

Kneitel_2010_algae_tukey2.R

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```
# Kneitel_2010_algae_tukey2.sas
# One-way ANOVA and Tukey method

# Load necessary libraries
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

# Read in data set
kndata <- read.table(header=T,colClasses=c("factor","numeric","numeric",
"numeric"),text="
treat richness total algae
Control    8    78     1
Control    5    84     7
Control   10   115    45
Control    7   200   100
Control    6    72    20
Low         8    73    15
Low         7   124    70
Low         8   116    50
Low         8    92     5
Low         7   138    60
Medium      7   124    85
Medium      8   116    80
Medium      8   145    60
Medium      6   154   100
Medium      7   129    90
High        6   134    95
High        7   138    95
```

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High      8 103 70
High      8 119 75
High      6 132 80
VeryHigh  6 148 95
VeryHigh  5 134 95
VeryHigh  5 119 100
VeryHigh  5 117 90
VeryHigh  5 129 80
")

```

```

# Apply transformations here
kndata <- transform(kndata,y=asin(sqrt(algae/100)))

```

```

# Print data
kndata

```

```

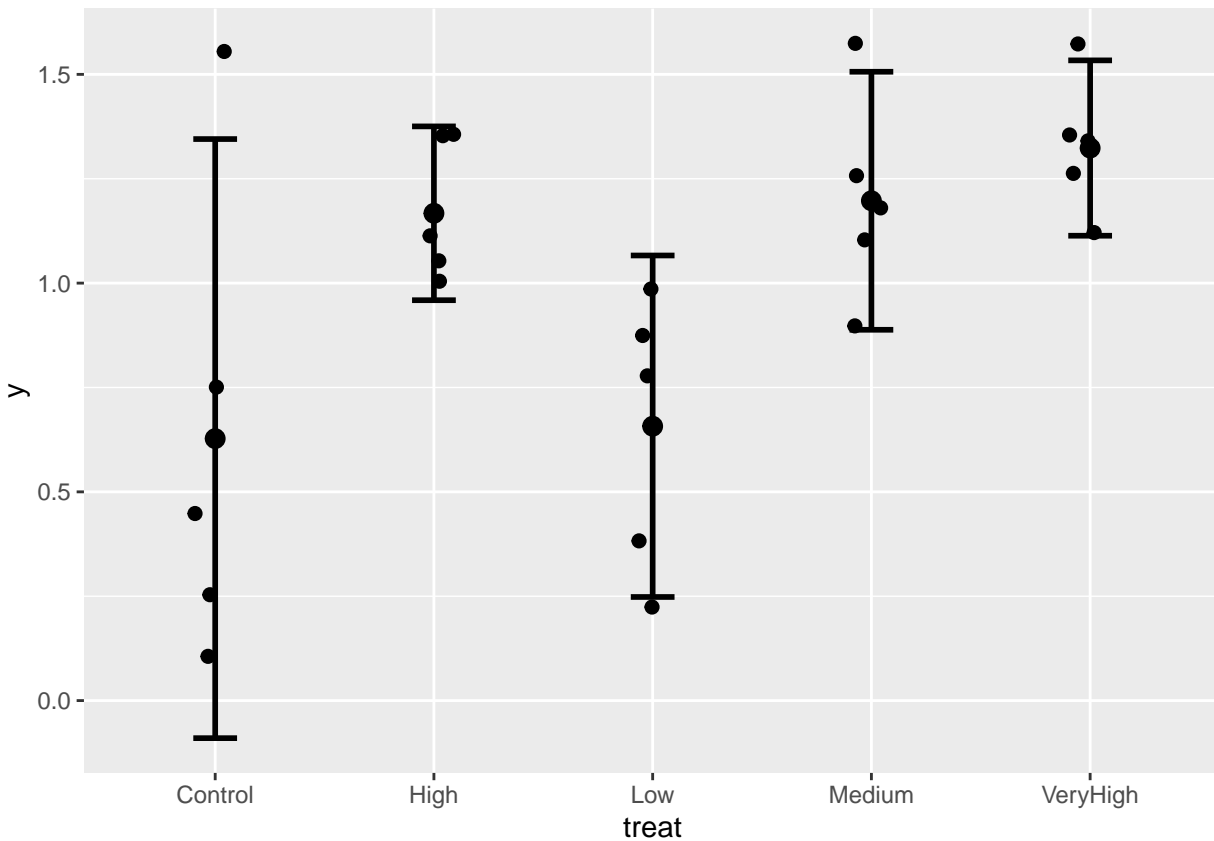
##      treat richness total algae      y
## 1 Control      8    78     1 0.1001674
## 2 Control      5    84     7 0.2677633
## 3 Control     10   115    45 0.7353145
## 4 Control      7   200   100 1.5707963
## 5 Control      6    72    20 0.4636476
## 6      Low      8    73    15 0.3976994
## 7      Low      7   124    70 0.9911566
## 8      Low      8   116    50 0.7853982
## 9      Low      8    92     5 0.2255134
## 10     Low      7   138    60 0.8860771
## 11 Medium      7   124    85 1.1730969
## 12 Medium      8   116    80 1.1071487
## 13 Medium      8   145    60 0.8860771
## 14 Medium      6   154   100 1.5707963
## 15 Medium      7   129    90 1.2490458
## 16      High      6   134    95 1.3452829
## 17      High      7   138    95 1.3452829
## 18      High      8   103    70 0.9911566
## 19      High      8   119    75 1.0471976
## 20      High      6   132    80 1.1071487
## 21 VeryHigh     6   148    95 1.3452829
## 22 VeryHigh     5   134    95 1.3452829
## 23 VeryHigh     5   119   100 1.5707963
## 24 VeryHigh     5   117    90 1.2490458
## 25 VeryHigh     5   129    80 1.1071487

```

```

# Graphics using ggplot2
ggplot(kndata,aes(treat,y))+
geom_jitter(size=2,position=position_jitter(width=0.1))+
stat_summary(fun="mean",geom="point",size=3)+
stat_summary(fun.data="mean_cl_normal",geom="errorbar",width=0.2,linewidth=1)

```



```
# One-way ANOVA
aovout <- aov(y~treat,data=kndata)
anova(aovout)

## Analysis of Variance Table
##
## Response: y
##          Df Sum Sq Mean Sq F value    Pr(>F)
## treat      4  2.1382  0.53454   4.7632 0.007295 **
## Residuals 20  2.2444  0.11222
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Obtain multiple comparison object
compout <- glht(aovout,linfct=mcp(treat="Tukey"))

# Tukey method - controls the EER
summary(compout)

##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
## Fit: aov(formula = y ~ treat, data = kndata)
##
```

```
## Linear Hypotheses:
##               Estimate Std. Error t value Pr(>|t|)
## High - Control == 0    0.53968   0.21187   2.547   0.1195
## Low - Control == 0     0.02963   0.21187   0.140   0.9999
## Medium - Control == 0   0.56970   0.21187   2.689   0.0913 .
## VeryHigh - Control == 0 0.69597   0.21187   3.285   0.0272 *
## Low - High == 0        -0.51004   0.21187  -2.407   0.1542
## Medium - High == 0      0.03002   0.21187   0.142   0.9999
## VeryHigh - High == 0    0.15630   0.21187   0.738   0.9450
## Medium - Low == 0       0.54006   0.21187   2.549   0.1191
## VeryHigh - Low == 0     0.66634   0.21187   3.145   0.0364 *
## VeryHigh - Medium == 0  0.12628   0.21187   0.596   0.9741
## ---
## 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 ~ treat, data = kndata)
##
## Quantile = 2.9928
## 95% family-wise confidence level
##
## Linear Hypotheses:
##               Estimate lwr      upr
## High - Control == 0    0.53968 -0.09440  1.17375
## Low - Control == 0     0.02963 -0.60444  0.66371
## Medium - Control == 0   0.56970 -0.06438  1.20377
## VeryHigh - Control == 0 0.69597  0.06190  1.33005
## Low - High == 0        -0.51004 -1.14412  0.12403
## Medium - High == 0      0.03002 -0.60406  0.66409
## VeryHigh - High == 0    0.15630 -0.47778  0.79037
## Medium - Low == 0       0.54006 -0.09401  1.17414
## VeryHigh - Low == 0     0.66634  0.03227  1.30042
## VeryHigh - Medium == 0  0.12628 -0.50780  0.76035
```

```
cld(compout)
```

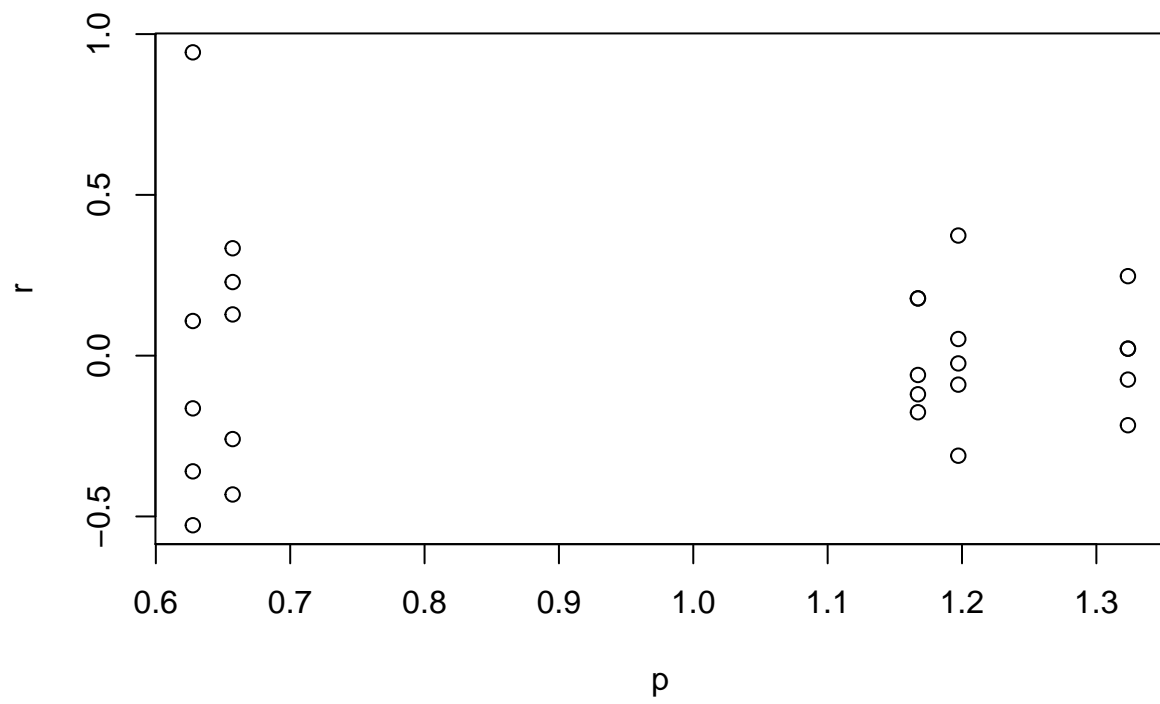
```
## Control      High      Low      Medium VeryHigh
##      "a"      "ab"      "a"      "ab"      "b"
```

```
# Diagnostic plots to check ANOVA assumptions
```

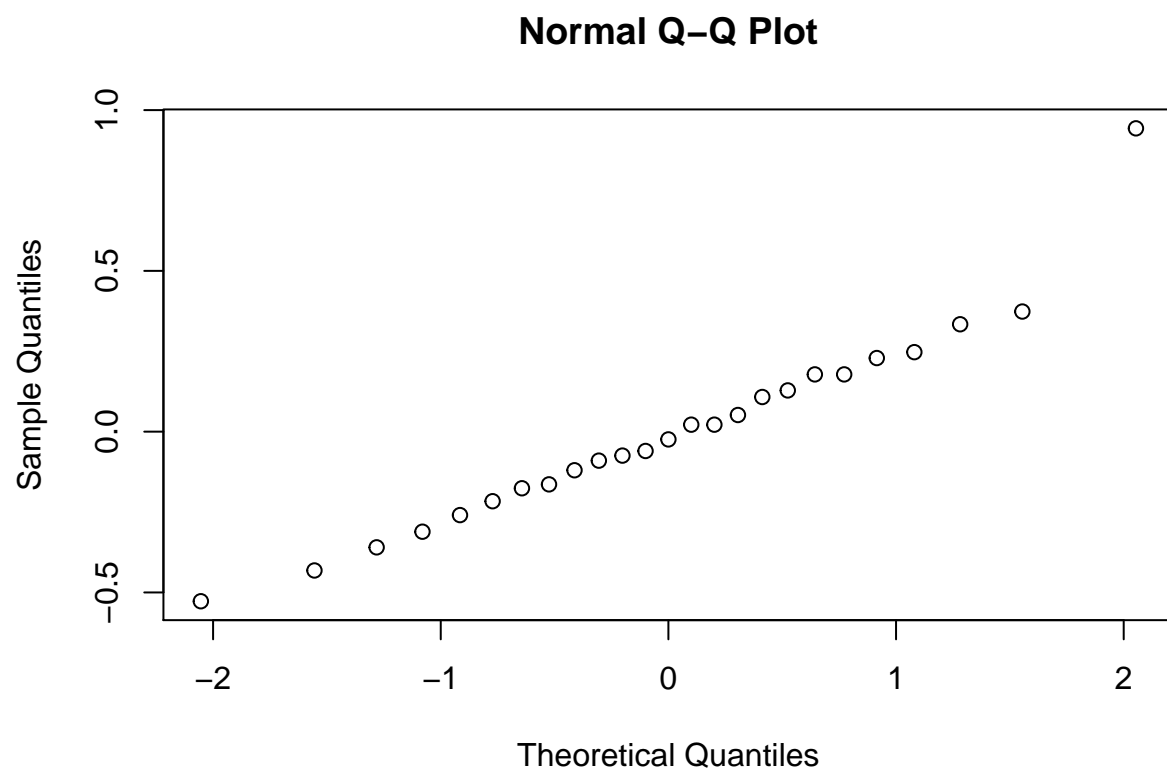
```
p <- predict(aovout)
```

```
r <- resid(aovout)
```

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



`qqnorm(r)`



```
?g
```

```
## No documentation for 'g' in specified packages and libraries:  
## you could try '??g'
```