

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.

```
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/main/original_dataset_2.csv")
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/main/original_dataset_1.csv")
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.

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

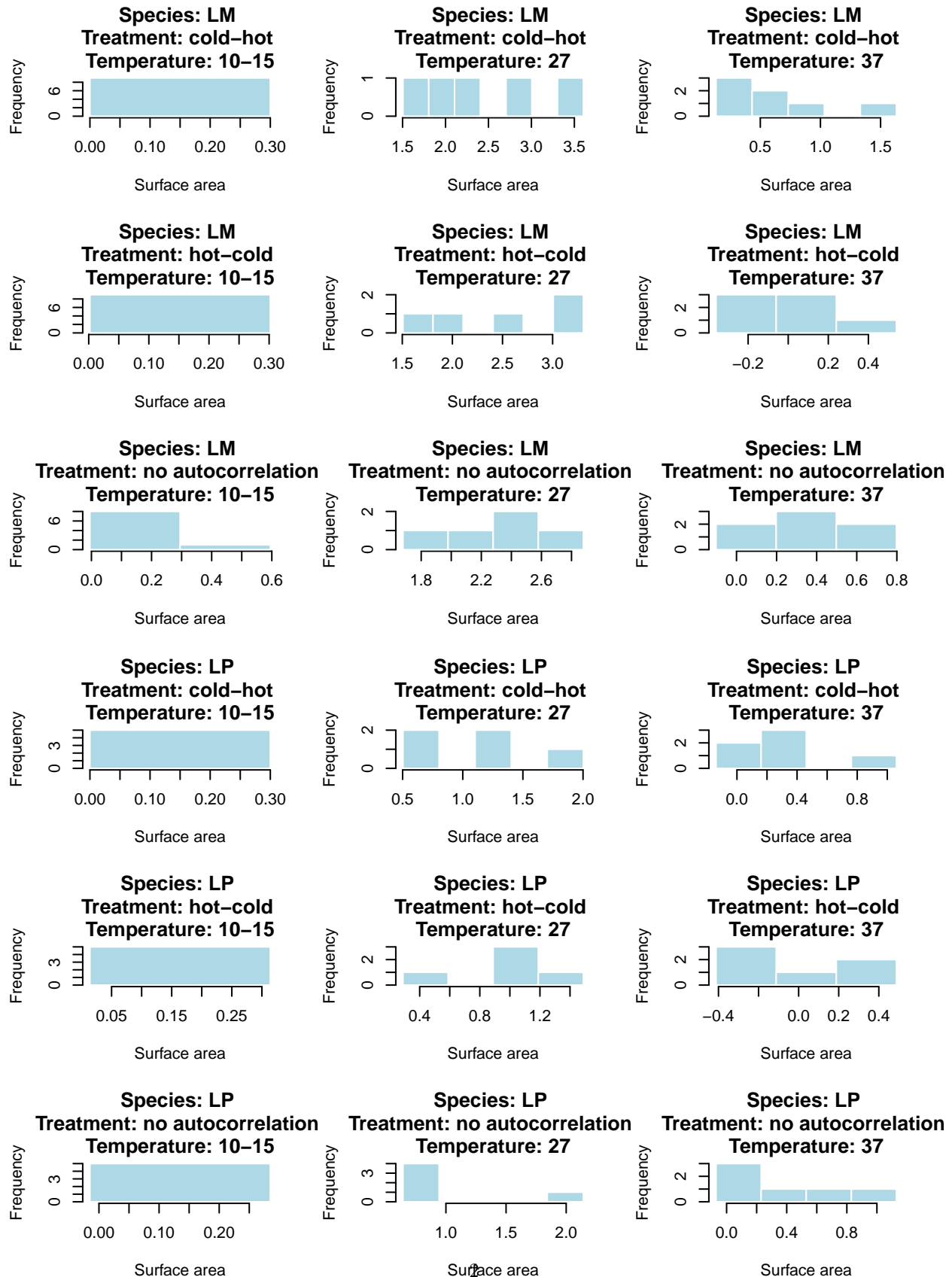
datin <- datin[!(datin$Treatment == 0 & (datin$Obs_sd <= 2.1 | datin$Obs_sd >= 2.9))
               &!(datin$Treatment == 0.95 & (datin$Obs_sd <= 2.1 | datin$Obs_sd >= 2.9)),]

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)



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

```
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 Comparison and Results

We compare the performance of the models and get results for best model.

```
## [1] "Model comparison for species: LM"
##
##
##           Name                AIC
## -----
## no random effects  no random effects  65.45
## experiment number  experiment number  73.14
##
## [1] "Model summary for species: LM"
##
## Call:
## lm(formula = SA ~ Treatment * Mean_temperature, data = species_data,
##     na.action = na.exclude)
##
## Coefficients:
##              (Intercept)              Treatmentcold-hot
##                   0.105889                   0.019556
##              Treatmenthot-cold              Mean_temperature27
##                   -0.002667                   2.115311
##              Mean_temperature37 Treatmentcold-hot:Mean_temperature27
##                   0.225683                   0.227644
## Treatmenthot-cold:Mean_temperature27 Treatmentcold-hot:Mean_temperature37
##                   0.226667                   0.211302
## Treatmenthot-cold:Mean_temperature37
##                   -0.314476
##
##
## [1] "Model comparison for species: LP"
##
##
##           Name                AIC
## -----
## no random effects  no random effects  38.94
## experiment number  experiment number  60.52
##
## [1] "Model summary for species: LP"
##
## Call:
## lm(formula = SA ~ Treatment * Mean_temperature, data = species_data,
##     na.action = na.exclude)
##
## Coefficients:
##              (Intercept)              Treatmentcold-hot
```

```
##              0.08600              0.01840
##      Treatmenthot-cold              Mean_temperature27
##      -0.01200              0.91140
##      Mean_temperature37 Treatmentcold-hot:Mean_temperature27
##              0.20100              0.09040
## Treatmenthot-cold:Mean_temperature27 Treatmentcold-hot:Mean_temperature37
##              -0.09440              -0.02453
## Treatmenthot-cold:Mean_temperature37
##              -0.26722
```

Model significance testing

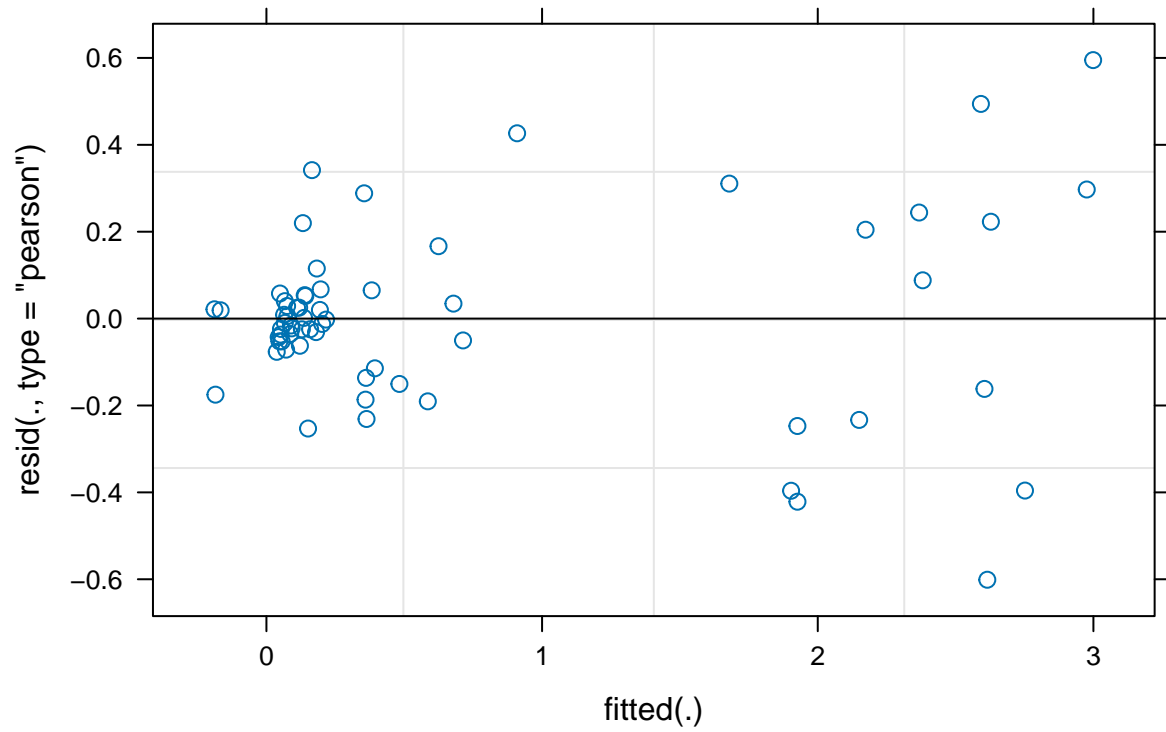
The best model selected in the step above is tested for significance, for each species

```
## [1] "Predictor significance - species LM : "
## Anova Table (Type III tests)
##
## Response: SA
##              Sum Sq Df F value              Pr(>F)
## (Intercept)      0.1009  1  0.7180              0.4005
## Treatment         0.0027  2  0.0094              0.9906
## Mean_temperature  15.6923  2 55.8276 0.0000000000000718 ***
## Treatment:Mean_temperature  0.8095  4  1.4400              0.2334
## Residuals         7.5893 54
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Residual degrees of freedom - species : LM : 54"
## [1] "Predictor significance - species LP : "
## Anova Table (Type III tests)
##
## Response: SA
##              Sum Sq Df F value      Pr(>F)
## (Intercept)      0.0370  1  0.3459 0.5598615
## Treatment         0.0023  2  0.0110 0.9890994
## Mean_temperature   2.3199  2 10.8483 0.0001795 ***
## Treatment:Mean_temperature  0.1375  4  0.3215 0.8618354
## Residuals         4.1701 39
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Residual degrees of freedom - species : LP : 39"
## [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)
```

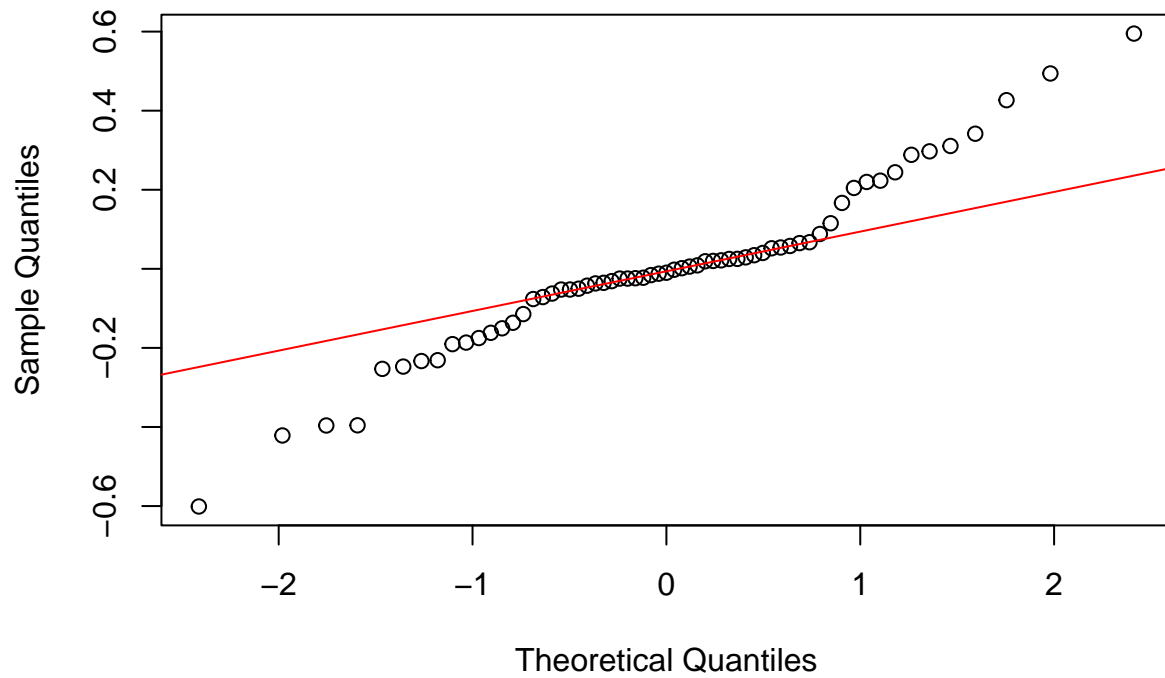
```
##
## Response: SA
##               Chisq Df Pr(>Chisq)
## (Intercept)    0.3459  1    0.5565
## Treatment      0.0222  2    0.9890
## Mean_temperature 21.6966  2 0.00001944 ***
## Treatment:Mean_temperature 1.2996  4    0.8614
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 '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

Model diagnostics

Residuals vs Fitted



Q-Q Plot



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
```