23C_aphid_cat_1_tt

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The purpose of this document is to display the results of the Power analysis for each mean temperature (15, 19, 23, 27) for the aphid data. For each temperature there will be 4 results total as follows.

1. T-test comparing 0 to 0.95 m<0, categorization based on whole sequence
2. T-test comparing 0 to 0.95 m>0, categorization based on whole sequence
3. T-test comparing 0 to 0.95 m<0, categorization based on first 1/4th of sequence
4. T-test comparing 0 to 0.95 m>0, categorization based on first 1/4th of sequence

In this document we'll focus on cat_1

##No. of acceptable samples per temperature

```
#Power analysis for autocorrelation experiments - duckweed
#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':    135 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/ 39 levels "02-Aug-20","03-Dec-21",..: 33 33 33 33 1 1 1 1 12 12 ...
##  $ Experiment_End   : Factor w/ 39 levels "02-Feb-22","02-Mar-22",..: 39 39 39 39 8 8 8 8 19 19 ...
##  $ Profile_name     : Factor w/ 118 levels "Simplelong 15_095_06",..: 21 34 27 35 45 47 48 50 52 53
##  $ 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
#(code for duckweeds, needs to be adapted for aphids)
datin <- subset(datin, Offspring_Plant1 != "NA" & Obs_sd < 2.7 & Obs_sd > 2.2 & Gaps != "y")

#Create new treatment label and check
table(datin$Autocorrelation, datin$cat_1)
```

```
##
##            N N/A  P
##   0     0  0  22  0
##   0.95  0 25   0 24
```

```
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
##      22      25      24
```

```
#Create new column including sum of fronds (sumFro)
datin$sumFro=datin$Offspring_Plant1+datin$Offspring_Plant2+datin$Offspring_Plant3
datin <- subset(datin, sumFro != "NA")
table(datin$Mean_Temp, datin$label)
```

```
##
##       0 0.95m<0 0.95m>0
##   15  6       5       6
##   19  0       1       1
##   23  3       5       5
##   27 13      14      12
```

23 deg C

```
#Select mean temp of 23C
dat27 <- subset(datin, Mean_Temp == 23)

#Perform power analysis based on preliminary data
#Source: https://med.und.edu/daccota/_files/pdfs/berdc_resource_pdfs/sample_size_r_module.pdf
library(pwr)
```

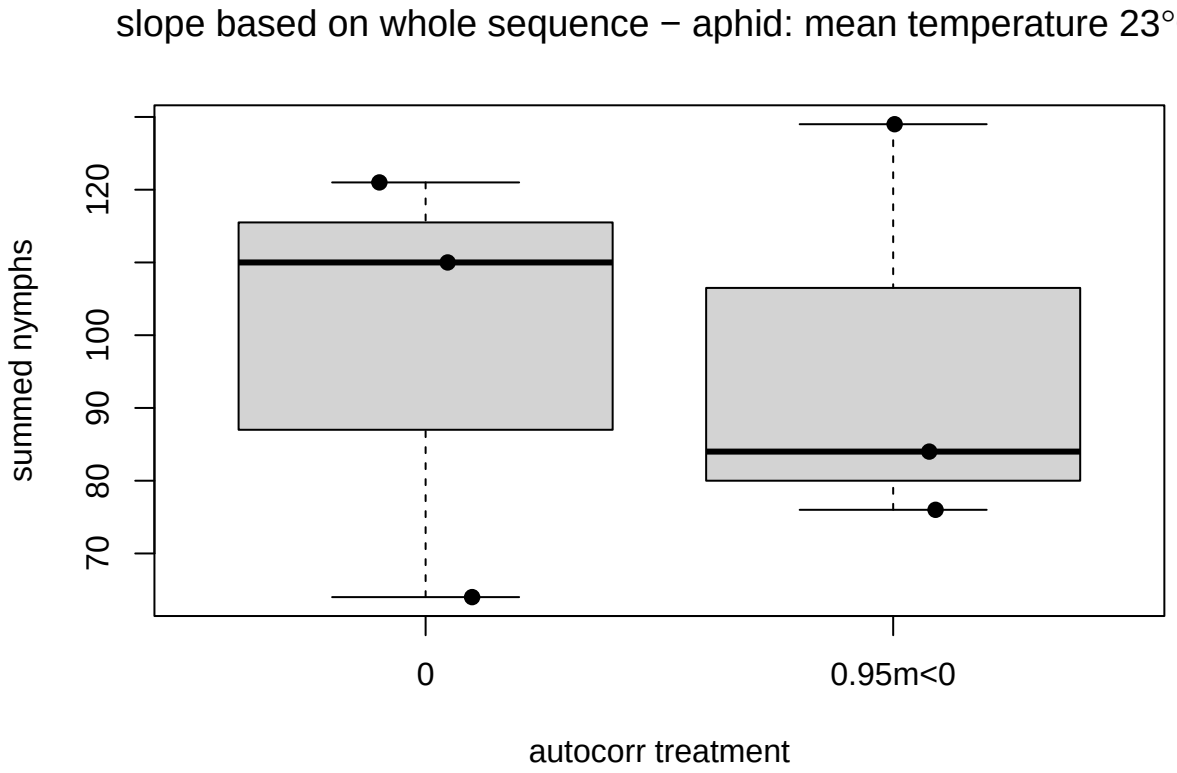
Categorization for whole sequence

checking 0 to 0.95m<0

```
#Subset data to include only one 0.95 autocorrelation group and control group
#Obtain same number of samples for each group
datpower <- rbind(dat27[ sample(which (dat27$label == "0") ,3), ],
                  dat27[ sample(which (dat27$label == "0.95m<0") ,3), ])
```

Producing boxplot

```
#BoxPlot
tr=boxplot(sumFro~label, data=datpower,main=expression(paste("slope based on whole sequence - aphid: mea
           xlab="autocorr treatment", ylab="summed nymphs",
           names = levels(as.factor(datpower$label)))
stripchart(sumFro~label, data=datpower,
           vertical = TRUE, method = "jitter",
           pch = 19, add = TRUE)
```



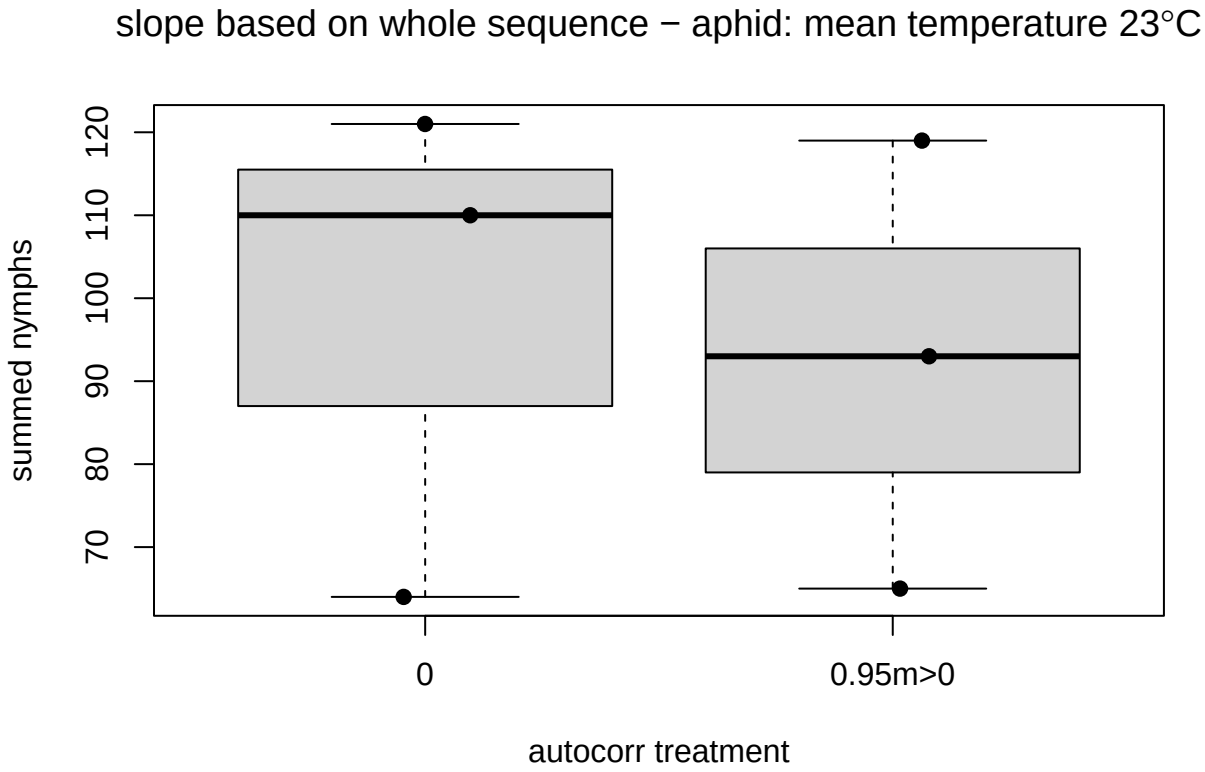
power analysis results

```
#Obtain effect size
treatmean <- mean(dat27[dat27$label == "0.95m<0", "sumFro"])
controlmean <- mean(dat27[dat27$label == "0", "sumFro"])
treatsd <- sd(dat27[dat27$label == "0.95m<0", "sumFro"])
controlsd <- sd(dat27[dat27$label == "0", "sumFro"])
effsize <- (treatmean-controlmean)/(sqrt((controlsd^2)+(treatsd^2))/2)

#Perform power test to obtain estimated "n" in each group based on effect size
pwr.t.test(d=effsize, sig.level=0.05, power=0.80, type="two.sample", alternative="two.sided")
```

```
##
##      Two-sample t test power calculation
##
##               n = 111.0276
##               d = 0.3776639
##       sig.level = 0.05
##           power = 0.8
##     alternative = two.sided
##
## NOTE: n is number in *each* group
```

checking 0 to 0.95m>0



producing boxplot

power analysis results

```
##
##      Two-sample t test power calculation
##
##               n = 130.5388
##               d = 0.3480677
##       sig.level = 0.05
##           power = 0.8
##     alternative = two.sided
##
## NOTE: n is number in *each* group
```

Note the code is not shown for the second iteration comparing 0 to 0.95 m>0 since it's the same as the other code, just the sample size is changed.