

Autocorrelation_stats: mortality - 10-day experiment

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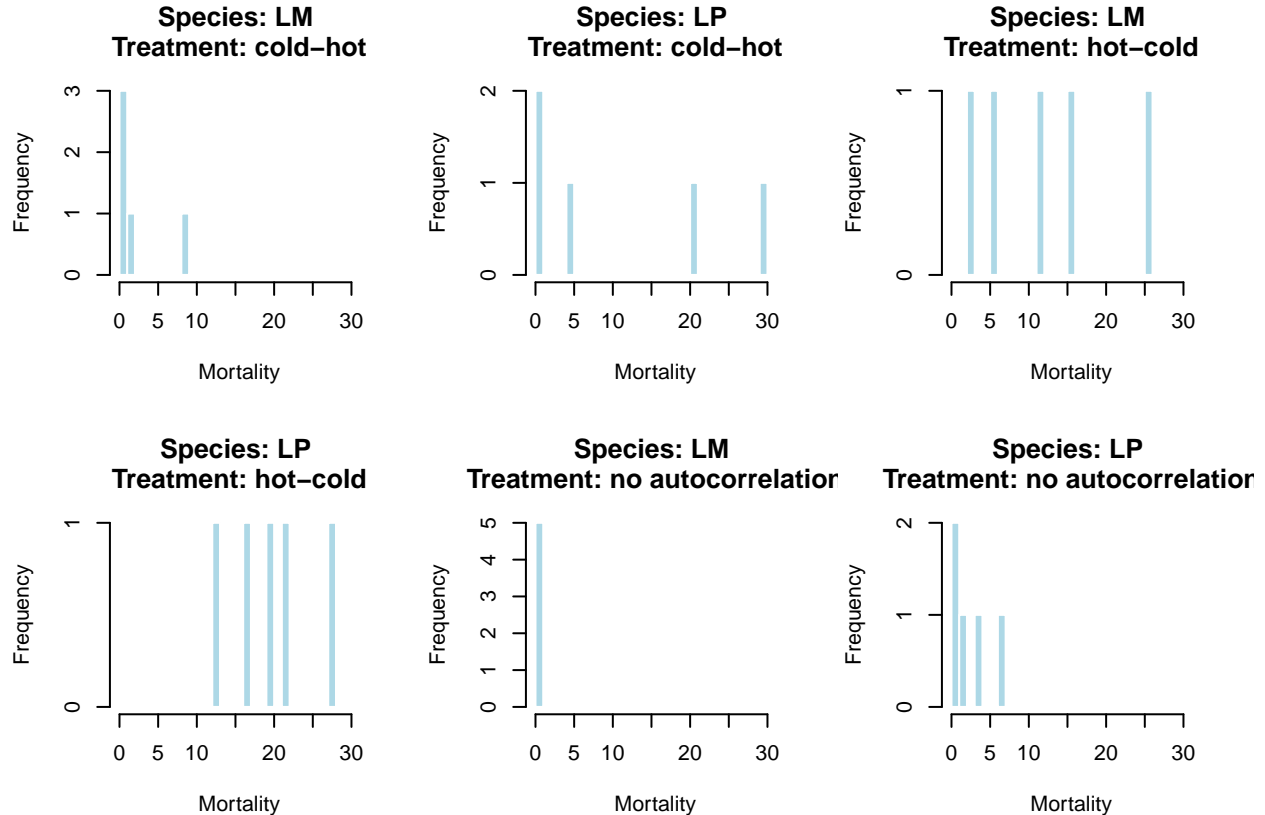
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Mortality analysis at 37 °C

Dataset

Exp_run	Treatment	Species	Fronde_count	Mortality	Total_fronde	Proportion
1	cold-hot	LM	56	0	56	1.000
1	cold-hot	LP	48	5	53	0.906
1	hot-cold	LM	0	16	16	0.000
1	hot-cold	LP	0	22	22	0.000
1	no autocorrelation	LM	40	0	40	1.000
1	no autocorrelation	LP	37	4	41	0.902

Overview of data distribution



Summary table: total sum of mortality across treatments

```
## Summary table for: LM
##
##
## | Treatment | Total.living.fronnd.count | Total.dead.fronnd.count | Average.proportion.of.survivor |
## |-----|:-----|:-----|:-----|
## | hot-cold | 67 | 63 | 0.52 |
## | no autocorrelation | 211 | 3 | 0.99 |
## | cold-hot | 287 | 11 | 0.96 |
##
## Summary table for: LP
##
##
## | Treatment | Total.living.fronnd.count | Total.dead.fronnd.count | Average.proportion.of.survivor |
## |-----|:-----|:-----|:-----|
## | hot-cold | 14 | 100 | 0.12 |
## | no autocorrelation | 165 | 15 | 0.92 |
## | cold-hot | 174 | 58 | 0.75 |
```

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)

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

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

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

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)
}

```

```

## Comparing simple x mixed model: LM
## p_value: 0.01803528
## Model assessment: LM
##
##
##           Model           AICc
## -----
## no random effects  no random effects  96.23
## experiment number  experiment number  91.96
## [1] "Model dispersion ratio for species LM : 4.00749817954252"
## 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 12.879  2   0.001598 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Comparing simple x mixed model: LP
## p_value: 0.00000004008947
## Model assessment: LP
##
##
##           Model           AICc
## -----
## no random effects   no random effects   141.71
## experiment number   experiment number   113.04
## [1] "Model dispersion ratio for species LP : 2.63701959933408"
## 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 19.306  2 0.00006425 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Visualization of Results

```
## [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
##    91.7    94.5   -41.8    83.7      11
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4207 -0.9646 -0.0791  0.6054  5.0922
##
## Random effects:
## Groups Name      Variance Std.Dev.
## Exp_run (Intercept) 0.133    0.3647
## Number of obs: 15, groups: Exp_run, 5
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -0.5761    0.5979  -0.964   0.3353
## Treatmentcold-hot  1.2993    0.6468   2.009   0.0445 *
## Treatmenthot-cold  3.0445    0.5868   5.189 0.000000212 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```

##
## Correlation of Fixed Effects:
##      (Intr) Trtmntc-
## Trtmntcld-h -0.850
## Trtmntht-cl -0.937  0.866
## [1] "Adjusted model summary - species : LM"
##      Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -0.58      1.20   -0.5    0.63
## Treatmentcold-hot    1.30      1.29    1.0    0.32
## Treatmenthot-cold    3.04      1.17    2.6    0.01 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Original model summary - species : LP"
## 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
##    112.7    115.6   -52.4    104.7      11
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.31215 -1.33208  0.09966  0.94961  2.01550
##
## Random effects:
## Groups Name      Variance Std.Dev.
## Exp_run (Intercept) 0.2389   0.4888
## Number of obs: 15, groups: Exp_run, 5
##
## Fixed effects:
##      Estimate Std. Error z value      Pr(>|z|)
## (Intercept)    0.9806    0.3395   2.888    0.00388 **
## Treatmentcold-hot  1.3524    0.2881   4.695 0.0000026724108 ***
## Treatmenthot-cold  1.8971    0.2754   6.889 0.0000000000056 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) Trtmntc-
## Trtmntcld-h -0.674
## Trtmntht-cl -0.705  0.831
## [1] "Adjusted model summary - species : LP"
##      Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.98      0.55    1.8   0.075 .
## Treatmentcold-hot  1.35      0.47    2.9   0.004 **
## Treatmenthot-cold  1.90      0.45    4.2 0.00002 ***
## ---
## 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 0.562 0.336 Inf      0.174      1.81
## cold-hot          2.061 0.709 Inf      1.050      4.05
## hot-cold          11.803 2.490 Inf      7.807     17.85
##
## 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) 0.2727 0.1764 Inf      1  -2.009  0.1100
## no autocorrelation / (hot-cold) 0.0476 0.0279 Inf      1  -5.189  <.0001
## (cold-hot) / (hot-cold)          0.1746 0.0567 Inf      1  -5.379  <.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 0.562 0.673 Inf      0.0538      5.87
## cold-hot          2.061 1.420 Inf      0.5340      7.95
## hot-cold          11.803 4.984 Inf      5.1591     27.00
##
## 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) 0.2727 0.3531 Inf      1  -1.004  0.5746
## no autocorrelation / (hot-cold) 0.0476 0.0559 Inf      1  -2.592  0.0258
## (cold-hot) / (hot-cold)          0.1746 0.1134 Inf      1  -2.687  0.0197
##
## 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 2.67 0.905 Inf      1.37      5.19
## cold-hot          10.31 2.656 Inf      6.22     17.08
## hot-cold          17.77 4.326 Inf     11.03     28.64
##
## 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) 0.259 0.0745 Inf    1 -4.695 <.0001
## no autocorrelation / (hot-cold) 0.150 0.0413 Inf    1 -6.889 <.0001
## (cold-hot) / (hot-cold)          0.580 0.0952 Inf    1 -3.319 0.0026
##
## 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  2.67 1.47 Inf    0.905    7.86
## cold-hot           10.31 4.31 Inf    4.540   23.41
## hot-cold           17.77 7.02 Inf    8.192   38.56
##
## 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) 0.259 0.1210 Inf    1 -2.891 0.0107
## no autocorrelation / (hot-cold) 0.150 0.0671 Inf    1 -4.243 0.0001
## (cold-hot) / (hot-cold)          0.580 0.1546 Inf    1 -2.044 0.1019
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## Tests are performed on the log scale
## Plot for LM

```