Autocorrelation_stats: mortality - 10-day experiment

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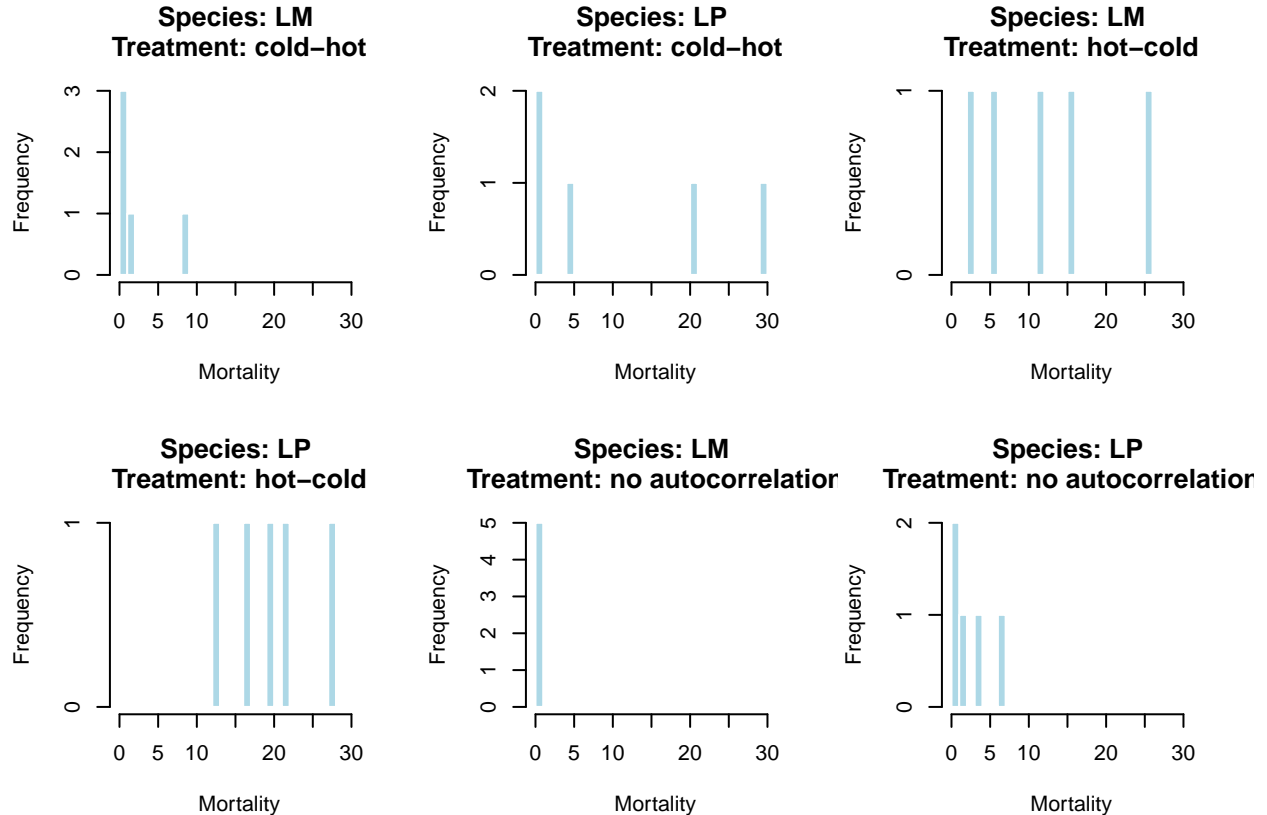
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Mortality analysis at 37 ºC

Dataset

Exp_run	Treatment	Species	Frond_count	Mortality	Total_frond	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.frond.count | Total.dead.frond.count | Average.proportion.of.surv
## |:-----------------:|:------------------------:|:----------------------:|:--------------------------
## |     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.frond.count | Total.dead.frond.count | Average.proportion.of.surv
## |:-----------------:|:------------------------:|:----------------------:|:--------------------------
## |     hot-cold      |           14             |         100            |                  0.12
## | no autocorrelation |          165            |          15            |                  0.92
## |     cold-hot      |          174             |          58            |                  0.75
```

Model Fitting

```r
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 = gl

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]] <- exp_number

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

```
## Comparing simple x mixed model: LM
## p_value: 0.01803528
## [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
## [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
```

Plot for LP