

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

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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("/Users/Angela/Library/Mobile Documents/com~apple~CloudDocs/research_limu/run5_1")
```

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
```

Make a new column that keeps only the numerical values for temperature (removes C)

```
run5_growth$temp_clean <- as.factor(substr(run5_growth$temperature, 1, 2))
```

## Change levels to factors

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

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

```
#assign run as a factor
```

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

## Create subset of the data to isolate the species

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

## Run the model

### ULVA

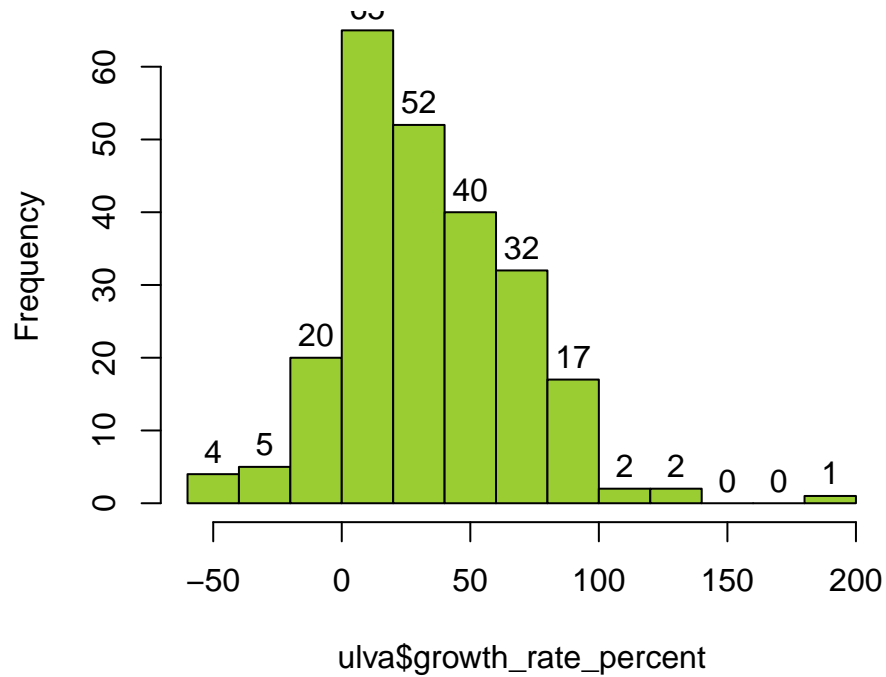
run model without interaction since interaction caused collinearity issues

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

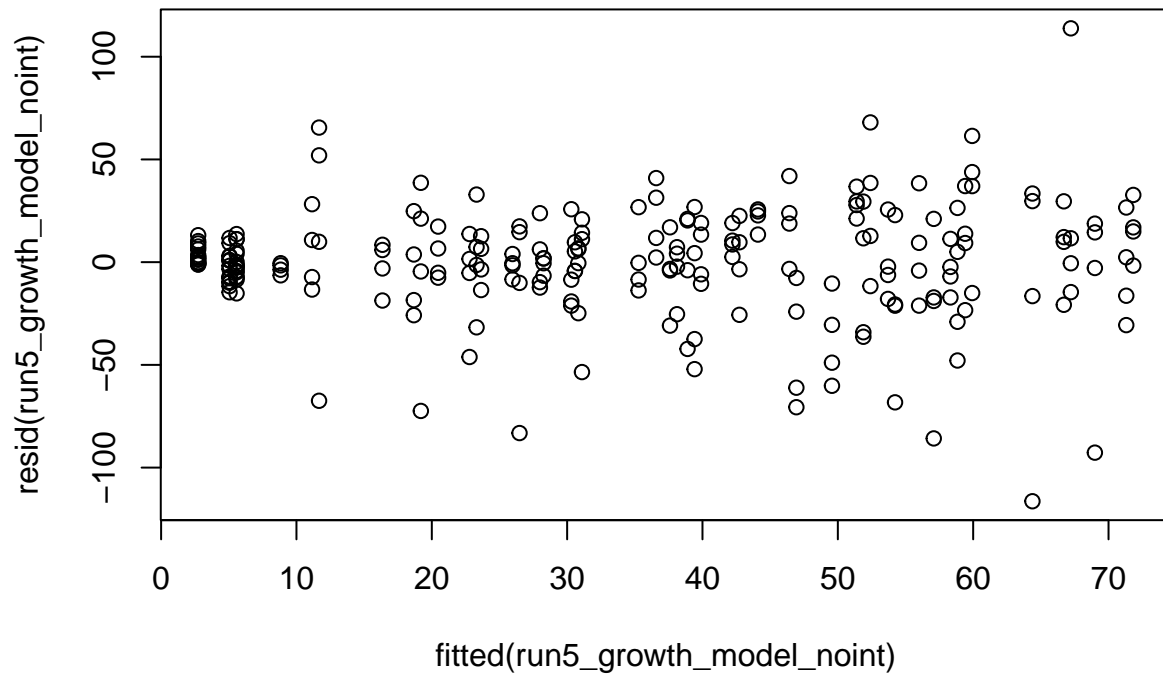
```
#make a histogram of the data for Ulva
```

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

## Ulva lactuca Growth Rate (%)

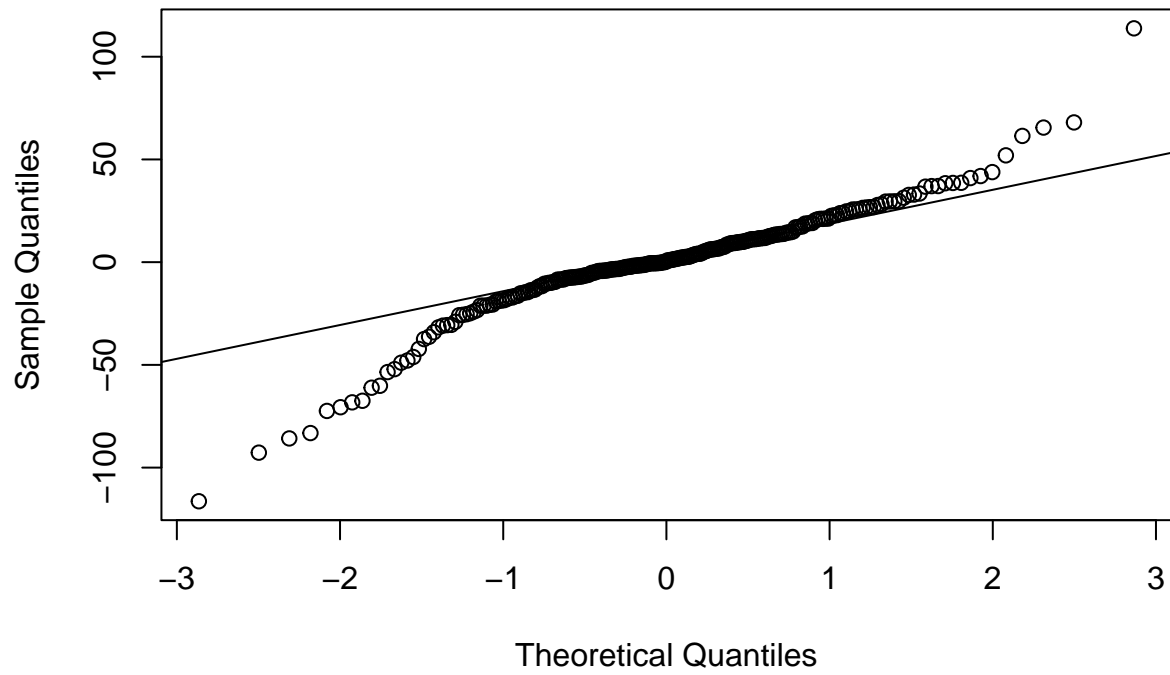


```
plot(resid(run5_growth_model_noint) ~ fitted(run5_growth_model_noint))
```



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

Normal Q-Q Plot

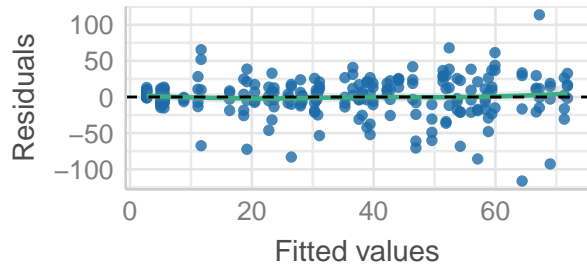


Check the performance of the model for Ulva

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

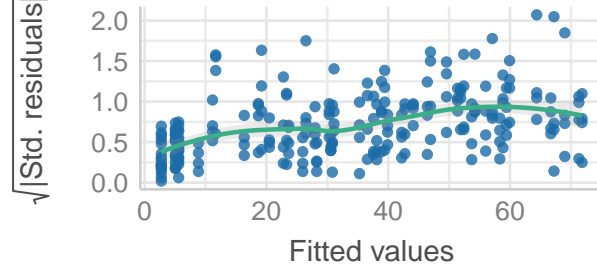
### Linearity

Reference line should be flat and horizontal



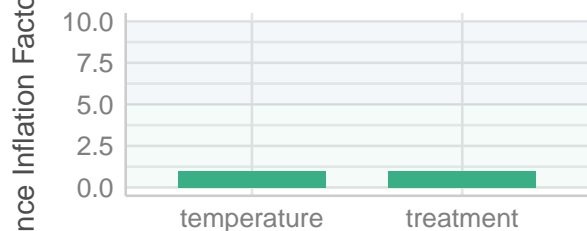
### Homogeneity of Variance

Reference line should be flat and horizontal



### Collinearity

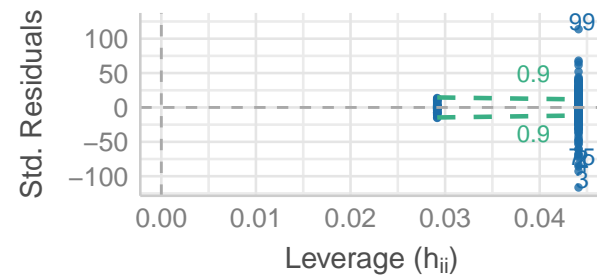
Higher bars (>5) indicate potential collinearity issue



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

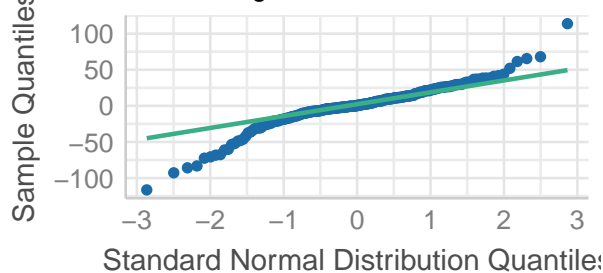
### Influential Observations

Points should be inside the contour lines



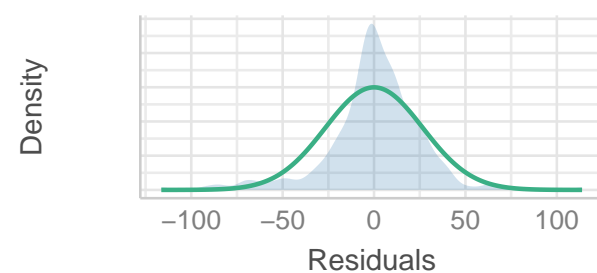
### Normality of Residuals

Dots should fall along the line



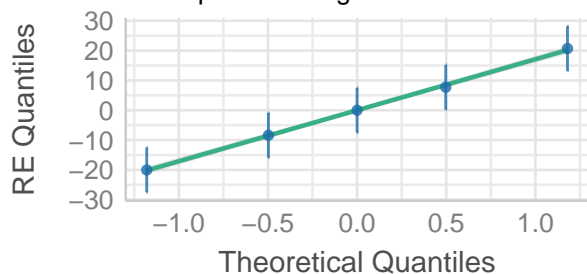
### Normality of Residuals

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

## Run ANOVA and Tukey's comparison

```
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  12681.6   3170.4     4     5.948   4.3074 0.05622 .
## temperature   365.4    182.7     2  230.000   0.2482 0.78042
## ---
## 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
## 1-0 26.122972  8.891291 43.35465 0.0004144
## 2-0 33.643252 16.411571 50.87493 0.0000019
## 3-0 40.933674 23.701993 58.16536 0.0000000
## 4-0 45.547350 28.315668 62.77903 0.0000000
## 2-1  7.520280 -9.711401 24.75196 0.7514921
## 3-1 14.810702 -2.420979 32.04238 0.1293111
## 4-1 19.424377  2.192696 36.65606 0.0183743
## 3-2  7.290422 -9.941259 24.52210 0.7723133
## 4-2 11.904098 -5.327584 29.13578 0.3206085
## 4-3  4.613675 -12.618006 21.84536 0.9478415
```

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

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

```
##           R2m           R2c
## [1,] 0.1953667 0.4468454
```

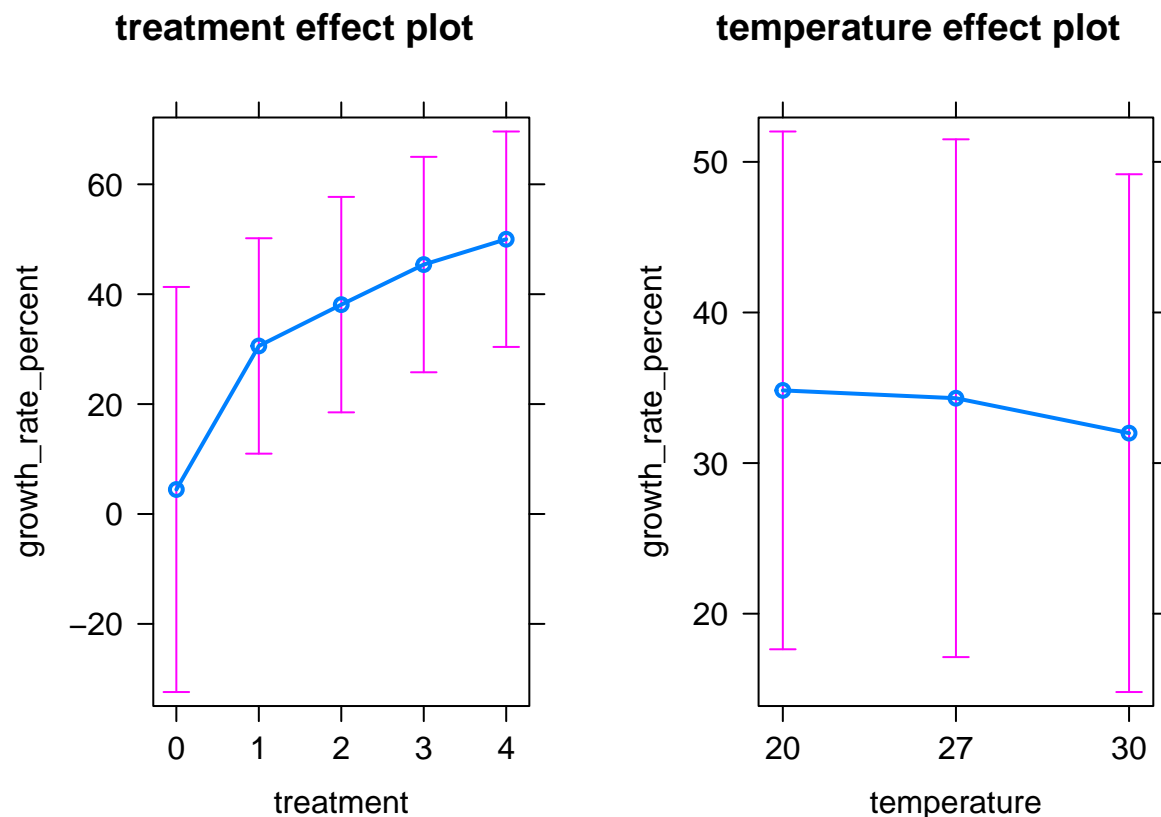
```
summary(run5_growth_model_noint)
```

```
## 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: 2235.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.2897 -0.3236  0.0169  0.4944  4.1949
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## run      (Intercept)    334.6      18.29
## Residual                    736.0      27.13
```

```
## Number of obs: 240, groups: run, 5
##
## Fixed effects:
##           Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   5.5765   18.8703    3.1061   0.296   0.786
## treatment1    26.1230   21.1882    3.1598   1.233   0.301
## treatment2    33.6433   21.1882    3.1598   1.588   0.206
## treatment3    40.9337   21.1882    3.1598   1.932   0.144
## treatment4    45.5473   21.1882    3.1598   2.150   0.116
## temperature27  -0.5186    4.2896  230.0000  -0.121   0.904
## temperature30  -2.8378    4.2896  230.0000  -0.662   0.509
##
## Correlation of Fixed Effects:
##           (Intr) trtmn1 trtmn2 trtmn3 trtmn4 tmpr27
## treatment1  -0.875
## treatment2  -0.875  0.966
## treatment3  -0.875  0.966  0.966
## treatment4  -0.875  0.966  0.966  0.966
## temperatur27 -0.114  0.000  0.000  0.000  0.000
## temperatur30 -0.114  0.000  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)
```

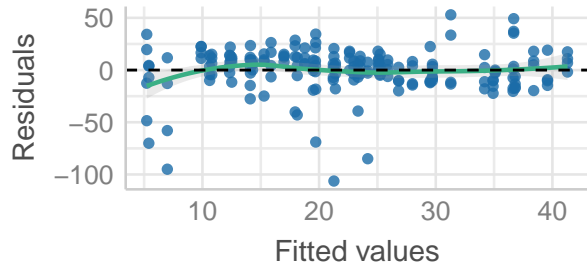
Check the performance of the model for Hypnea

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



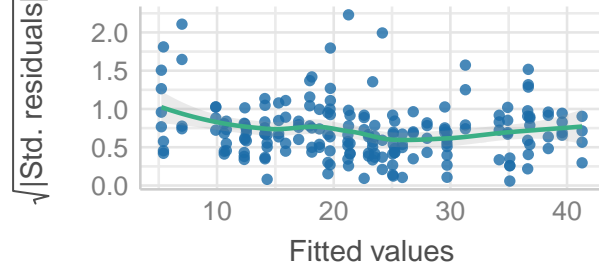
### Linearity

Reference line should be flat and horizontal



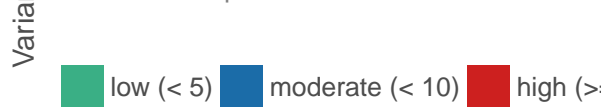
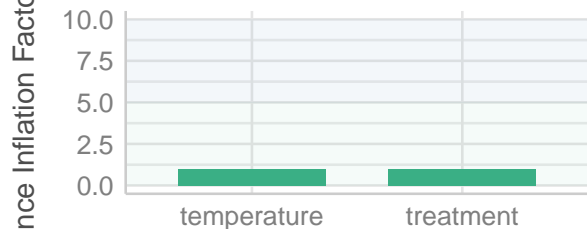
### Homogeneity of Variance

Reference line should be flat and horizontal



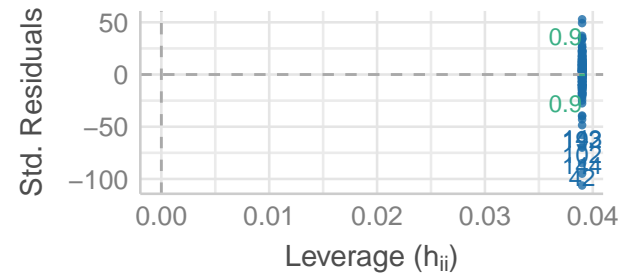
### Collinearity

Higher bars (>5) indicate potential collinearity issue



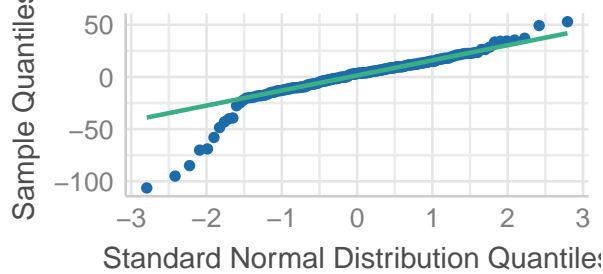
### Influential Observations

Points should be inside the contour lines



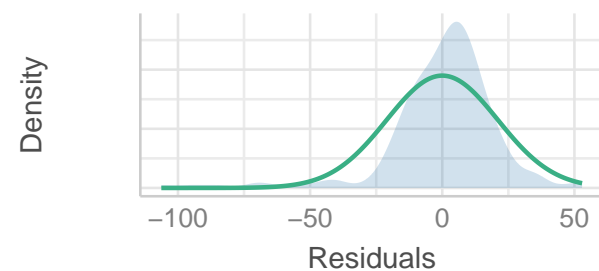
### Normality of Residuals

Dots should fall along the line



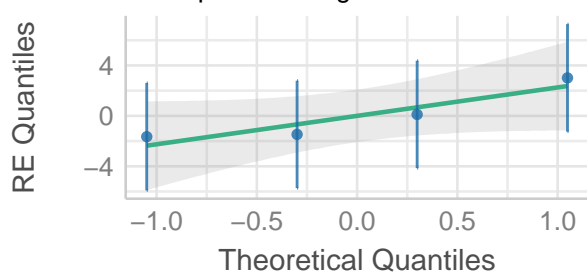
### Normality of Residuals

Distribution should be close to the normal curve



### Normality of Random Effects (run)

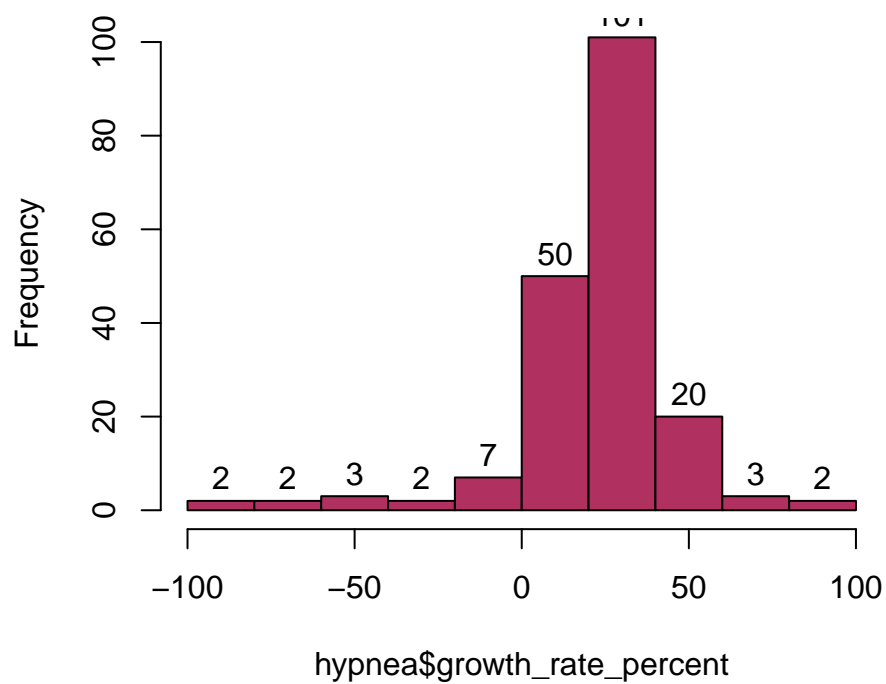
Dots should be plotted along the line



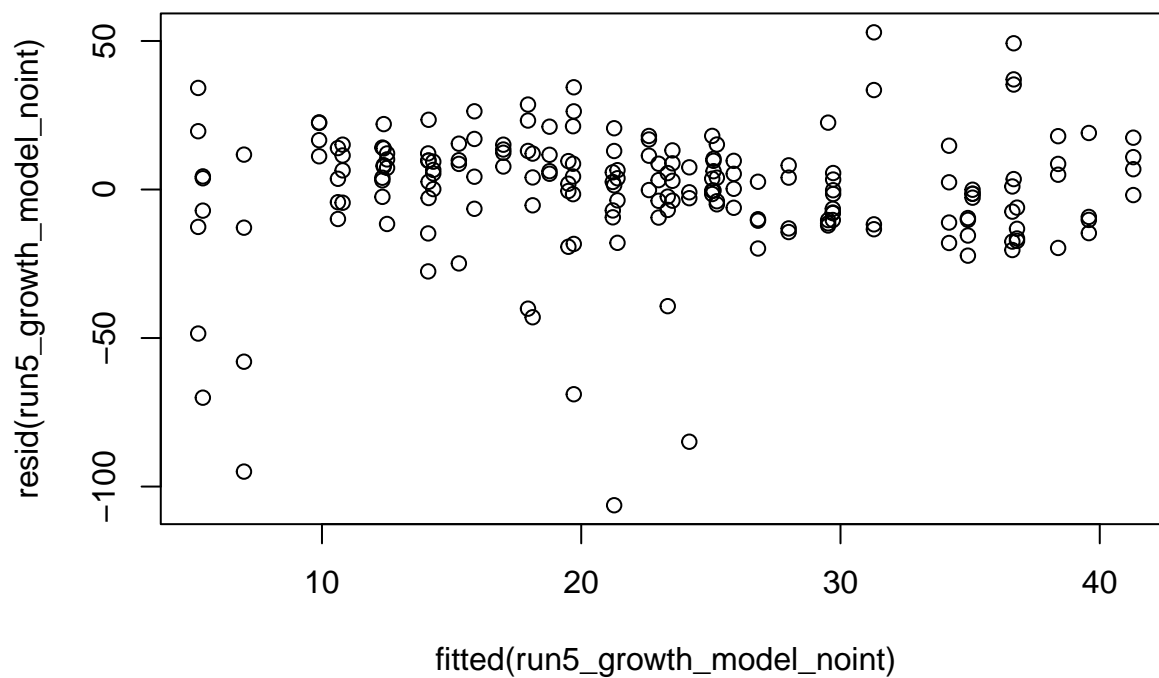
These outputs show the model is acceptable for the data

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

## Hypnea musciformis Growth Rate (%)

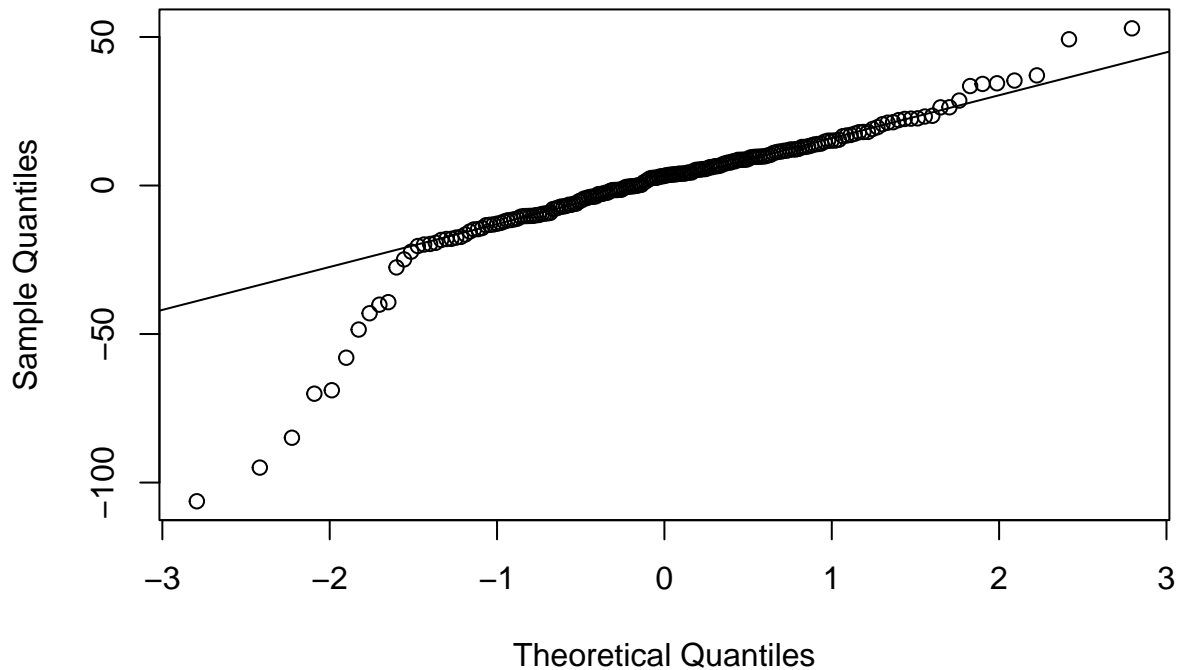


```
plot(resid(run5_growth_model_noint) ~ fitted(run5_growth_model_noint))
```



```
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
## 2-1 -15.410092 -26.810063 -4.0101220 0.0031917
## 3-1 -11.576913 -22.976883 -0.1769428 0.0450335
## 4-1 -24.297854 -35.697825 -12.8978839 0.0000007
## 3-2  3.833179 -7.566791 15.2331495 0.8194889
## 4-2 -8.887762 -20.287732 2.5122084 0.1839285
## 4-3 -12.720941 -24.120911 -1.3209708 0.0220255
```

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

```
##           R2m           R2c
## [1,] 0.1552732 0.1722819
```

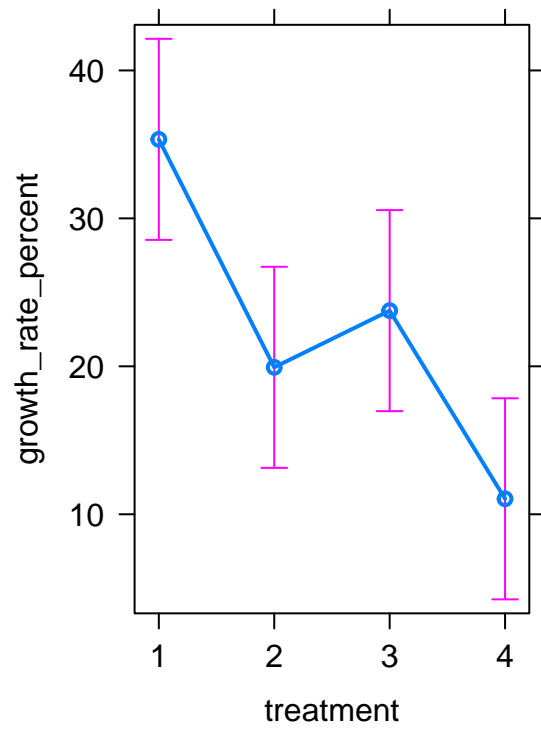
```
summary(run5_growth_model_noint)
```

```
## 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) 36.567 4.077 33.620 8.969 1.94e-10 ***
## treatment2 -15.410 4.363 183.000 -3.532 0.000522 ***
## treatment3 -11.577 4.363 183.000 -2.654 0.008667 **
## treatment4 -24.298 4.363 183.000 -5.569 9.02e-08 ***
## temperature27 1.714 3.778 183.000 0.454 0.650624
## temperature30 -5.391 3.778 183.000 -1.427 0.155331
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) trtmn2 trtmn3 trtmn4 tmpr27
## treatment2 -0.535
## treatment3 -0.535 0.500
## treatment4 -0.535 0.500 0.500
## temperatur27 -0.463 0.000 0.000 0.000
## temperatur30 -0.463 0.000 0.000 0.000 0.500
```

## Effects Plots

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

**treatment effect plot**



**temperature effect plot**

