

# bark\_beetle\_random.R

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

# Load necessary libraries
library(ggplot2)
library(lme4)

## Loading required package: Matrix

# Read in data set
bbdata <- read.table(header=T,
colClasses=c("factor","numeric"),text="site count
1 137
1 101
1 113
1 48
1 155
2 156
2 165
2 652
2 179
2 757
3 278
3 197
3 95
3 395
3 83
4 2540
4 613
4 200
4 251
4 390
5 18
5 16
5 11
5 21
5 14
")

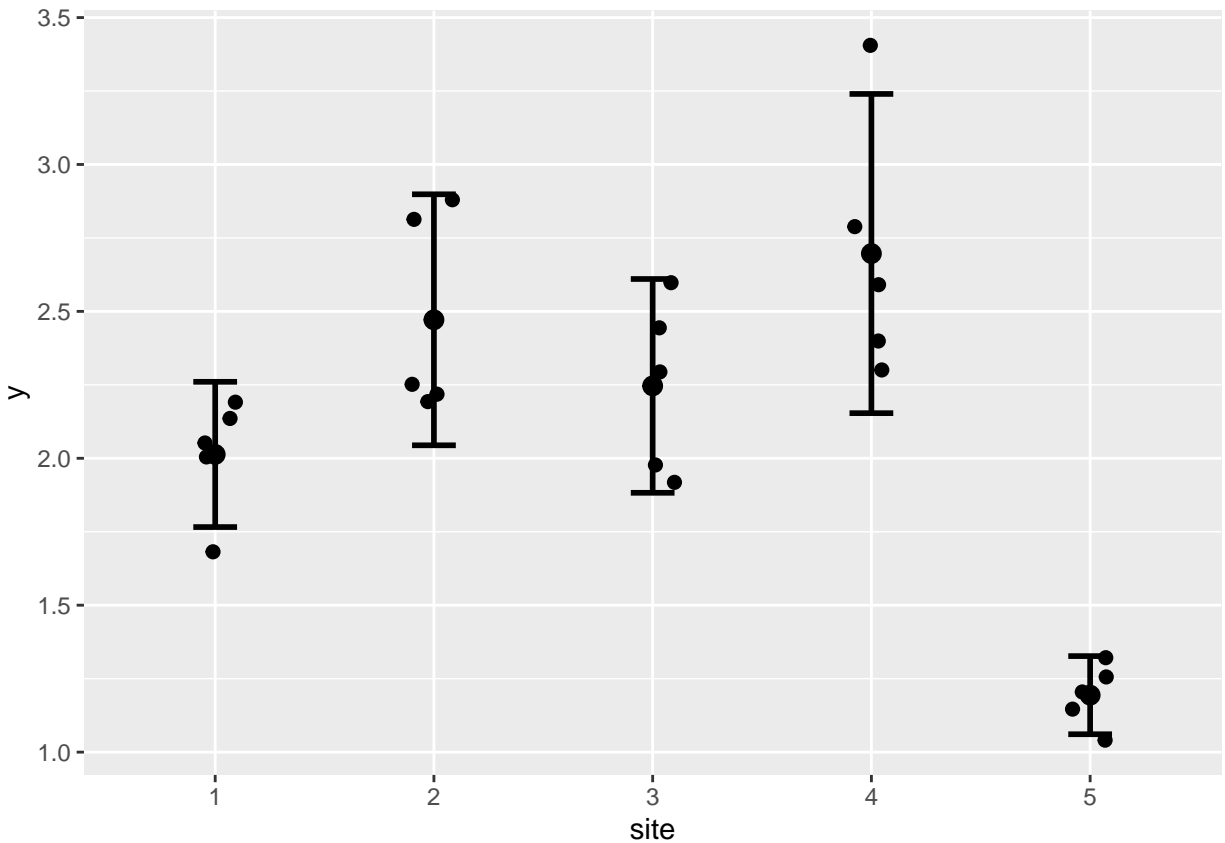
# Apply transformations here
bbdata <- transform(bbdata,y=log10(count))

# Print data
```

```
bbdata
```

```
##      site count      y
## 1      1   137 2.136721
## 2      1   101 2.004321
## 3      1   113 2.053078
## 4      1    48 1.681241
## 5      1   155 2.190332
## 6      2   156 2.193125
## 7      2   165 2.217484
## 8      2   652 2.814248
## 9      2   179 2.252853
## 10     2   757 2.879096
## 11     3   278 2.444045
## 12     3   197 2.294466
## 13     3    95 1.977724
## 14     3   395 2.596597
## 15     3    83 1.919078
## 16     4  2540 3.404834
## 17     4   613 2.787460
## 18     4   200 2.301030
## 19     4   251 2.399674
## 20     4   390 2.591065
## 21     5    18 1.255273
## 22     5    16 1.204120
## 23     5    11 1.041393
## 24     5    21 1.322219
## 25     5    14 1.146128
```

```
# Graphics using ggplot2
ggplot(bbdata,aes(site,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)
```



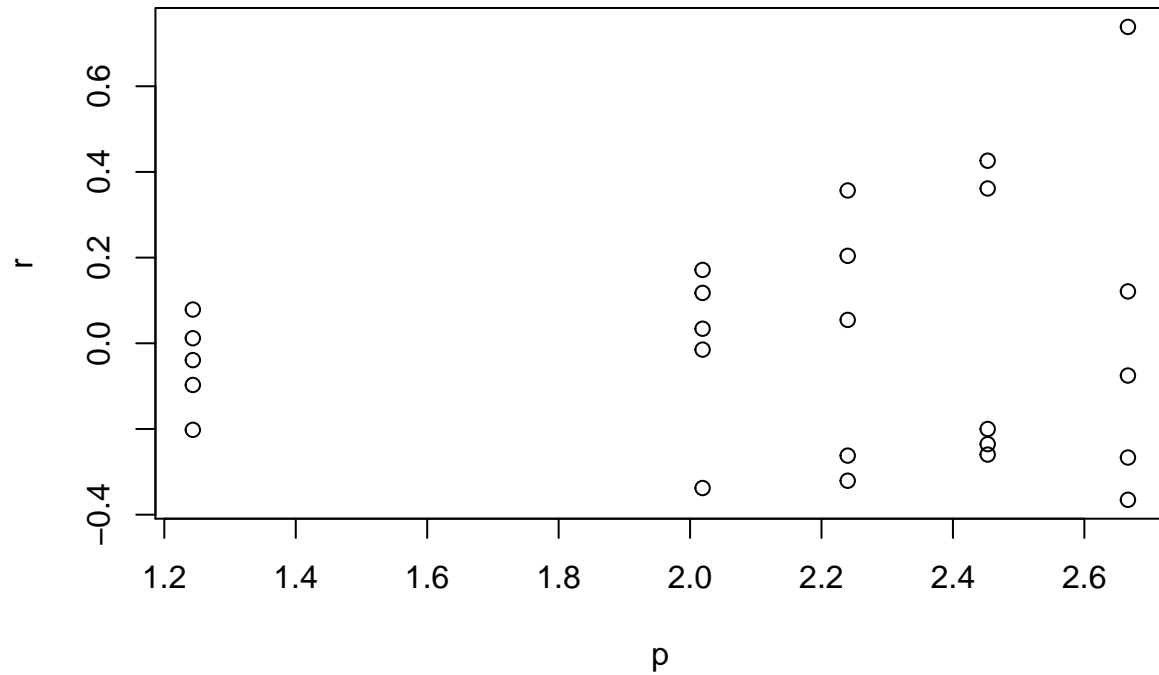
```
# One-way ANOVA with random effects - F test
aovout <- aov(y~site,data=bbdata)
anova(aovout)

## Analysis of Variance Table
##
## Response: y
##          Df Sum Sq Mean Sq F value    Pr(>F)
## site       4  6.7063  1.67658   18.767 1.511e-06 ***
## Residuals 20  1.7868  0.08934
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# One-way ANOVA with random effects - variance components
lmerout <- lmer(y~(1|site),data=bbdata)
summary(lmerout)

## Linear mixed model fit by REML ['lmerMod']
## Formula: y ~ (1 | site)
##      Data: bbdata
##
## REML criterion at convergence: 25.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.22208 -0.78751 -0.04932  0.40534  2.47085
##
```

```
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   site     (Intercept) 0.31745  0.5634
##   Residual              0.08934  0.2989
## Number of obs: 25, groups:  site, 5
##
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)    2.124      0.259    8.203
# Diagnostic plots to check ANOVA assumptions
p <- fitted(lmerout)
r <- resid(lmerout)
plot(p,r)
```



```
qqnorm(r)
```

Normal Q-Q Plot

