

# Autocorrelation experiment - 5 days - Mortality

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## Load and Preprocess Datasets

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

```
options(scipen=999)
# 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/ma

# 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/ma
```

## Combine and clean up datasets

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)),]

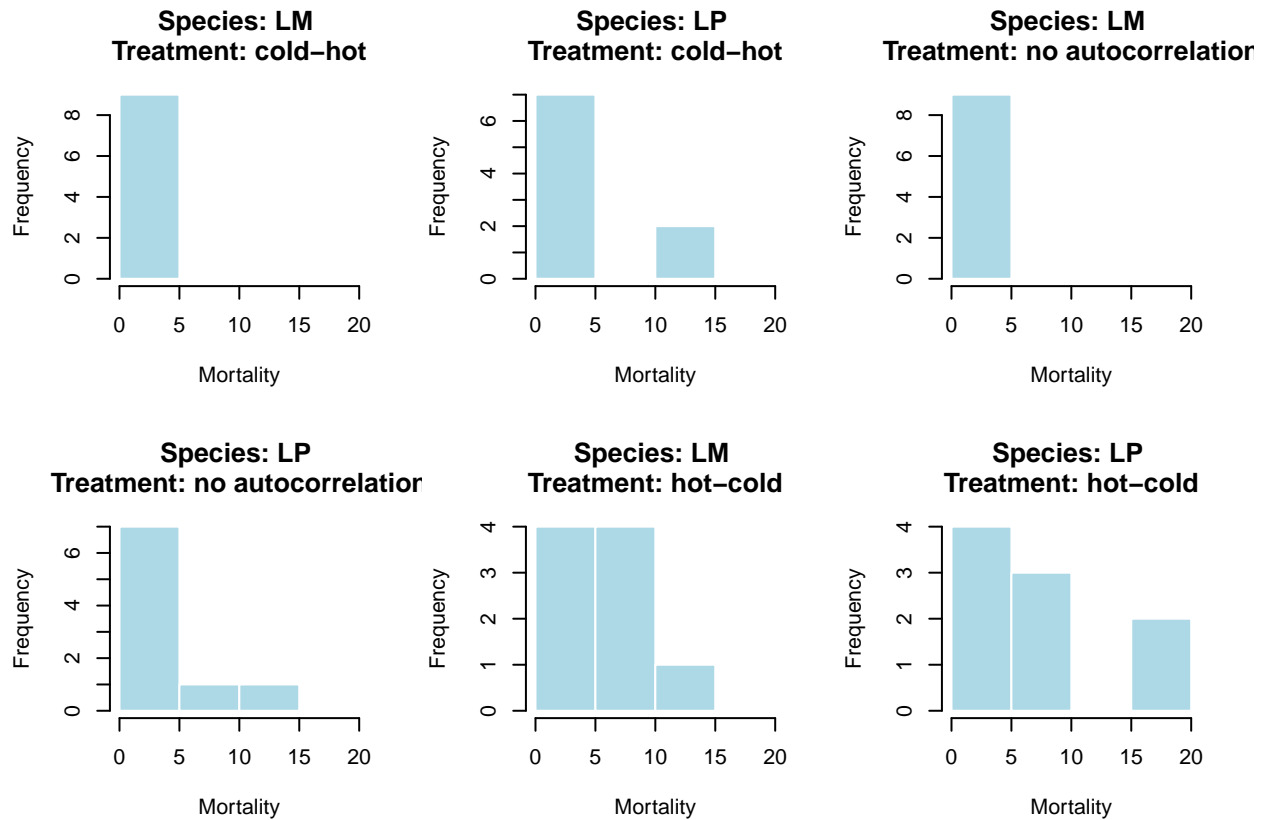
datin <- datin[!(datin$Treatment == 0 & (datin$Obs_ac <= -0.2 | datin$Obs_ac >= 0.2))
               &!(datin$Treatment == 0.95 & (datin$Obs_ac <= 0.92 | datin$Obs_ac >= 0.98)),]

datin <- subset(datin, !Errors == "y"|is.na(Errors))
datin <- subset(datin, !Treatment == "constant")
```

**Dataset:** each row of the dataset corresponds to a replicate; here we are showing 3 experiment runs, each including 3 treatments

	Exp_run	Treatment	Species	Frond_count	Mortality	Total_fron
190	9	cold-hot	LP	22	2	24
191	9	cold-hot	LM	35	0	35
192	9	no autocorrelation	LP	18	4	22
193	9	no autocorrelation	LM	21	2	23
194	9	hot-cold	LP	17	7	24
195	9	hot-cold	LM	17	5	22

## Overview of data distribution



## Summary table: total sum of mortality across treatments

```
##
##
## Treatment          Common duckweed   Dotted duckweed
## -----
## no autocorrelation  14                31
## cold-hot            1                 33
## hot-cold            54                60
```

## Model Fitting

```
results_list <- list()
compare_results <- list()

for (species in unique(datins$Species)) {

  species_data <- subset(datins, Species == species)

  simple <- glm(Mortality ~ Treatment, data = species_data, family = poisson)
  library(lme4)
  exp_number <- glmer(Mortality ~ Treatment + (1|Exp_run), data=species_data, family=poisson, control = g

  # Store models
```

```

results_list[[species]] <- list(simple = simple, exp_number = exp_number)

# Mixed models were selected for all analyses, as likelihood-ratio tests indicated that the random effects
results_list[[species]] <- exp_number

best_model <- results_list[[species]]

model_dispersion <- sum(residuals(best_model, type = "pearson")^2) / df.residual(best_model)
print(paste("Model dispersion ratio for species", species, ":", model_dispersion))

cat("Wald test type 2 for significance of predictor:", species, "\n")
library(car)
phi <- sum(residuals(best_model, type="pearson")^2) / df.residual(best_model)
anova_table <- Anova(best_model, type = "II")

# Adjusting chi-square values (quasipoisson)
anova_table$`Chisq` <- anova_table$`Chisq` / phi

# Recalculating p-values using chi-square distribution
anova_table$`Pr(>Chisq)` <- pchisq(anova_table$`Chisq`, anova_table$Df, lower.tail = FALSE)

print(paste("Adjusted predictor significance", species, ":"))
print(anova_table)
}

```

```

## [1] "Model dispersion ratio for species LP : 2.27711234930369"
## Wald test type 2 for significance of predictor: LP
## [1] "Adjusted predictor significance LP :"
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Mortality
##           Chisq Df Pr(>Chisq)
## Treatment 5.5482  2    0.06241 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Model dispersion ratio for species LM : 1.09452335724362"
## Wald test type 2 for significance of predictor: LM
## [1] "Adjusted predictor significance LM :"
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Mortality
##           Chisq Df   Pr(>Chisq)
## Treatment 32.008  2 0.0000001121 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Original model summary - species : LM"
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: Mortality ~ Treatment + (1 | Exp_run)
## Data: species_data
## Control: glmerControl(optimizer = "nloptwrap")
##

```

```

##      AIC      BIC   logLik deviance df.resid
##    101.1    106.3    -46.5    93.1      23
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.4999 -0.4380 -0.2976  0.6142  2.3798
##
## Random effects:
##   Groups Name            Variance Std.Dev.
##   Exp_run (Intercept) 0.4273    0.6537
## Number of obs: 27, groups: Exp_run, 9
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.2621     0.3563   0.736   0.46199
## Treatmentcold-hot -2.6391     1.0172  -2.594   0.00947 **
## Treatmenthot-cold  1.3499     0.2947   4.580 0.00000464 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Trtmntc-
## Trtmntcld-h -0.190
## Trtmntht-cl -0.657  0.230
## [1] "Adjusted model summary - species : LM"
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.26     0.37     0.7     0.48
## Treatmentcold-hot -2.64     1.06    -2.5     0.01 *
## Treatmenthot-cold  1.35     0.31     4.4 0.00001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

## Post-hoc test for common duckweed

```

## Non-adjusted post-hoc for species: LM
## $emmeans
##   Treatment      rate      SE df asymp.LCL asymp.UCL
## no autocorrelation 1.2996 0.4630 Inf    0.6465    2.613
## cold-hot           0.0928 0.0939 Inf    0.0128    0.674
## hot-cold           5.0128 1.3805 Inf    2.9219    8.600
##
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
##
## $contrasts
##   contrast              ratio      SE df null z.ratio p.value
## no autocorrelation / (cold-hot) 14.0001 14.2409 Inf    1    2.594 0.0257
## no autocorrelation / (hot-cold)  0.2593  0.0764 Inf    1   -4.580 <.0001
## (cold-hot) / (hot-cold)          0.0185  0.0184 Inf    1   -4.022 0.0002
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## Tests are performed on the log scale
##
##

```

```

## Adjusted post-hoc for species: LM
## $emmeans
##   Treatment      rate      SE  df asymp.LCL asymp.UCL
## no autocorrelation 1.2996 0.4844 Inf    0.6259    2.698
## cold-hot           0.0928 0.0983 Inf    0.0117    0.739
## hot-cold           5.0128 1.4443 Inf    2.8499    8.817
##
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
##
## $contrasts
##   contrast      ratio      SE  df null z.ratio p.value
## no autocorrelation / (cold-hot) 14.0001 14.8987 Inf    1   2.480 0.0351
## no autocorrelation / (hot-cold)  0.2593  0.0799 Inf    1  -4.378 <.0001
## (cold-hot) / (hot-cold)          0.0185  0.0192 Inf    1  -3.845 0.0004
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## Tests are performed on the log scale

```