

# Autocorrelation experiment - 10 days - Reproduction

Debora

2025-06-16

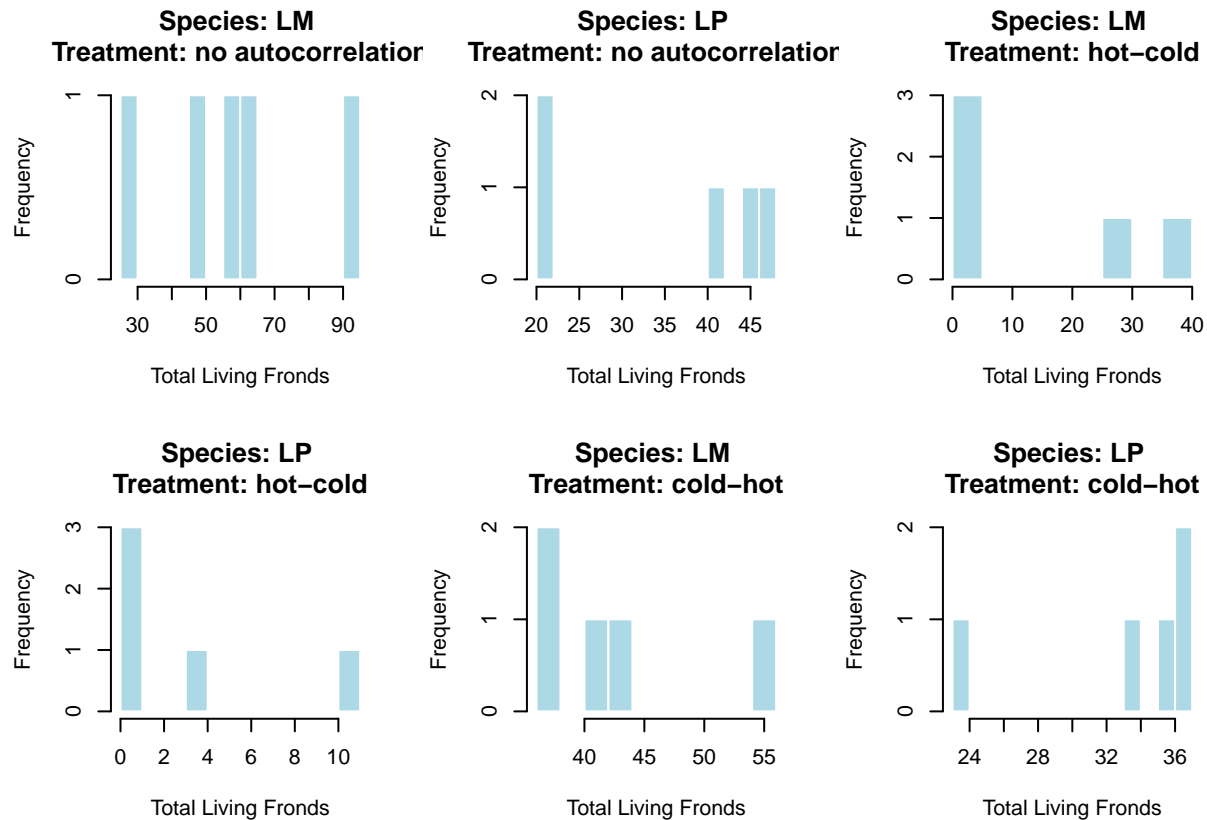
## Load and Preprocess Datasets

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="broyden"))

  #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)
```

```

# Compare models by AIC
Cand.modsF <- list("no random effects" = model_results[[species]]$simple,
                  "experiment number" = model_results[[species]]$exp_number)

# Get AIC for each model and store it
AIC_values <- sapply(Cand.modsF, function(model) AIC(model))

# Function to compute AICc
compute_AICc <- function(model, n) {
  aic <- AIC(model)
  k <- length(coef(model)) # Number of parameters
  aicc <- aic + (2 * k * (k + 1)) / (n - k - 1) # AICc formula
  return(aicc)
}

n <- nrow(species_data)

# Compute AICc for each model
AICc_values <- sapply(Cand.modsF, compute_AICc, n = n)

# Create a summary table using AICc
compare_results[[species]] <- knitr::kable(data.frame(Model = names(AICc_values), AICc = AICc_values),
cat("Model assessment:", species, "\n")
print(compare_results[[species]])

# Find the best model based on AICc
best_model_name <- names(AICc_values)[which.min(AICc_values)]
model_results[[species]] <- Cand.modsF[[best_model_name]]

best_model <- model_results[[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("Predictor significance", species, ":"))
print(anova_table)
}

## Comparing simple x mixed model for LM
## p_value: 0.00206983
## Model assessment: LM
##

```

```
##
##               Model               AICc
## -----
## no random effects    no random effects    218.80
## experiment number    experiment number    210.71
## [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
## Model assessment: LP
##
##
##               Model               AICc
## -----
## no random effects    no random effects    125.23
## experiment number    experiment number    119.16
## [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
```

