

# 15C\_duckweeds\_2022\_P\_cat\_1

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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/exp_metafi  
                  header=TRUE, stringsAsFactors = TRUE)  
str(datin)
```

```
## 'data.frame': 39 obs. of 23 variables:  
## $ Experiment_Number: int 60 60 60 61 61 61 62 62 63 63 ...  
## $ Mean_Temp : int 27 27 27 27 27 27 27 27 27 27 ...  
## $ Experiment_Start : Factor w/ 10 levels "04-Feb-22","04-Mar-22",...: 5 5 5 8 8 8 10 10 1 1 ...  
## $ Experiment_End : Factor w/ 10 levels "02-Feb-22","02-Mar-22",...: 7 7 7 10 10 10 1 1 3 3 ...  
## $ Profile_name : Factor w/ 38 levels "Simplelong15_000_10",...: 14 15 16 17 18 19 20 21 25 32 ..  
## $ Autocorrelation : num 0 0 0 0 0 0 0 0 0.95 0.95 ...  
## $ Incubator : int 4 5 6 4 5 6 5 6 2 3 ...  
## $ Offspring_Plant1 : int 4 4 6 1 0 7 18 33 NA NA ...  
## $ Offspring_Plant2 : int 5 4 6 0 0 6 18 10 NA NA ...  
## $ Offspring_Plant3 : int 6 0 4 2 4 7 9 33 NA NA ...  
## $ Duckweed_Rep1 : int 14 14 12 10 9 12 8 NA 10 11 ...  
## $ Duckweed_Rep2 : int 11 12 12 11 9 10 8 NA 9 13 ...  
## $ Duckweed_Rep3 : int 11 11 13 12 10 10 8 NA 11 13 ...  
## $ cat_1 : Factor w/ 3 levels "N","N/A","P": 2 2 2 2 2 2 2 2 1 3 ...  
## $ cat_1_4 : Factor w/ 3 levels "N","N/A","P": 2 2 2 2 2 2 2 2 1 1 ...  
## $ Program_mean : num 26.9 26.9 26.9 26.9 26.9 ...  
## $ Obs_mean : num 26.9 26.9 26.9 26.9 26.9 ...  
## $ Program_sd : num 2.98 2.97 2.97 2.95 2.95 ...  
## $ Obs_sd : num 2.95 2.92 2.92 2.92 2.92 ...  
## $ Program_ac : num -0.00283 0.00482 -0.00386 0.00281 -0.01334 ...  
## $ Obs_ac : num 0.01605 0.026283 0.014053 0.018468 0.000767 ...  
## $ Gaps : Factor w/ 1 level "n": 1 1 1 1 1 1 1 1 1 1 ...  
## $ Gap_size : logi NA NA NA NA NA NA ...
```

```
#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)
```

```
##
```

```
##           N N/A  P
##      0      0   6   0
##    0.95 13     0  12
```

```
levels(datin$cat_1) = c("m<0","", "m>0" )
datin$label<-paste0(datin$Autocorrelation, datin$cat_1)
table(datin$label)
```

```
##
##           0 0.95m<0 0.95m>0
##           6      13      12
```

```
#Create new column including sum of fronds (sumFro)
#duckweed:
datin$sumFro=datin$Duckweed_Rep1+datin$Duckweed_Rep2+datin$Duckweed_Rep2
#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 3           5           5
##      27 3           6           6
```

Selecting the temperature

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

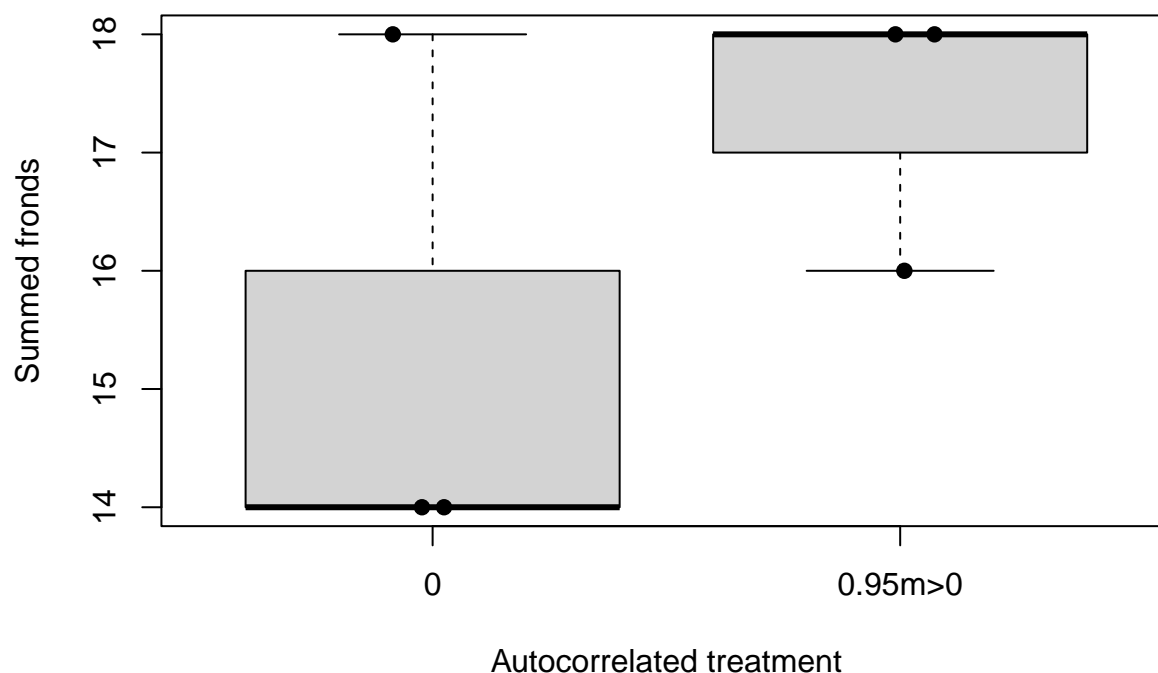
#Select experiments in which all treatments occurred in the same week
datunique <- dat27[!duplicated(dat27[c("Experiment_Number", "cat_1")]),]
datunique <- datunique[unsplit(table(datunique$Experiment_Number), datunique$Experiment_Number) >= 3, ]
```

0 x 0.95P

```
#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 fronds",
                        names = levels(as.factor(datunique$label)))
stripchart(sumFro~label, data=datunique,
            vertical = TRUE, method = "jitter",
            pch = 19, add = TRUE)
```

## Autocorrelated temperature regimes: mean temperature 27°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      1    6.00    6.000      1.8  0.251
## Residuals  4   13.33    3.333
```

```
#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 1      0.2 0.6779
##      4
```

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

*#Histograms*

```
library(ggplot2)
ggplot(datunique, aes(x = sumFro)) +
  geom_histogram(fill = "white", colour = "black", binwidth = 5) +
  facet_grid(label ~ .)
```

