Ulva and Hypnea Photosynthesis and Growth Run5 - Sept-Nov 2021

Angela Richards Donà

1/28/2022

Run5 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.

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 growth/weight dataset

```
run5_growth <- read.csv("data/run5_growth_all_012422.csv")
```

Make a new column for weight change (difference final from initial)

```
run5_growth$growth_rate_percent <-
  (run5_growth$final.weight - run5_growth$Inital.weight) / run5_growth$Inital.weight * 100
```

Also make a new column for daily growth rate from 8 day study (steady growth rate assumed rather than exponential), which may or may not be used

```
run5_growth$steady_growth_daily <- run5_growth$growth_rate_percent / 8
```

Change levels to factors

```
run5_growth$temperature <- as.factor(run5_growth$temperature)
run5_growth$run <- as.factor(run5_growth$run)

run5_growth$treatment <- as.factor(as.character(run5_growth$treatment))

hypnea <- subset(run5_growth, Species == "Hm")
ulva <- subset(run5_growth, Species == "Ul")
```
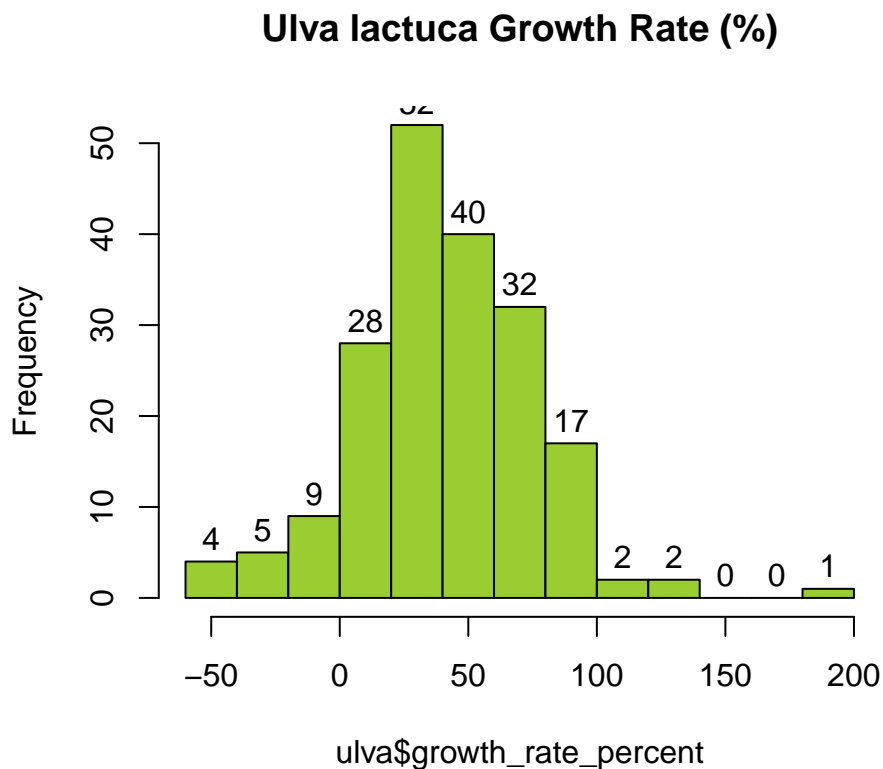
Run the model

ULVA

run model without interaction (0 in model permits display of four levels of treatments - no intercept)
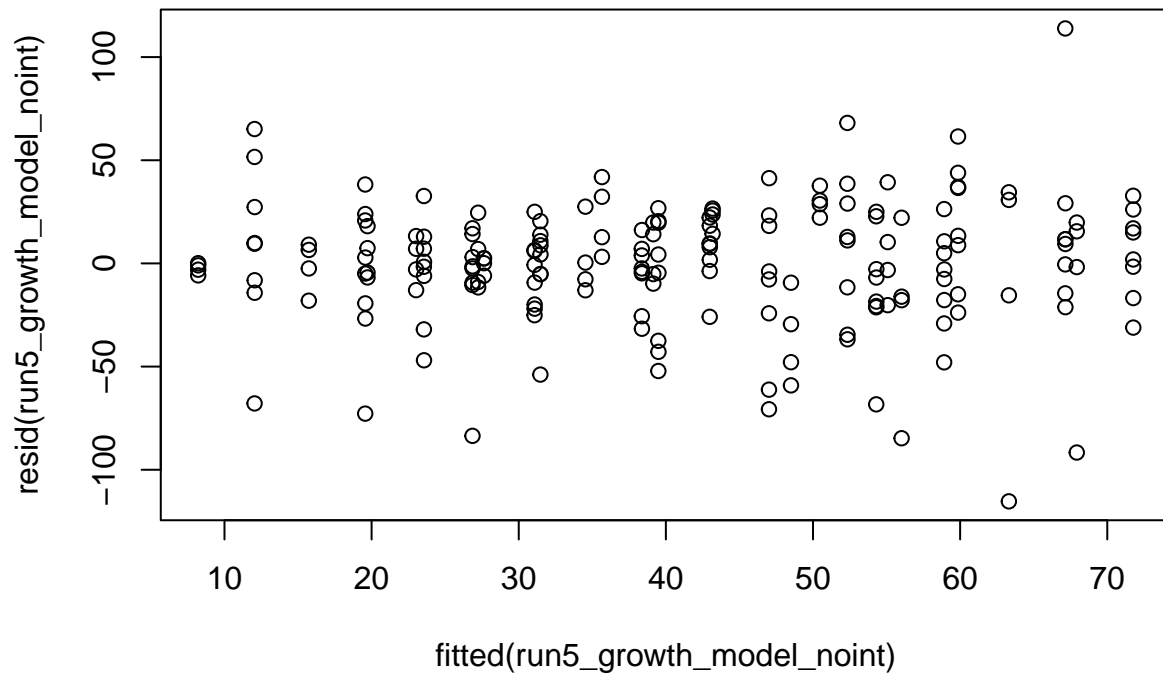
```
run5_growth_model_noint <- lmer(formula = growth_rate_percent ~ treatment + temperature + (1 | run),
                                data = ulva)
```

#make a histogram of the data for Ulva

```
hist(ulva$growth_rate_percent, main = paste("Ulva lactuca Growth Rate (%)"),
     col = "olivedrab3", labels = TRUE)
```


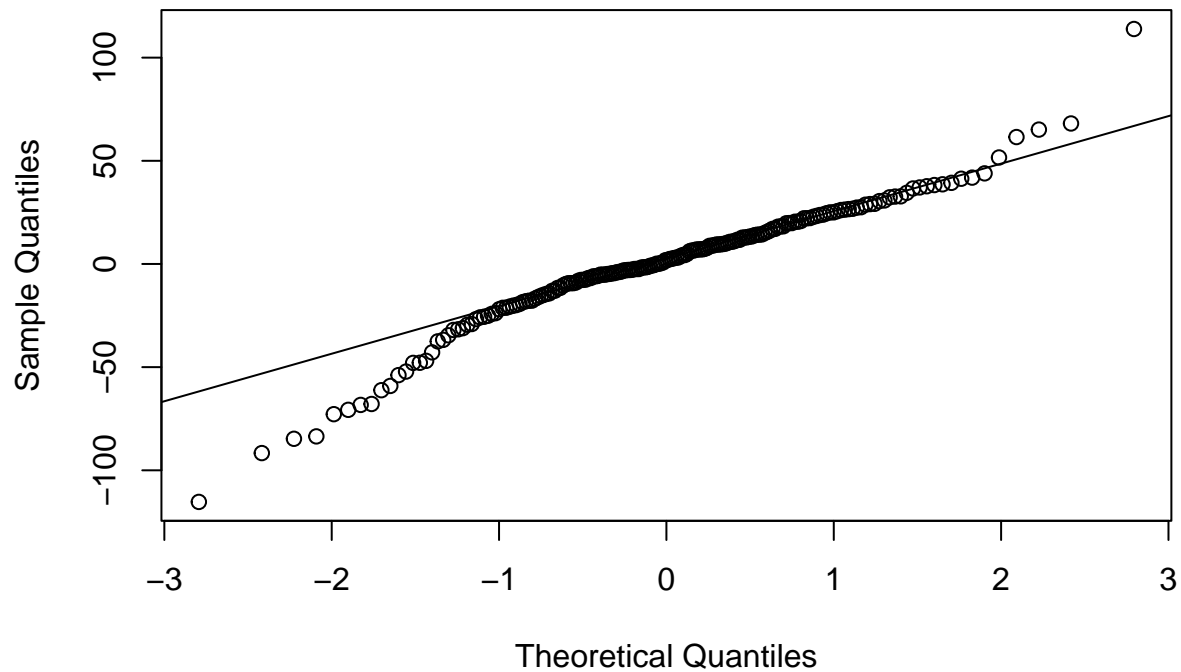**Ulva lactuca Growth Rate (%)**

```
plot(resid(run5_growth_model_noint) ~ fitted(run5_growth_model_noint))
```



```
qqnorm(resid(run5_growth_model_noint))
qqline(resid(run5_growth_model_noint))
```
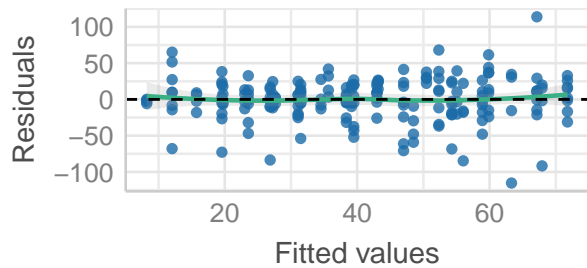
Normal Q–Q Plot

Check the performance of the model for Ulva

```
performance::check_model(run5_growth_model_noint)
```
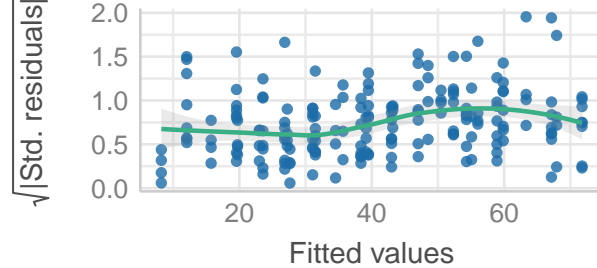
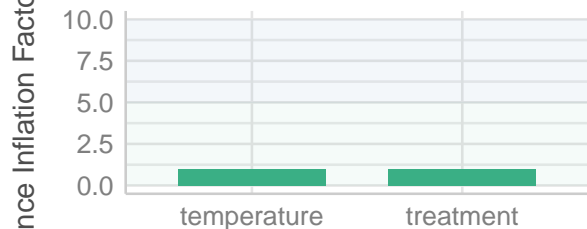## Linearity
Reference line should be flat and horizontal

Homogeneity of Variance
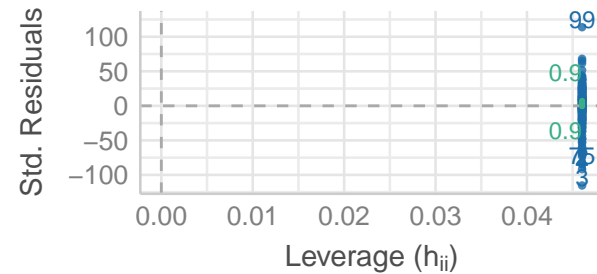Reference line should be flat and horizontal

Collinearity
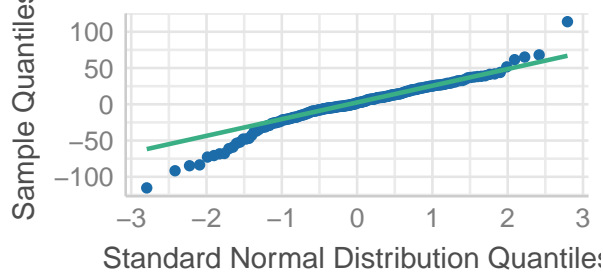Higher bars (>5) indicate potential collinearity issu

Influential Observations
Points should be inside the contour lines
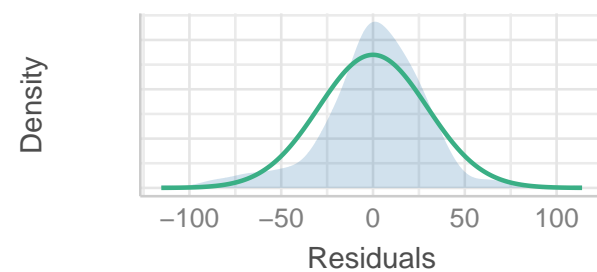
low (< 5)   moderate (< 10)   high (>

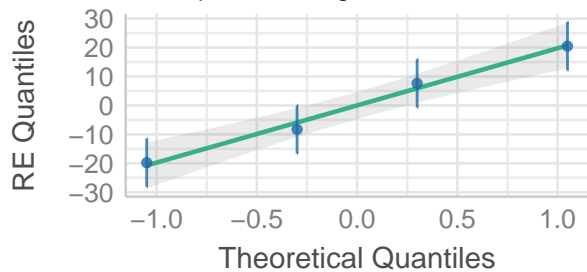## Normality of Residuals
Dots should fall along the line

Normality of Residuals
Distribution should be close to the normal curve

Normality of Random Effects (run)
Dots should be plotted along the line

These outputs show the model is acceptable

```
anova(run5_growth_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   10432.3  3477.4     3   183  3.8151 0.01103 *
## temperature   628.1   314.1     2   183  0.3445 0.70900
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ulva_growth_model_aov <- aov(growth_rate_percent ~ treatment + temperature, data = ulva)
TukeyHSD(ulva_growth_model_aov, "treatment", ordered = FALSE)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = growth_rate_percent ~ treatment + temperature, data = ulva)
##
## $treatment
##                     diff       lwr       upr     p adj
## 18 ppt-11 ppt  -4.613675 -22.69656 13.469205 0.9113928
## 28 ppt-11 ppt -11.904098 -29.98698  6.178783 0.3231502
## 35 ppt-11 ppt -19.424377 -37.50726 -1.341497 0.0298857
## 28 ppt-18 ppt  -7.290422 -25.37330 10.792459 0.7230962
## 35 ppt-18 ppt -14.810702 -32.89358  3.272179 0.1495161
## 35 ppt-28 ppt  -7.520280 -25.60316 10.562601 0.7033053
```

```
r.squaredGLMM(run5_growth_model_noint)
```

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

```
##             R2m       R2c
## [1,] 0.0445322 0.2990482
```

```
summary(run5_growth_model_noint)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: growth_rate_percent ~ treatment + temperature + (1 | run)
##    Data: ulva
##
## REML criterion at convergence: 1826.9
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.8195 -0.4297  0.0612  0.5993  3.7719
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  run      (Intercept) 331.0    18.19
##  Residual             911.5    30.19
```

```
## Number of obs: 192, groups:  run, 4
##
## Fixed effects:
##                   Estimate Std. Error         df t value Pr(>|t|)
## (Intercept)      51.279813  10.546330   4.842874   4.862  0.00503 **
## treatment18 ppt  -4.613675   6.162701 183.000000  -0.749  0.45503
## treatment28 ppt -11.904098   6.162701 183.000000  -1.932  0.05495 .
## treatment35 ppt -19.424377   6.162701 183.000000  -3.152  0.00190 **
## temperature27 C   0.008408   5.337056 183.000000   0.002  0.99874
## temperature30 C  -3.832627   5.337056 183.000000  -0.718  0.47360
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) trt18p trt28p trt35p tmp27C
## trtmnt18ppt -0.292
## trtmnt28ppt -0.292  0.500
## trtmnt35ppt -0.292  0.500  0.500
## tempertr27C -0.253  0.000  0.000  0.000
## tempertr30C -0.253  0.000  0.000  0.000  0.500
```

Effects Plots

```
plot(allEffects(run5_growth_model_noint))
```


treatment effect plot

temperature effect plot
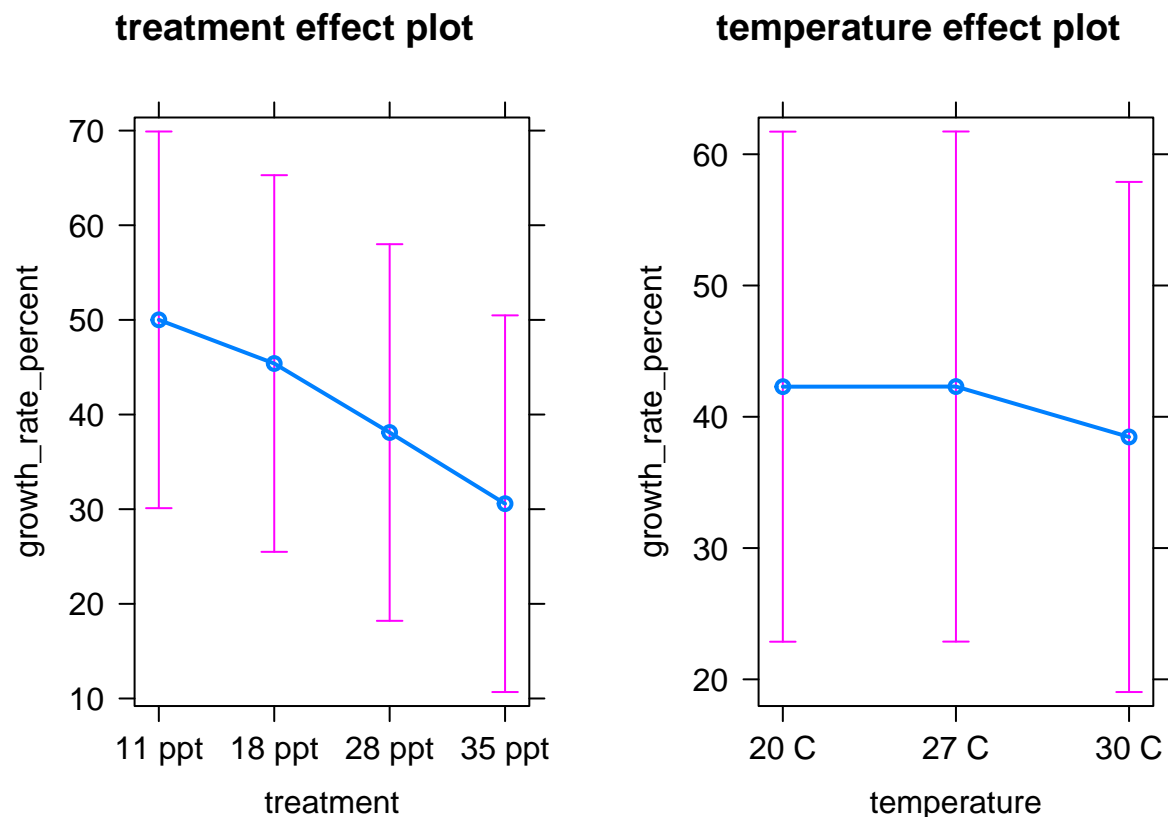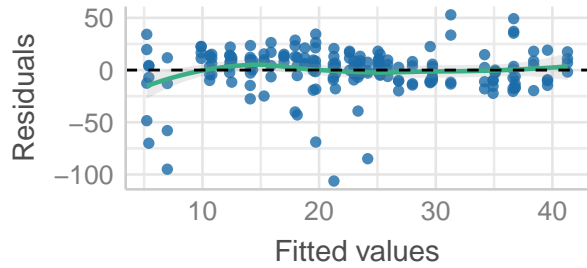
HYPNEA

```
run5_growth_model_noint <- lmer(formula = growth_rate_percent ~ treatment + temperature + (1 | run),
                                data = hypnea)
```

Check the performance of the model for Hypnea

```
performance::check_model(run5_growth_model_noint)
```
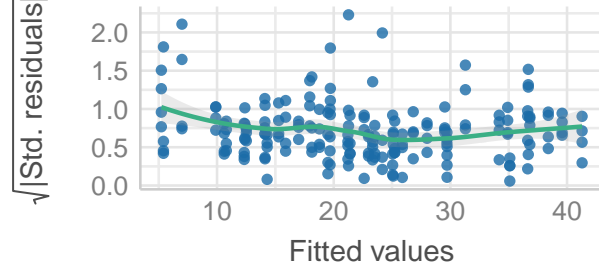
Linearity
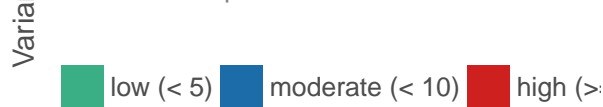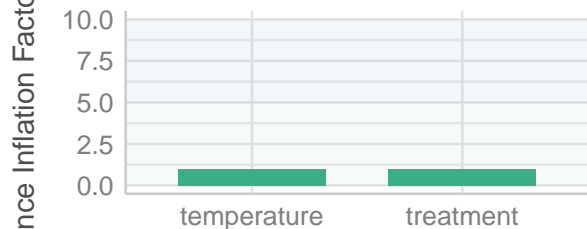Reference line should be flat and horizontal

Homogeneity of Variance
Reference line should be flat and horizontal

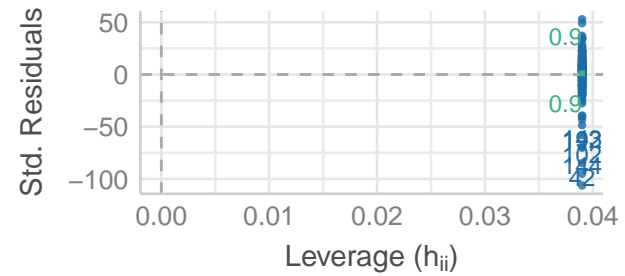## Collinearity
Higher bars (>5) indicate potential collinearity issu
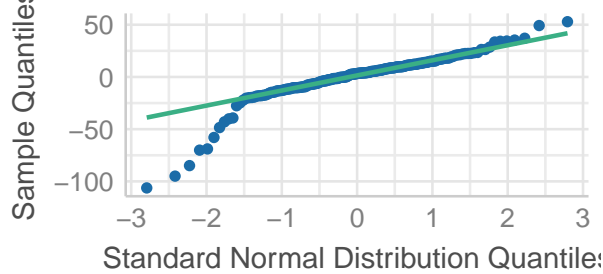

low (< 5)   moderate (< 10)   high (>

Influential Observations
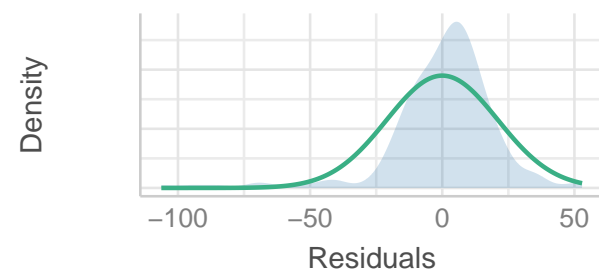Points should be inside the contour lines

Normality of Residuals
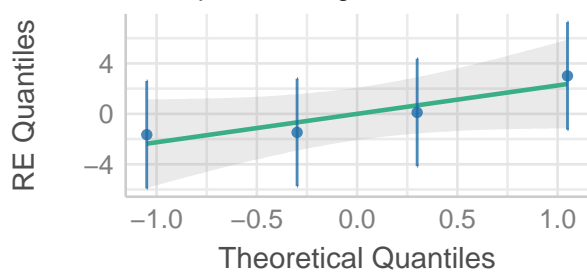Dots should fall along the line

Normality of Residuals
Distribution should be close to the normal curve

Normality of Random Effects (run)
Dots should be plotted along the line

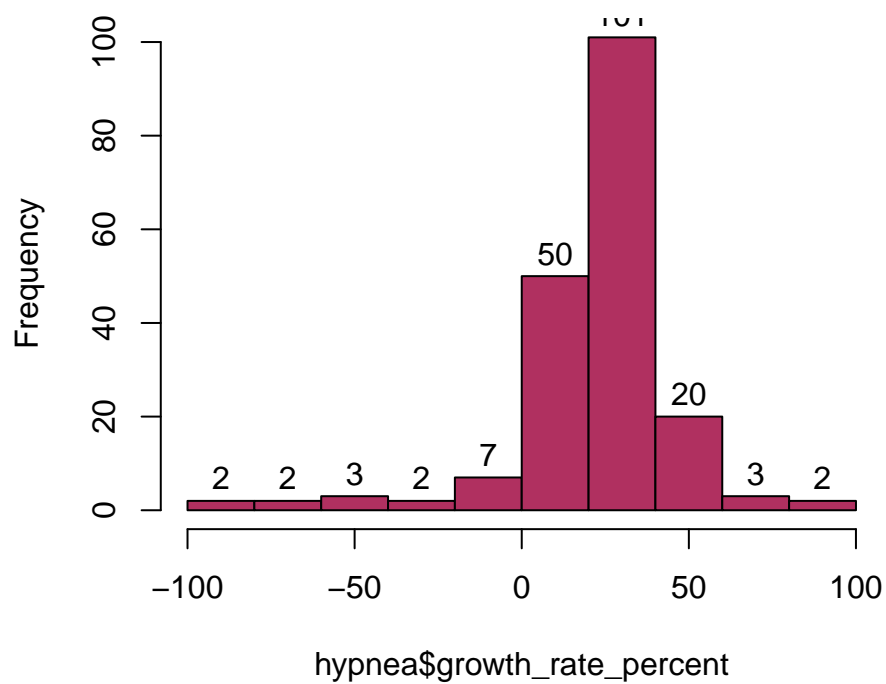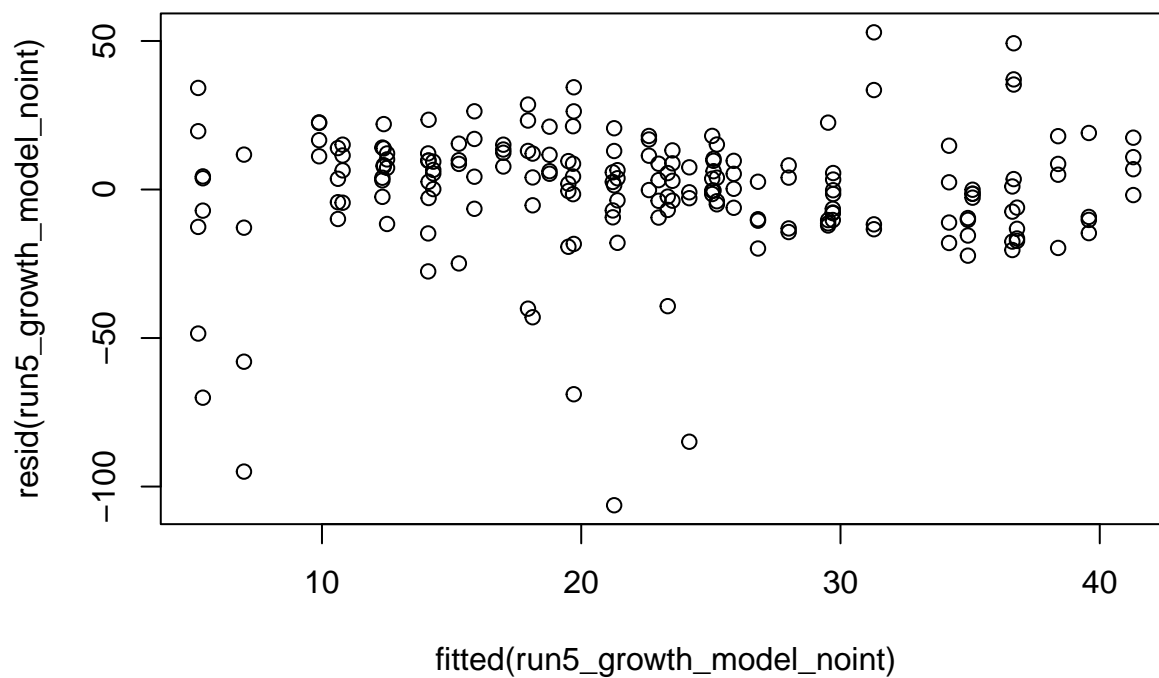

These outputs show the model is acceptable for the data

```
hist(hypnea$growth_rate_percent, main = paste("Hypnea musciformis Growth Rate (%)"),
     col = "maroon", labels = TRUE)
```
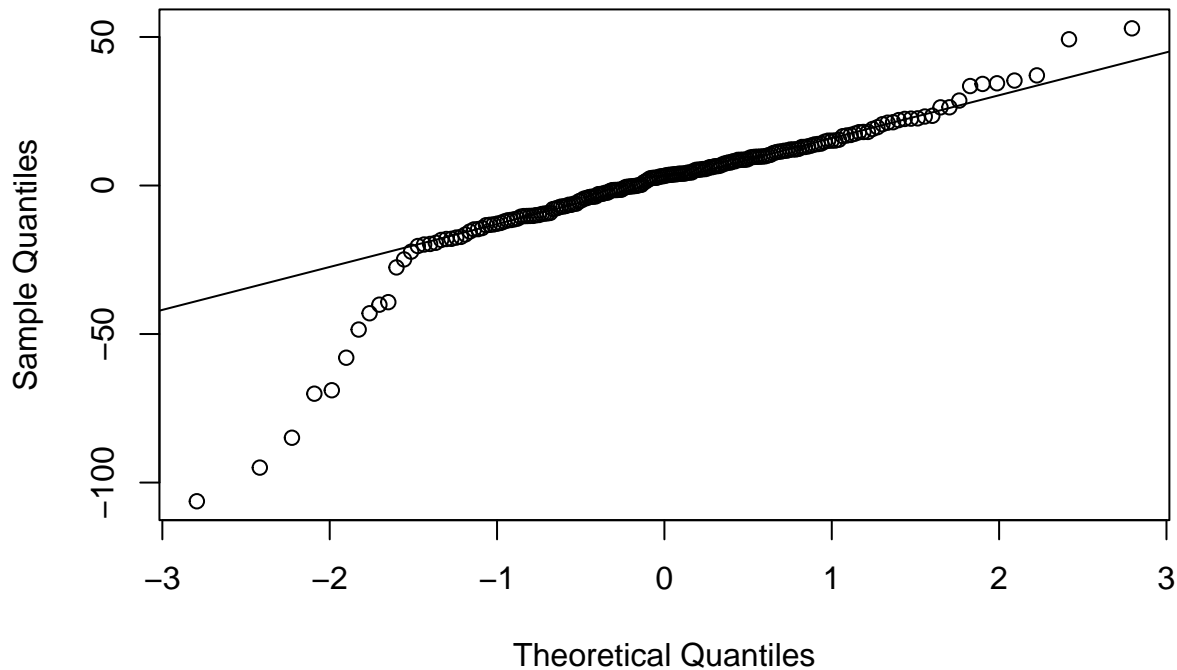
Hypnea musciformis Growth Rate (%)


```
plot(resid(run5_growth_model_noint) ~ fitted(run5_growth_model_noint))
```



```
qqnorm(resid(run5_growth_model_noint))
qqline(resid(run5_growth_model_noint))
```

Normal Q–Q Plot


```r
anova(run5_growth_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   14608.7  4869.6     3   183  10.659 1.715e-06 ***
## temperature  1759.7   879.8     2   183   1.926    0.1487
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
hypnea_growth_model_aov <- aov(growth_rate_percent ~ treatment + temperature, data = hypnea)
TukeyHSD(hypnea_growth_model_aov, "treatment", ordered = FALSE)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = growth_rate_percent ~ treatment + temperature, data = hypnea)
##
## $treatment
##                   diff        lwr       upr     p adj
## 18 ppt-11 ppt 12.720941   1.3209708 24.120911 0.0220255
## 28 ppt-11 ppt  8.887762  -2.5122084 20.287732 0.1839285
## 35 ppt-11 ppt 24.297854  12.8978839 35.697825 0.0000007
## 28 ppt-18 ppt -3.833179 -15.2331495  7.566791 0.8194889
## 35 ppt-18 ppt 11.576913   0.1769428 22.976883 0.0450335
## 35 ppt-28 ppt 15.410092   4.0101220 26.810063 0.0031917
```

```
r.squaredGLMM(run5_growth_model_noint)
```

```
##              R2m        R2c
## [1,] 0.1552732 0.1722819
```
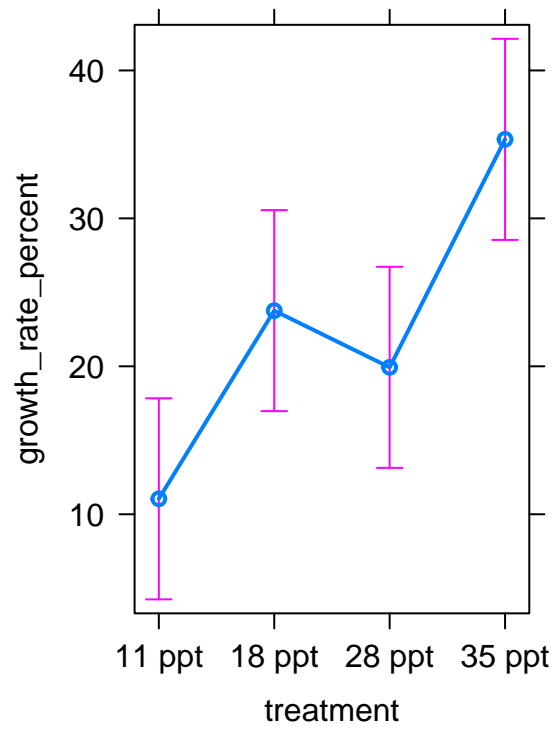
```
summary(run5_growth_model_noint)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: growth_rate_percent ~ treatment + temperature + (1 | run)
##    Data: hypnea
##
## REML criterion at convergence: 1691.7
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.9728 -0.3868  0.1524  0.5253  2.4751
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  run      (Intercept)   9.387   3.064
##  Residual             456.833  21.374
## Number of obs: 192, groups:  run, 4
##
## Fixed effects:
##                Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      12.269      4.077  33.620   3.009  0.00494 **
## treatment18 ppt  12.721      4.363 183.000   2.916  0.00399 **
## treatment28 ppt   8.888      4.363 183.000   2.037  0.04308 *
## treatment35 ppt  24.298      4.363 183.000   5.569 9.02e-08 ***
## temperature27 C   1.714      3.778 183.000   0.454  0.65062
## temperature30 C  -5.391      3.778 183.000  -1.427  0.15533
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) trt18p trt28p trt35p tmp27C
## trtmnt18ppt -0.535
## trtmnt28ppt -0.535  0.500
## trtmnt35ppt -0.535  0.500  0.500
## tempertr27C -0.463  0.000  0.000  0.000
## tempertr30C -0.463  0.000  0.000  0.000  0.500
```

Effects Plots

```
plot(allEffects(run5_growth_model_noint))
```

treatment effect plot

temperature effect plot