

Kneitel_2010_algae_Westfall2.R

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```
# Kneitel_2010_algae_Westfall2.sas
# One-way ANOVA and Westfall 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
```

```

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

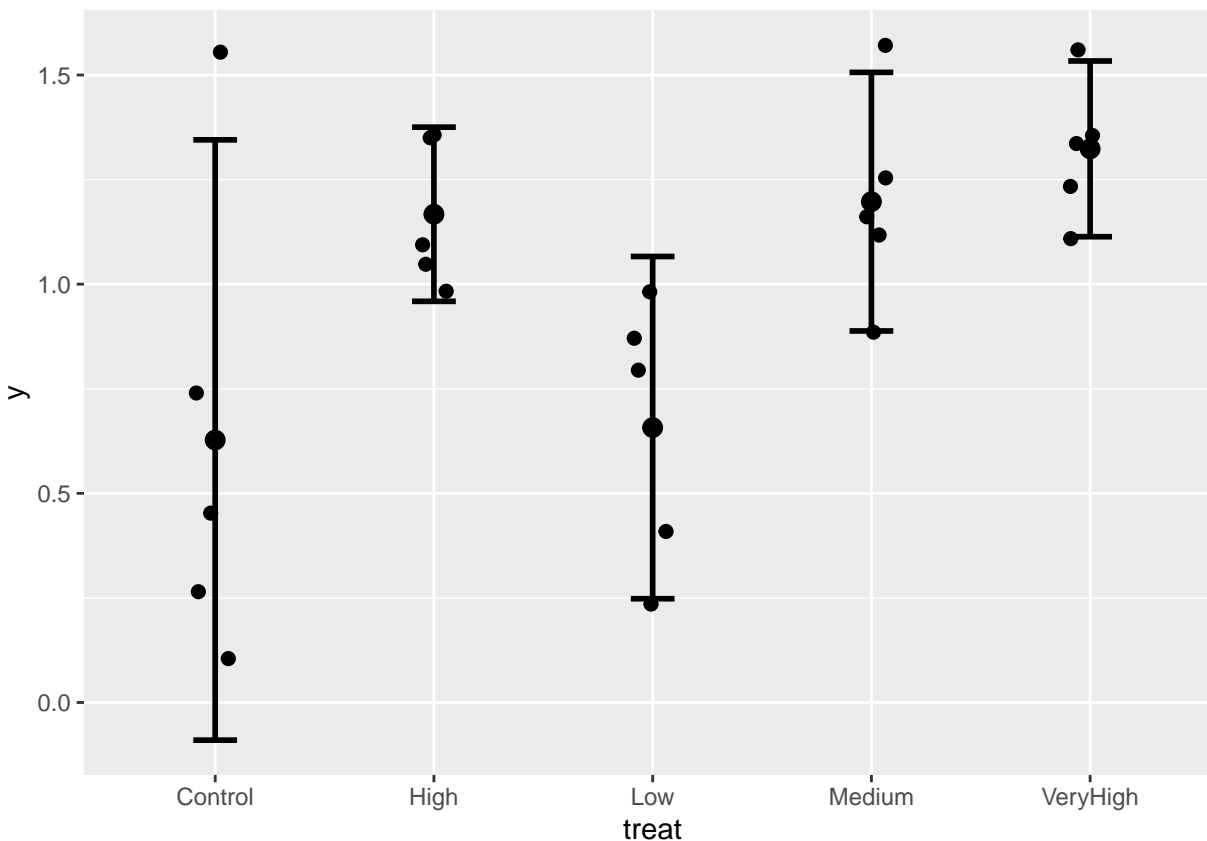
```

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"))

# Westfall method - controls the EER
westout <- summary(compout,test=adjusted(type="Westfall"))
westout

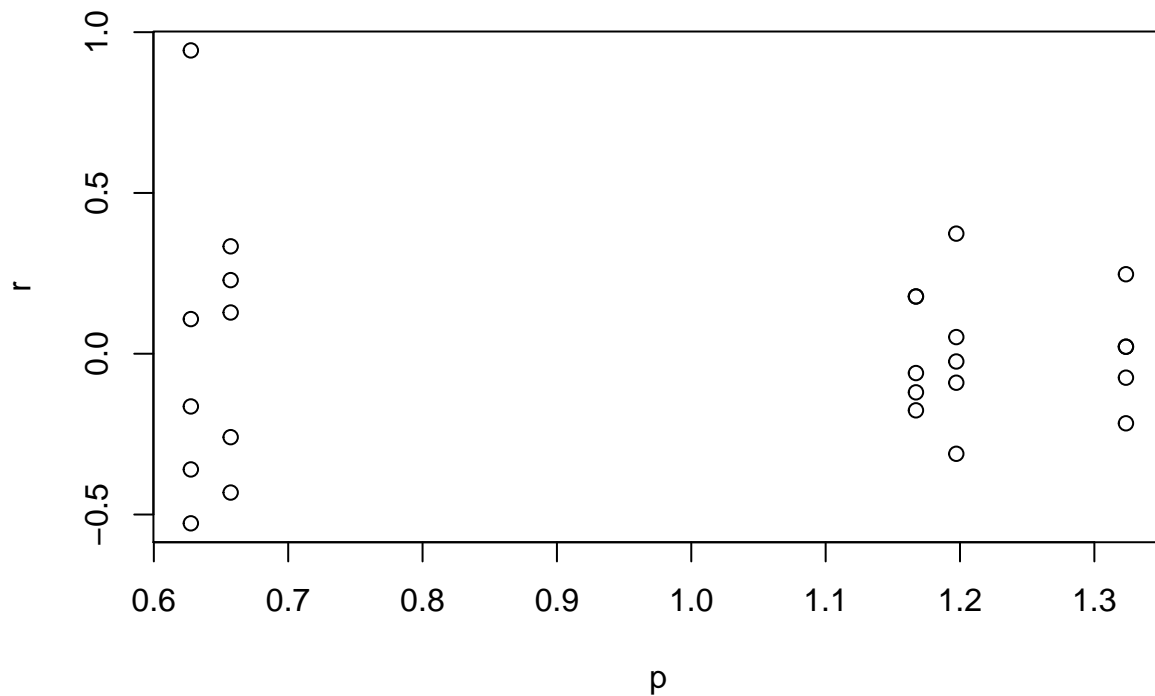
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: aov(formula = y ~ treat, data = kndata)
##
```

```
## Linear Hypotheses:
##               Estimate Std. Error t value Pr(>|t|)
## High - Control == 0    0.53968    0.21187   2.547  0.0656 .
## Low - Control == 0     0.02963    0.21187   0.140  0.9873
## Medium - Control == 0   0.56970    0.21187   2.689  0.0625 .
## VeryHigh - Control == 0 0.69597    0.21187   3.285  0.0271 *
## Low - High == 0        -0.51004    0.21187  -2.407  0.0656 .
## Medium - High == 0      0.03002    0.21187   0.142  0.9873
## VeryHigh - High == 0    0.15630    0.21187   0.738  0.8595
## Medium - Low == 0       0.54006    0.21187   2.549  0.0625 .
## VeryHigh - Low == 0     0.66634    0.21187   3.145  0.0271 *
## VeryHigh - Medium == 0  0.12628    0.21187   0.596  0.8595
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- Westfall method)
```

```
cld(westout)
```

```
## 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)
```

