27C_duckweed

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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_me
                  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)
```

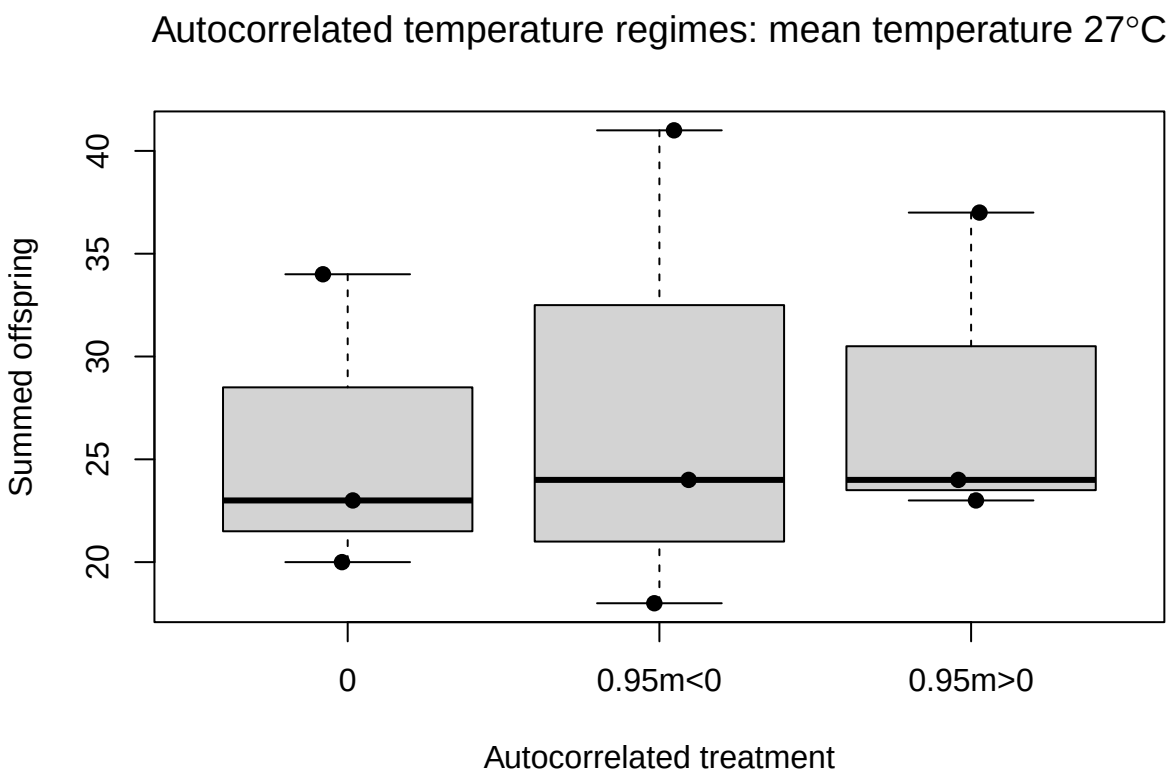
```
##
##       0 0.95m<0 0.95m>0
##      28      28      32
```

```
#Create new column including sum of fronds (sumFro)
#duckweed:
datin$sumFro=datin$Duckweed_Rep1+datin$Duckweed_Rep2+datin$Duckweed_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  2       4       3
##   23  2       5       3
##   27 11       7       9
```

Selecting the temperature

```
#Select mean temp
dat27 <- subset(datin, Mean_Temp == 27)

#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)
```



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    9.6    4.78   0.056  0.946
## Residuals    6  515.3   85.89
```

```
#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
```

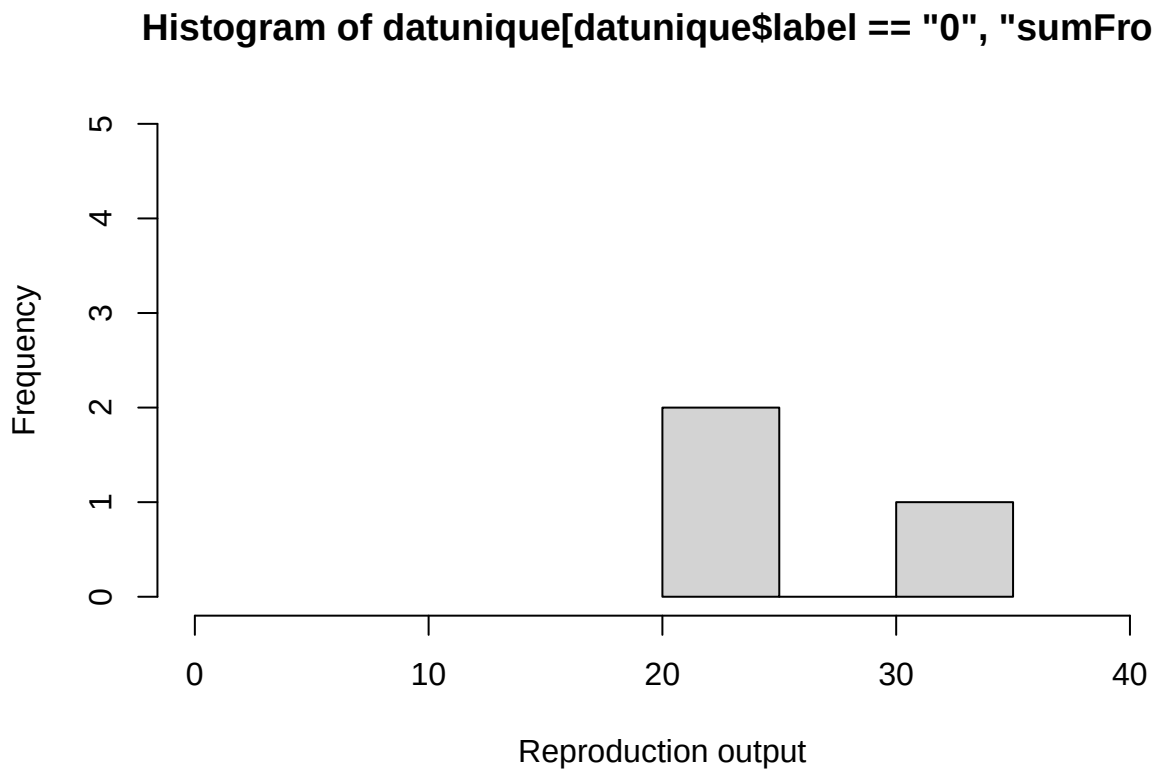
```
## Warning: package 'carData' was built under R version 4.1.3
```

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

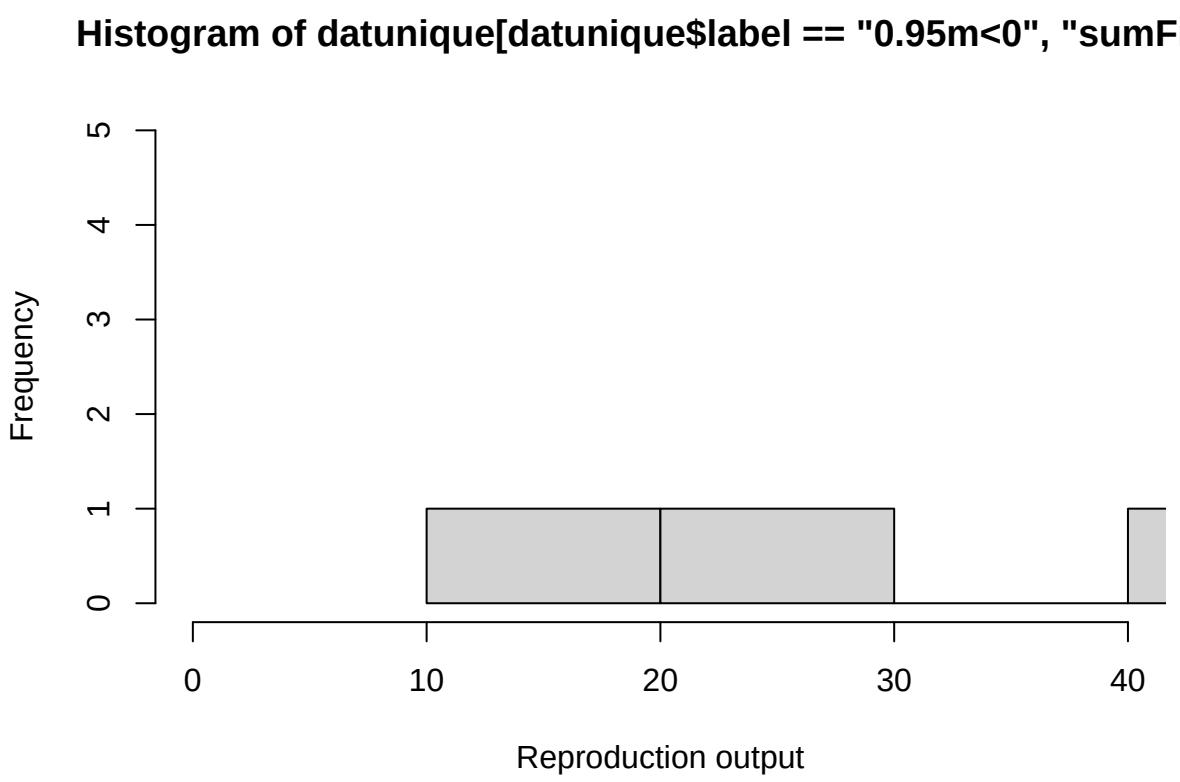
```
## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  2  0.1698 0.8477
##        6
```

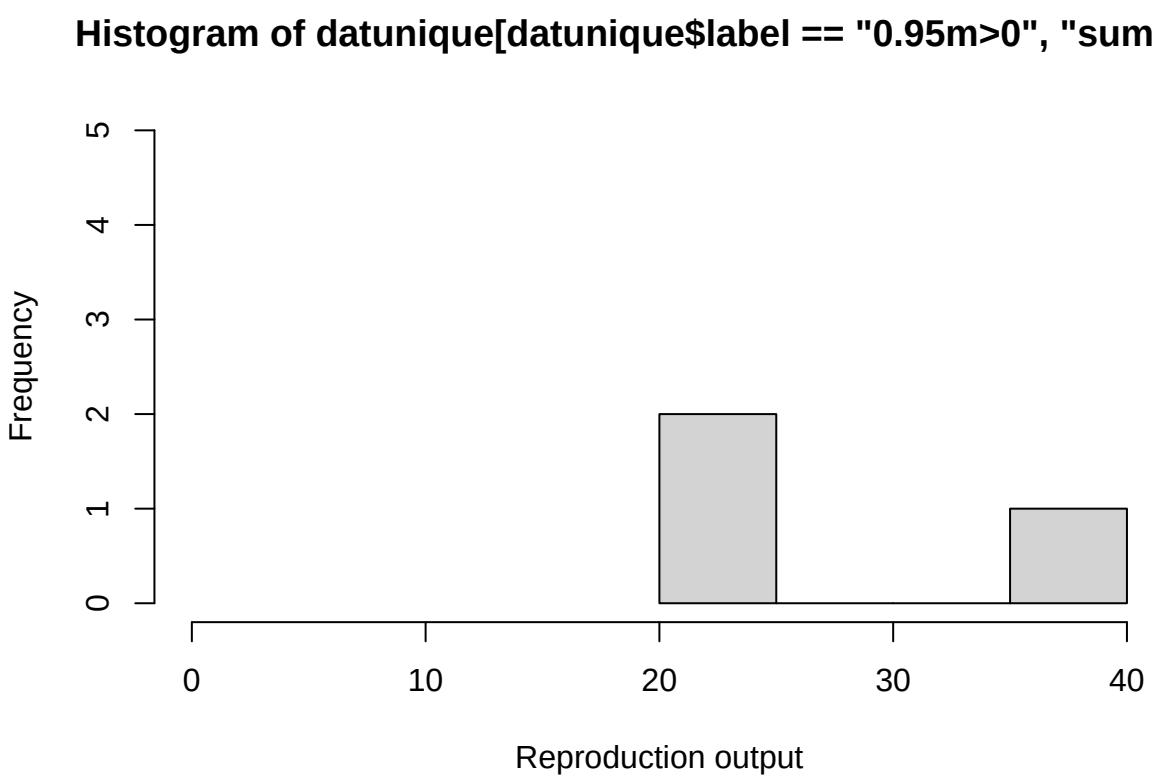
```
#http://www.sthda.com/english/wiki/compare-multiple-sample-variances-in-r

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




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




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


Histogram of datunique[datunique$label == "0.95m>0", "sumFro"]
Frequency
0
1
2
3
4
5
0
10
20
30
40
Reproduction output