

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

Angela Richards Donà

1/28/2022

Run5 GROWTH RATE 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.

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))
```

Create subset of the data to isolate the species

```
hypnea <- subset(run5_growth, Species == "Hm")
ulva <- subset(run5_growth, Species == "U1")
```

Run the model

ULVA

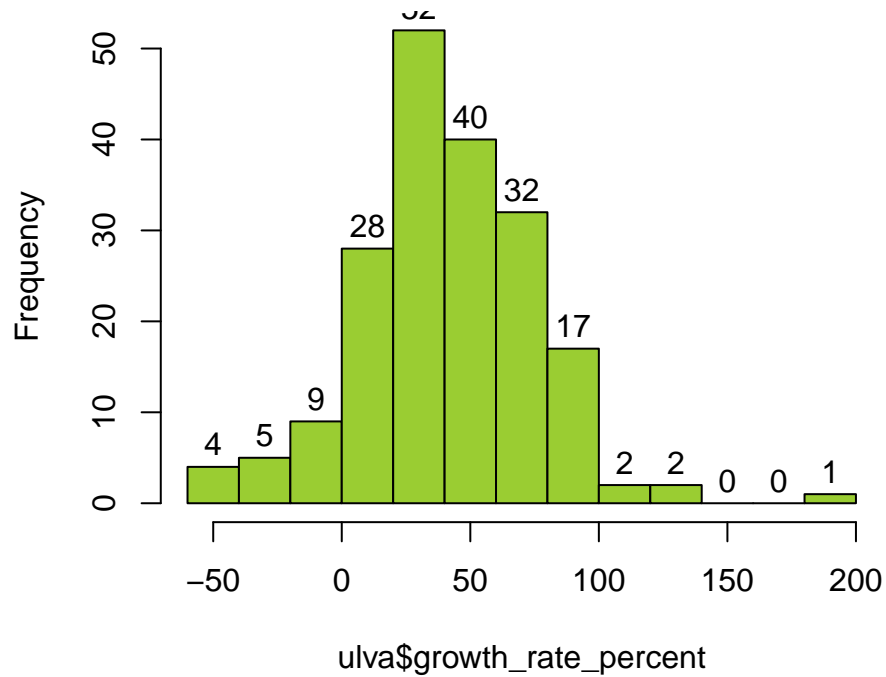
run model without interaction since interaction caused collinearity issues

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

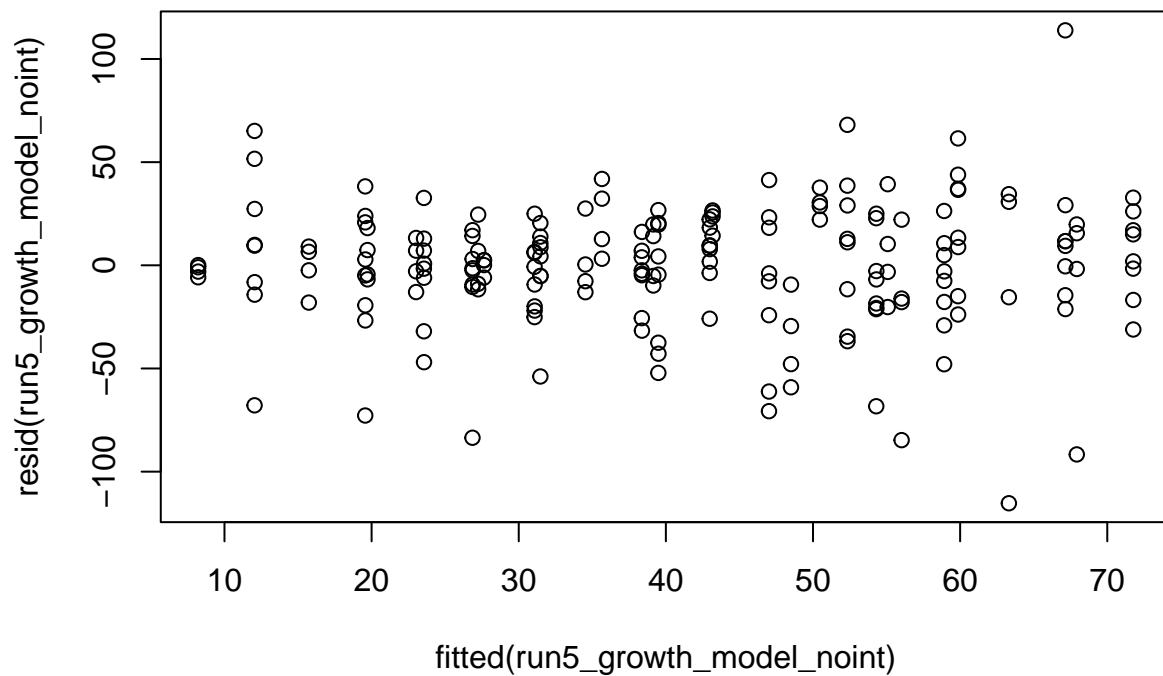
#make a histogram of the data for Ulva

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

Ulva lactuca Growth Rate (%)

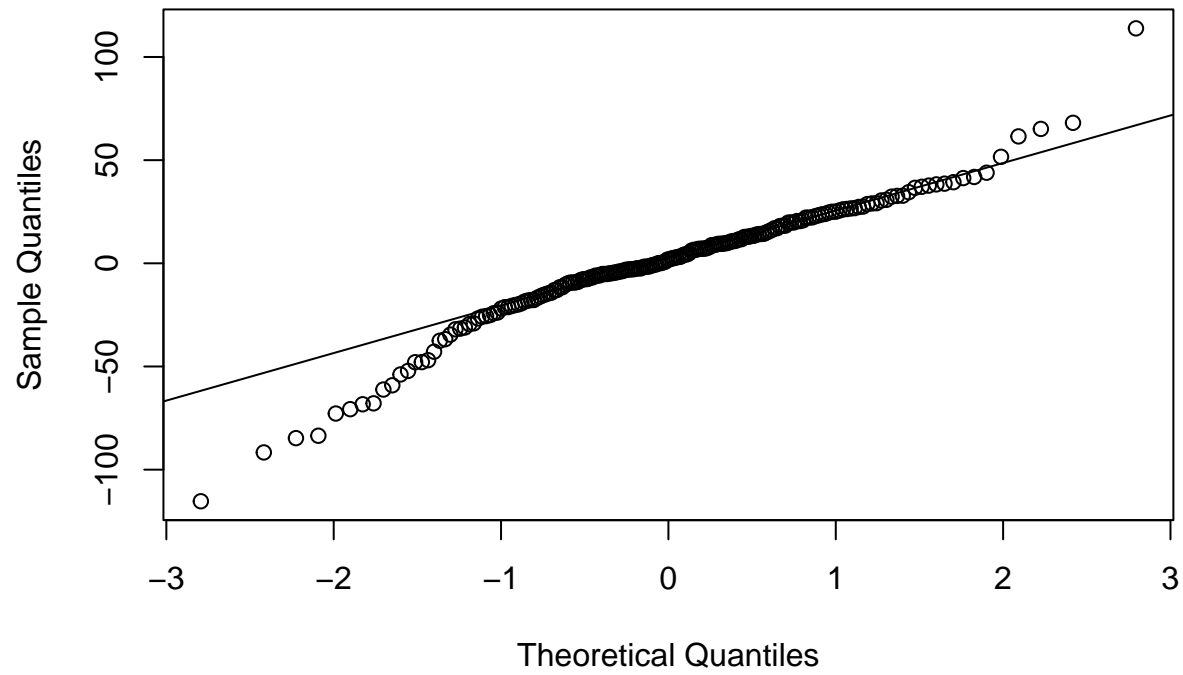


```
plot(resid(run5_growth_model_noint) ~ fitted(run5_growth_model_noint))
```



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

Normal Q-Q Plot

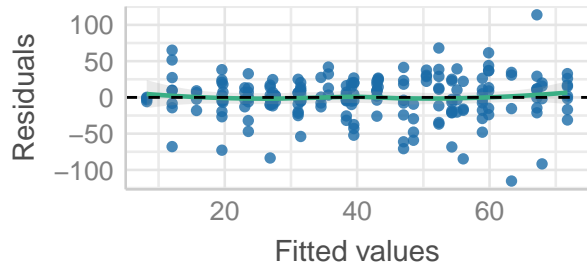


Check the performance of the model for Ulva

```
performance::check_model(run5_growth_model_noint)
```

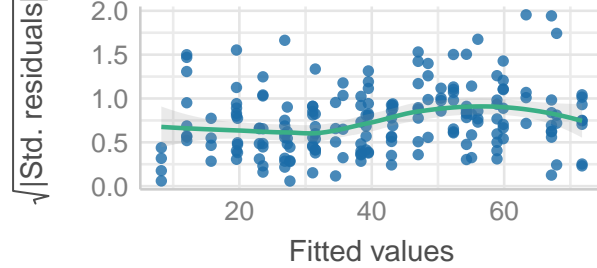
Linearity

Reference line should be flat and horizontal



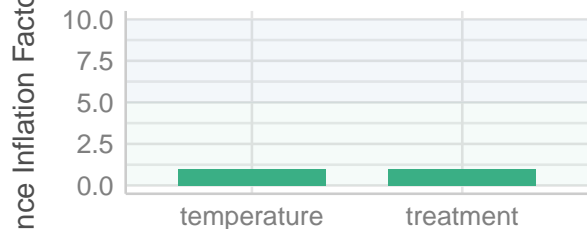
Homogeneity of Variance

Reference line should be flat and horizontal



Collinearity

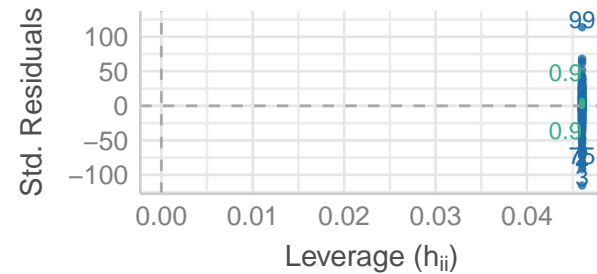
Higher bars (>5) indicate potential collinearity issue



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

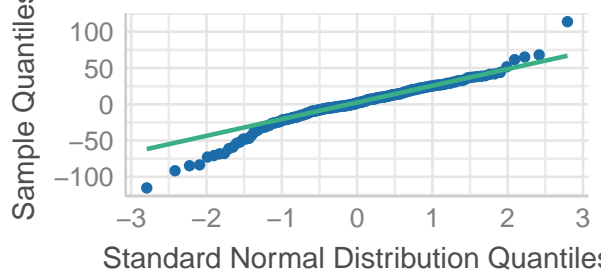
Influential Observations

Points should be inside the contour lines



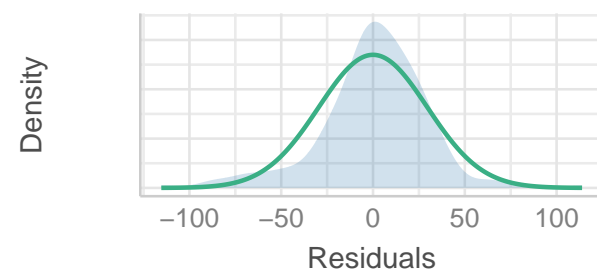
Normality of Residuals

Dots should fall along the line



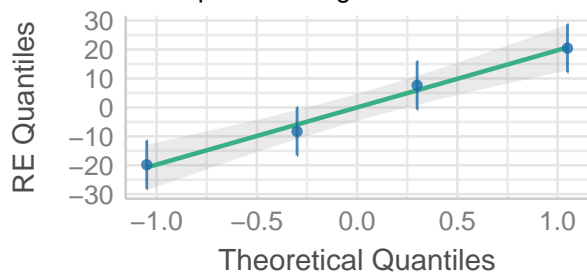
Normality of Residuals

Distribution should be close to the normal curve



Normality of Random Effects (run)

Dots should be plotted along the line



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)

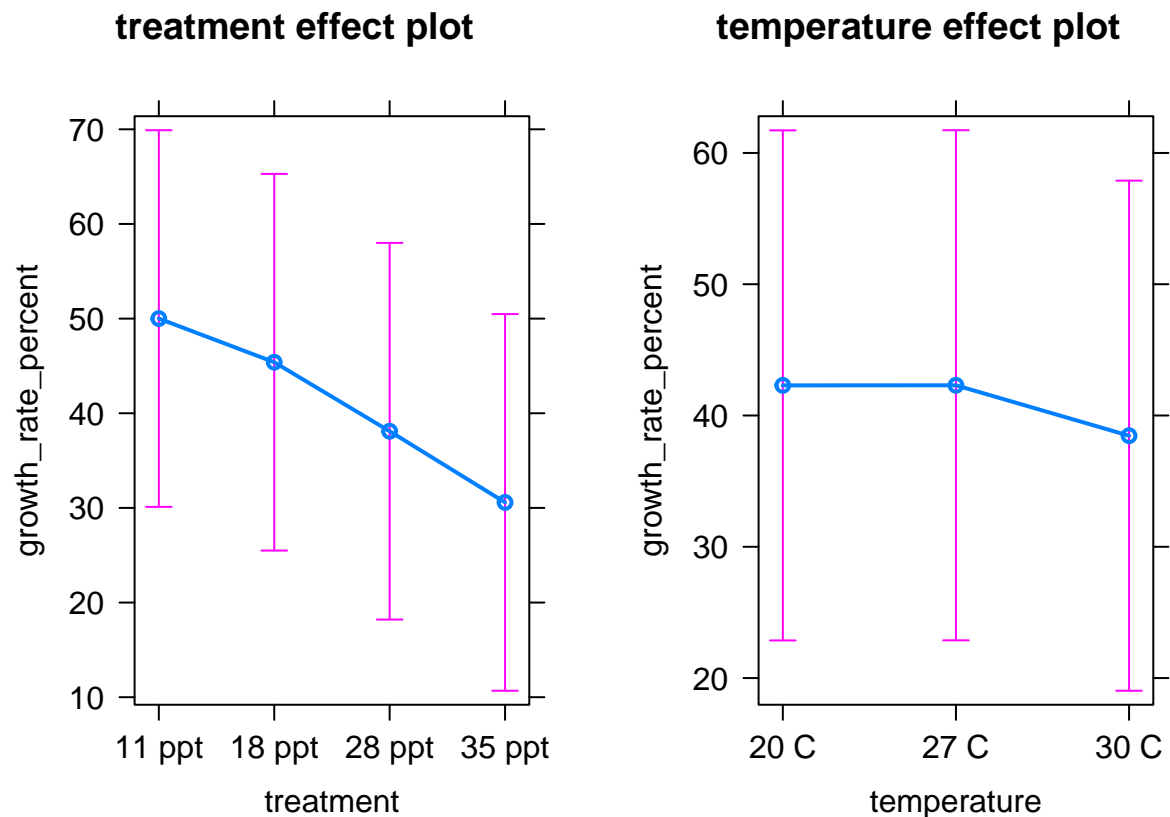
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: growth_rate_percent ~ treatment + temperature + (1 | run)
## Data: ulva
##
## REML criterion at convergence: 1826.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.8195 -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))
```



HYPNEA

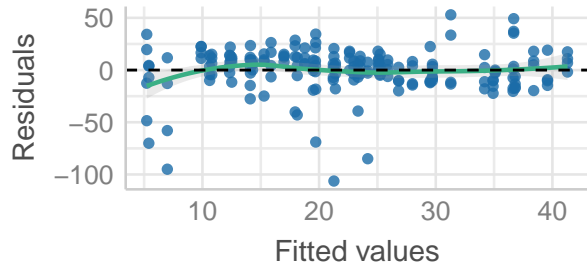
```
run5_growth_model_noint <- lmer(formula = growth_rate_percent ~ treatment + temperature + (1 | run),  
                                data = hypnea)
```

Check the performance of the model for Hypnea

```
performance::check_model(run5_growth_model_noint)
```

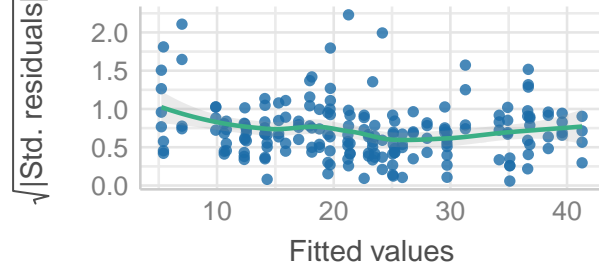

Linearity

Reference line should be flat and horizontal



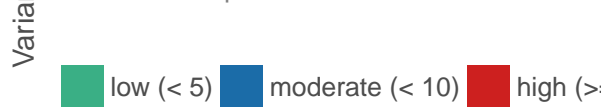
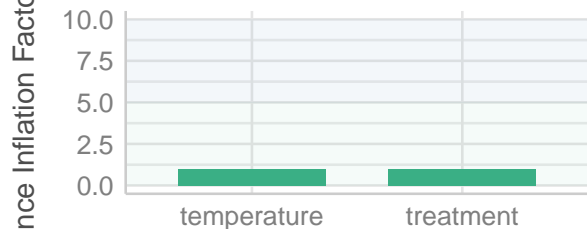
Homogeneity of Variance

Reference line should be flat and horizontal



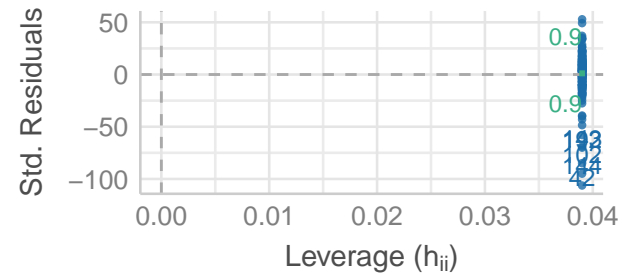
Collinearity

Higher bars (>5) indicate potential collinearity issue



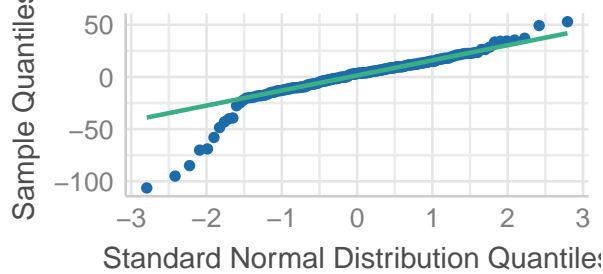
Influential Observations

Points should be inside the contour lines



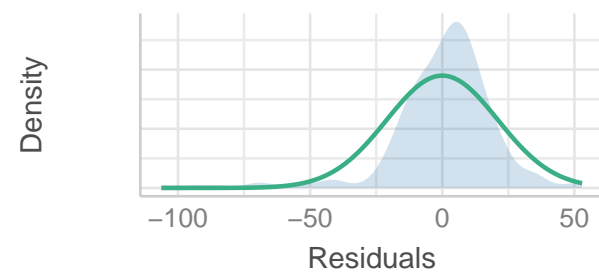
Normality of Residuals

Dots should fall along the line



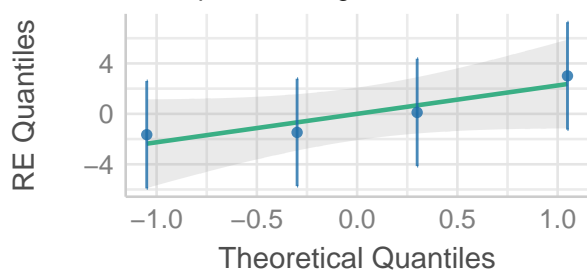
Normality of Residuals

Distribution should be close to the normal curve



Normality of Random Effects (run)

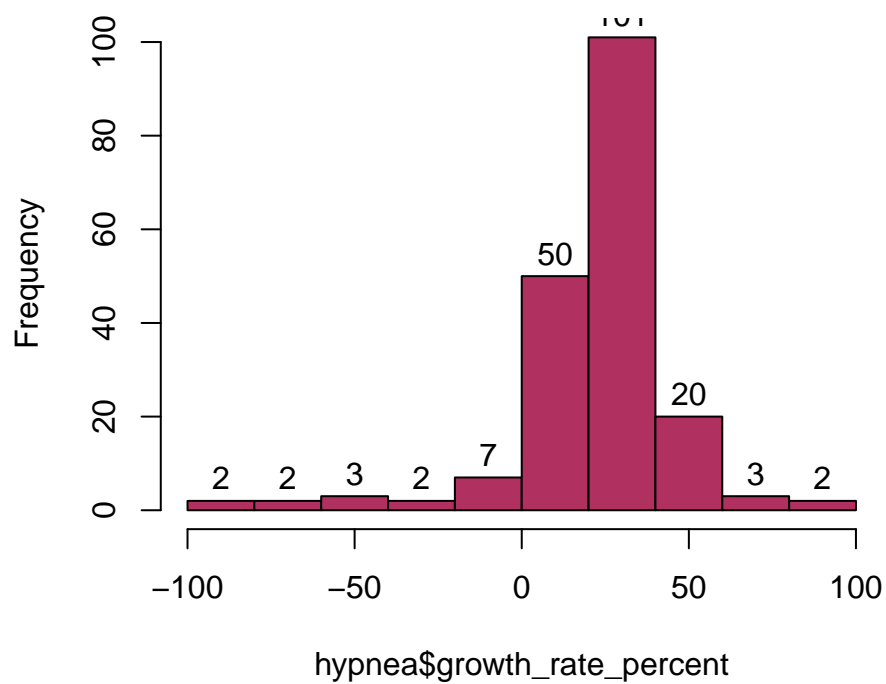
Dots should be plotted along the line



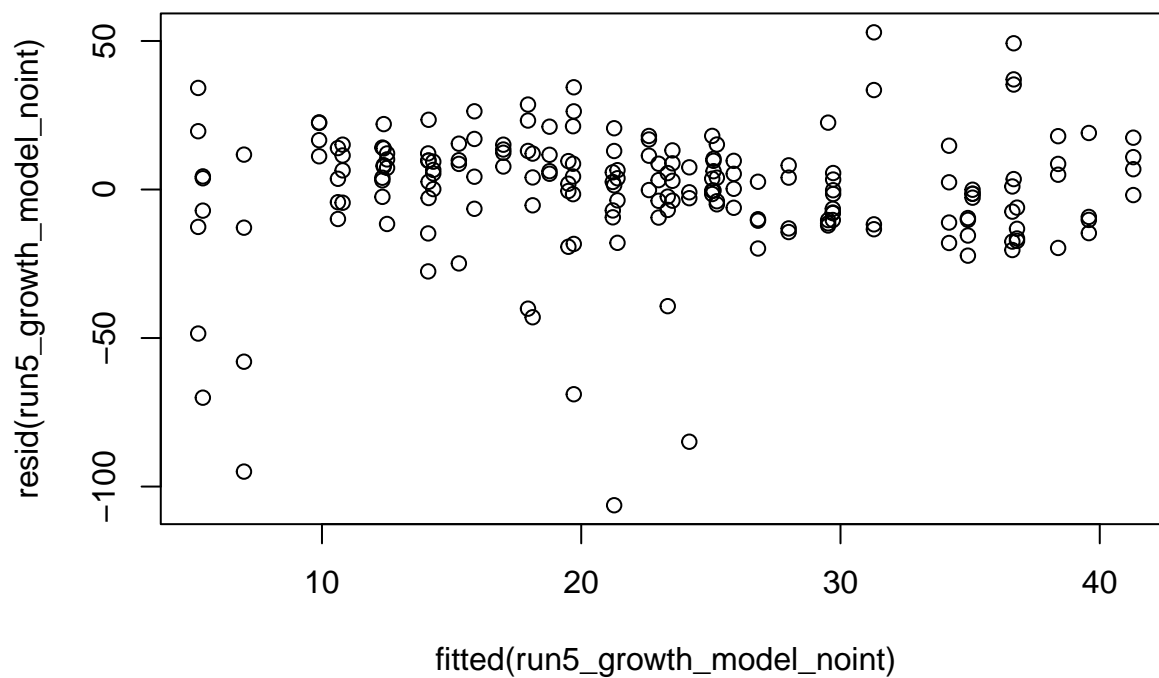
These outputs show the model is acceptable for the data

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

Hypnea musciformis Growth Rate (%)

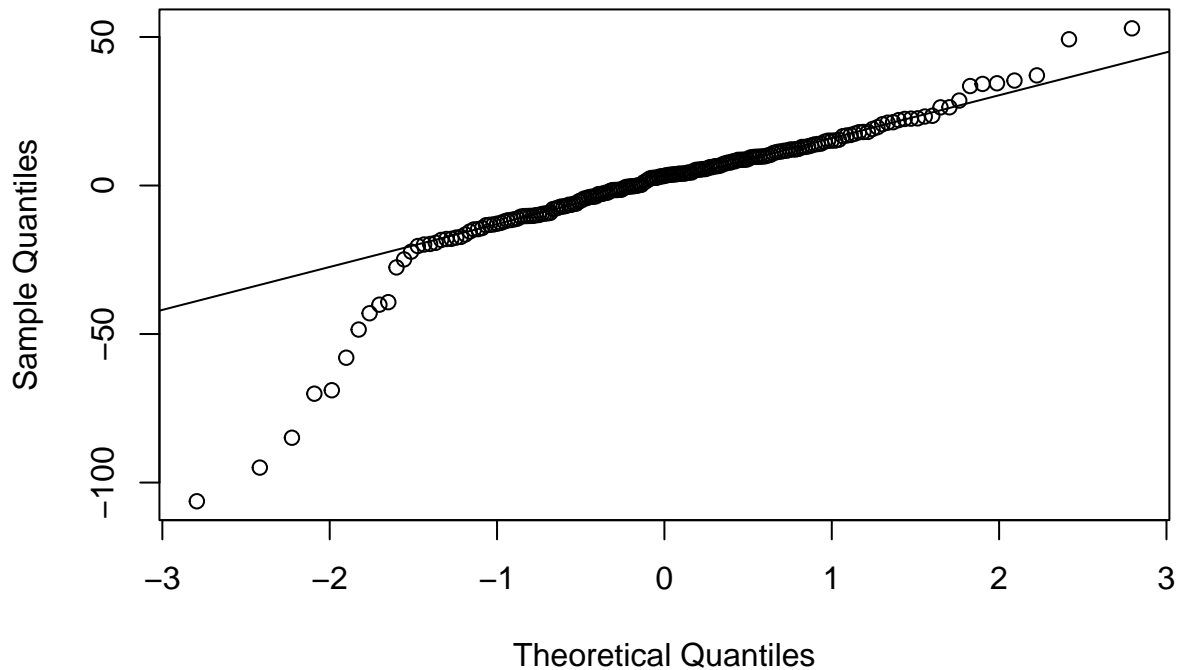


```
plot(resid(run5_growth_model_noint) ~ fitted(run5_growth_model_noint))
```



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

Normal Q-Q Plot



```
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
```

```
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
```

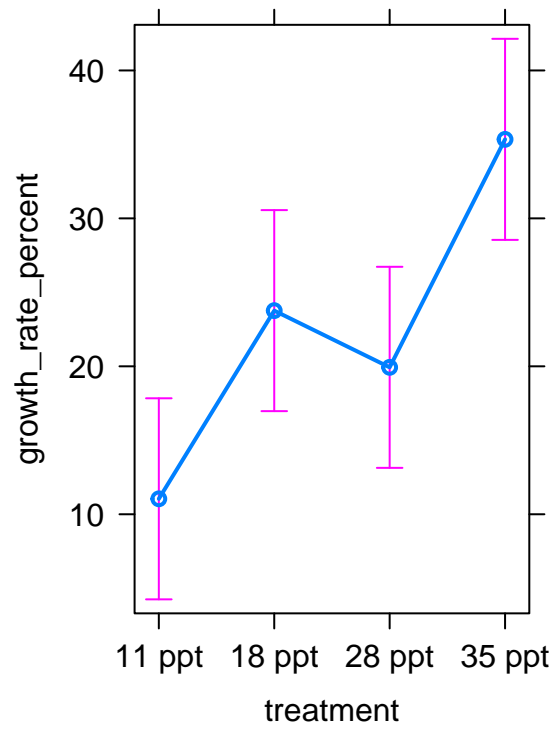
```
summary(run5_growth_model_noint)
```

```
## 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

