

# Autocorrelation experiment - 10 days - Surface area

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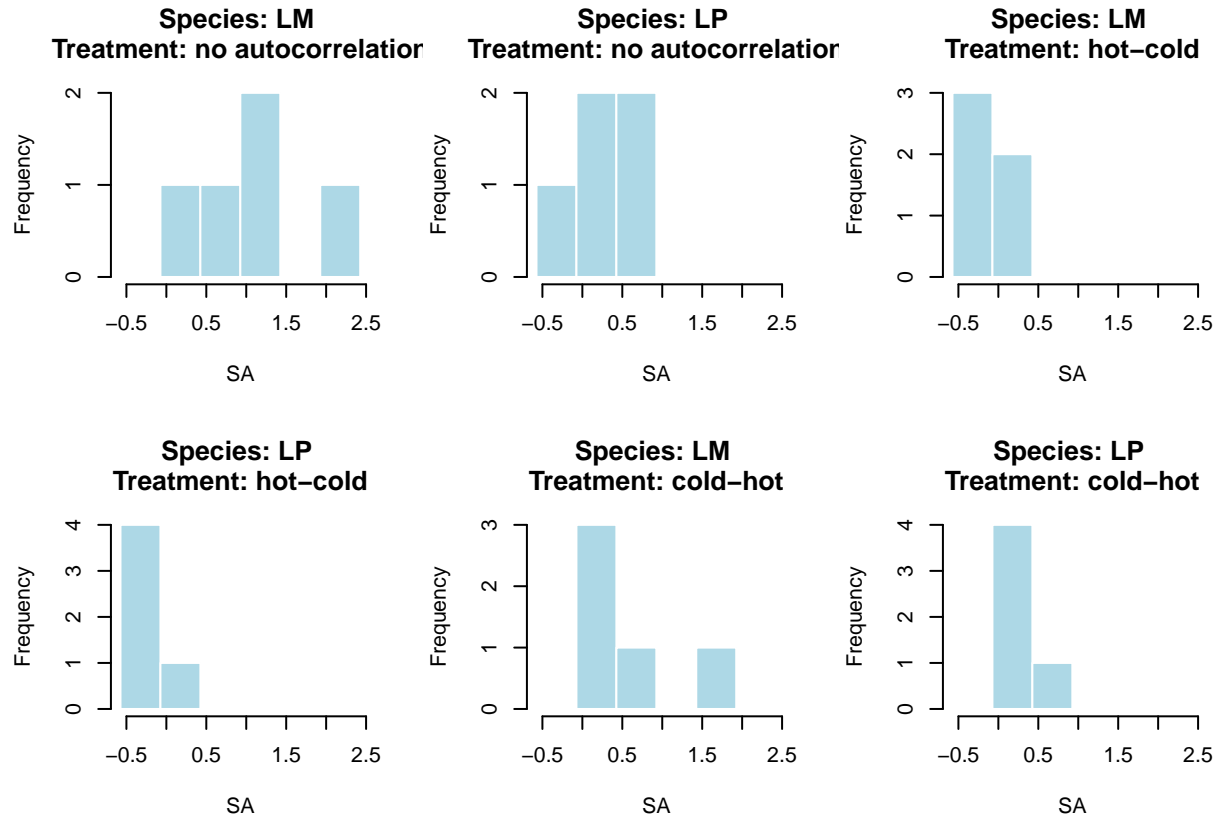
## Load and Preprocess Datasets

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

## View dataset and response variable (SA = change in surface area)

Exp_run	Mean_temperature	Treatment	Species	Initial_area	Final_area	SA
1	37	no autocorrelation	LM	0.648	1.678	1.030
1	37	no autocorrelation	LP	0.456	0.782	0.326
1	37	hot-cold	LM	0.574	0.000	-0.574
1	37	hot-cold	LP	0.399	0.000	-0.399
1	37	cold-hot	LM	0.644	0.994	0.350
1	37	cold-hot	LP	0.409	0.464	0.055

## Histogram of surface areas for each species



## Mixed-Effects Model Fitting

```
results_list <- list()

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

  species_data <- subset(dataset, Species == species)
  library(lme4)

  simple <- lm(SA ~ Treatment,
               data = species_data)

  exp_number <- lmer(SA ~ Treatment + (1 | Exp_run),
                    data = species_data)

  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)
  print(paste("Comparing simple x mixed model:"))
  cat("p_value:", p_value, "\n")

  results_list[[species]] <- list(simple = simple, exp_number = exp_number)
```

```

}

## [1] "Comparing simple x mixed model:"
## p_value: 0.5
## [1] "Comparing simple x mixed model:"
## p_value: 0.5

```

## Model Comparison and Results

We compare the performance of the models and extract estimates, confidence intervals, and p values.

```

## [1] "Model comparison for species: LM"
##
##
##           Name                AIC
## -----
## no random effects  no random effects  34.12
## experiment number  experiment number  38.40
##
## [1] "Model summary for species: LM"
##
## Call:
## lm(formula = SA ~ Treatment, data = species_data)
##
## Coefficients:
##      (Intercept)  Treatmentcold-hot  Treatmenthot-cold
##           1.1150           -0.5124           -1.2788
##
##
## [1] "Model comparison for species: LP"
##
##
##           Name                AIC
## -----
## no random effects  no random effects   9.49
## experiment number  experiment number  18.69
##
## [1] "Model summary for species: LP"
##
## Call:
## lm(formula = SA ~ Treatment, data = species_data)
##
## Coefficients:
##      (Intercept)  Treatmentcold-hot  Treatmenthot-cold
##           0.2636           0.0582           -0.4902

```

## Model significance testing

The best model selected in the step above is tested for significance, for each species

```

## Residual degrees of freedom for species LM : 12
## [1] "Predictor significance - species LM :"
## Analysis of Variance Table
##
## Response: SA

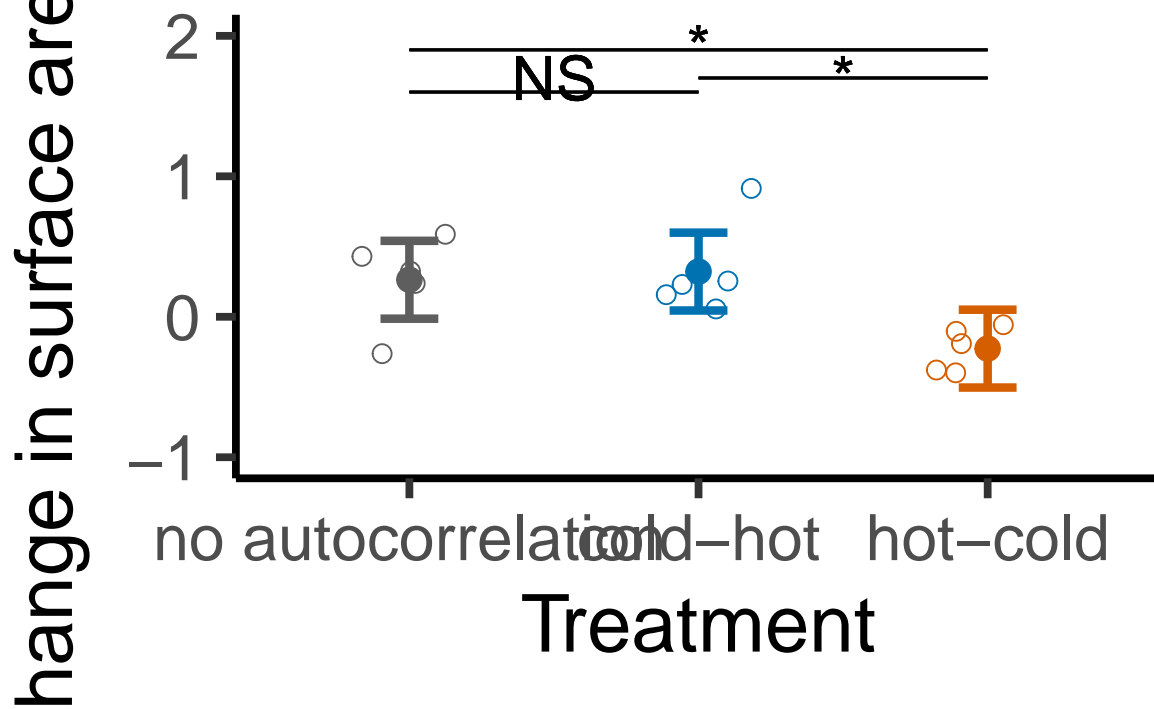
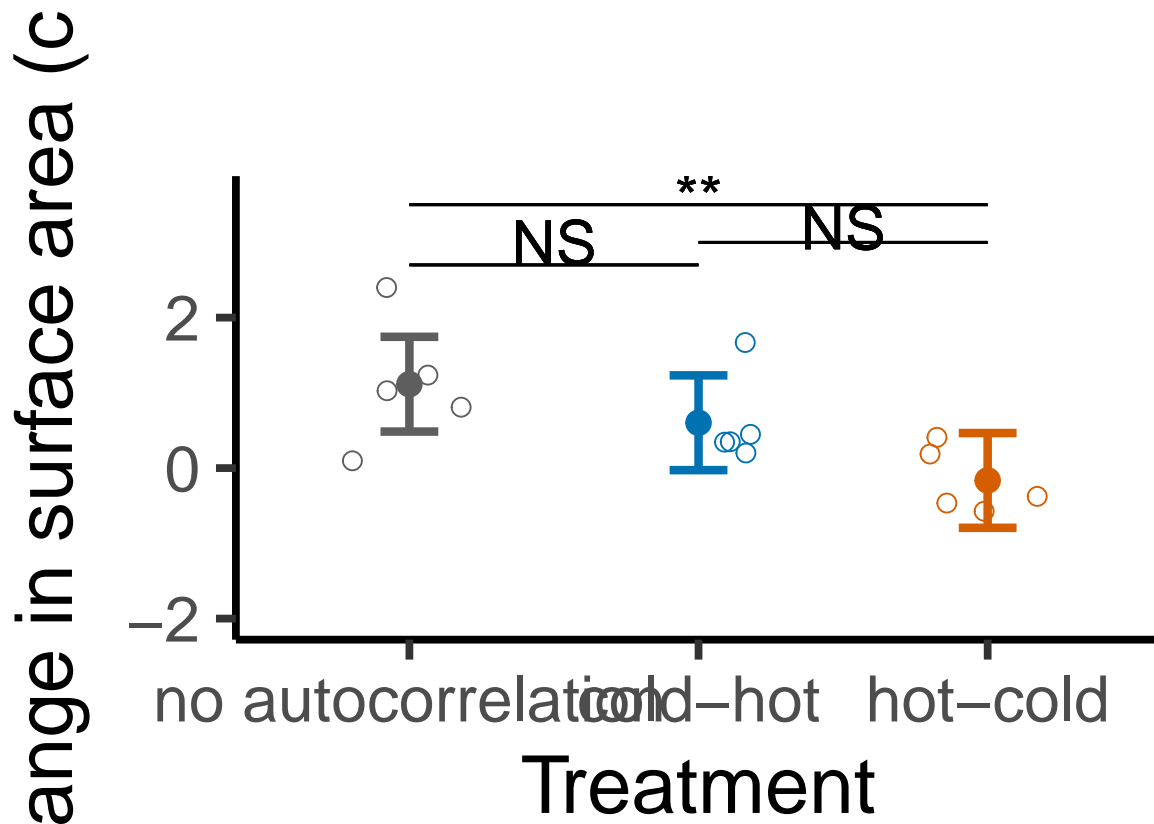
```

```

##           Df Sum Sq Mean Sq F value  Pr(>F)
## Treatment  2 4.1421  2.07104   4.9591 0.04587 *
## Residuals 12 5.0115  0.41763
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Residual degrees of freedom for species LP : 12
## [1] "Predictor significance - species LP :"
## Analysis of Variance Table
##
## Response: SA
##           Df Sum Sq Mean Sq F value  Pr(>F)
## Treatment  2 0.90738  0.45369   5.6113 0.03548 *
## Residuals 12 0.97022  0.08085
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

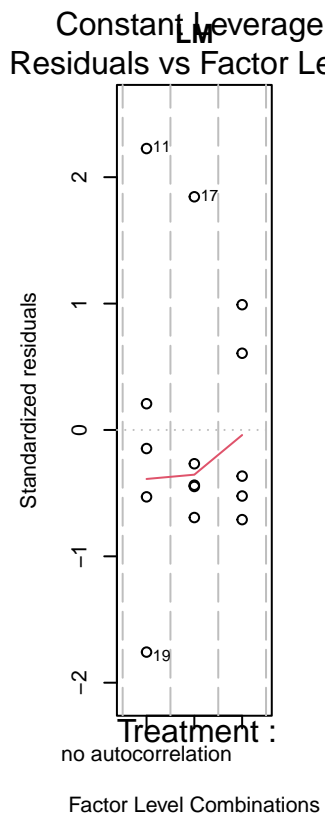
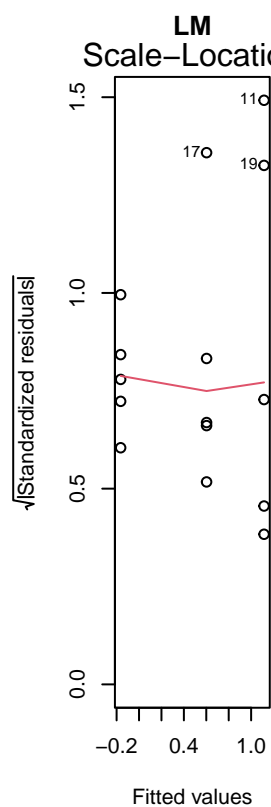
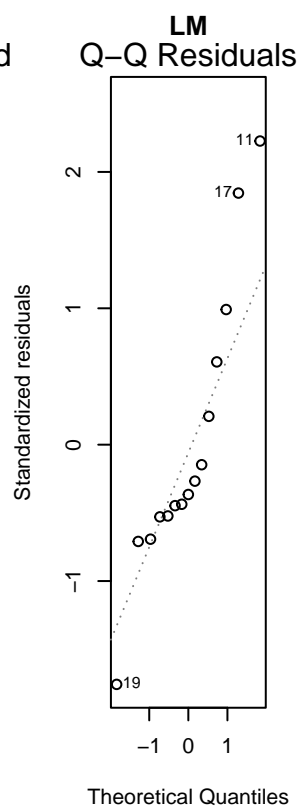
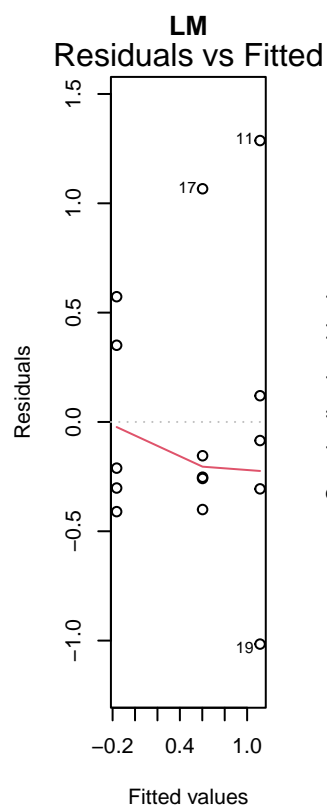
```

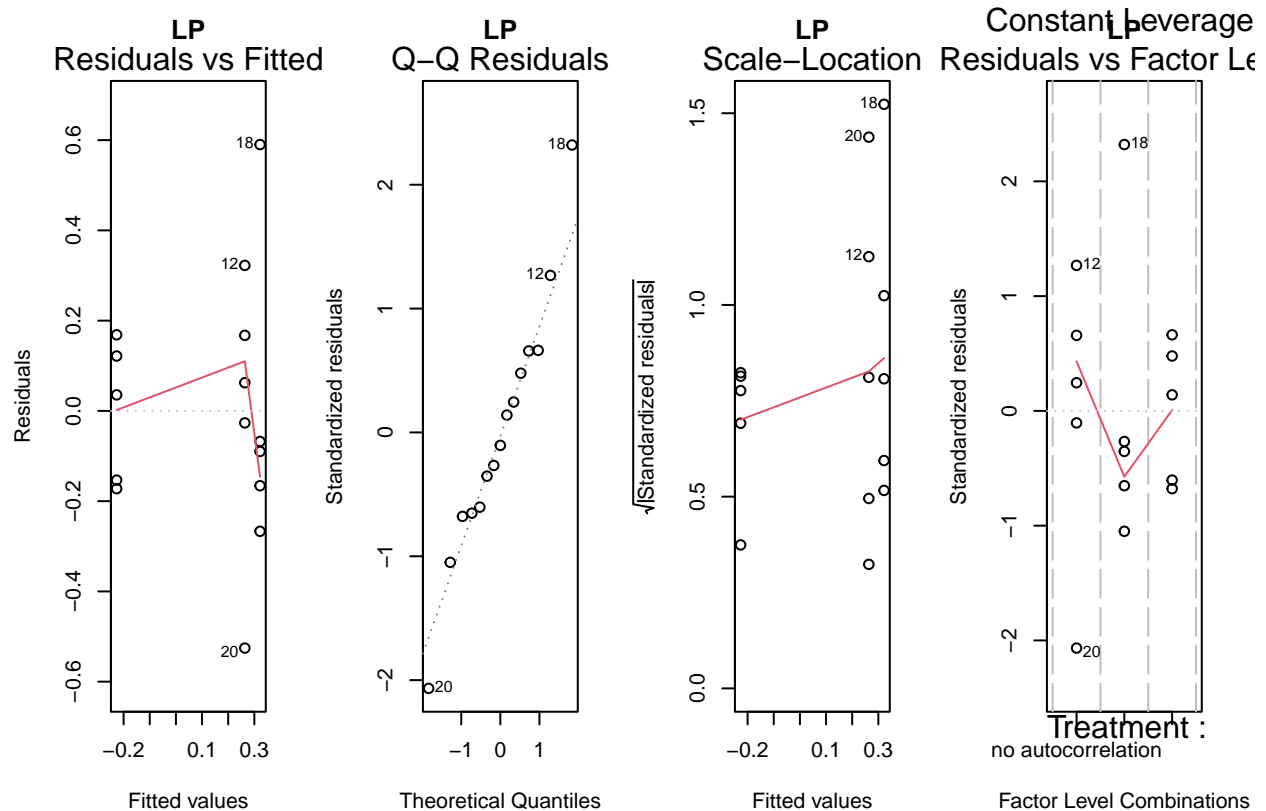
# Visualization of Results



## Model diagnostics

```
## Processing simple linear model for LM
## NULL
## Shapiro-Wilk test for normality of residuals for LM :
##
##   Shapiro-Wilk normality test
##
## data:  model_residuals
## W = 0.89437, p-value = 0.07812
##
## Breusch-Pagan test for heteroscedasticity for LM :
##
##   studentized Breusch-Pagan test
##
## data:  best_model
## BP = 1.7915, df = 2, p-value = 0.4083
##
## Processing simple linear model for LP
## NULL
## Shapiro-Wilk test for normality of residuals for LP :
##
##   Shapiro-Wilk normality test
##
## data:  model_residuals
## W = 0.97429, p-value = 0.9157
##
## Breusch-Pagan test for heteroscedasticity for LP :
##
##   studentized Breusch-Pagan test
##
## data:  best_model
## BP = 1.501, df = 2, p-value = 0.4721
```





```
## Post-hoc Test Results for Species: LM
```

```
##
```

```
##
```

## 1	estimate	SE	df	t.ratio	p.value
## no autocorrelation - (cold-hot)	0.512	0.409	12	1.254	0.446
## no autocorrelation - (hot-cold)	1.279	0.409	12	3.129	0.022
## (cold-hot) - (hot-cold)	0.766	0.409	12	1.875	0.188

```
## Post-hoc Test Results for Species: LP
```

```
##
```

```
##
```

## 1	estimate	SE	df	t.ratio	p.value
## no autocorrelation - (cold-hot)	-0.058	0.18	12	-0.324	0.944
## no autocorrelation - (hot-cold)	0.490	0.18	12	2.726	0.045
## (cold-hot) - (hot-cold)	0.548	0.18	12	3.049	0.025

If I had used mixed linear models, these would be the results

```
## [1] "Anova - linear mixed model - species LM :"
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
```

```
##
```

```
## Response: SA
```

```
## Chisq Df Pr(>Chisq)
```

```
## Treatment 10.212 2 0.00606 **
```



```

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Summary - linear mixed model - species LM :"
## Linear mixed model fit by REML ['lmerMod']
## Formula: SA ~ Treatment + (1 | Exp_run)
##   Data: species_data
##
## REML criterion at convergence: 28.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.5558 -0.4756 -0.3029  0.3518  1.9958
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   Exp_run  (Intercept) 0.01202  0.1096
##   Residual                0.40561  0.6369
## Number of obs: 15, groups:  Exp_run, 5
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)      1.1150     0.2890   3.858
## Treatmentcold-hot -0.5124     0.4028  -1.272
## Treatmenthot-cold -1.2788     0.4028  -3.175
##
## Correlation of Fixed Effects:
##              (Intr) Trtmntc-
## Trtmntcld-h -0.697
## Trtmntht-cl -0.697  0.500
## Post-hoc Test Results for Species: LM
##
##
## 1              estimate      SE      df    t.ratio    p.value
## -----
## no autocorrelation - (cold-hot)      0.512   0.403   491.053     1.272     0.412
## no autocorrelation - (hot-cold)      1.279   0.403   491.053     3.175     0.005
## (cold-hot) - (hot-cold)      0.766   0.403   491.053     1.903     0.139
##
## [1] "Anova - linear mixed model - species LP :"
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: SA
##           Chisq Df Pr(>Chisq)
## Treatment 11.563  2  0.003084 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Summary - linear mixed model - species LP :"
## Linear mixed model fit by REML ['lmerMod']
## Formula: SA ~ Treatment + (1 | Exp_run)
##   Data: species_data
##
## REML criterion at convergence: 8.7
##
## Scaled residuals:

```

```

##      Min      1Q  Median      3Q      Max
## -1.8197 -0.5454 -0.1676  0.5099  2.0342
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   Exp_run  (Intercept) 0.002379 0.04877
##   Residual                0.078473 0.28013
## Number of obs: 15, groups:  Exp_run, 5
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)      0.2636     0.1272   2.073
## Treatmentcold-hot  0.0582     0.1772   0.328
## Treatmenthot-cold -0.4902     0.1772  -2.767
##
## Correlation of Fixed Effects:
##              (Intr) Trtmntc-
## Trtmntcld-h -0.697
## Trtmntht-cl -0.697  0.500
## Post-hoc Test Results for Species: LP
##
##
## 1              estimate      SE    df    t.ratio    p.value
## -----
## no autocorrelation - (cold-hot)    -0.058    0.177    8    -0.328    0.943
## no autocorrelation - (hot-cold)     0.490    0.177    8     2.767    0.057
## (cold-hot) - (hot-cold)            0.548    0.177    8     3.095    0.035

```