

Kneitel_2010_cover2.R

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2023-11-14

```
# Kneitel_2010_cover2.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
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,vcover=total-algae)
kndata <- transform(kndata,y=asin(sqrt(vcover/100)))

```

```
# Print data
```

```
kndata
```

```

##      treat richness total algae vcover      y
## 1 Control        8    78     1    77 1.0706167
## 2 Control        5    84     7    77 1.0706167
## 3 Control       10   115    45    70 0.9911566
## 4 Control        7   200   100   100 1.5707963
## 5 Control        6    72    20    52 0.8054035
## 6      Low        8    73    15    58 0.8657435
## 7      Low        7   124    70    54 0.8254410
## 8      Low        8   116    50    66 0.9482629
## 9      Low        8    92     5    87 1.2019333
## 10     Low        7   138    60    78 1.0825911
## 11   Medium       7   124    85    39 0.6744909
## 12   Medium       8   116    80    36 0.6435011
## 13   Medium       8   145    60    85 1.1730969
## 14   Medium       6   154   100    54 0.8254410
## 15   Medium       7   129    90    39 0.6744909
## 16     High       6   134    95    39 0.6744909
## 17     High       7   138    95    43 0.7151675
## 18     High       8   103    70    33 0.6119397
## 19     High       8   119    75    44 0.7252532
## 20     High       6   132    80    52 0.8054035
## 21 VeryHigh       6   148    95    53 0.8154162
## 22 VeryHigh       5   134    95    39 0.6744909
## 23 VeryHigh       5   119   100    19 0.4510268
## 24 VeryHigh       5   117    90    27 0.5464006
## 25 VeryHigh       5   129    80    49 0.7753975

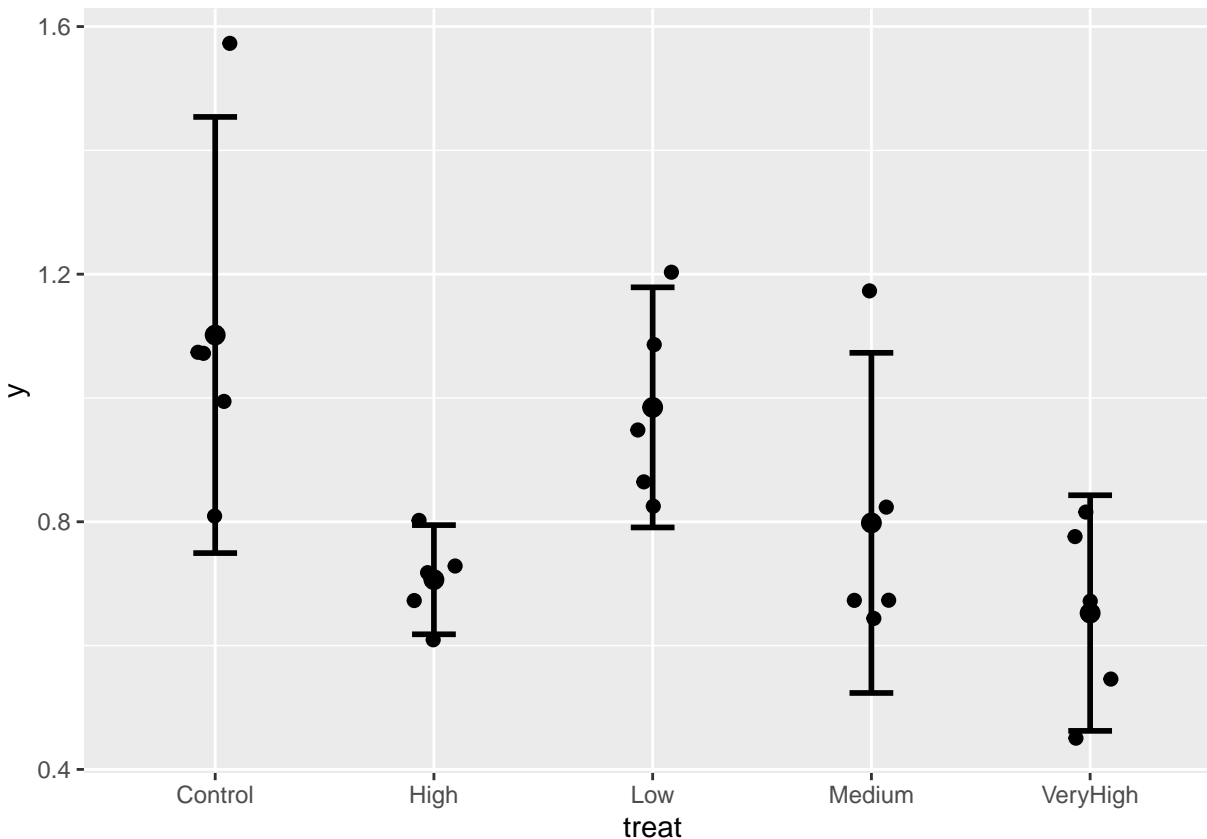
```

```
# 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  0.71900  0.17975   4.9274 0.006264 **
## Residuals 20  0.72959  0.03648
## ---
## 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   -0.39527    0.12080   -3.272   0.0278 *
## Low - Control == 0    -0.11692    0.12080   -0.968   0.8662
## Medium - Control == 0 -0.30351    0.12080   -2.513   0.1274
## VeryHigh - Control == 0 -0.44917    0.12080   -3.718   0.0106 *
## Low - High == 0       0.27834    0.12080    2.304   0.1846
## Medium - High == 0     0.09175    0.12080    0.760   0.9392
## VeryHigh - High == 0  -0.05390    0.12080   -0.446   0.9911
## Medium - Low == 0     -0.18659    0.12080   -1.545   0.5473
## VeryHigh - Low == 0   -0.33225    0.12080   -2.750   0.0810 .
## VeryHigh - Medium == 0 -0.14566    0.12080   -1.206   0.7481
## ---
## 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 = 2.9912
## 95% family-wise confidence level
##
## Linear Hypotheses:
##               Estimate lwr      upr
## High - Control == 0   -0.39527 -0.75659 -0.03394
## Low - Control == 0    -0.11692 -0.47825  0.24440
## Medium - Control == 0 -0.30351 -0.66484  0.05781
## VeryHigh - Control == 0 -0.44917 -0.81050 -0.08785
## Low - High == 0       0.27834 -0.08298  0.63967
## Medium - High == 0     0.09175 -0.26957  0.45308
## VeryHigh - High == 0  -0.05390 -0.41523  0.30742
## Medium - Low == 0     -0.18659 -0.54791  0.17473
## VeryHigh - Low == 0   -0.33225 -0.69357  0.02908
## VeryHigh - Medium == 0 -0.14566 -0.50698  0.21567
```

```
cld(compout)
```

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

```
# Obtain multiple comparison object
```

```
compout2 <- glht(aovout, linfct=mcp(treat="Dunnett"))
```

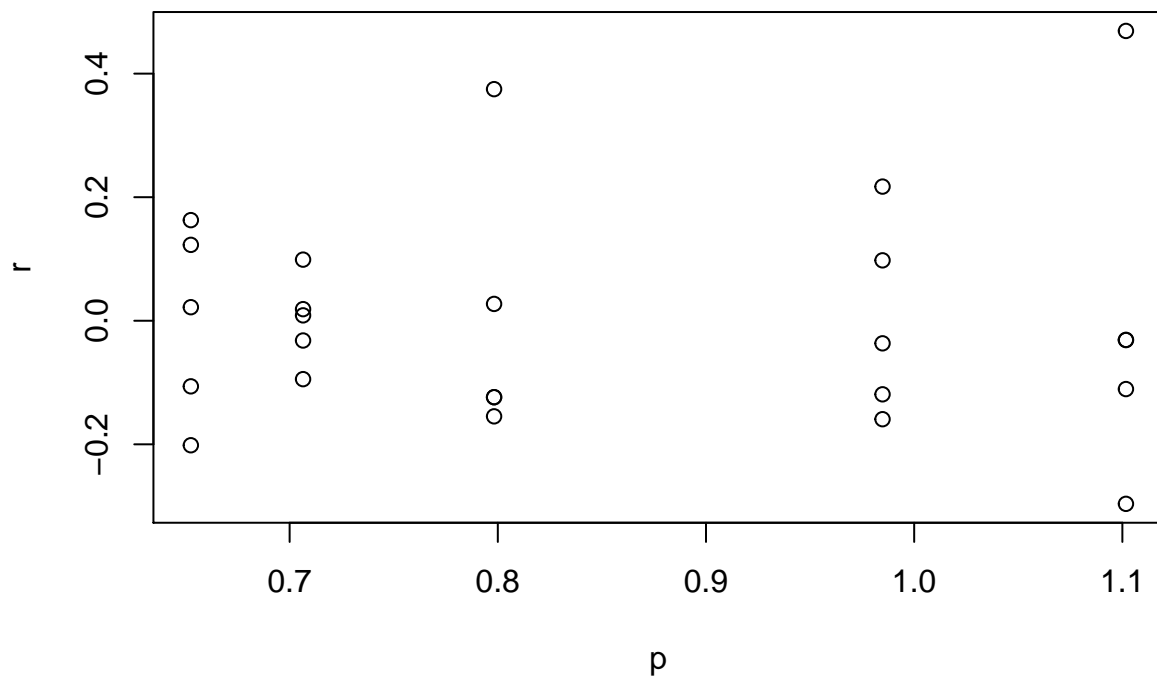
```
# Dunnett's method - controls the EER for comparisons with a control
```

```
dunnout <- summary(compout2)
```

```
confint(dunnout)
```

```
##
```

```
## Simultaneous Confidence Intervals
##
## Multiple Comparisons of Means: Dunnett Contrasts
##
##
## Fit: aov(formula = y ~ treat, data = kndata)
##
## Quantile = 2.6509
## 95% family-wise confidence level
##
## Linear Hypotheses:
##               Estimate lwr      upr
## High - Control == 0   -0.39527 -0.71549 -0.07505
## Low - Control == 0    -0.11692 -0.43714  0.20330
## Medium - Control == 0 -0.30351 -0.62373  0.01671
## VeryHigh - Control == 0 -0.44917 -0.76939 -0.12895
# Diagnostic plots to check ANOVA assumptions
p <- predict(aovout)
r <- resid(aovout)
plot(p,r)
```



```
qqnorm(r)
```

Normal Q-Q Plot

