total_tube_growth_results

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25/11/2021

```
library(mgcv)
library(fitdistrplus)
library(goft)
library(gamlss)
library(here)
library(patchwork)
library(LambertW)
library(scales)
library(viridis)
library(performance)
library(dplyr)
library(tidyverse)
library(readr)

# import data set
tube_growth <- read_csv("tube-growth.csv")
```

Load required libraries and data set

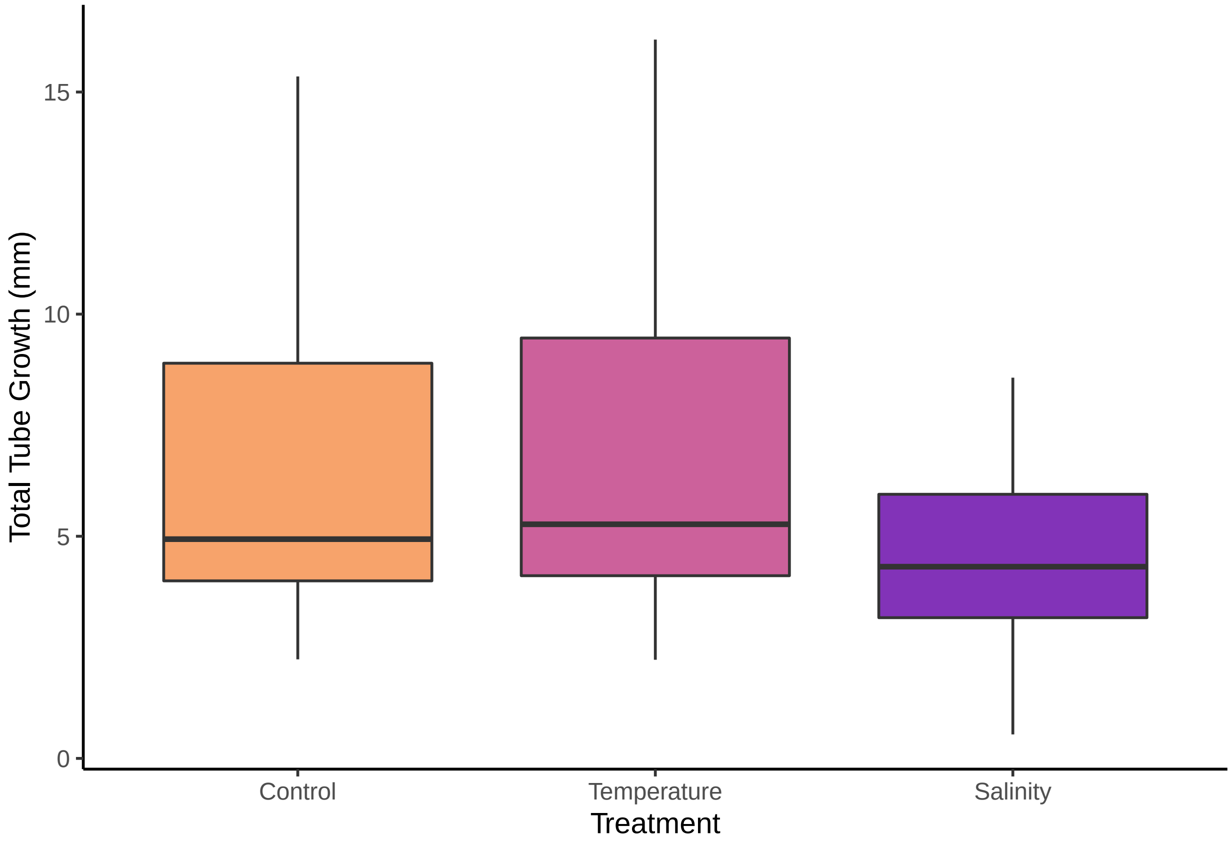
```
# Manipulated data for intial visualization
clean_growth <- tube_growth %>%
select(total_growth, treatment)

# Manipulated data for GAMLSS Model (Important note; Could not get the model to run using worm_id and s
model_growth <- tube_growth %>%
  dplyr::select(c(treatment,total_growth,mortality, amt_cut_mm, worm_id)) %>%
  mutate(worm_id = as.factor(worm_id))
```

Cleaning Data Sheet

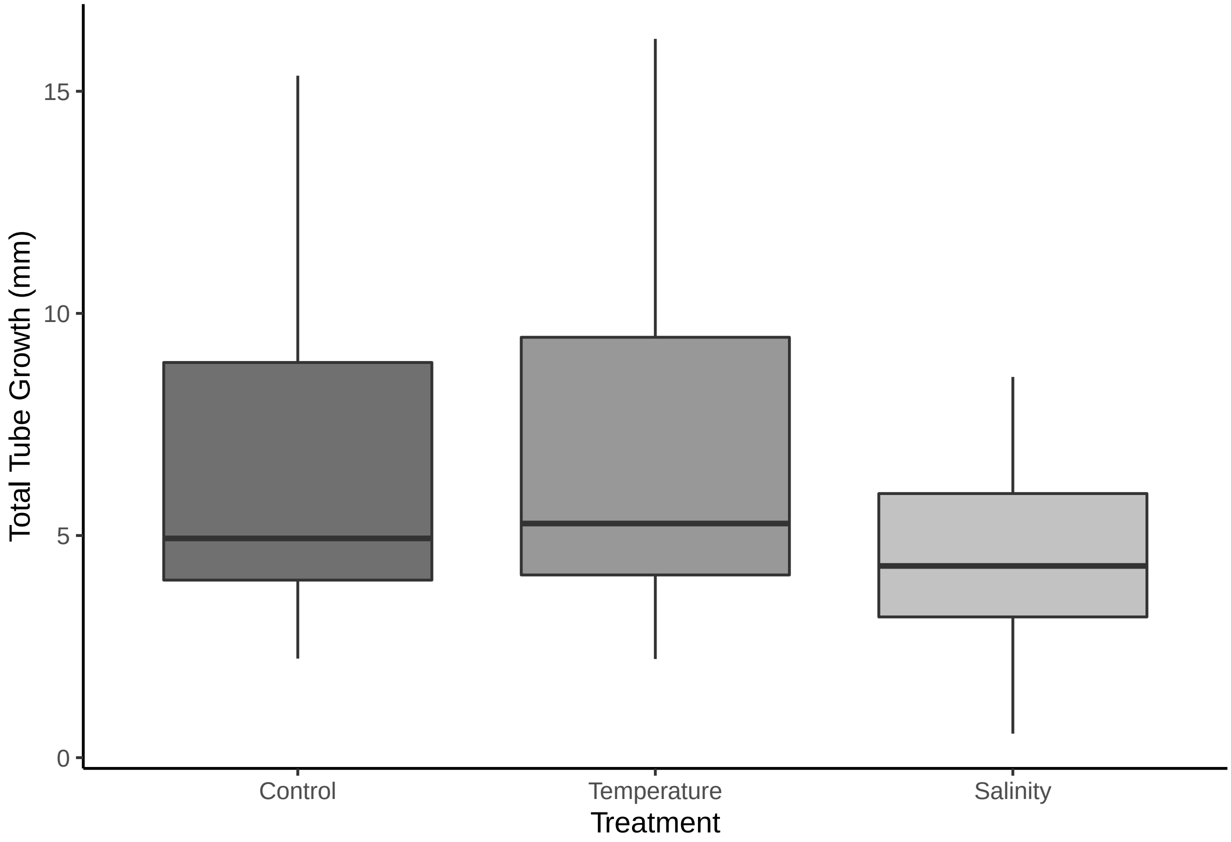
Visualizing Total Tube Growth Data with a boxplot

```
#colour version
my_cols = c("low_salinity" = "#6300A7FF", "high_temp" = "#C03A83FF", "control" = "#F58C46FF")
```

```
ggplot(clean_growth, aes(x = treatment, y = total_growth, fill = treatment)) +
  geom_boxplot(alpha = 0.8) +
  theme_classic() +
  ylab("Total Tube Growth (mm)") +
  xlab("Treatment") +
  scale_fill_manual(values = my_cols) +
  scale_colour_manual(values = my_cols) +
  theme(legend.position="none") +
  scale_x_discrete(labels = c('Control','Temperature','Salinity'))
```



```
ggsave(plot = last_plot(), filename = "total_tube_growth_boxplot_colourized.pdf")

#grey scale version
my_cols_grey = c("low_salinity" = "grey70", "high_temp" = "grey50", "control" = "grey30")
ggplot(clean_growth, aes(x = treatment, y = total_growth, fill = treatment)) +
  geom_boxplot(alpha = 0.8) +
  theme_classic() +
  ylab("Total Tube Growth (mm)") +
  xlab("Treatment") +
  scale_fill_manual(values = my_cols_grey) +
  scale_colour_manual(values = my_cols_grey) +
  theme(legend.position="none") +
  scale_x_discrete(labels = c('Control','Temperature','Salinity'))
```



```
ggsave(plot = last_plot(), filename = "total_tube_growth_boxplot_greyscale.pdf")
```

Finding Mean Values for Each Treatment

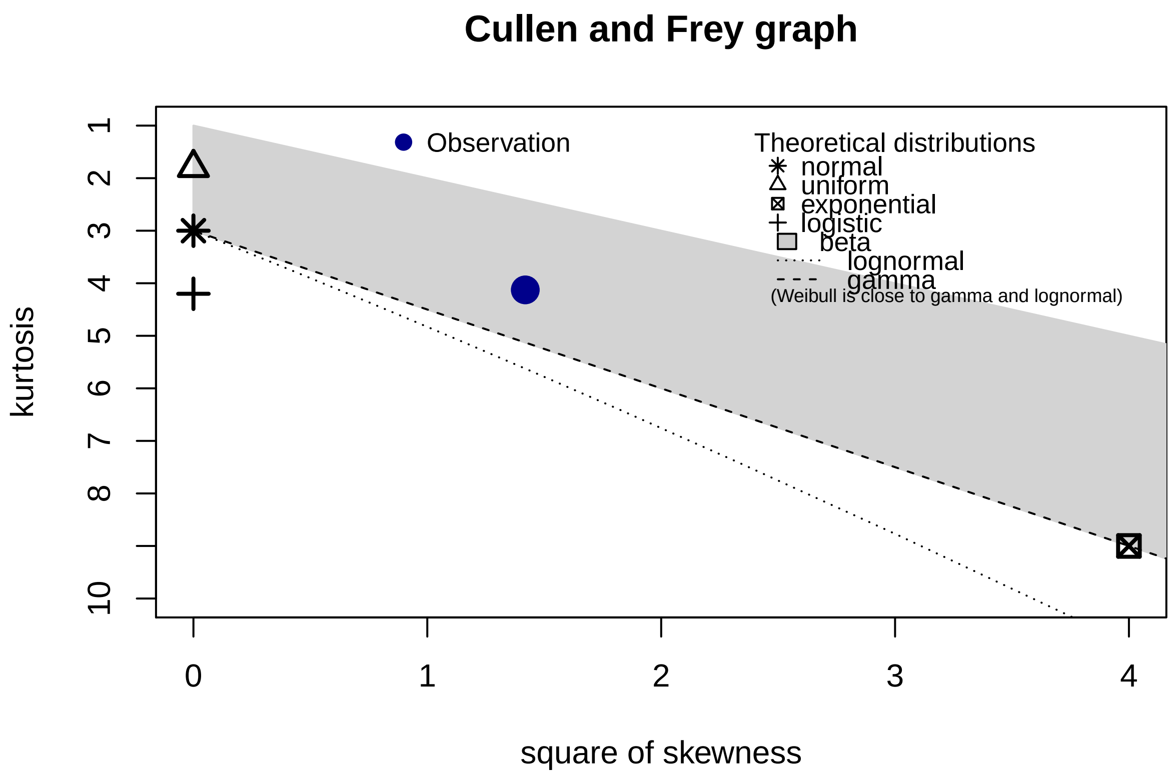
```
mean_growth <- clean_growth %>%
group_by(treatment) %>%
summarise_at(vars(total_growth), list(mean = mean))
```

Checking Distributions For Normality

```
# Original

shapiro.test(clean_growth$total_growth) # P value = 2.292e-06
```

```
##
##  Shapiro-Wilk normality test
##
## data:  clean_growth$total_growth
## W = 0.89439, p-value = 2.292e-06
```

```
descdist(clean_growth$total_growth)
```



```
## summary statistics
## ------
## min:  0.54   max:  16.18 
## median:  4.92 
## mean:  5.879944 
## estimated sd:  3.207908 
## estimated skewness:  1.191188 
## estimated kurtosis:  4.126008
```

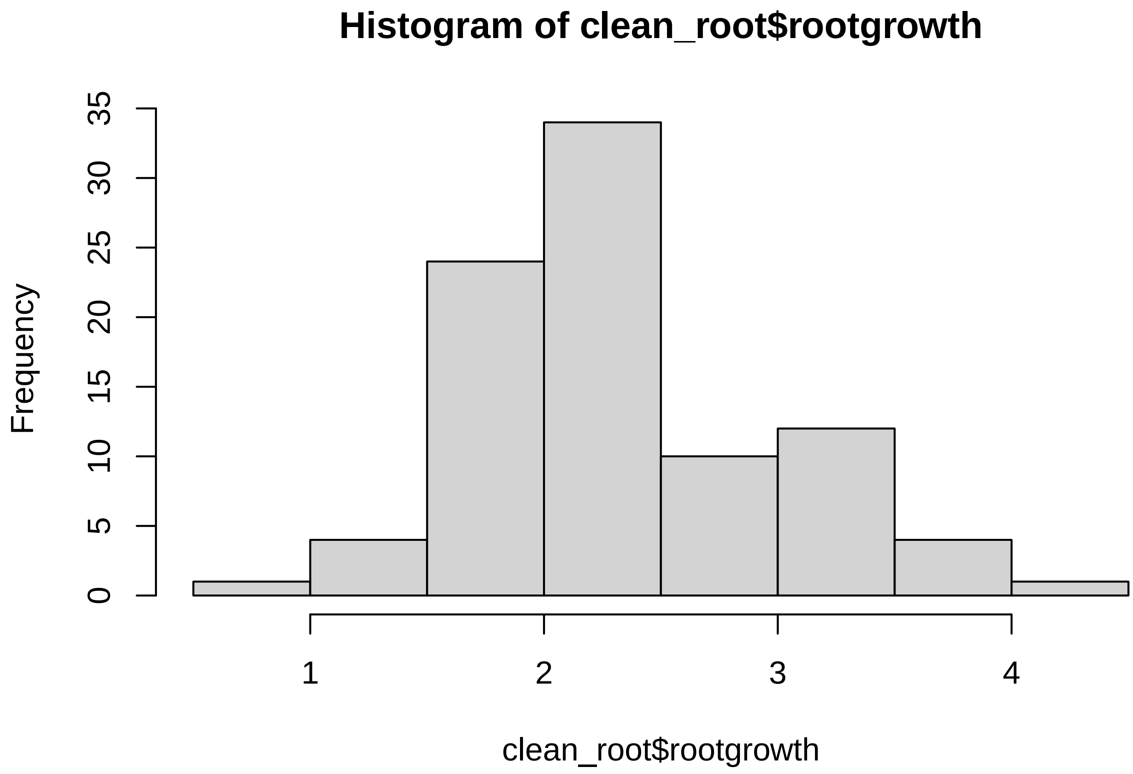
```
# trying log transform

clean_log <- clean_growth %>%
  mutate(loggrowth = log2(total_growth))
shapiro.test(clean_log$loggrowth) # P value 0.006626
```

```
## 
##  Shapiro-Wilk normality test
## 
## data:  clean_log$loggrowth
## W = 0.95936, p-value = 0.006626
```

```
# trying to square root transform

clean_root <- clean_growth %>%
  mutate(rootgrowth = sqrt(total_growth))
shapiro.test(clean_root$rootgrowth) # P value = 0.008449
```

```
##
##  Shapiro-Wilk normality test
##
## data:  clean_root$rootgrowth
## W = 0.96095, p-value = 0.008449
```

```
# All attempts show our data varies significantly from normal, now trying fist dist function to find th

hist(clean_root$rootgrowth)
```



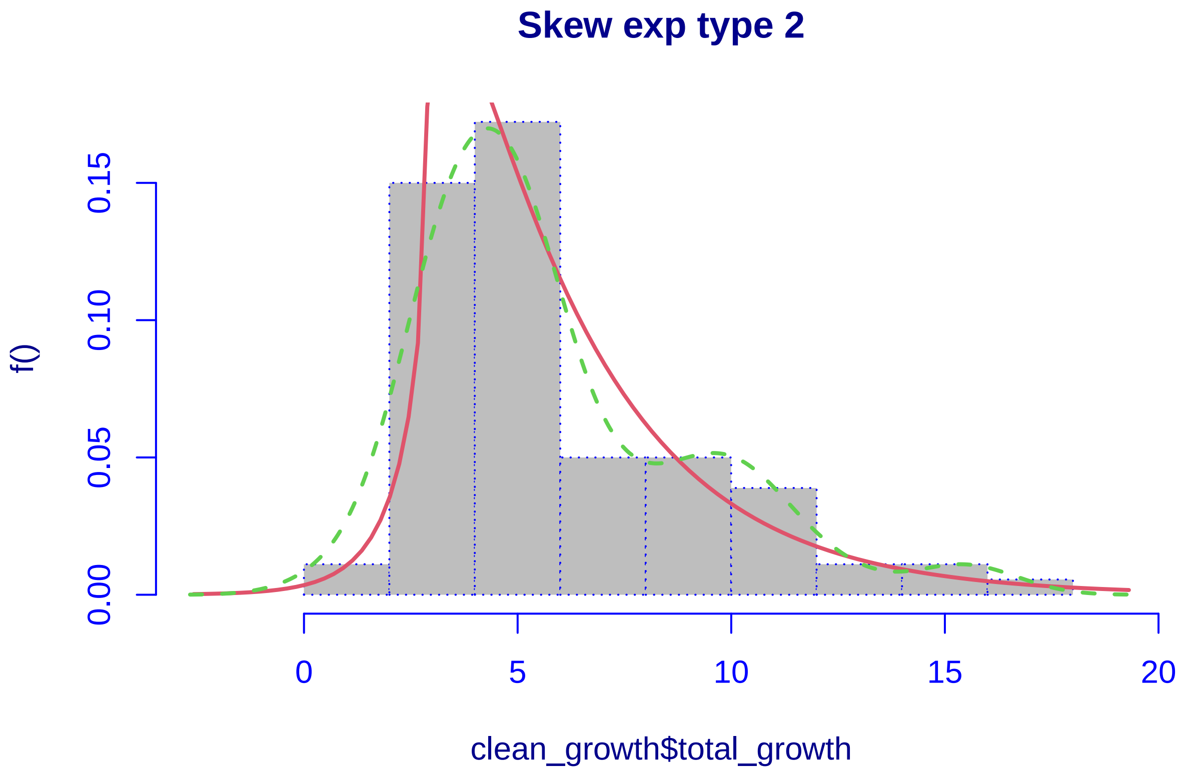
```
fitDist(rootgrowth, data = clean_root, type = "realAll", try.gamlss = T)
```

```
##   |                                                                              |
## Call:  gamlssML(formula = y, family = DIST[i])
##
## Mu Coefficients:
## [1]  1.728
## Sigma Coefficients:
## [1]  -0.2874
## Nu Coefficients:
## [1]  1.427
## Tau Coefficients:
## [1]  0.2958
##
##  Degrees of Freedom for the fit: 4 Residual Deg. of Freedom   86
## Global Deviance:     161.898
##             AIC:     169.898
##             SBC:     179.897
```

```
fitDist(total_growth, data = clean_growth, type = "realAll", try.gamlss = T)
```

```
##   |                                                                              |
```

```
### Both show the best distribution is Skew Exponential Power type 2

mSEP2 <- histDist(clean_growth$total_growth, "SEP2", density = T, main = "Skew exp type 2")
```



```
# Running a Gamlss Model

gamlss.mod <- gamlss(total_growth ~ treatment + amt_cut_mm + mortality,
               family = SEP2(),
               data = model_growth,
               control = gamlss.control(n.cyc = 25))
```

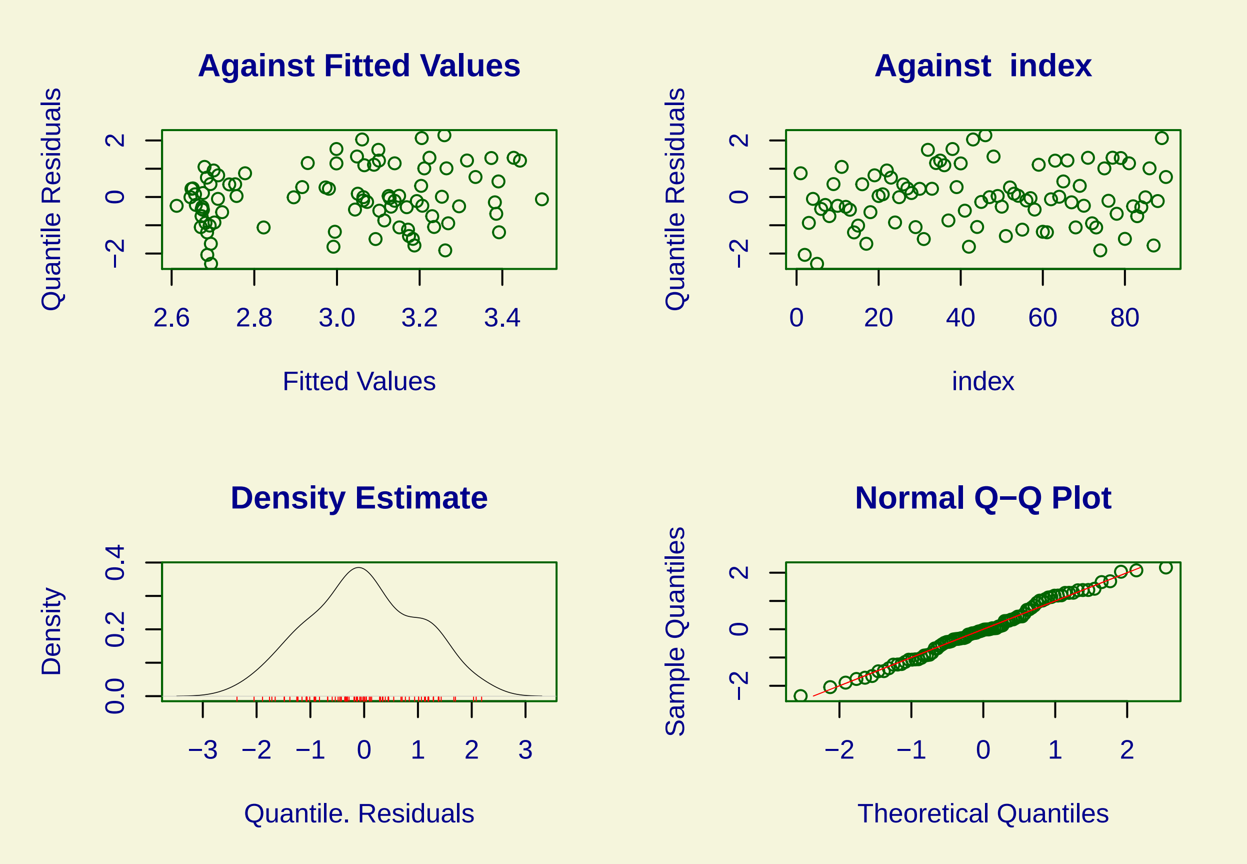
Modelling

```
## GAMLSS-RS iteration 1: Global Deviance = 453.4377
## GAMLSS-RS iteration 2: Global Deviance = 453.1597
## GAMLSS-RS iteration 3: Global Deviance = 452.7278
## GAMLSS-RS iteration 4: Global Deviance = 452.0642
## GAMLSS-RS iteration 5: Global Deviance = 450.5416
## GAMLSS-RS iteration 6: Global Deviance = 446.3317
## GAMLSS-RS iteration 7: Global Deviance = 440.7388
## GAMLSS-RS iteration 8: Global Deviance = 436.1565
## GAMLSS-RS iteration 9: Global Deviance = 434.69
## GAMLSS-RS iteration 10: Global Deviance = 434.5907
## GAMLSS-RS iteration 11: Global Deviance = 431.9027
## GAMLSS-RS iteration 12: Global Deviance = 431.7732
## GAMLSS-RS iteration 13: Global Deviance = 431.7615
## GAMLSS-RS iteration 14: Global Deviance = 431.7486
## GAMLSS-RS iteration 15: Global Deviance = 431.7276
## GAMLSS-RS iteration 16: Global Deviance = 430.3352
## GAMLSS-RS iteration 17: Global Deviance = 429.6759
## GAMLSS-RS iteration 18: Global Deviance = 429.2198
## GAMLSS-RS iteration 19: Global Deviance = 429.195
## GAMLSS-RS iteration 20: Global Deviance = 429.1835
## GAMLSS-RS iteration 21: Global Deviance = 429.1772
## GAMLSS-RS iteration 22: Global Deviance = 429.1733
## GAMLSS-RS iteration 23: Global Deviance = 429.1709
## GAMLSS-RS iteration 24: Global Deviance = 429.169
## GAMLSS-RS iteration 25: Global Deviance = 429.1683
```

```
# ran after 25 iterations when we removed worm_id as a random effect as per Dans advice

# Checking model

summary(gamlss.mod)
```

```
## ******************************************************************
## Family:  c("SEP2", "Skew Exponential Power type 2")
##
## Call:  gamlss(formula = total_growth ~ treatment + amt_cut_mm +
##     mortality, family = SEP2(), data = model_growth,
##     control = gamlss.control(n.cyc = 25))
##
## Fitting method: RS()
##
## ------------------------------------------------------------------
## Mu link function:  identity
## Mu Coefficients:
##                        Estimate Std. Error t value Pr(>|t|)
## (Intercept)             2.53051    3.19413   0.792    0.431
## treatmenthigh_temp     -0.22516    0.57646  -0.391    0.697
## treatmentlow_salinity -0.58452    0.48038  -1.217    0.227
## amt_cut_mm              0.04937    0.18162   0.272    0.786
## mortality              -0.47564    0.86336  -0.551    0.583
##
## ------------------------------------------------------------------
## Sigma link function:  log
## Sigma Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.1062     0.1435   7.706 2.66e-11 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## ------------------------------------------------------------------
## Nu link function:  identity
## Nu Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.3141     0.3875   3.391  0.00107 **
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## ------------------------------------------------------------------
## Tau link function:  log
## Tau Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.009221   0.187175  -0.049    0.961
##
## ------------------------------------------------------------------
## No. of observations in the fit:  90
## Degrees of Freedom for the fit:  8
##       Residual Deg. of Freedom:  82
##                       at cycle:  25
##
## Global Deviance:     429.1683
##             AIC:     445.1683
##             SBC:     465.1668
## ******************************************************************
```

```
plot(gamlss.mod)
```



```
## ******************************************************************
##        Summary of the Quantile Residuals
##                            mean   =  -0.008825433
##                        variance   =  1.044282
##                coef. of skewness  =  0.01144696
##                coef. of kurtosis  =  2.371234
## Filliben correlation coefficient  =  0.9951015
## ******************************************************************
```

```
residuals(gamlss.mod)
```

```
##  [1]  0.838960862 -2.047339013 -0.916710769 -0.067464758 -2.364455626
##  [6] -0.422950781 -0.281456827 -0.677165248  0.455626250 -0.312873678
## [11]  1.064725857 -0.349493941 -0.452182053 -1.252259762 -1.012323587
## [16]  0.449801457 -1.654619011 -0.536965177  0.766453321  0.034539369
## [21]  0.095120663  0.938065669  0.683733039 -0.901385708 -0.007972099
## [26]  0.445195612  0.303373896  0.139121611 -1.066117676  0.288316415
## [31] -1.488011156  1.667333949  0.290758974  1.200868837  1.287646114
## [36]  1.122586402 -0.830306879  1.697027090  0.349462926  1.187410707
## [41] -0.484304664 -1.759936020  2.034002880 -1.061255026 -0.175730681
## [46]  2.183857071 -0.007199967  1.431848792  0.035371520 -0.342589088
## [51] -1.381315876  0.337992601  0.115772439  0.041008263 -1.155764022
## [56] -0.122999227 -0.040834372 -0.445376254  1.139933093 -1.230697496
## [61] -1.248460965 -0.081508799  1.285579078  0.008589324  0.550034181
## [66]  1.290809698 -0.188914759 -1.076372566  0.393228763 -0.310015635
## [71]  1.386082658 -0.931032063 -1.077950260 -1.889465248  1.011927085
## [76] -0.134408652  1.388776962 -0.594228105  1.378184718 -1.481703121
## [81]  1.191151024 -0.329595938 -0.679137247 -0.362066468 -0.011803696
## [86]  1.013277669 -1.715732592 -0.144736767  2.082785294  0.706558254
```