

# Ulva and Hypnea PHOTOSYNTHESIS and Growth Run5 - Sept-Nov 2021

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1/31/2022

## Run5 rETRmax Analysis, Script Chunks, and Plots

This is the analysis of the final run of the Ulva and Hypnea salinity and nutrient experiments conducted on the lanai in St. John 616. These experiments incorporated three temperature levels. Model was run on parameter rETRmax

Packages loaded:

```
library(lme4)
library(lmerTest)
library(effects)
library(car)
library(MuMIn)
library(dplyr)
library(emmeans)
library(DHARMA)
library(performance)
library(patchwork)
```

## Load and prepare the dataset

Open the photosynthesis dataset that was created in R using the package “Phytotools” Several parameters are available but are not independent of one another thus for this analysis, we chose to use rETRmax to represent the results for photosynthetic efficiency

```
run5_photosyn_data <- read.csv("data/run5_hyp_ulv_final_alpha_ek_rounded.csv")
```

## Write function that returns the run number based on the range of dates input

```
get_run_number <- function(d) {
  # returns the run number based on the input date
  run = NA
  if ("2021-09-20" <= d && d <= "2021-09-29") {
    run <- 1
  }
}
```

```

} else if ("2021-09-30" <= d && d <= "2021-10-09") {
  run <- 2
} else if ("2021-10-11" <= d && d <= "2021-10-29") {
  run <- 3
} else if ("2021-11-01" <= d && d <= "2021-11-12") {
  run <- 4
} else {
  print("The date is %s not in a recognized range", d)
}
run
}

```

Make new column adding run to the dataset

```

run5_photosyn_data$run <- sapply(run5_photosyn_data$Date, get_run_number)
run5_photosyn_data$run <- as.factor(run5_photosyn_data$run)

```

Change levels to factors

```

run5_photosyn_data$Temperature <- as.factor(run5_photosyn_data$Temperature)
run5_photosyn_data$Treatment <- as.factor(as.character(run5_photosyn_data$Treatment))

```

Make a subset of the data to isolate the species and use only Day 9 (final day) results

```

hypnea <- subset(run5_photosyn_data, Species == "hm" & RLC.Day == 9)
ulva <- subset(run5_photosyn_data, Species == "ul" & RLC.Day == 9)

```

ULVA

Run model without interaction between the dependent variables

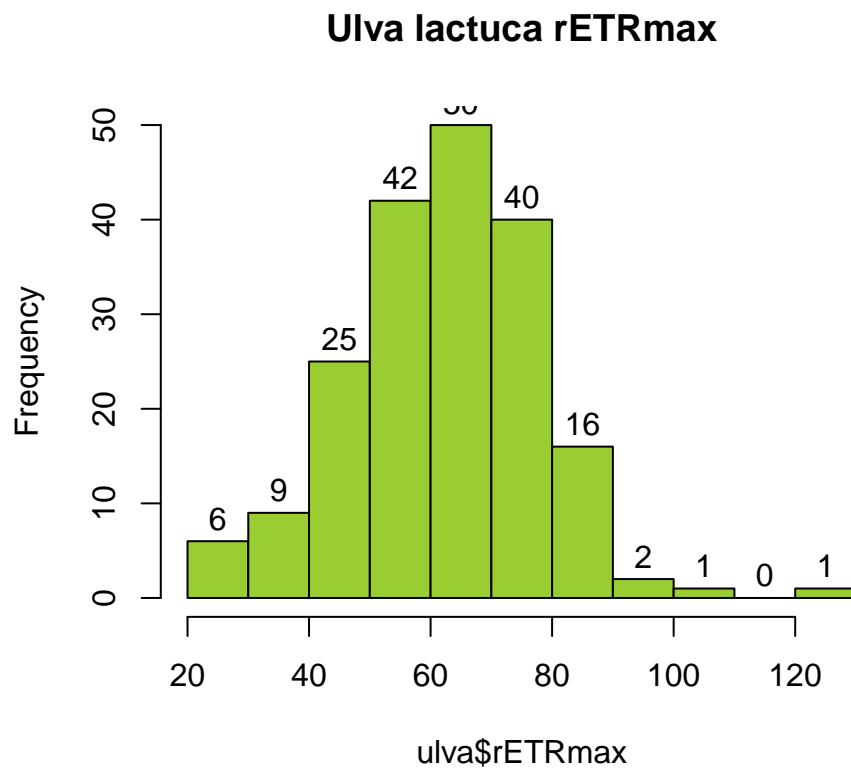
```

run5_photosyn_model_noint <- lmer(formula = rETRmax ~ Treatment + Temperature + (1 | run), data = ulva)

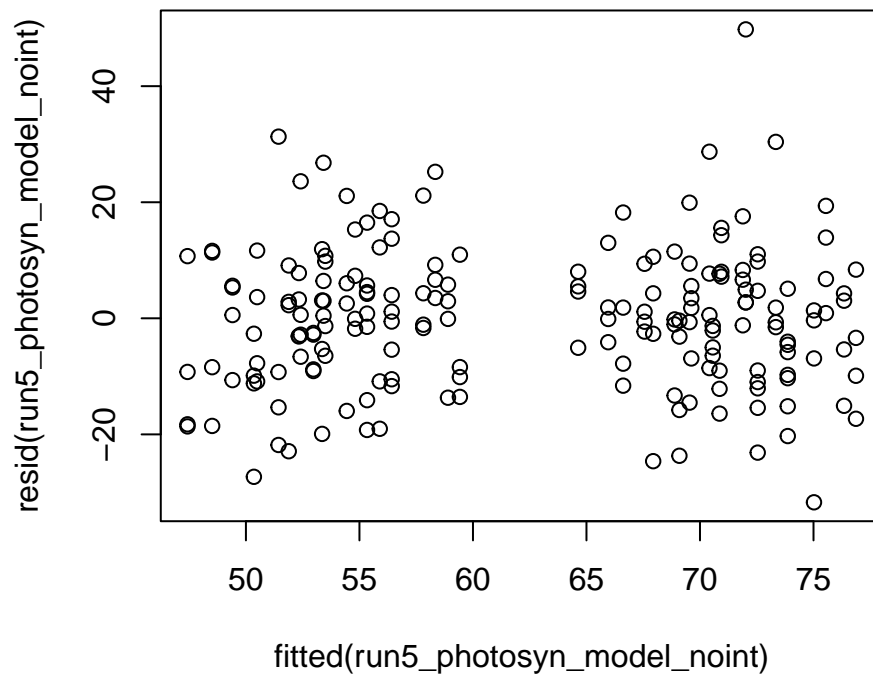
```

Make a histogram and Normal and residual plots of the data for ulva

```
hist(ulva$rETRmax, main = paste("Ulva lactuca rETRmax"), col = "olivedrab3", labels = TRUE)
```

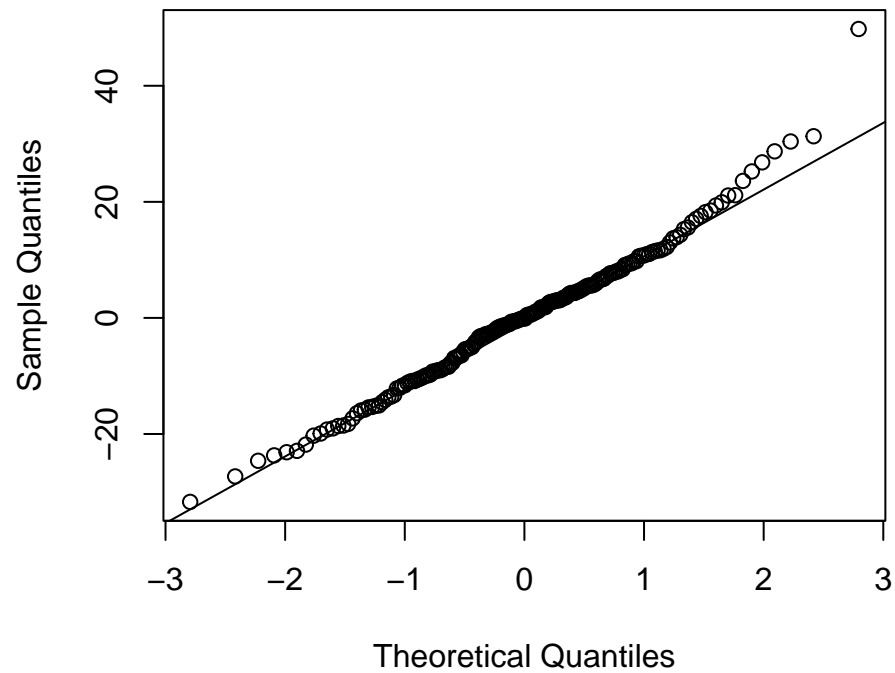


```
plot(resid(run5_photosyn_model_noint) ~ fitted(run5_photosyn_model_noint))
```



```
qqnorm(resid(run5_photosyn_model_noint))  
qqline(resid(run5_photosyn_model_noint))
```

### Normal Q–Q Plot

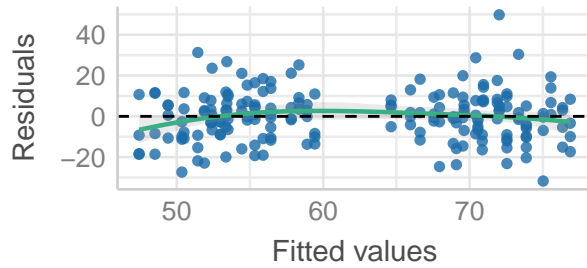


### Check the performance of the model

```
performance::check_model(run5_photosyn_model_noint)
```

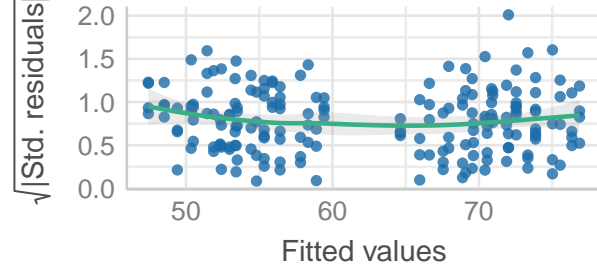
### Linearity

Reference line should be flat and horizontal



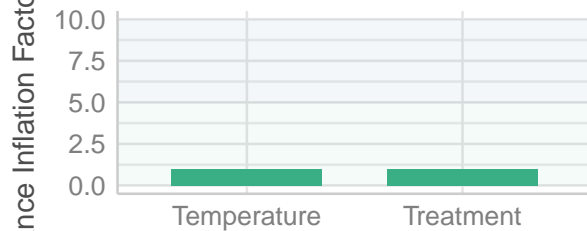
### Homogeneity of Variance

Reference line should be flat and horizontal



### Collinearity

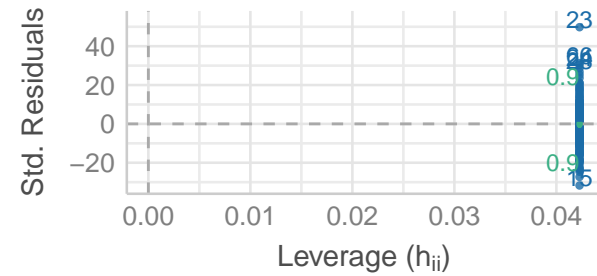
Higher bars (>5) indicate potential collinearity issue



low (< 5) moderate (< 10) high (>= 10)

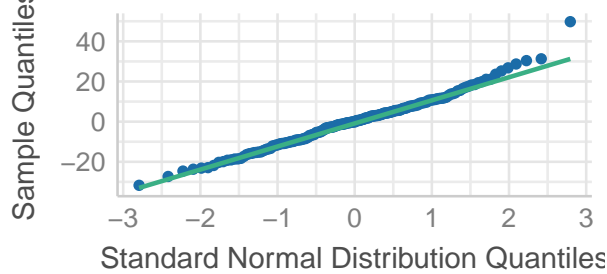
### Influential Observations

Points should be inside the contour lines



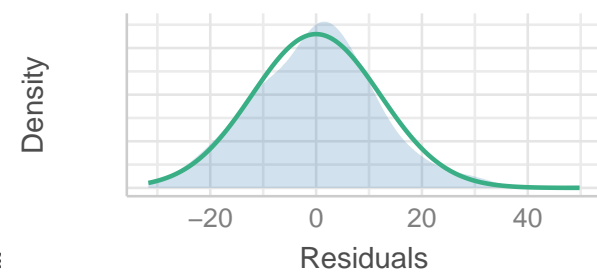
### Normality of Residuals

Dots should fall along the line



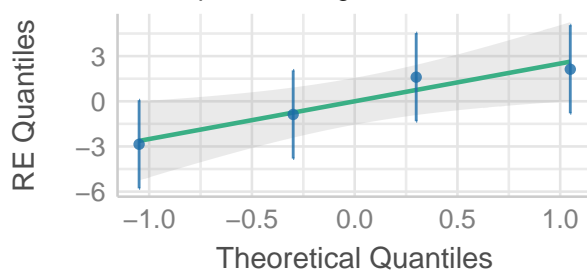
### Normality of Residuals

Distribution should be close to the normal curve



### Normality of Random Effects (run)

Dots should be plotted along the line



```
r.squaredGLMM(run5_photosyn_model_noint)
```

```
## Warning: 'r.squaredGLMM' now calculates a revised statistic. See the help page.
```

```
##           R2m           R2c
## [1,] 0.3387438 0.3701439
```

```
summary(run5_photosyn_model_noint)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: rETRmax ~ Treatment + Temperature + (1 | run)
## Data: ulva
##
## REML criterion at convergence: 1488.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.5721 -0.7004 -0.0077  0.5577  4.0391
##
## Random effects:
## Groups Name Variance Std.Dev.
## run (Intercept) 7.573 2.752
## Residual 151.913 12.325
## Number of obs: 192, groups: run, 4
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 74.742 2.577 17.726 29.004 < 2e-16 ***
## Treatment18 ppt -1.324 2.516 183.000 -0.526 0.59947
## Treatment28 ppt -17.445 2.516 183.000 -6.934 6.80e-11 ***
## Treatment35 ppt -18.531 2.516 183.000 -7.366 5.83e-12 ***
## Temperature27 -5.928 2.179 183.000 -2.721 0.00714 **
## Temperature30 -3.005 2.179 183.000 -1.379 0.16957
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) Trt18p Trt28p Trt35p Tmpr27
## Trtmnt18ppt -0.488
## Trtmnt28ppt -0.488 0.500
## Trtmnt35ppt -0.488 0.500 0.500
## Temperatr27 -0.423 0.000 0.000 0.000
## Temperatr30 -0.423 0.000 0.000 0.000 0.500
```

```
#run ANOVA and pairwise comparisons (sig differences for both random variables)
```

```
anova(run5_photosyn_model_noint, type = c("III"), ddf = "Satterthwaite")
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
## Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## Treatment 14480.0 4826.7 3 183 31.773 < 2e-16 ***
## Temperature 1124.8 562.4 2 183 3.702 0.02654 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ulva_photosyn_model_aov <- aov(rETRmax ~ Treatment + Temperature, data = ulva)
TukeyHSD(ulva_photosyn_model_aov, "Treatment", ordered = FALSE)
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = rETRmax ~ Treatment + Temperature, data = ulva)
##
## $Treatment
##           diff           lwr           upr           p adj
## 18 ppt-11 ppt -1.323542 -7.970429  5.323345 0.9551327
## 28 ppt-11 ppt -17.445417 -24.092304 -10.798530 0.0000000
## 35 ppt-11 ppt -18.530833 -25.177720 -11.883946 0.0000000
## 28 ppt-18 ppt -16.121875 -22.768762  -9.474988 0.0000000
## 35 ppt-18 ppt -17.207292 -23.854179 -10.560405 0.0000000
## 35 ppt-28 ppt  -1.085417  -7.732304   5.561470 0.9744337
```

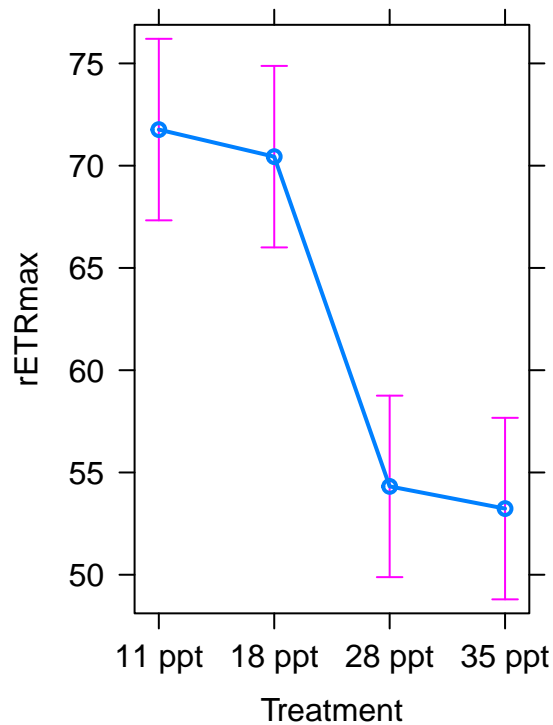
```
TukeyHSD(ulva_photosyn_model_aov, "Temperature", ordered = FALSE)
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = rETRmax ~ Treatment + Temperature, data = ulva)
##
## $Temperature
##           diff           lwr           upr           p adj
## 27-20 -5.928438 -11.174592 -0.6822827 0.0223906
## 30-20 -3.004687  -8.250842  2.2414673 0.3677644
## 30-27  2.923750  -2.322405  8.1699048 0.3876698
```

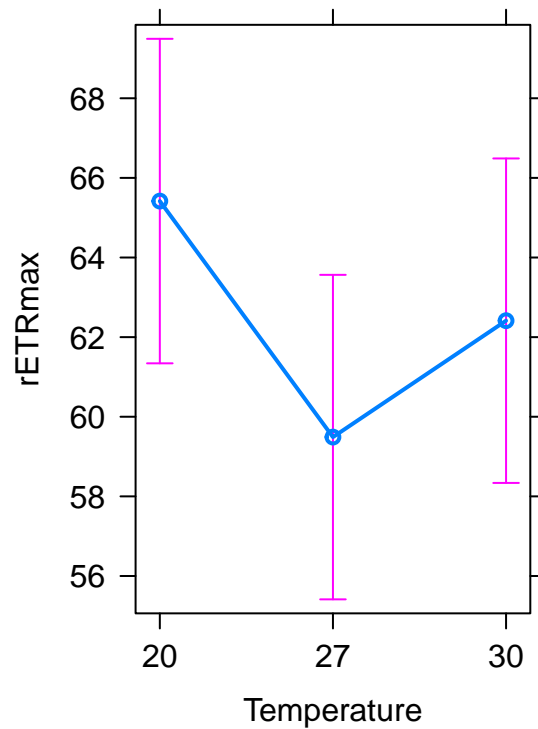
## Plot the random effects for Ulva

```
plot(allEffects(run5_photosyn_model_noint))
```

**Treatment effect plot**



**Temperature effect plot**



## HYPNEA

Run model without interaction between the dependent variables

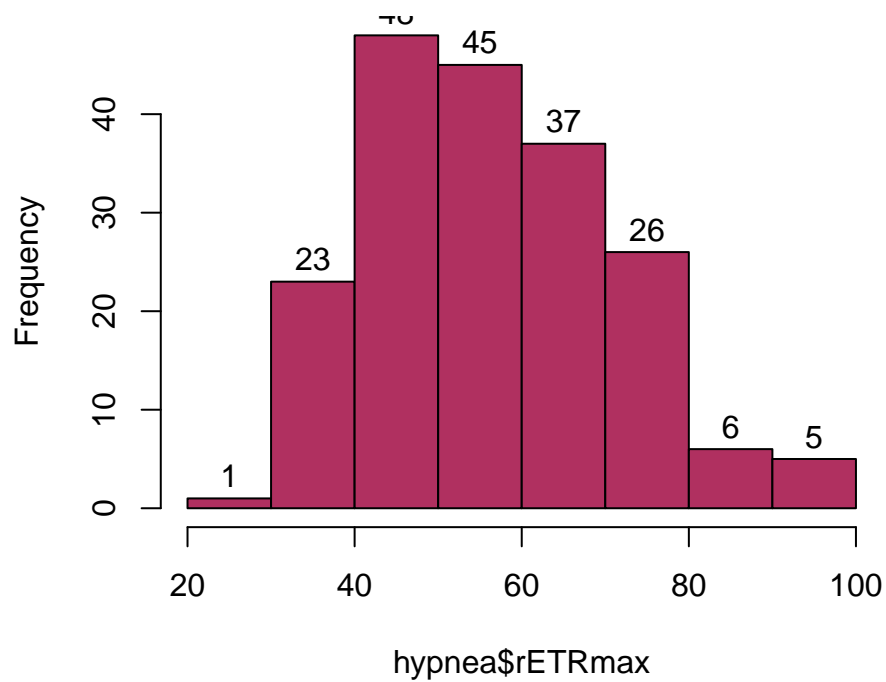
```
run5_photosyn_model_noint <- lmer(formula = rETRmax ~ Treatment + Temperature + (1 | run),
                                   data = hypnea)
```

Make a histogram and Normal and residual plots of the data for hypnea

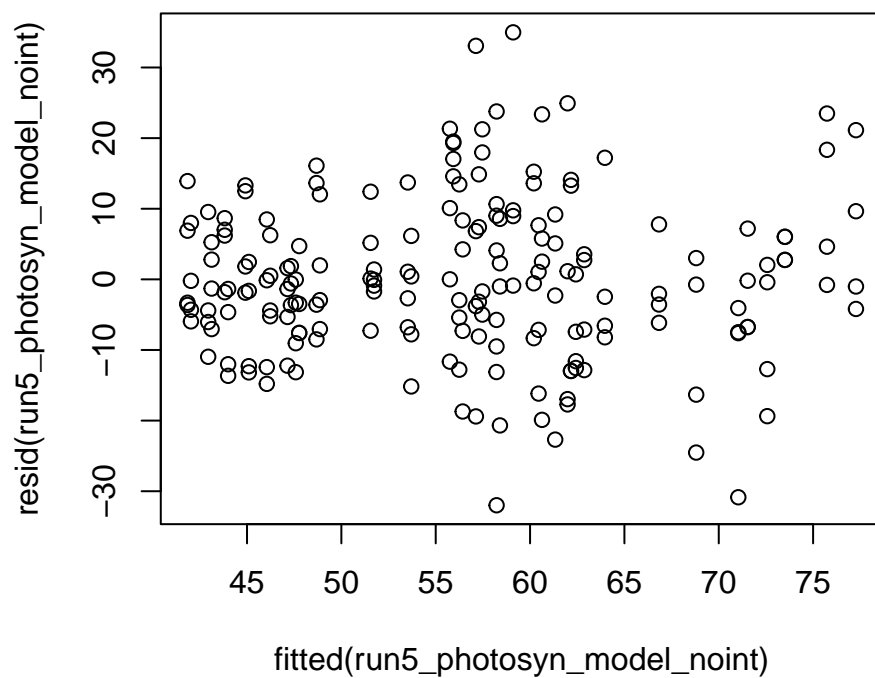
```
hist(hypnea$rETRmax, main = paste("Hypnea musciformis rETRmax"), col = "maroon", labels = TRUE)
```



## Hypnea musciformis rETRmax

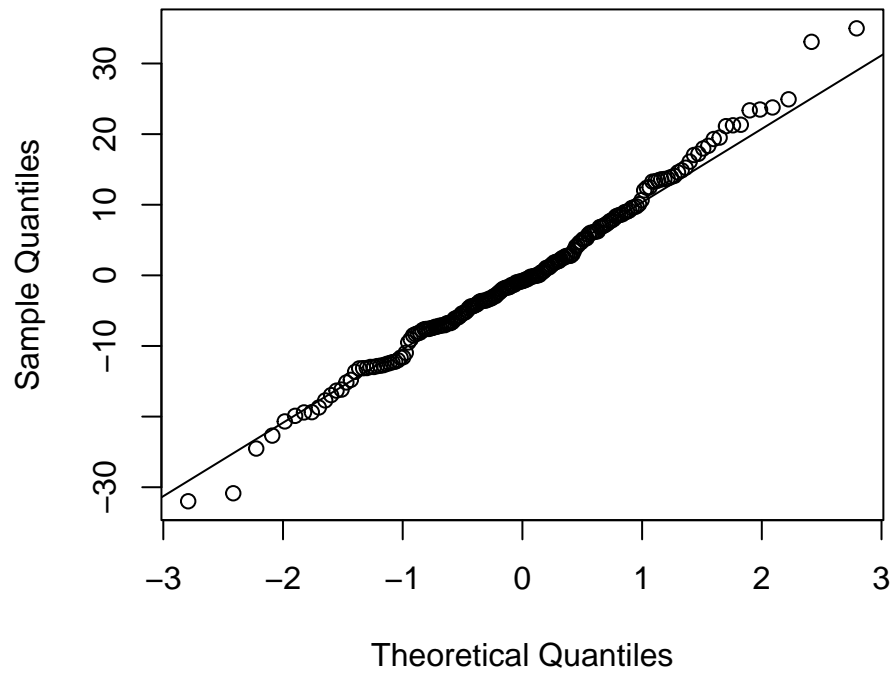


```
plot(resid(run5_photosyn_model_noint) ~ fitted(run5_photosyn_model_noint))
```



```
qqnorm(resid(run5_photosyn_model_noint))
qqline(resid(run5_photosyn_model_noint))
```

### Normal Q-Q Plot

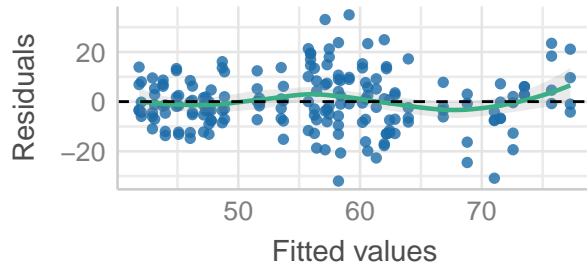


Check the performance of the model

```
performance::check_model(run5_photosyn_model_noint)
```

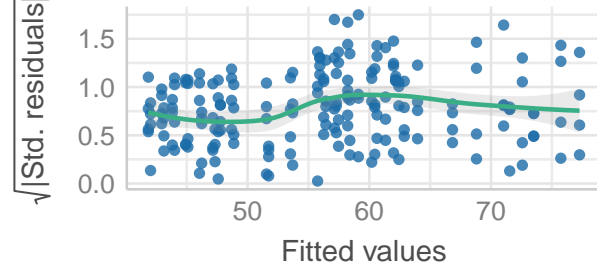
### Linearity

Reference line should be flat and horizontal



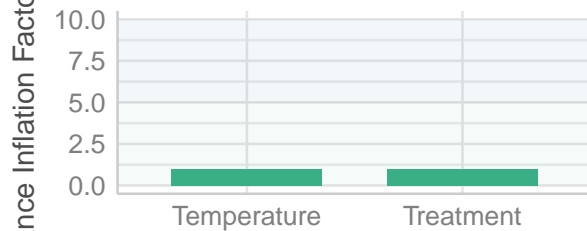
### Homogeneity of Variance

Reference line should be flat and horizontal



### Collinearity

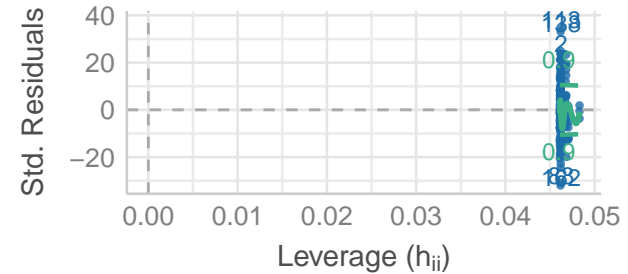
Higher bars (>5) indicate potential collinearity issue



low (< 5) moderate (< 10) high (>= 10)

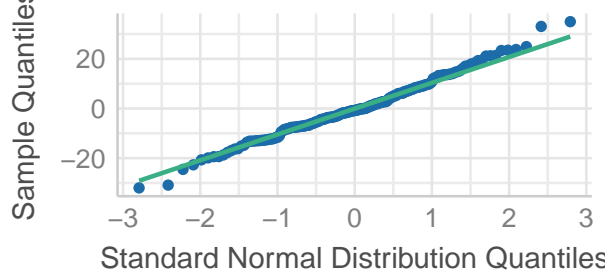
### Influential Observations

Points should be inside the contour lines



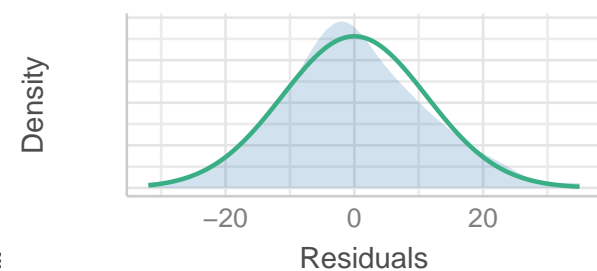
### Normality of Residuals

Dots should fall along the line



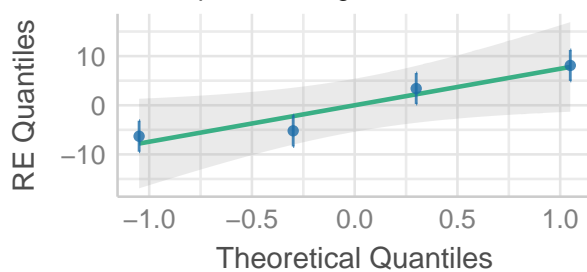
### Normality of Residuals

Distribution should be close to the normal curve



### Normality of Random Effects (run)

Dots should be plotted along the line



```
r.squaredGLMM(run5_photosyn_model_noint)
```

```
##           R2m           R2c
## [1,] 0.2375505 0.4500714
```

```
summary(run5_photosyn_model_noint)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: rETRmax ~ Treatment + Temperature + (1 | run)
## Data: hypnea
##
## REML criterion at convergence: 1458.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.79523 -0.61841 -0.06864  0.60795  3.05660
##
## Random effects:
## Groups Name Variance Std.Dev.
## run (Intercept) 50.61 7.114
## Residual 130.95 11.443
## Number of obs: 191, groups: run, 4
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 67.633 4.096 4.743 16.512 2.26e-05 ***
## Treatment18 ppt 1.537 2.349 182.004 0.654 0.5138
## Treatment28 ppt -4.202 2.349 182.004 -1.789 0.0752 .
## Treatment35 ppt -2.230 2.349 182.004 -0.950 0.3436
## Temperature27 -15.283 2.023 182.000 -7.555 1.97e-12 ***
## Temperature30 -15.102 2.031 182.003 -7.435 3.96e-12 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) Trt18p Trt28p Trt35p Tmpr27
## Trtmnt18ppt -0.288
## Trtmnt28ppt -0.288 0.505
## Trtmnt35ppt -0.288 0.505 0.505
## Temperatr27 -0.247 0.000 0.000 0.000
## Temperatr30 -0.242 -0.009 -0.009 -0.009 0.498
```

```
#run ANOVA and pairwise comparisons (only significant diff for Temperature)
```

```
anova(run5_photosyn_model_noint, type = c("III"), ddf = "Satterthwaite")
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
## Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## Treatment 910.4 303.5 3 182 2.3175 0.07712 .
## Temperature 9823.9 4912.0 2 182 37.5106 2.287e-14 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
hypnea_photosyn_model_aov <- aov(rETRmax ~ Treatment + Temperature, data = hypnea)
TukeyHSD(hypnea_photosyn_model_aov, "Temperature", ordered = FALSE)
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = rETRmax ~ Treatment + Temperature, data = hypnea)
##
## $Temperature
##          diff          lwr          upr      p adj
## 27-20 -15.2834375 -20.732092 -9.834783 0.0000000
## 30-20 -15.0172137 -20.487447 -9.546981 0.0000000
## 30-27  0.2662238  -5.204009  5.736457 0.9927371
```

## Plot the random effects for Hypnea

```
plot(allEffects(run5_photosyn_model_noint))
```

