Autocorrelation_stats

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Load and Preprocess Datasets

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

```
# 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/ma
original_dataset_2$prep <- rep("yes",times=length(original_dataset_2$Experiment_Number))

# This dataset contains replicates of experiments performed without a preparation technique
original_dataset_1 <- read.csv("https://raw.githubusercontent.com/Cuddington-Lab/thermal-experiments/ma
original_dataset_1$prep <- rep("no",times=length(original_dataset_1$Experiment_Number))
```

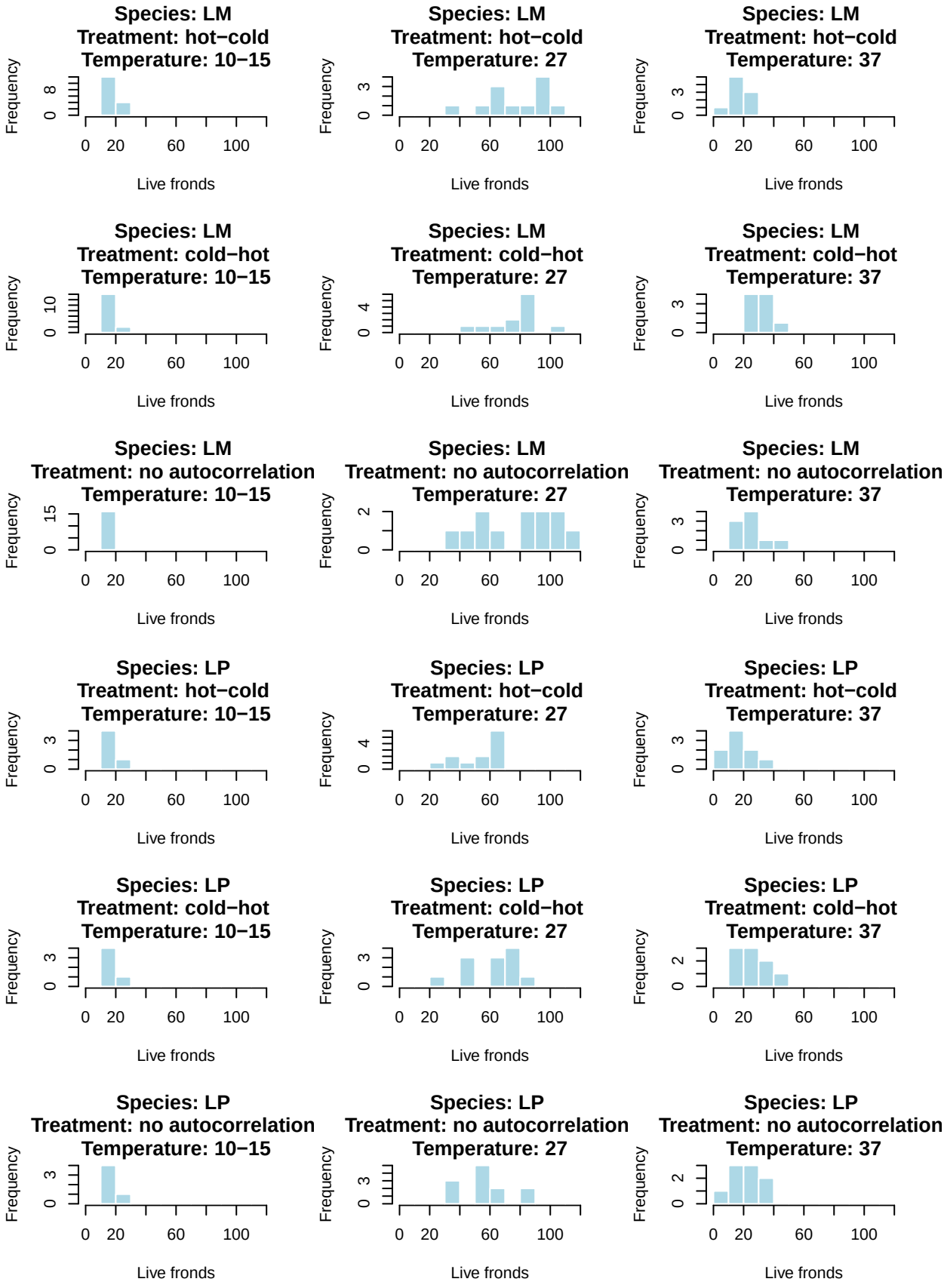
Combine Datasets

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")
```

View dataset and response variable

	Species	Exp_run	Treatment	total_living_fronds
395	LM	2733	cold-hot	90
396	LP	2733	cold-hot	74
397	LM	2733	hot-cold	91
398	LP	2733	hot-cold	63
399	LM	2733	no autocorrelation	101
400	LP	2733	no autocorrelation	88


Species: LM
Treatment: hot−cold
Temperature: 10−15
Species: LM
Treatment: hot−cold
Temperature: 27
Species: LM
Treatment: hot−cold
Temperature: 37
Species: LM
Treatment: cold−hot
Temperature: 10−15
Species: LM
Treatment: cold−hot
Temperature: 27
Species: LM
Treatment: cold−hot
Temperature: 37
Species: LM
Treatment: no autocorrelation
Temperature: 10−15
Species: LM
Treatment: no autocorrelation
Temperature: 27
Species: LM
Treatment: no autocorrelation
Temperature: 37
Species: LP
Treatment: hot−cold
Temperature: 10−15
Species: LP
Treatment: hot−cold
Temperature: 27
Species: LP
Treatment: hot−cold
Temperature: 37
Species: LP
Treatment: cold−hot
Temperature: 10−15
Species: LP
Treatment: cold−hot
Temperature: 27
Species: LP
Treatment: cold−hot
Temperature: 37
Species: LP
Treatment: no autocorrelation
Temperature: 10−15
Species: LP
Treatment: no autocorrelation
Temperature: 27
Species: LP
Treatment: no autocorrelation
Temperature: 37
Frequency
Live fronds
0
20
60
100

View number of replicates

LM

```
##
##         no autocorrelation cold-hot hot-cold
##   10-15                 16       16       16
##   27                    12       12       12
##   37                     9        9        9
```

LP

```
##
##         no autocorrelation cold-hot hot-cold
##   10-15                  5        5        5
##   27                    12       12       12
##   37                     9        9        9
```

Mixed-Effects Model Fitting

We fit candidate simple or mixed-effects models to the data, including random effects for Experiment run (`Exp_run`).

```
## [1] "Comparing simple x mixed model:"
## p_value: 0
## [1] "Comparing simple x mixed model:"
## p_value: 0
```

Model significance testing

```
## Wald test type 3 for significance of predictor: LM
## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: total_living_fronds
##                               Chisq Df            Pr(>Chisq)
## (Intercept)                1317.9353  1 < 0.00000000000000022 ***
## Treatment                     0.6144  2                0.7355
## Mean_temperature            240.9907  2 < 0.00000000000000022 ***
## Treatment:Mean_temperature   35.9543  4          0.0000002957 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Residual degrees of freedom - species : LM : 101"
## Wald test type 3 for significance of predictor: LP
## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: total_living_fronds
##                               Chisq Df            Pr(>Chisq)
## (Intercept)                1317.9353  1 < 0.00000000000000022 ***
## Treatment                     0.6144  2                0.7355
## Mean_temperature            240.9907  2 < 0.00000000000000022 ***
## Treatment:Mean_temperature   35.9543  4          0.0000002957 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Residual degrees of freedom - species : LP : 101"
```

Visualization of Results for common duckweeds

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: total_living_fronds ~ Treatment * Mean_temperature + (1 | Exp_run)
##    Data: dataset_species
## Control: glmerControl(optimizer = "nloptwrap")
##
##      AIC      BIC   logLik deviance df.resid
##    772.1    799.2   -376.1    752.1      101
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.3375 -0.3678 -0.0017  0.3794  3.6435
##
## Random effects:
##  Groups  Name        Variance Std.Dev.
##  Exp_run (Intercept) 0.03766  0.1941
## Number of obs: 111, groups:  Exp_run, 37
##
## Fixed effects:
##                                      Estimate Std. Error z value
## (Intercept)                           2.82097    0.07771  36.303
## Treatmentcold-hot                     0.05397    0.08459   0.638
## Treatmenthot-cold                     0.06070    0.08446   0.719
## Mean_temperature27                    1.51541    0.10126  14.965
## Mean_temperature37                    0.46435    0.11965   3.881
## Treatmentcold-hot:Mean_temperature27 -0.05601    0.09635  -0.581
## Treatmenthot-cold:Mean_temperature27 -0.05632    0.09619  -0.585
## Treatmentcold-hot:Mean_temperature37  0.07823    0.12134   0.645
## Treatmenthot-cold:Mean_temperature37 -0.55293    0.13329  -4.148
##                                                  Pr(>|z|)
## (Intercept)                          < 0.0000000000000002 ***
## Treatmentcold-hot                                 0.523492
## Treatmenthot-cold                                 0.472348
## Mean_temperature27                   < 0.0000000000000002 ***
## Mean_temperature37                                0.000104 ***
## Treatmentcold-hot:Mean_temperature27              0.560991
## Treatmenthot-cold:Mean_temperature27              0.558218
## Treatmentcold-hot:Mean_temperature37              0.519091
## Treatmenthot-cold:Mean_temperature37             0.0000335 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##               (Intr) Trtmntc- Trtmnth- Mn_t27 Mn_t37 Trtmntc-:M_27
## Trtmntcld-h   -0.559
## Trtmntht-cl   -0.560  0.514
## Mn_tmprtr27   -0.767  0.429    0.430
## Mn_tmprtr37   -0.649  0.363    0.364    0.498
## Trtmntc-:M_27  0.491 -0.878   -0.452   -0.486 -0.319
## Trtmnth-:M_27  0.492 -0.452   -0.878   -0.486 -0.319  0.511
## Trtmntc-:M_37  0.390 -0.697   -0.359   -0.299 -0.531  0.612
```

```
## Trtmnth-:M_37  0.355 -0.326   -0.634   -0.272 -0.483  0.286
##               Trtmnth-:M_27 Trtmntc-:M_37
## Trtmntcld-h
## Trtmntht-cl
## Mn_tmprtr27
## Mn_tmprtr37
## Trtmntc-:M_27
## Trtmnth-:M_27
## Trtmntc-:M_37  0.315
## Trtmnth-:M_37  0.556         0.477
## optimizer (nloptwrap) convergence code: 0 (OK)
## Model failed to converge with max|grad| = 0.00674263 (tol = 0.002, component 1)
```

Model validation for common duckweeds

```
## [1] "Model dispersion ratio : 0.780382048699719"
```

```
## [1] "Shapiro test for normality of random factors 0.051"
```

Post-hoc test for common duckweeds

```
## [1] "Pairwise interactions"
```

```
## Mean_temperature = 10-15:
##  Treatment              rate       SE  df asymp.LCL asymp.UCL
##  no autocorrelation 16.79316 1.304921 Inf  14.42080  19.55580
##  cold-hot           17.72437 1.355084 Inf  15.25786  20.58959
##  hot-cold           17.84400 1.361503 Inf  15.36545  20.72236
##
## Mean_temperature = 27:
##  Treatment              rate       SE  df asymp.LCL asymp.UCL
##  no autocorrelation 76.43063 4.964703 Inf  67.29395  86.80784
##  cold-hot           76.27457 4.955841 Inf  67.15434  86.63343
##  hot-cold           76.76596 4.983742 Inf  67.59391  87.18258
##
## Mean_temperature = 37:
##  Treatment              rate       SE  df asymp.LCL asymp.UCL
##  no autocorrelation 26.71753 2.431967 Inf  22.35195  31.93574
##  cold-hot           30.49379 2.690734 Inf  25.65089  36.25103
##  hot-cold           16.33133 1.701186 Inf  13.31540  20.03035
##
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
```

```
## Mean_temperature = 10-15:
##  contrast                        ratio     SE  df null z.ratio p.value
##  no autocorrelation / (cold-hot) 0.947 0.0801 Inf    1  -0.638  0.7992
##  no autocorrelation / (hot-cold) 0.941 0.0795 Inf    1  -0.719  0.7524
##  (cold-hot) / (hot-cold)         0.993 0.0827 Inf    1  -0.081  0.9964
##
## Mean_temperature = 27:
##  contrast                        ratio     SE  df null z.ratio p.value
##  no autocorrelation / (cold-hot) 1.002 0.0462 Inf    1   0.044  0.9989
##  no autocorrelation / (hot-cold) 0.996 0.0458 Inf    1  -0.095  0.9950
##  (cold-hot) / (hot-cold)         0.994 0.0458 Inf    1  -0.139  0.9893
##
```

```
## Mean_temperature = 37:
##  contrast                        ratio     SE  df null z.ratio p.value
##  no autocorrelation / (cold-hot) 0.876 0.0762 Inf    1  -1.520  0.2816
##  no autocorrelation / (hot-cold) 1.636 0.1687 Inf    1   4.774  <.0001
##  (cold-hot) / (hot-cold)         1.867 0.1880 Inf    1   6.203  <.0001
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## Tests are performed on the log scale
```