

# 15C\_aphids

nbutool

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```
#Statistical analyses for autocorrelation experiments - duckweeds and aphids  
#based on file named simpleanovathermal.Rmd
```

```
#Download the data from github repo and check import
```

```
datin <- read.csv("https://raw.githubusercontent.com/Cuddington-Lab/thermal-experiments/main/expdata_merged.csv",  
                  header=TRUE, stringsAsFactors = TRUE)  
str(datin)
```

```
## 'data.frame': 140 obs. of 23 variables:  
## $ Experiment_Number: int 2 2 2 2 3 3 3 3 4 4 ...  
## $ Mean_Temp : int 15 15 15 15 19 19 19 19 23 23 ...  
## $ Experiment_Start : Factor w/ 40 levels "02-Aug-20","03-Dec-21",...: 34 34 34 34 1 1 1 1 13 13 ...  
## $ Experiment_End : Factor w/ 40 levels "02-Feb-22","02-Mar-22",...: 40 40 40 40 8 8 8 8 20 20 ...  
## $ Profile_name : Factor w/ 121 levels "Simplelong 15_095_06",...: 21 35 28 36 50 52 53 55 57 58 ...  
## $ Autocorrelation : num 0 0.9 0.6 0.9 0 0.6 0.95 0.95 0 0.6 ...  
## $ Incubator : int 1 3 5 6 1 3 5 6 1 3 ...  
## $ Offspring_Plant1 : int 0 6 0 0 12 19 22 19 21 23 ...  
## $ Offspring_Plant2 : int 8 6 3 0 16 16 23 17 21 26 ...  
## $ Offspring_Plant3 : int 1 0 4 1 21 14 8 8 22 20 ...  
## $ Duckweed_Rep1 : int NA NA NA NA NA NA NA NA NA NA ...  
## $ Duckweed_Rep2 : int NA NA NA NA NA NA NA NA NA NA ...  
## $ Duckweed_Rep3 : int NA NA NA NA NA NA NA NA NA NA ...  
## $ cat_1 : Factor w/ 4 levels "", "N", "N/A", "P": 3 1 3 1 3 3 2 4 3 3 ...  
## $ cat_1_4 : Factor w/ 4 levels "", "N", "N/A", "P": 3 1 3 1 3 3 4 2 3 3 ...  
## $ Program_mean : num NA NA NA NA NA ...  
## $ Obs_mean : num NA NA NA NA NA ...  
## $ Program_sd : num NA NA NA NA NA ...  
## $ Obs_sd : num NA NA NA NA NA ...  
## $ Program_ac : num NA NA NA NA NA ...  
## $ Obs_ac : num NA NA NA NA NA ...  
## $ Gaps : Factor w/ 3 levels "", "n", "y": 2 2 2 2 1 2 2 2 2 2 ...  
## $ Gap_size : Factor w/ 8 levels "", "35h", "36h",...: 1 1 1 1 1 1 1 1 1 1 ...
```

```
#Exclude NAs and samples with standard deviations too different from set value of 2.5  
datin <- subset(datin, Gaps != "y" & (Obs_sd >= 2.2 & Obs_sd <= 2.8))
```

```
#Create new treatment label (cat_1_4: if investigating effect of initial  
#sequence slope; cat_1: whole sequence)  
table(datin$Autocorrelation, datin$cat_1_4)
```

```
##
```

```
##           N N/A  P
##    0      0  0  28  0
##   0.95  0  28   0 32
```

```
levels(datin$cat_1_4) = c("", "m<0", "", "m>0" )
datin$label<-paste0(datin$Autocorrelation, datin$cat_1_4)
table(datin$label)
```

```
##
##      0 0.95m<0 0.95m>0
##    28      28      32
```

```
#Create new column including sum of fronds (sumFro)
#duckweed:
#datin$sumFro=datin$Duckweed_Rep1+datin$Duckweed_Rep2+datin$Duckweed_Rep3
#aphids:
datin$sumFro=datin$Offspring_Plant1+datin$Offspring_Plant2+datin$Offspring_Plant3

#Exclude missing data
datin <- subset(datin, sumFro != "NA")
table(datin$Mean_Temp, datin$label)
```

```
##
##      0 0.95m<0 0.95m>0
##   15  7      6      7
##   19  0      1      1
##   23  3      6      4
##   27 16     10     18
```

Selecting the temperature

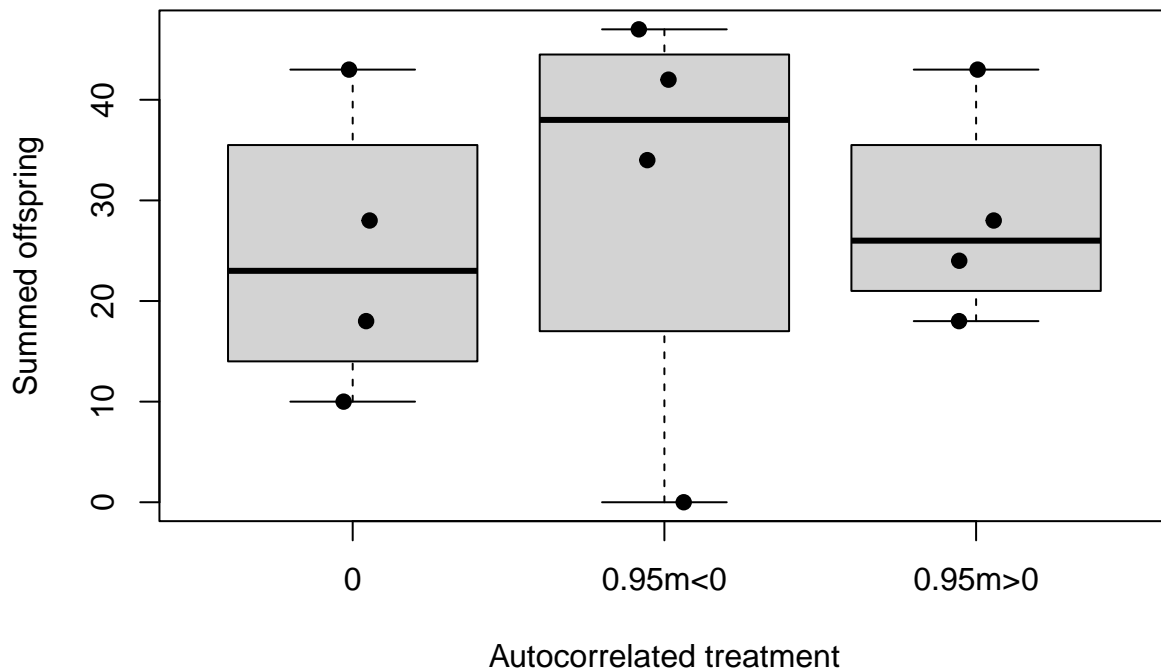
```
#Select mean temp
dat27 <- subset(datin, Mean_Temp == 15)

#Select experiments in which all treatments occurred in the same week
datunique <- dat27[!duplicated(dat27[c("Experiment_Number", "cat_1_4")]),]
datunique <- datunique[unsplit(table(datunique$Experiment_Number), datunique$Experiment_Number) >= 3, ]

#If investigating whole sequence (cat_1), remove one of the 2 autocorrelated regimes
#datunique <- subset(datunique, label != "0.95m>0")

#BoxPlot
tr=boxplot(sumFro~label, data=datunique, main=expression(paste("Autocorrelated temperature regimes: mean",
  xlab="Autocorrelated treatment", ylab="Summed offspring",
  names = levels(as.factor(datunique$label)))
stripchart(sumFro~label, data=datunique,
  vertical = TRUE, method = "jitter",
  pch = 19, add = TRUE)
```

## Autocorrelated temperature regimes: mean temperature 15°C



### Anova Analysis

```
#Anova (Are average performances significantly different across groups?)
anova=aov(sumFro~label, data=datunique)
summary(anova)
```

```
##           Df Sum Sq Mean Sq F value Pr(>F)
## label      2   72.7    36.33   0.143  0.869
## Residuals  9 2294.2    254.92
```

```
#Equality of variances (Is distribution of performances significantly different across groups?)
library(car)
```

```
## Warning: package 'car' was built under R version 4.1.3
```

```
## Loading required package: carData
```

```
## Warning: package 'carData' was built under R version 4.1.3
```

```
leveneTest(sumFro ~ label, data = datunique)
```

```
## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.
```

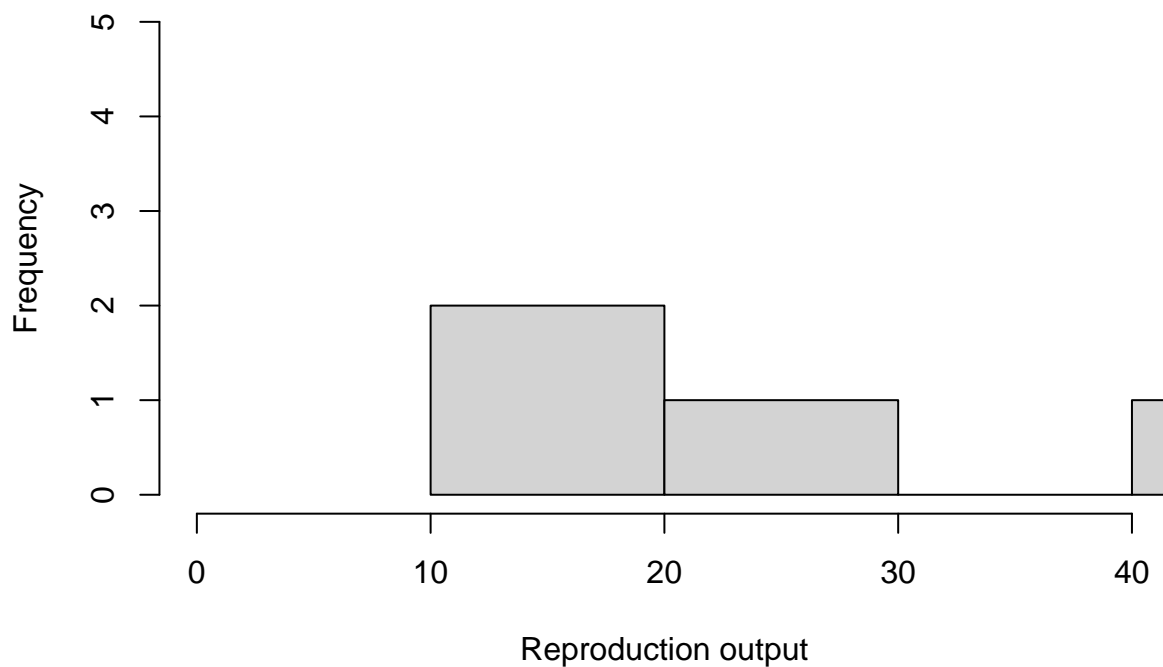
```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 2  0.3438  0.718
##      9
```

<http://www.sthda.com/english/wiki/compare-multiple-sample-variances-in-r>

*#Histograms*

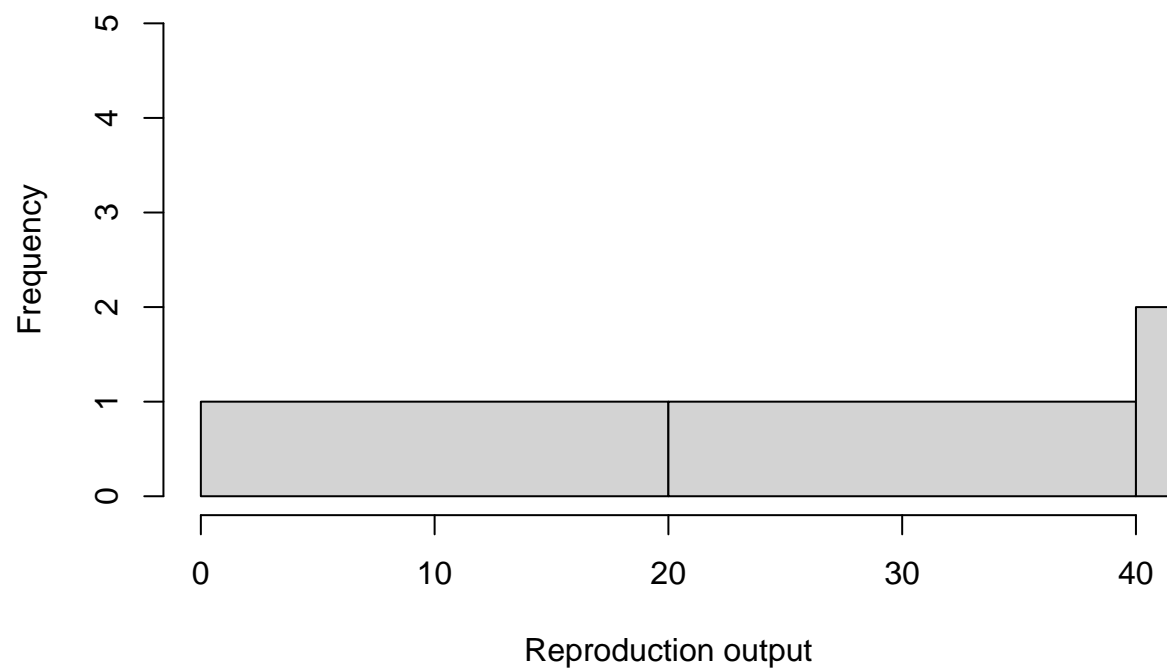
```
hist(datunique[datunique$label == "0", "sumFro"], xlab="Reproduction output",xlim=c(0,40),ylim=c(0,5))
```

## Histogram of datunique[datunique\$label == "0", "sumFro"]



```
hist(datunique[datunique$label == "0.95m<0", "sumFro"], xlab="Reproduction output",xlim=c(0,40),ylim=c(0,5))
```

**Histogram of datunique[datunique\$label == "0.95m<0", "sumFro"]**



```
hist(datunique[datunique$label == "0.95m>0", "sumFro"], xlab="Reproduction output",xlim=c(0,40),ylim=c(0,5))
```

**Histogram of datunique[datunique\$label == "0.95m>0", "sumFro"]**

