

# bark\_beetle\_experiment.R

SIU850486795

2023-11-14

```
# bark_beetle_experiment.R
# One-way ANOVA for bark beetle trapping experiment

# Load necessary libraries
library(ggplot2)

# Read in data set
bbdata <- read.table(header=T,colClasses=c("factor","numeric"),text="
treat count
A 373
A 126
A 255
A 138
A 379
B 25
B 64
B 62
B 71
B 54
C 449
C 249
C 69
C 199
C 84
")

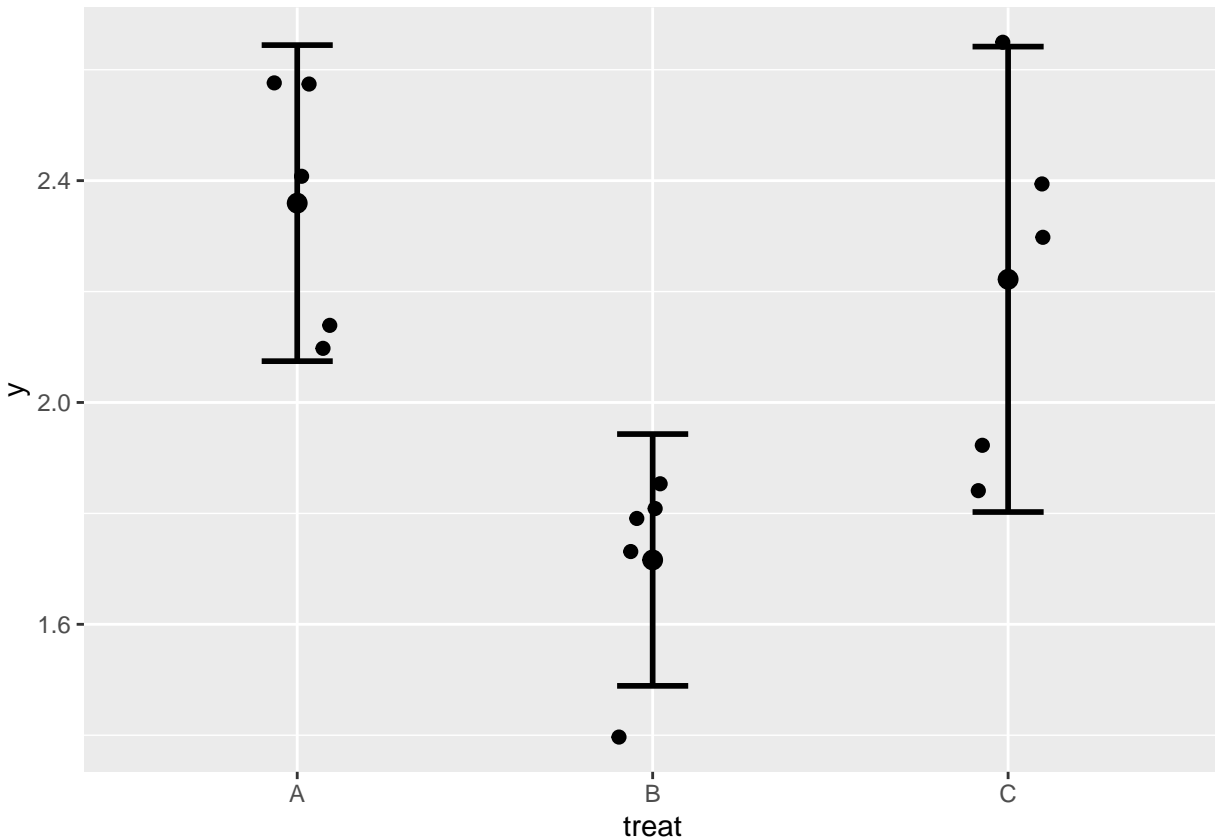
# Apply transformations here
bbdata <- transform(bbdata,y=log10(count))

# Print data
bbdata
```

##	treat	count	y
## 1	A	373	2.571709
## 2	A	126	2.100371
## 3	A	255	2.406540
## 4	A	138	2.139879
## 5	A	379	2.578639
## 6	B	25	1.397940
## 7	B	64	1.806180
## 8	B	62	1.792392
## 9	B	71	1.851258
## 10	B	54	1.732394

```
## 11      C    449 2.652246
## 12      C    249 2.396199
## 13      C     69 1.838849
## 14      C    199 2.298853
## 15      C     84 1.924279
```

```
# Graphics using ggplot2
ggplot(bdata,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)
```

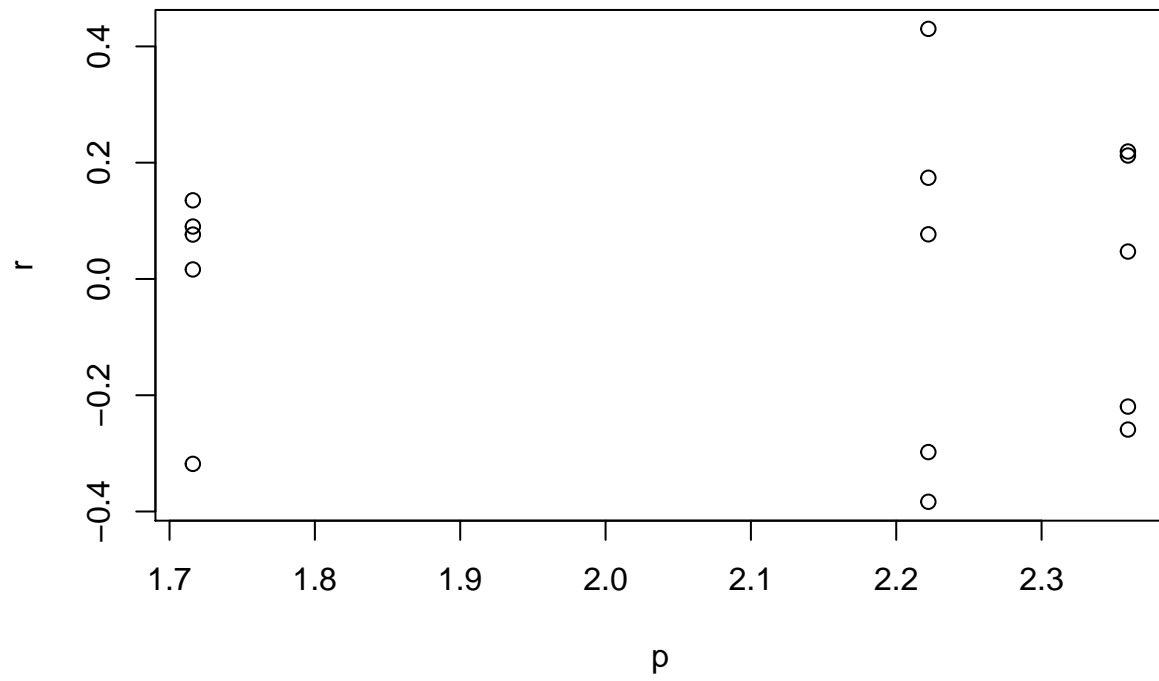


```
# One-way ANOVA
aovout <- aov(y~treat,data=bdata)
anova(aovout)
```

```
## Analysis of Variance Table
##
## Response: y
##          Df Sum Sq Mean Sq F value    Pr(>F)
## treat      2  1.14818  0.57409   8.599 0.004819 **
## Residuals 12  0.80115  0.06676
## ---
## 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**

