

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)

##
## Attaching package: 'lmerTest'
## The following object is masked from 'package:lme4':
##
##     lmer
## The following object is masked from 'package:stats':
##
##     step
library(multcomp)

## Loading required package: mvtnorm
## Loading required package: survival
## Loading required package: TH.data
## 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

```

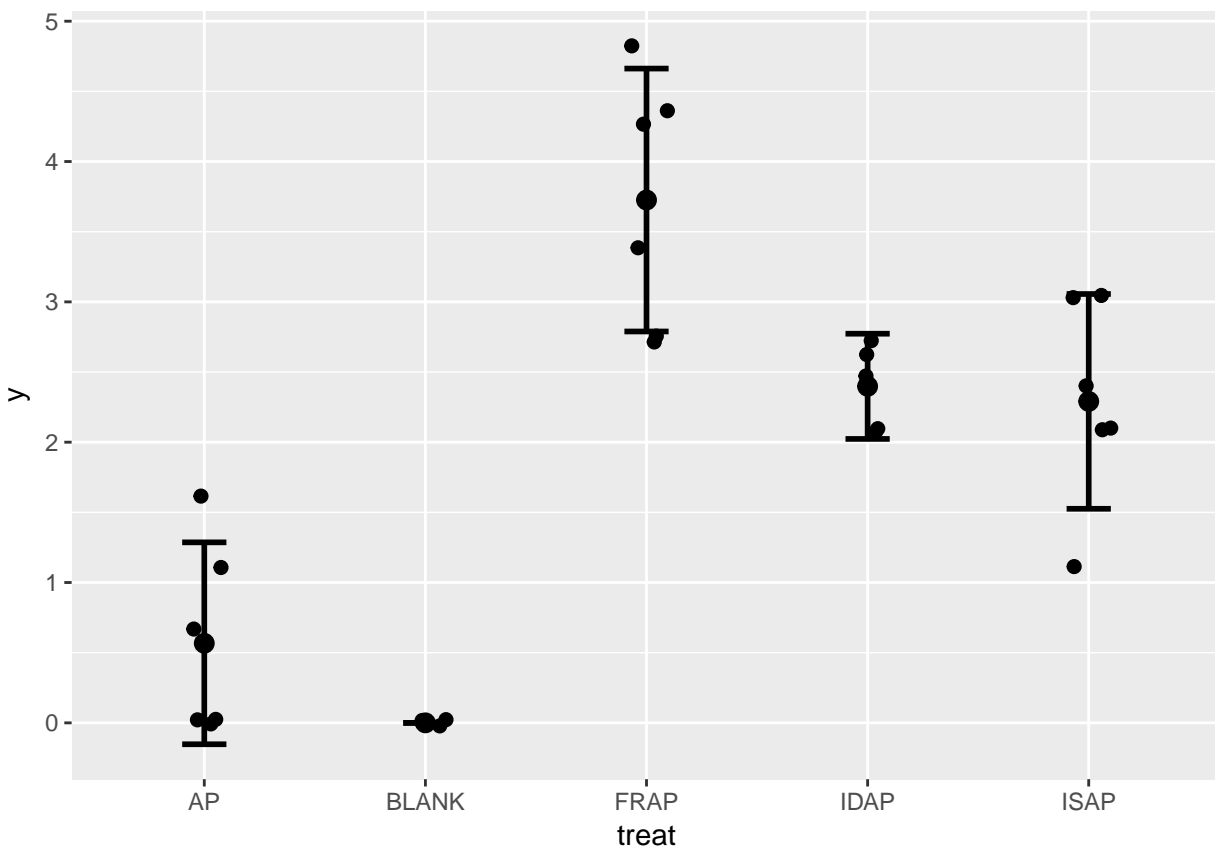
```
## 27      6 BLANK      0 0.0000000
## 28      6 FRAP      70 4.2626799
## 29      6 IDAP      14 2.7080502
## 30      6 ISAP      20 3.0445224
```

```
# Plot treatment means and confidence intervals
ggplot(trapdata,aes(treat,y))+
  geom_jitter(size=2,position=position_jitter(width=0.1))+
  stat_summary(fun.y="mean",geom="point",size=3)+
  stat_summary(fun.data="mean_cl_normal",geom="errorbar",width=0.2,size=1)
```

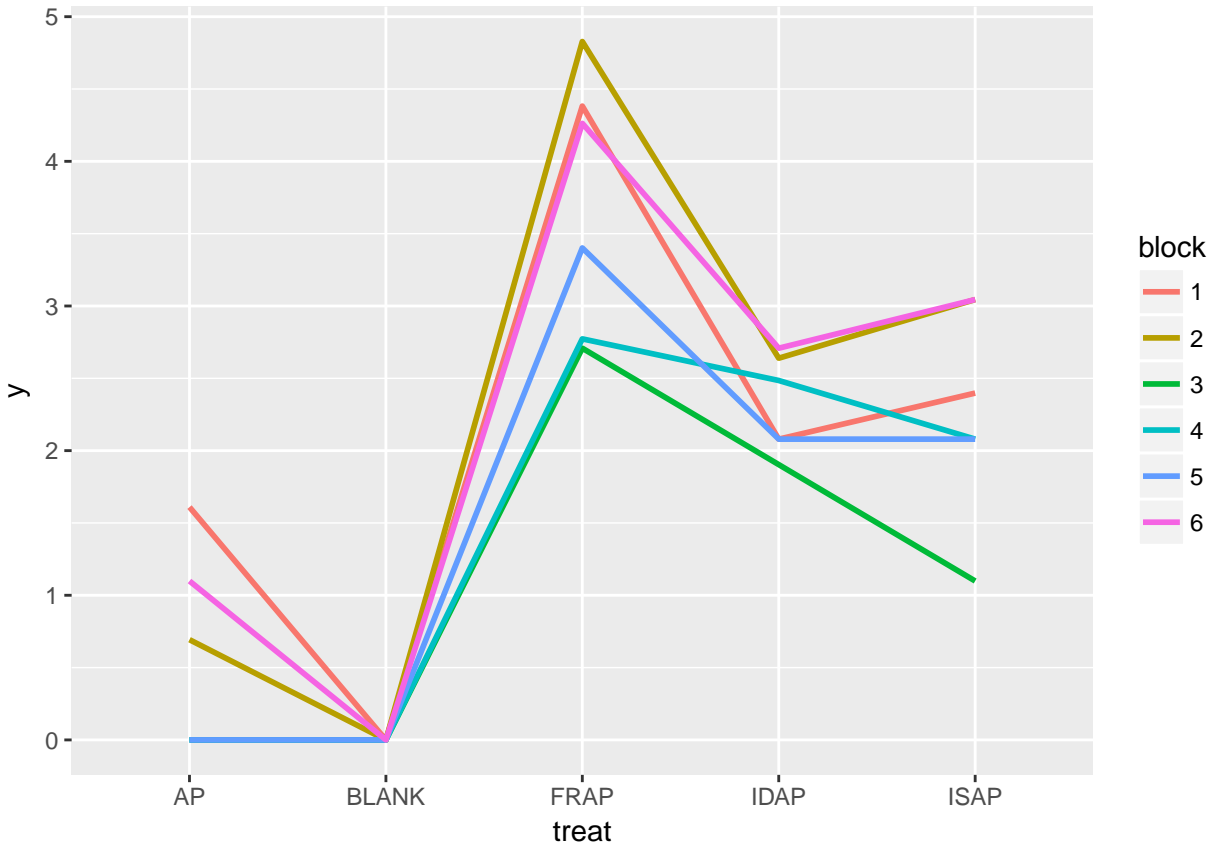
```
## Warning: Removed 1 rows containing non-finite values (stat_summary).
```

```
## Warning: Removed 1 rows containing non-finite values (stat_summary).
```

```
## Warning: Removed 1 rows containing missing values (geom_point).
```



```
# 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(size=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)
```

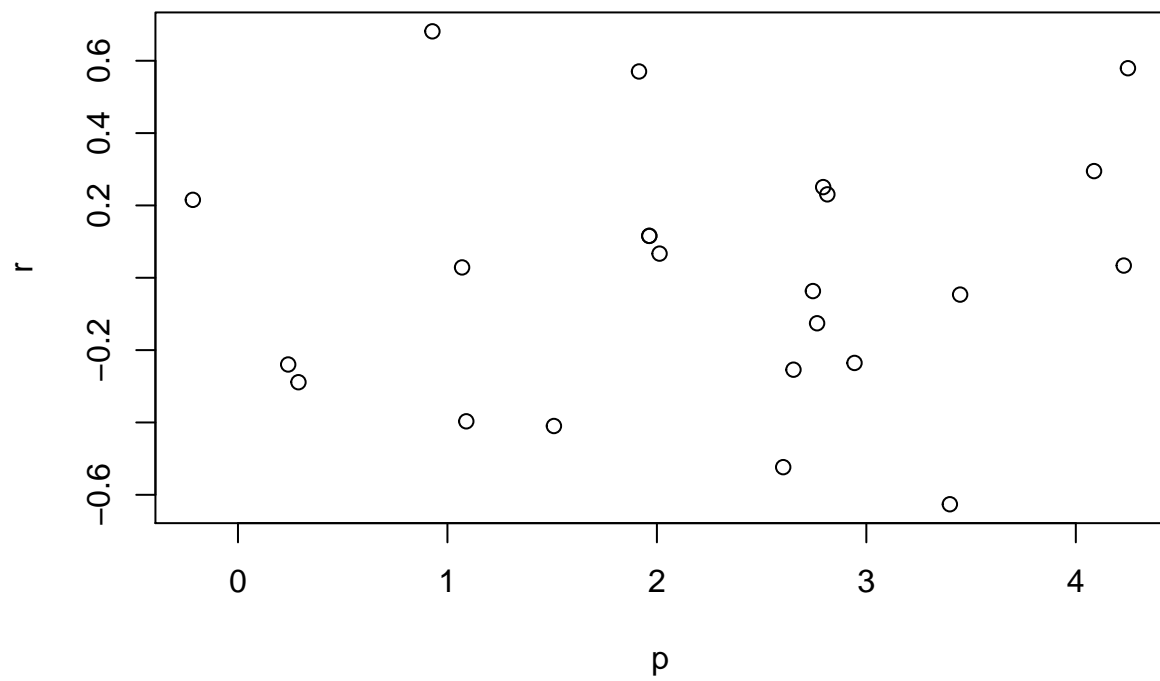
```
##
## Simultaneous Confidence Intervals
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lmer(formula = y ~ treat + (1 | block), data = trapdata2)
##
## Quantile = 2.5688
## 95% family-wise confidence level
##
## Linear Hypotheses:
##           Estimate lwr      upr
## FRAP - AP == 0    3.15894 2.52439 3.79350
## IDAP - AP == 0    1.67485 1.00085 2.34884
## ISAP - AP == 0    1.72387 1.08932 2.35843
## IDAP - FRAP == 0 -1.48410 -2.15809 -0.81010
## ISAP - FRAP == 0 -1.43507 -2.06963 -0.80052
## ISAP - IDAP == 0 0.04903 -0.62497 0.72302
```

```
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

