Autocorrelation_stats

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Load and Preprocess Datasets

We load two datasets: one with a preparation technique (repeated frond selection) and one without.

```r
library(interactions)
library(ggplot2)

# This dataset contains replicates for which a preparation technique was performed (repeated first born
original_dataset_2 <- read.csv("https://raw.githubusercontent.com/Cuddington-Lab/thermal-experiments/ma
original_dataset_2$prep <- rep("yes",times=length(original_dataset_2$Experiment_Number))

# This dataset contains replicates of experiments performed without a preparation technique
original_dataset_1 <- read.csv("https://raw.githubusercontent.com/Cuddington-Lab/thermal-experiments/ma
original_dataset_1$prep <- rep("no",times=length(original_dataset_1$Experiment_Number))
```

Combine datasets and do data validation

We combine both datasets and filter out rows based on specific conditions for standard deviation (`Obs_sd`) and autocorrelation (`Obs_ac`) to clean the data.

```r
# Blending both datasets, as there are no significant differences between preparation methods (probably
datin <- rbind(original_dataset_1,original_dataset_2)

datin <- datin[!(datin$Treatment == 0 & (datin$Obs_sd <= 2.1 | datin$Obs_sd >= 2.9))
               &!(datin$Treatment == 0.95 & (datin$Obs_sd <= 2.1 | datin$Obs_sd >= 2.9)),]

datin <- datin[!(datin$Treatment == 0 & (datin$Obs_ac <= -0.2 | datin$Obs_ac >= 0.2))
               &!(datin$Treatment == 0.95 & (datin$Obs_ac <= 0.92 | datin$Obs_ac >= 0.98)),]

datin <- subset(datin, !Errors == "y"|is.na(Errors))
datin <- subset(datin, !Treatment == "constant")
```
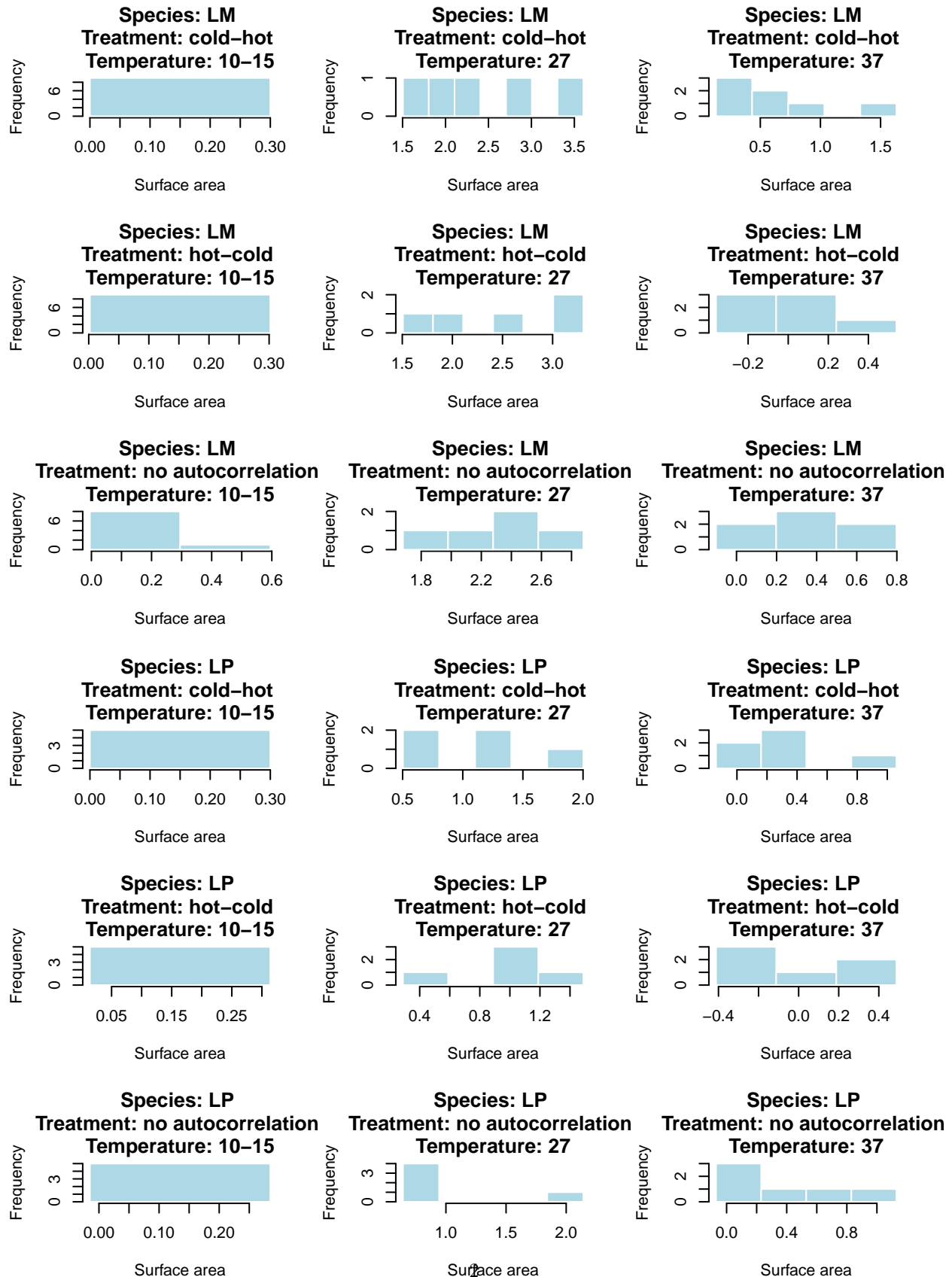
Surface area measurement used: change in surface area

Histogram of data (SA = change in surface area)

Species: LM
Treatment: cold–hot
Temperature: 10–15

Species: LM
Treatment: cold–hot
Temperature: 27

Species: LM
Treatment: cold–hot
Temperature: 37

Species: LM
Treatment: hot–cold
Temperature: 10–15

Species: LM
Treatment: hot–cold
Temperature: 27

Species: LM
Treatment: hot–cold
Temperature: 37

Species: LM
Treatment: no autocorrelation
Temperature: 10–15

Species: LM
Treatment: no autocorrelation
Temperature: 27

Species: LM
Treatment: no autocorrelation
Temperature: 37

Species: LP
Treatment: cold–hot
Temperature: 10–15

Species: LP
Treatment: cold–hot
Temperature: 27

Species: LP
Treatment: cold–hot
Temperature: 37

Species: LP
Treatment: hot–cold
Temperature: 10–15

Species: LP
Treatment: hot–cold
Temperature: 27

Species: LP
Treatment: hot–cold
Temperature: 37

Species: LP
Treatment: no autocorrelation
Temperature: 10–15

Species: LP
Treatment: no autocorrelation
Temperature: 27

Species: LP
Treatment: no autocorrelation
Temperature: 37

View dataset and response variable (SA = change in surface area)

	Exp_run	Treatment	Initial_area	Final_area	Frond_count	SA
65	1510	cold-hot	0.530	0.723	18	0.193
66	1510	hot-cold	0.549	0.693	17	0.144
67	1510	no autocorrelation	0.608	0.667	14	0.059
68	1511	cold-hot	0.549	0.683	15	0.134
69	1511	hot-cold	0.556	0.694	15	0.138
70	1511	no autocorrelation	0.532	0.725	16	0.193

View number of replicates

LM

```
## 
##        no autocorrelation cold-hot hot-cold
##   10-15                 9        9        9
##   27                    5        5        5
##   37                    7        7        7
```

LP

```
## 
##        no autocorrelation cold-hot hot-cold
##   10-15                 5        5        5
##   27                    5        5        5
##   37                    6        6        6
```

Mixed-Effects Model Fitting

```r
species_list <- c("LM", "LP")
model_results <- list()

for (sp in species_list) {
  species_data <- subset(dataset, Species == sp)
  library(lme4)
simple <- lm(SA ~ Treatment * Mean_temperature,
              data = species_data,
              na.action = na.exclude)

exp_number <- lmer(SA ~ Treatment * Mean_temperature + (1 | Exp_run),
                    data = species_data,
                    na.action = na.exclude)

#anova(exp_number, simple, test = "Chisq")
L0 <- logLik(simple)
L1 <- logLik(exp_number)
L.ratio <- as.vector(- 2 * (L0 - L1))
p_value <- 0.5 * (1 - pchisq(L.ratio, 1))
options(scipen = 999)
cat("Comparing simple x mixed model for ", sp, "\n")
cat("p_value:", p_value, "\n")

model_results[[sp]] <- list(simple = simple, exp_number = exp_number)
```

```
}
```

```
## Comparing simple x mixed model for  LM
## p_value: 0.5
## Comparing simple x mixed model for  LP
## p_value: 0.5
```

Model significance testing

Mixed models were selected for all analyses, as likelihood-ratio tests indicated that the random effects were significant in most cases

```
## [1] "Predictor significance - species LM :"
## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: SA
##                            Chisq Df          Pr(>Chisq)
## (Intercept)                0.718  1             0.39679
## Treatment                  0.039  2             0.98068
## Mean_temperature         111.655  2 < 0.0000000000000002 ***
## Treatment:Mean_temperature 11.917  4             0.01798 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Residual degrees of freedom - species : LM : 52"
## [1] "Predictor significance - species LP :"
## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: SA
##                            Chisq Df Pr(>Chisq)
## (Intercept)               0.3459  1     0.5565
## Treatment                 0.0222  2     0.9890
## Mean_temperature         21.6966  2 0.00001944 ***
## Treatment:Mean_temperature 1.2996  4     0.8614
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Residual degrees of freedom - species : LP : 37"

## [1] "Showing predictor significance for linear mixed model for LM"

## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: SA
##                            Chisq Df          Pr(>Chisq)
## (Intercept)                0.718  1             0.39679
## Treatment                  0.039  2             0.98068
## Mean_temperature         111.655  2 < 0.0000000000000002 ***
## Treatment:Mean_temperature 11.917  4             0.01798 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Showing predictor significance for linear mixed model for LP"

## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: SA
##                            Chisq Df Pr(>Chisq)
```

```
## (Intercept)                0.3459  1      0.5565
## Treatment                  0.0222  2      0.9890
## Mean_temperature          21.6966  2 0.00001944 ***
## Treatment:Mean_temperature 1.2996  4      0.8614
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model summary for common duckweeds

```
## character(0)
```

Post-hoc test for common duckweeds

```
## [1] "Pairwise interactions:"

## $emmeans
## Mean_temperature = 10-15:
##  Treatment         emmean    SE   df lower.CL upper.CL
##  no autocorrelation 0.1059 0.125 1.43  -0.7016    0.913
##  cold-hot           0.1254 0.125 1.43  -0.6820    0.933
##  hot-cold           0.1032 0.125 1.43  -0.7043    0.911
##
## Mean_temperature = 27:
##  Treatment         emmean    SE   df lower.CL upper.CL
##  no autocorrelation 2.2212 0.168 4.63   1.7795    2.663
##  cold-hot           2.4684 0.168 4.63   2.0267    2.910
##  hot-cold           2.4452 0.168 4.63   2.0035    2.887
##
## Mean_temperature = 37:
##  Treatment         emmean    SE   df lower.CL upper.CL
##  no autocorrelation 0.3316 0.142 3.40  -0.0909    0.754
##  cold-hot           0.5624 0.142 3.40   0.1400    0.985
##  hot-cold           0.0144 0.142 3.40  -0.4080    0.437
##
## Degrees-of-freedom method: satterthwaite
## Confidence level used: 0.95
##
## $contrasts
## Mean_temperature = 10-15:
##  contrast                       estimate    SE   df t.ratio p.value
##  no autocorrelation - (cold-hot) -0.01956 0.123 11.6  -0.159  0.9861
##  no autocorrelation - (hot-cold)  0.00267 0.123 11.6   0.022  0.9997
##  (cold-hot) - (hot-cold)          0.02222 0.123 11.6   0.181  0.9822
##
## Mean_temperature = 27:
##  contrast                       estimate    SE   df t.ratio p.value
##  no autocorrelation - (cold-hot) -0.24720 0.165 37.5  -1.500  0.3026
##  no autocorrelation - (hot-cold) -0.22400 0.165 37.5  -1.359  0.3724
##  (cold-hot) - (hot-cold)          0.02320 0.165 37.5   0.141  0.9891
##
## Mean_temperature = 37:
##  contrast                       estimate    SE   df t.ratio p.value
##  no autocorrelation - (cold-hot) -0.23086 0.139 27.6  -1.657  0.2396
##  no autocorrelation - (hot-cold)  0.31714 0.139 27.6   2.276  0.0762
##  (cold-hot) - (hot-cold)          0.54800 0.139 27.6   3.934  0.0014
```

Degrees-of-freedom method: satterthwaite
P value adjustment: tukey method for comparing a family of 3 estimates