

Autocorrelation experiment - 10 days - Reproduction

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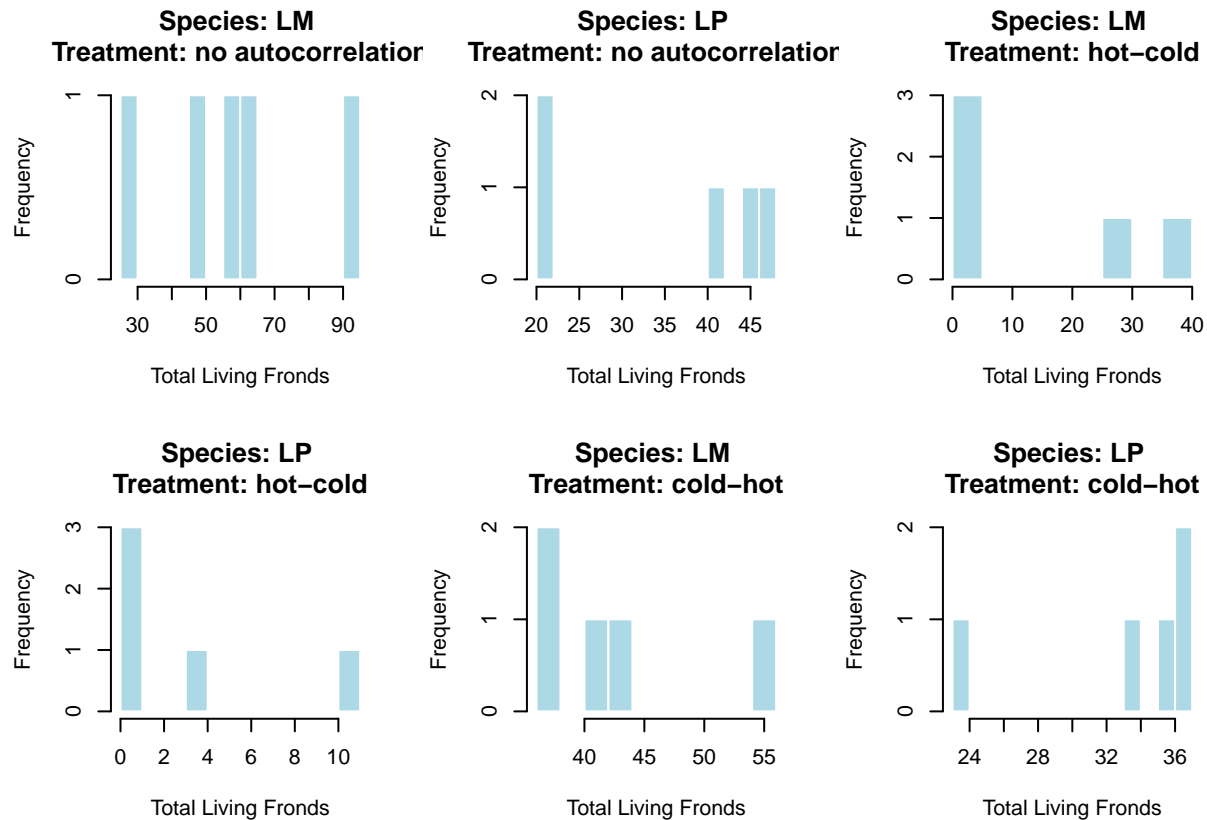
Load and Preprocess Datasets

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

```
# Load dataset  
original_dataset <- read.csv("https://raw.githubusercontent.com/Cuddington-Lab/thermal-experiments/main,
```

View dataset and response variable

Exp_run	Mean_temperature	Species	Treatment	total_living_fronds
1	37	LM	no autocorrelation	56
1	37	LP	no autocorrelation	48
1	37	LM	hot-cold	0
1	37	LP	hot-cold	0
1	37	LM	cold-hot	40
1	37	LP	cold-hot	37



Mixed-Effects Model Fitting

```
model_results <- list()
compare_results <- list()

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

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

  simple <- glm(total_living_fronds ~ Treatment, data = species_data, family = poisson)
  library(lme4)
  exp_number <- glmer(total_living_fronds ~ Treatment + (1|Exp_run), data=species_data, family=poisson, control=glmerControl(optimizer="Nelder-Mead"))

  #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 ", species, "\n")
  cat("p_value:", p_value, "\n")

  # Store models
  model_results[[species]] <- list(simple = simple, exp_number = exp_number)
```

```

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

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("Predictor significance", species, ":"))
print(anova_table)
}

```

```

## Comparing simple x mixed model for  LM
## p_value: 0.00206983
## [1] "Model dispersion ratio for species LM : 10.1020126500838"
## Wald test type 2 for significance of predictor: LM
## [1] "Predictor significance LM :"
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: total_living_fronds
##           Chisq Df Pr(>Chisq)
## Treatment 11.422  2   0.003309 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Comparing simple x mixed model for  LP
## p_value: 0.006429144
## [1] "Model dispersion ratio for species LP : 3.9249724942641"
## Wald test type 2 for significance of predictor: LP
## [1] "Predictor significance LP :"
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: total_living_fronds
##           Chisq Df Pr(>Chisq)
## Treatment 21.452  2 0.00002197 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Visualization of model results

```

## [1] "Adjusted model summary - species : LM"
##           Estimate Std. Error z value      Pr(>|z|)
## (Intercept)      4.04      0.30    13.4 <0.0000000000000002 ***
## Treatmentcold-hot  -0.31      0.29     -1.1        0.3
## Treatmenthot-cold  -1.45      0.43     -3.4      0.0007 ***

```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Adjusted model summary - species : LP"
##           Estimate Std. Error z value      Pr(>|z|)
## (Intercept)      3.530      0.234    15.1 < 0.0000000000000002 ***
## Treatmentcold-hot -0.053      0.215     -0.2         0.8
## Treatmenthot-cold -2.520      0.549     -4.6    0.000004 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Post-hoc test

```
## Non-adjusted post-hoc for species: LM
## $emmeans
## Treatment      rate    SE df asymp.LCL asymp.UCL
## no autocorrelation 56.6 5.36 Inf      47.05      68.2
## cold-hot           41.6 4.21 Inf      34.16      50.7
## hot-cold           13.2 1.89 Inf       9.99      17.5
##
## 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) 1.36 0.123 Inf    1  3.396 0.0020
## no autocorrelation / (hot-cold) 4.28 0.580 Inf    1 10.735 <.0001
## (cold-hot) / (hot-cold)         3.15 0.441 Inf    1  8.191 <.0001
##
## 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 56.6 17.0 Inf      31.41     102.1
## cold-hot           41.6 13.4 Inf      22.19      78.1
## hot-cold           13.2  6.0 Inf       5.43      32.2
##
## 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) 1.36 0.392 Inf    1  1.069 0.5336
## no autocorrelation / (hot-cold) 4.28 1.845 Inf    1  3.378 0.0021
## (cold-hot) / (hot-cold)         3.15 1.402 Inf    1  2.577 0.0269
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## Tests are performed on the log scale
##
##
## Non-adjusted post-hoc for species: LP
## $emmeans
```

```

## Treatment      rate    SE  df asymp.LCL asymp.UCL
## no autocorrelation 34.14 4.032 Inf    27.08    43.03
## cold-hot          32.37 3.866 Inf    25.61    40.91
## hot-cold           2.75 0.774 Inf     1.58     4.77
##
## 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)  1.05 0.114 Inf    1  0.490  0.8762
## no autocorrelation / (hot-cold) 12.43 3.446 Inf    1  9.089 <.0001
## (cold-hot) / (hot-cold)         11.79 3.274 Inf    1  8.879 <.0001
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## Tests are performed on the log scale
##
##
## Adjusted post-hoc for species: LP
## $emmeans
## Treatment      rate    SE  df asymp.LCL asymp.UCL
## no autocorrelation 34.14 7.99 Inf    21.58    54.0
## cold-hot          32.37 7.66 Inf    20.36    51.5
## hot-cold           2.75 1.53 Inf     0.92     8.2
##
## 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)  1.05 0.227 Inf    1  0.247  0.9669
## no autocorrelation / (hot-cold) 12.43 6.827 Inf    1  4.588 <.0001
## (cold-hot) / (hot-cold)         11.79 6.487 Inf    1  4.482 <.0001
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## Tests are performed on the log scale

```

