

# TrapRCBD\_clerids.R

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```
# TrapRCBD_clerids.R - trapping experiment data
# Randomized block mixed model and Tukey method

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

## Loading required package: Matrix
library(lmerTest)

## Warning: package 'lmerTest' was built under R version 4.0.4
##
## Attaching package: 'lmerTest'
## The following object is masked from 'package:lme4':
##
##      lmer
## The following object is masked from 'package:stats':
##
##      step
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
trapdata <- read.table(header=T,colClasses=c("factor","factor","numeric"),text="
block treat count
1  AP      4
1  BLANK   0
```

```

1  FRAP      79
1  IDAP       7
1  ISAP      10
2  AP         1
2  BLANK      0
2  FRAP    124
2  IDAP      13
2  ISAP      20
3  AP         0
3  BLANK      0
3  FRAP      14
3  IDAP      NA
3  ISAP       2
4  AP         0
4  BLANK      0
4  FRAP      15
4  IDAP      11
4  ISAP       7
5  AP         0
5  BLANK      0
5  FRAP      29
5  IDAP       7
5  ISAP       7
6  AP         2
6  BLANK      0
6  FRAP      70
6  IDAP      14
6  ISAP      20
")

```

*# Apply transformations here*

```
trapdata <- transform(trapdata,y=log(count+1))
```

*# Print data*

```
trapdata
```

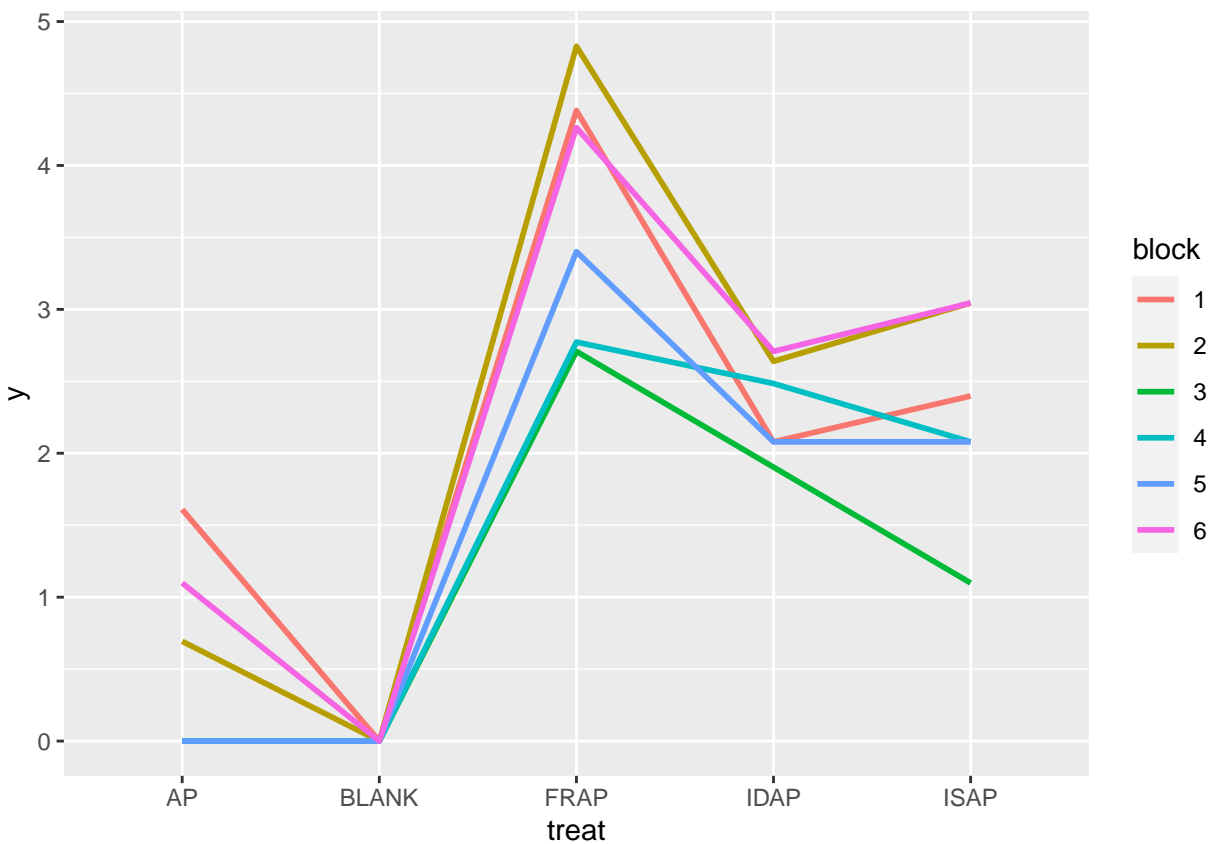
```

##      block treat count      y
## 1      1    AP      4 1.6094379
## 2      1 BLANK      0 0.0000000
## 3      1  FRAP     79 4.3820266
## 4      1  IDAP      7 2.0794415
## 5      1  ISAP     10 2.3978953
## 6      2    AP      1 0.6931472
## 7      2 BLANK      0 0.0000000
## 8      2  FRAP    124 4.8283137
## 9      2  IDAP     13 2.6390573
## 10     2  ISAP     20 3.0445224
## 11     3    AP      0 0.0000000
## 12     3 BLANK      0 0.0000000
## 13     3  FRAP     14 2.7080502
## 14     3  IDAP     NA      NA
## 15     3  ISAP      2 1.0986123
## 16     4    AP      0 0.0000000
## 17     4 BLANK      0 0.0000000

```

```
## 18      4  FRAP      15 2.7725887
## 19      4  IDAP      11 2.4849066
## 20      4  ISAP       7 2.0794415
## 21      5    AP       0 0.0000000
## 22      5 BLANK       0 0.0000000
## 23      5  FRAP      29 3.4011974
## 24      5  IDAP       7 2.0794415
## 25      5  ISAP       7 2.0794415
## 26      6    AP       2 1.0986123
## 27      6 BLANK       0 0.0000000
## 28      6  FRAP      70 4.2626799
## 29      6  IDAP      14 2.7080502
## 30      6  ISAP      20 3.0445224
```

```
# Plot treatments and blocks
# Remove missing values using is.na
ggplot(trapdata[!is.na(trapdata$y),],aes(treat,y,group=block,color=block))+
  geom_line(linewidth=1)
```



```
# Delete blank traps before analysis
trapdata2 <- subset(trapdata,subset=treat!="BLANK")

# Mixed model
lmerout <- lmer(y~treat+(1|block),data=trapdata2)
summary(lmerout)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
```

```
## lmerModLmerTest]
## Formula: y ~ treat + (1 | block)
## Data: trapdata2
##
## REML criterion at convergence: 39
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.46335 -0.57717  0.06696  0.52134  1.59231
##
## Random effects:
## Groups Name Variance Std.Dev.
## block (Intercept) 0.3332  0.5773
## Residual 0.1831  0.4279
## Number of obs: 23, groups: block, 6
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 0.5669 0.2933 8.5925 1.932 0.0869 .
## treatFRAP 3.1589 0.2470 13.8768 12.788 4.57e-09 ***
## treatIDAP 1.6748 0.2624 14.0029 6.383 1.70e-05 ***
## treatISAP 1.7239 0.2470 13.8768 6.979 6.78e-06 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) trFRAP trIDAP
## treatFRAP -0.421
## treatIDAP -0.396 0.471
## treatISAP -0.421 0.500 0.471
```

```
anova(lmerout)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
## Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## treat 30.029 10.009 3 13.936 54.68 5.926e-08 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Calculate least squares means
```

```
lsmeansLT(lmerout)
```

```
## Least Squares Means table:
##
## Estimate Std. Error df t value lower upper Pr(>|t|)
## treatAP 0.56687 0.29334 8.6 1.9324 -0.10155 1.23528 0.08687 .
## treatFRAP 3.72581 0.29334 8.6 12.7012 3.05739 4.39423 7.294e-07 ***
## treatIDAP 2.24171 0.30638 9.8 7.3167 1.55745 2.92597 2.798e-05 ***
## treatISAP 2.29074 0.29334 8.6 7.8091 1.62232 2.95916 3.490e-05 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Confidence level: 95%
## Degrees of freedom method: Satterthwaite
```

```

# All pairwise comparisons - Tukey method
compout <- glht(lmerout, linfct=mcp(treat="Tukey"))
summary(compout)

##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lmer(formula = y ~ treat + (1 | block), data = trapdata2)
##
## Linear Hypotheses:
##              Estimate Std. Error z value Pr(>|z|)
## FRAP - AP == 0    3.15894    0.24702  12.788 <1e-07 ***
## IDAP - AP == 0    1.67485    0.26237   6.383 <1e-07 ***
## ISAP - AP == 0    1.72387    0.24702   6.979 <1e-07 ***
## IDAP - FRAP == 0 -1.48410    0.26237  -5.656 <1e-07 ***
## ISAP - FRAP == 0 -1.43507    0.24702  -5.810 <1e-07 ***
## ISAP - IDAP == 0  0.04903    0.26237   0.187  0.998
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)

confint(compout)

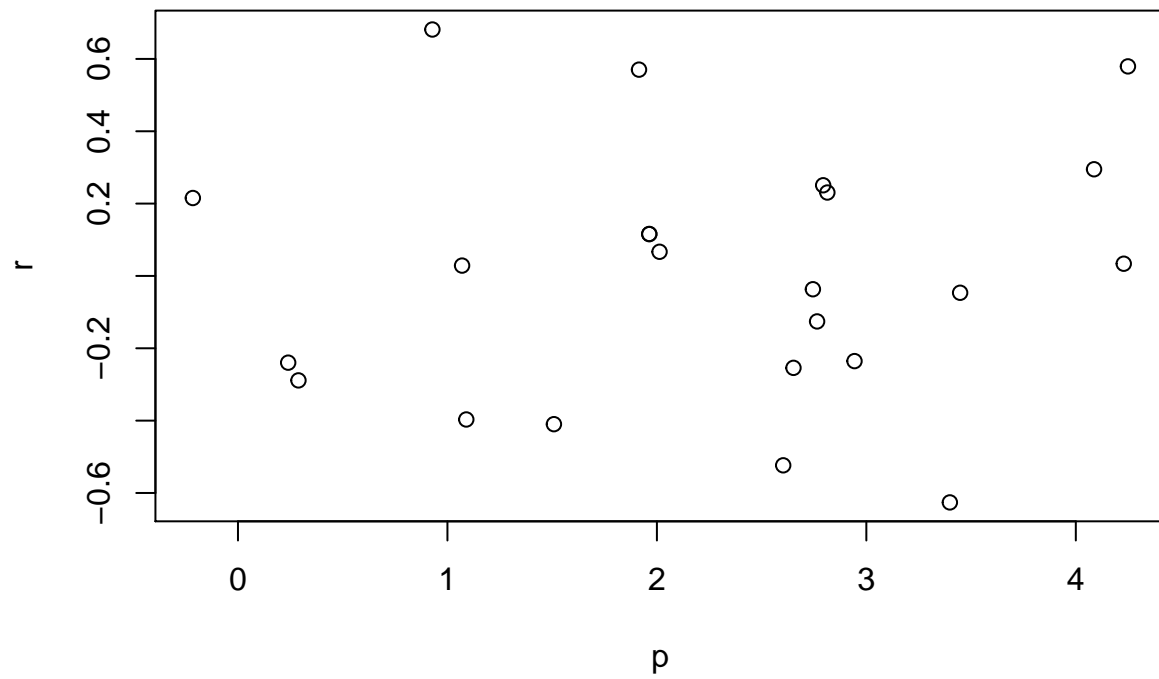
##
## Simultaneous Confidence Intervals
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lmer(formula = y ~ treat + (1 | block), data = trapdata2)
##
## Quantile = 2.568
## 95% family-wise confidence level
##
##
## Linear Hypotheses:
##              Estimate lwr      upr
## FRAP - AP == 0    3.15894 2.52459 3.79329
## IDAP - AP == 0    1.67485 1.00107 2.34863
## ISAP - AP == 0    1.72387 1.08952 2.35822
## IDAP - FRAP == 0 -1.48410 -2.15788 -0.81032
## ISAP - FRAP == 0 -1.43507 -2.06942 -0.80072
## ISAP - IDAP == 0  0.04903 -0.62475 0.72281

cld(compout)

## AP FRAP IDAP ISAP
## "a" "c" "b" "b"

# Diagnostic plots to check ANOVA assumptions
p <- fitted(lmerout)
r <- resid(lmerout)
plot(p,r)

```



`qqnorm(r)`

Normal Q-Q Plot

