	0.14873	1	144.1426	< 2.2e-16 ***
## nitrogen	0.26767	2	129.7083	< 2.2e-16 ***
## water	1.35578	2	656.9966	< 2.2e-16 ***
## nitrohet:nitrogen	0.00191	2	0.9277	0.4017
## nitrohet:water	0.02702	2	13.0956	2.308e-05 ***
## nitrogen:water	0.05326	4	12.9039	1.933e-07 ***
## nitrohet:nitrogen:water	0.00574	4	1.3914	0.2492
## Residuals	0.05572	54		

```
## ---
```

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

```
# MODEL WITH ONLY SIGNIFICANT INTERACTIONS
```

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

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

```
Anova(aovout_nonsint)
```



```
## Anova Table (Type II tests)
##
## Response: y
##           Sum Sq Df F value    Pr(>F)
## nitrohet      0.14873  1 140.808 < 2.2e-16 ***
## nitrogen      0.26767  2 126.707 < 2.2e-16 ***
## water         1.35578  2 641.795 < 2.2e-16 ***
## nitrohet:water 0.02702  2  12.793 2.358e-05 ***
## nitrogen:water 0.05326  4  12.605 1.660e-07 ***
## Residuals      0.06337 60
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Calculate least squares means
emmeans(aovout_nonsint,~nitrohet:water)

##   nitrohet water emmean      SE df lower.CL upper.CL
## N         125    0.659 0.00938 60    0.641    0.678
## Y         125    0.802 0.00938 60    0.783    0.821
## N         250    0.951 0.00938 60    0.933    0.970
## Y         250    1.001 0.00938 60    0.983    1.020
## N         375    1.012 0.00938 60    0.994    1.031
## Y         375    1.092 0.00938 60    1.073    1.111
##
## Results are averaged over the levels of: nitrogen
## Confidence level used: 0.95

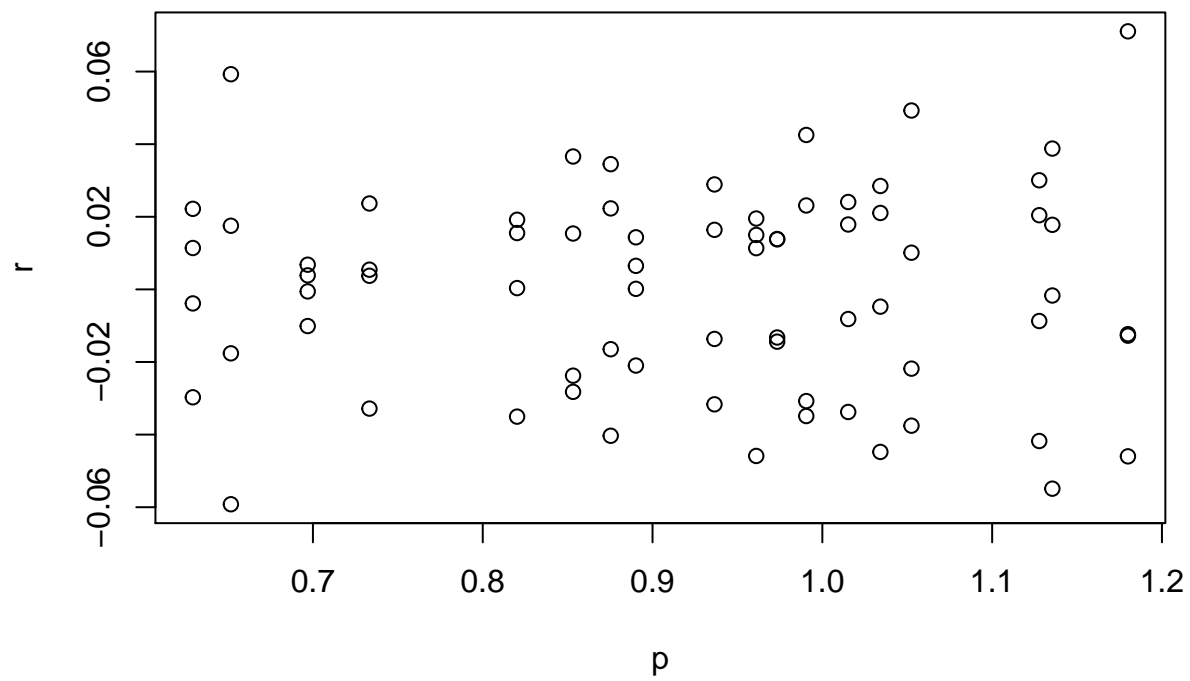
# Tests for simple effects
testInteractions(aovout_nonsint,fixed="water",across="nitrohet",adjustment="none")

## F Test:
## P-value adjustment method: none
##           Value Df Sum of Sq      F    Pr(>F)
## 125         -0.142941  1  0.122592 116.065 1.181e-15 ***
## 250         -0.050021  1  0.015013  14.213 0.0003752 ***
## 375         -0.079734  1  0.038145  36.114 1.185e-07 ***
## Residuals              60  0.063374
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

testInteractions(aovout_nonsint,fixed="nitrohet",across="water",adjustment="none")

## F Test:
## P-value adjustment method: none
##           water1   water2 Df Sum of Sq      F    Pr(>F)
## N         -0.35313 -0.061056  2  0.85496 404.72 < 2.2e-16 ***
## Y         -0.28993 -0.090769  2  0.52784 249.87 < 2.2e-16 ***
## Residuals              60  0.06337
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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



`qqnorm(r)`

Normal Q-Q Plot

