Introduction:
Orange is a small data set in the nlme package in R consisting of measurements of the growth of orange trees including their 'circumference' and 'age' and the identification number of the 'tree'. The aims of this analysis is to determine how the circumference (response variable) depends on the age (explanatory variable) of the tree.

Methodology:
First the orange data set was imported from the nlme package in R. Then the data was analysed and this consisted of creating a brief summary of the data ensuring no outliers or data entry errors were present. This was supported by a scatter plot of circumference against age and a line graph showing the differences in circumference between the different trees. With no apparent outliers and a visible linear trend in the data a linear model was fitted plotting circumference against age. From here the model was analysed via the summary statistics (p-value of age) and the Adjusted R-squared value as well as a residuals vs fitted values plot, Normal Q-Q plot, and a histogram of residuals. To improve the model two new modelling approaches were compared, gls and lme. Both plotted circumference against age however the lme had a random effects structure that meant the intercept and slope for age vary randomly across trees. Also due to the data not being able to converge for the lme model due to the small size and the variance in the data a weighted structure was applied to the lme model. Due to continuous errors with multiple variance structures only one was used for the lme data.

Because of this the gls was created and then a number of variance structures were applied to determine the best fit. These gls models were compared using anova tests where the smallest AIC value was picked when the models were significantly different and when they weren't the simpler model (less parameters) was picked. The best gls model with a variance structure was compared to the lme and the lme was significantly better. From here three different correlation structures were applied to the lme model and using anova the final model was the lme with a variance power structure and no correlation structure.

Analysing the quality of the final model a standardized residual vs fitted values plot was generated, a histogram of the residuals, a normal Q-Q plot, and summary statistics were generated such as the significance levels of the intercept and age as well as the AIC, BIC, and log likelihood values.

Results:
Based on the methodology the final model selected was circumference(ij) = 17.1 + 0.107*age(ij) + b0(i) + b1(i) * age + e(ij). In this equation b0 and b1 are the random effects representing the deviations of the intercept and slope for the ith tree, also j represents the jth time point. The random intercept has a standard deviation of 1.890 and the random slope has a standard deviation of 0.0239. The intercept is not correlated with any other random effect while age is negatively correlated with the intercept with a correlation coefficient of -0.999. The standard deviations appear to be quite small implying that there is some variance between the response variable, circumference, across the different trees in the dataset which is not accounted for by the fixed effects age but it is not a lot. When looking at the fixed effects both the intercept and the age have extremely small p-values much smaller then the significance level of 0.05.

The standardised residuals vs fitted values graph shows that the majority of the points sit between 1 and -2, a small range implying an ideal fit due to a lack of variation in residuals. The histogram of residuals resembles a normal distribution and combining this with the Q-Q plot (figure 1) it can be seen that the tails tend to drag on. The model has a relatively low AIC value of 289 and relatively low BIC value of 299 and a relatively high log likelihood value of -137.

Discussion:
Based on the analysis performed in this study a positive significant final model was found: circumference(ij) = 17.1 + 0.107*age(ij) + b0(i) + b1(i) * age + e(ij). Based on the results that the fixed effects were significant the conclusion can be reached that age has a statistically significant positive effect on circumference with an increase estimate of 0.107mm per day. With a relatively low AIC, BIC, a relatively high log likelihood value, residuals that fell within a small range it appears as though the model is a relatively good fit. Since the QQ-plot ends are slightly too heavy with the ones around the bottom deviating below and the ones at the top deviating up there is evidence of some heteroscedasticity. The random effects small standard deviation shows how the fixed variables explain most of the change in circumference. Using this knowledge the findings of this research may be beneficial to farmers who may want to know when their Oranges are the ideal size. The experiment can be improved by sourcing more data since only 35 observations were taken and only 3 variables were present.

Introduction:
The phlebitis dataset contains 60 observations and 4 variables: **Y** the difference in temperature between two ears, **Treatment** a categorical variable that consists of T1 the drug in solution, T2 is the carrier solution and T3 is a saline solution, **Animal** consisting of 15 different types, and **Time** measured at 0, 30, 60, 90 minutes. The aim is to investigate if there is any difference between the treated and untreated ears for the three treatments.

Methodology:
First the data was read in and Animal, Time and Treatment were all converted to factors. Next a summary of the data and two box plots, one plotting Y against treatment, and the other plotting y against time were generated to see if there were any anomalies or data entry errors as well as getting an idea as to the differences between the different groups. An initial linear model is of Y (the response variable) plotted against treatment, time, and their interaction was created and summarised. To improve upon this initial model the stepAIC function that performs backwards elimination was applied to the model but nothing was removed. From here a linear mixed effects model (lme) and a generalised least squares model (gls) were used to map the relationship between Y and the same explanatory variables. After creating the lme and gls and comparing them via an anova test the lme and gls were then given variance structures and compared via anova testing. Next correlation structures were applied and once again compared using anova testing. The best performing model was selected. Evaluating this model a histogram of the residuals, a Q-Q plot, a summary containing information such as the AIC and BIC values was calculated, and finally a standardises residual against fitted value plot was created.

Results:
Selecting a model was difficult. Three different variance structures and three different correlation structures were applied, the initial anova test between the gls and lme model showed no significant difference so variance structures were applied to both. After using anova to decide the best fitting model, this was done by; when a significant difference occurred selecting the model with the lowest AIC value but when there was no significant difference the simplest model was selected (containing less variables). From this process it was determined that both the lme and gls with no variance structures were still the best options. From here correlation structures were applied to both and the same process of anova testing took place, once again it was determined that the original gls and lme models with no correlation structures performed better. Because of this the model selected was the gls, because it's AIC in the initial anova test between the two was slightly smaller and it also contained one less parameter making it the simpler model. The selected model can be represented by the equation:
Y = -0.24 + 1.62(Time30) + 2.12(Time60) + 2.82(Time) -0.34(Treatment2) -0.44(Treatment3) -1.56 (Time30:Treatment2) -1.60(Time60:Treatment2) -2.24(Time90:Treatment2) - 0.70(Time30:Treatment3) -1.86(Time60:Treatment3) -1.92(Time90:Treatment3). The standard residual vs fitted values plot show the standardised residuals are in a small range mostly existing between 2 and -2. The histogram of residuals and the Normal Q-Q plot show that the residuals deviate from a normal distribution on the left side as there's two many of them at the negative end of the distribution as well as some deviation (although not a lot) from the line in the middle and the top (figure 2). The summary shows that the intercept, Treatment2, and Treatment3 are not significant. The AIC value is small at 161.7, BIC is small at 186, the log likelihood is quite high with a value of -67.9, and a low residual standard error of 0.813.

Discussion
Based on the complexity of the final model, containing twelve parameters there is a strong chance that while this module fits quite well according to the AIC, BIC and log likelihood, and residual standard error values that it could actually suffer from overfitting especially since there is only 60 observations. However, this can only be tested by applying the model to a new dataset and assessing its accuracy. Analysing the histogram of the residuals and the QQ-plot the model is not perfect and there is heteroscedasticity as the variance of the residuals is not constant across all values of the predictor variables. Based on the final model, it appears as though temperature increased as time increased and the relationship between time and treatments 2 and 3 was negative implying that over time the change in temperature was negative for those two treatments and it was also found it was positive for treatment 1. Using this knowledge it appears as though the drug in a solution does cause a change in temperature. Whether this is a safe change or not needs to be decided by professionals. In general by time 90 a 2.82 degrees change in temperature has occurred for Treatment1. To improve this model the use of more variables and data from the source as well as testing other methods of plotting the data.
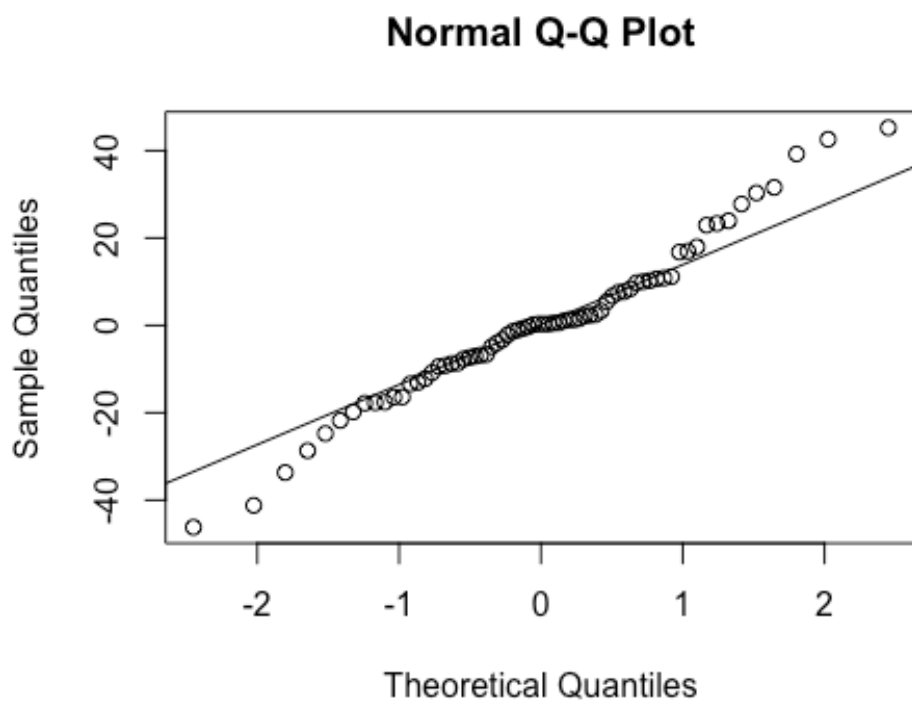
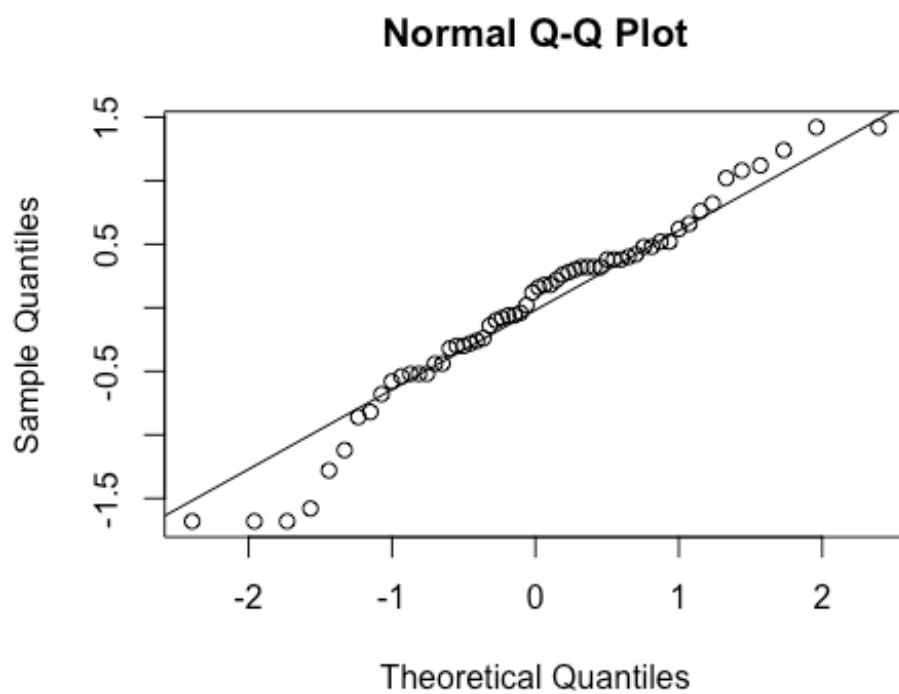Figure 1: Normal Q-Q plot for the final lme model
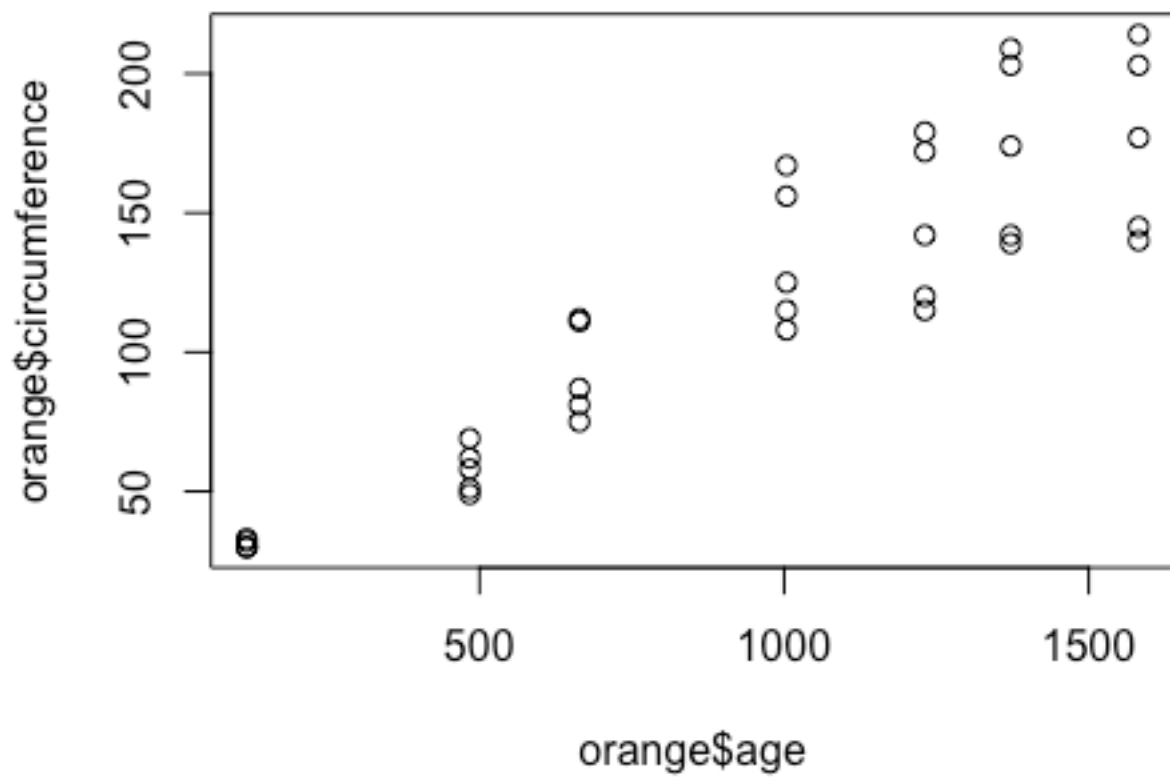

Figure 2: Normal Q-Q plot for the final gls model

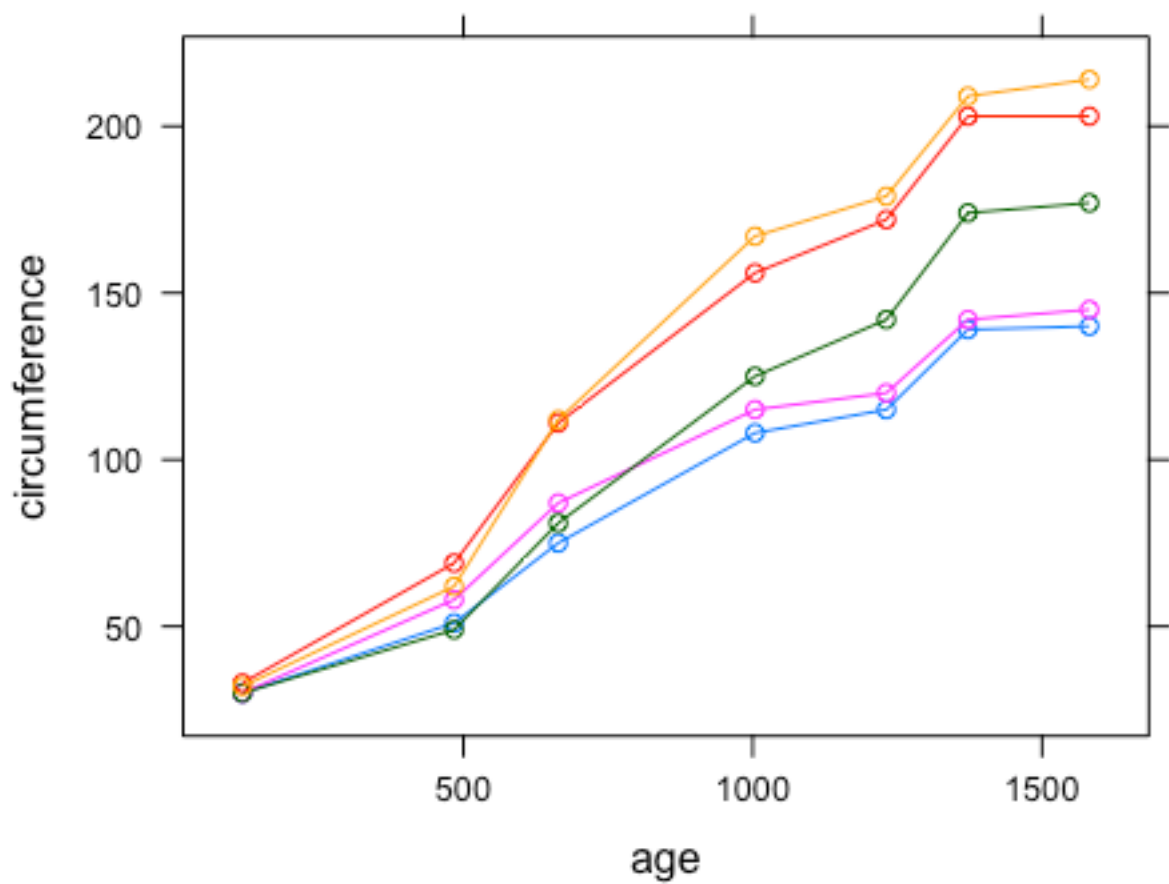# Project 1 Orange

2023-04-02

```
library(nlme)
library(lattice)
orange = Orange
summary(orange)
```

```
## Tree       age          circumference
## 3:7   Min.  : 118.0   Min.  : 30.0
## 1:7   1st Qu.: 484.0   1st Qu.: 65.5
## 5:7   Median :1004.0   Median :115.0
## 2:7   Mean  : 922.1   Mean  :115.9
## 4:7   3rd Qu.:1372.0   3rd Qu.:161.5
##        Max.  :1582.0   Max.  :214.0
```

```
plot(orange$circumference ~ orange$age)
```

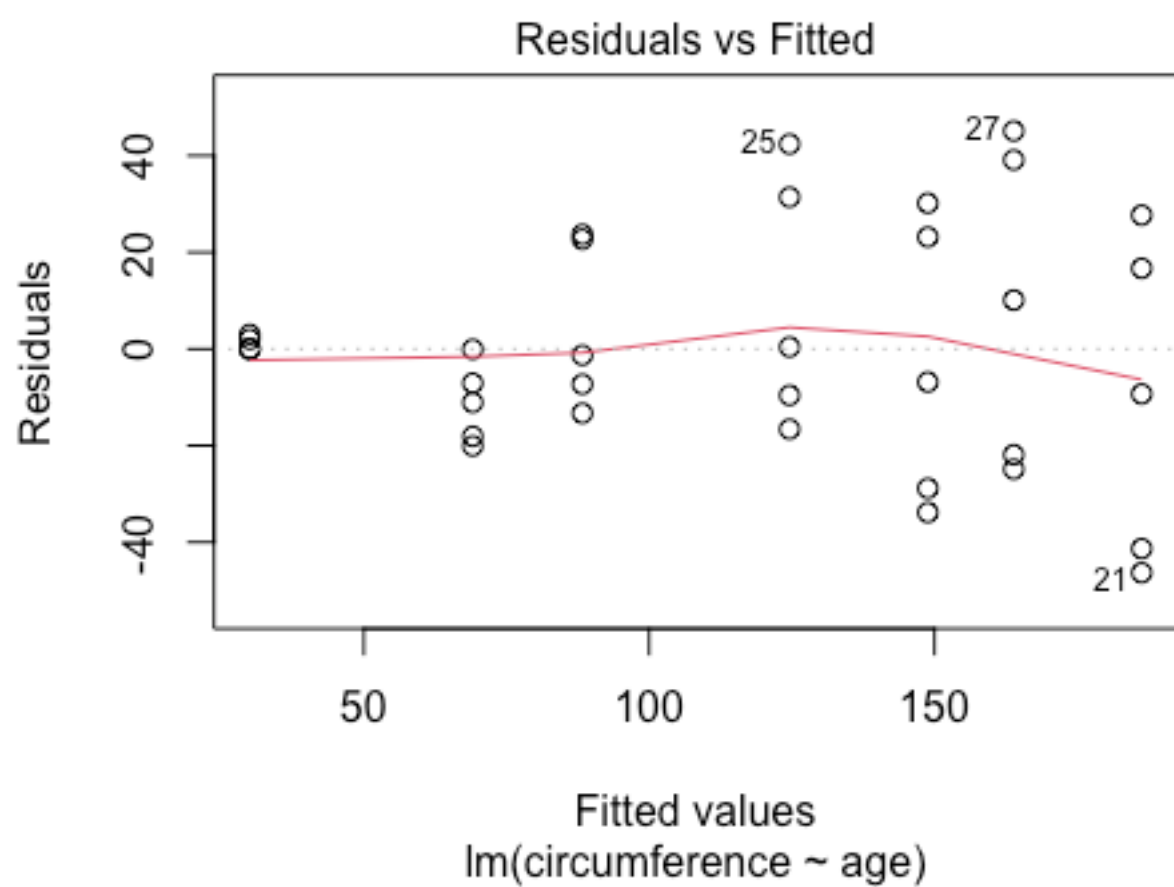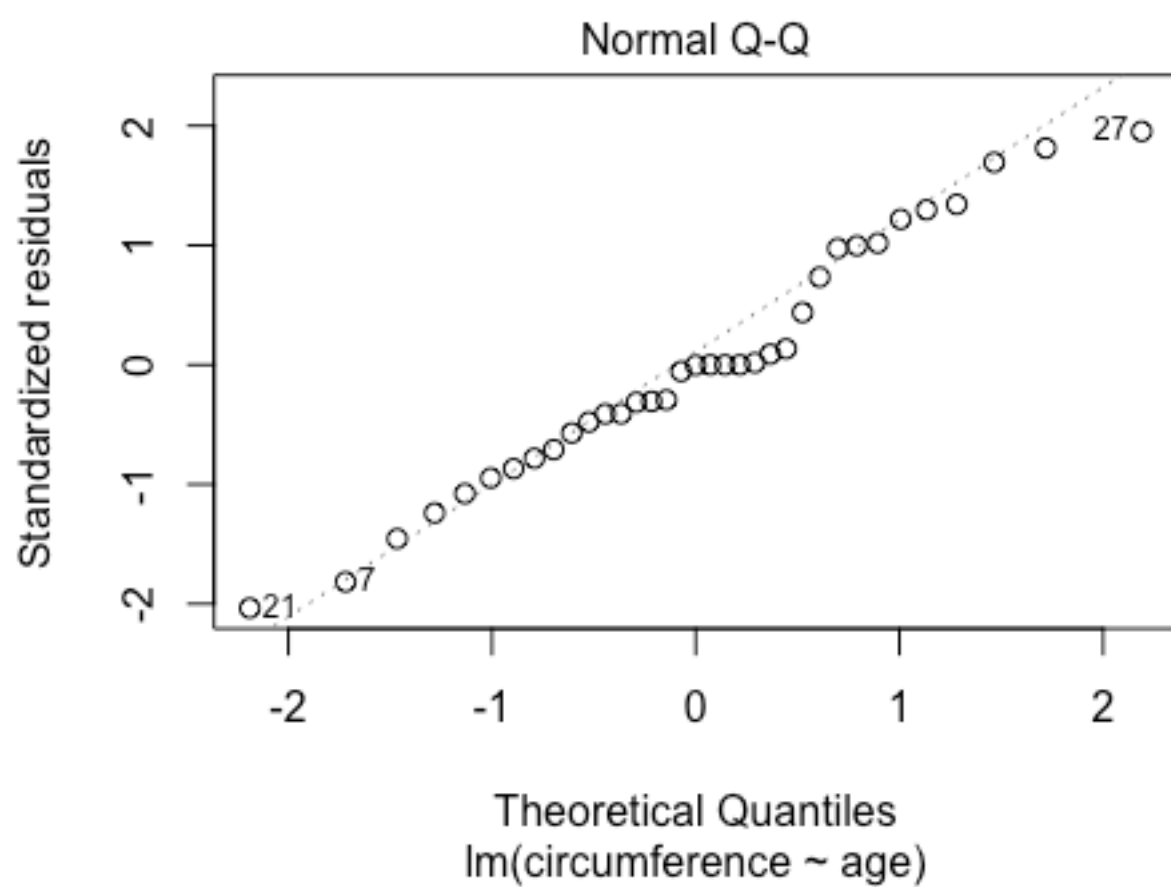**xyplot**(circumference ~ age, data=orange, groups = Tree, type="b")

```
orange.lm = lm(circumference ~ age, data = Orange)
summary(orange.lm)
```
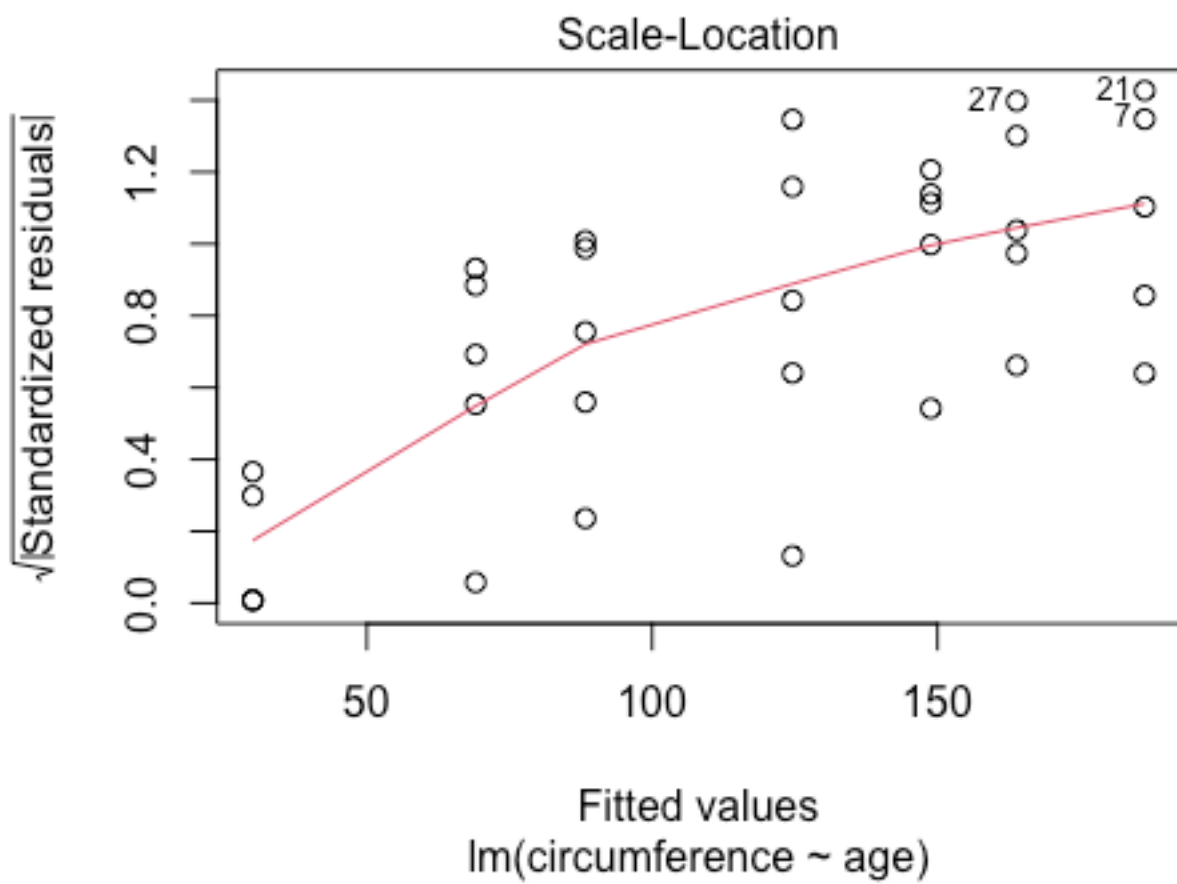
```
##
## Call:
## lm(formula = circumference ~ age, data = Orange)
##
## Residuals:
##    Min     1Q  Median     3Q    Max
## -46.310 -14.946  -0.076  19.697  45.111
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 17.399650   8.622660   2.018   0.0518 .
## age          0.106770   0.008277  12.900 1.93e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```
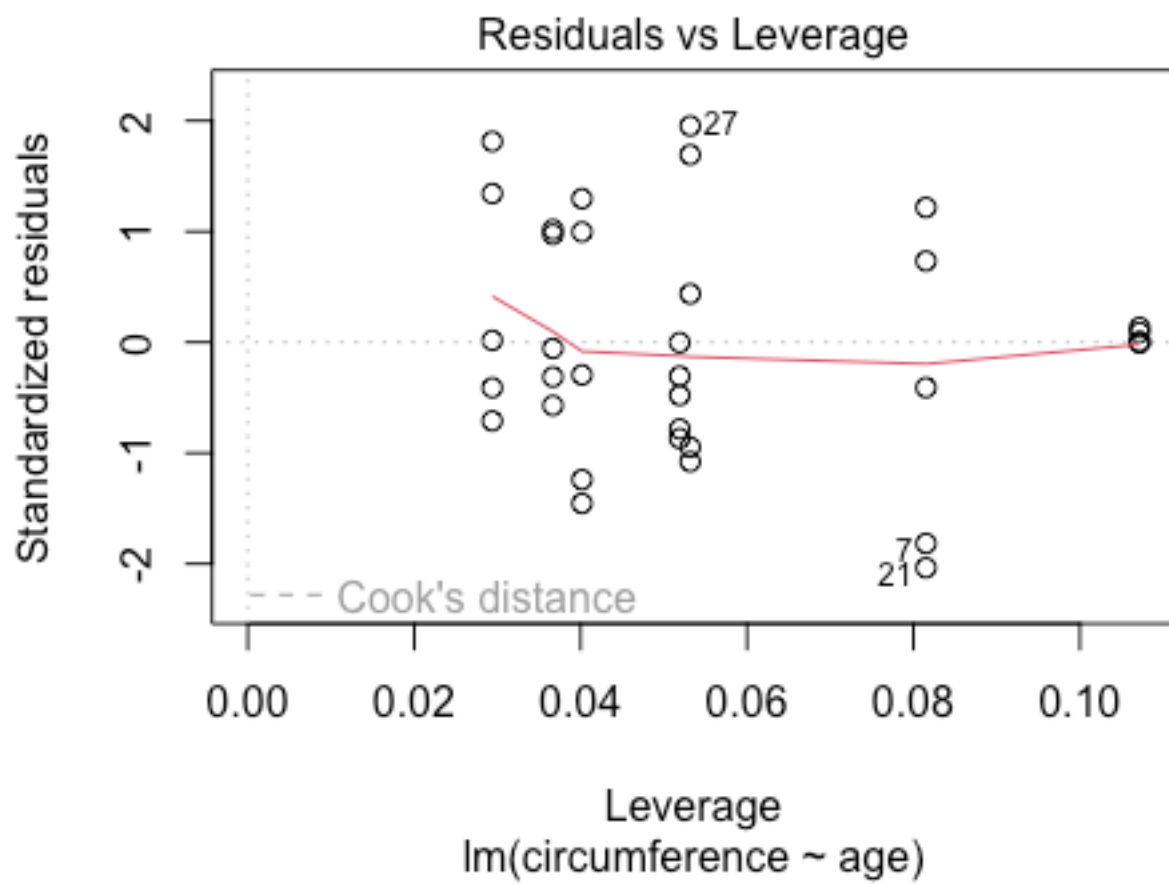
```
## Residual standard error: 23.74 on 33 degrees of freedom
## Multiple R-squared:  0.8345, Adjusted R-squared:  0.8295
## F-statistic: 166.4 on 1 and 33 DF,  p-value: 1.931e-14
```

plot(orange.lm)
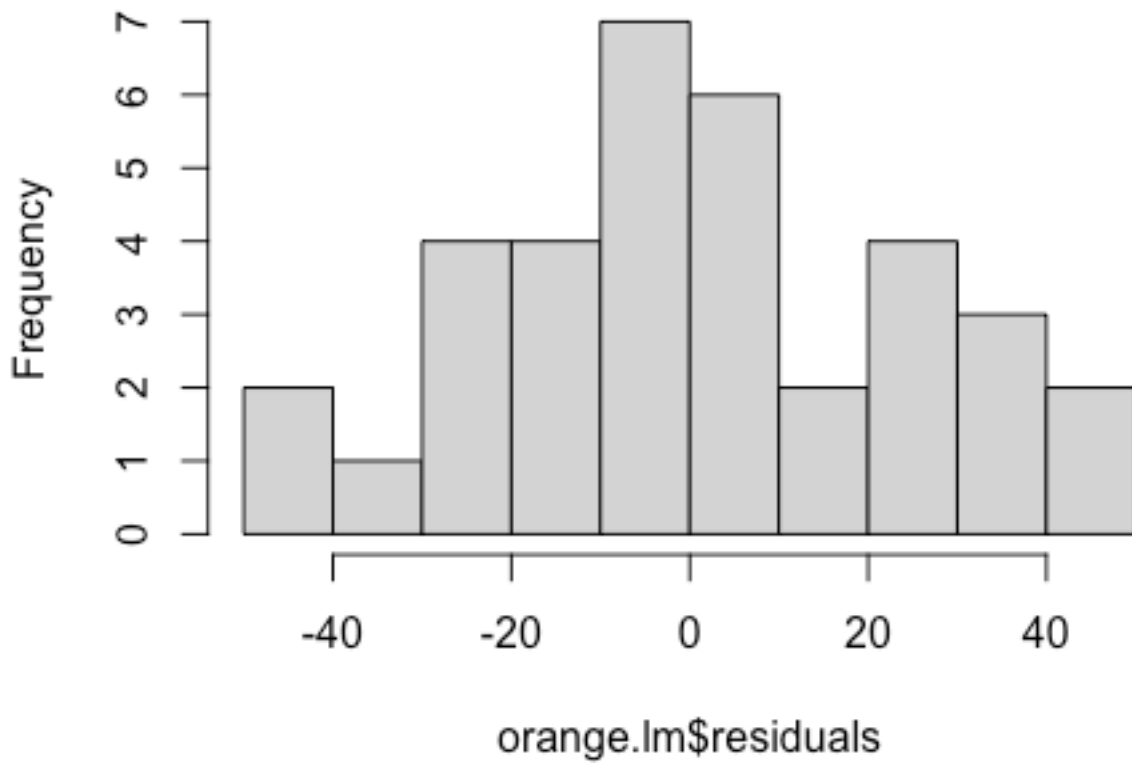
Residuals vs Fitted

Normal Q-Q

Standardized residuals

Theoretical Quantiles
lm(circumference ~ age)

Scale-Location

Fitted values
lm(circumference ~ age)

Residuals vs Leverage

lm(circumference ~ age)

hist(orange.lm$residuals)

Histogram of orange.lm$residuals


```
orange.gls = gls(circumference ~ age, data = Orange)
summary(orange.gls)

## Generalized least squares fit by REML
##   Model: circumference ~ age
##   Data: Orange
##      AIC     BIC   logLik
##   328.1542 332.6438 -161.0771
##
## Coefficients:
##              Value Std.Error   t-value p-value
## (Intercept) 17.39965  8.622660  2.017898  0.0518
## age          0.10677  0.008277 12.900228  0.0000
##
##  Correlation:
##     (Intr)
## age -0.885
##
```

```
## Standardized residuals:
##         Min         Q1         Med         Q3         Max
## -1.950920177 -0.629636341 -0.003222202  0.829789635  1.900416458
##
## Residual standard error: 23.73767
## Degrees of freedom: 35 total; 33 residual
```

orange.lme = **lme**(circumference ~ age, random = ~ age | Tree, data = orange, weights = **varPower**(),)

summary(orange.lme)

```
## Linear mixed-effects model fit by REML
##   Data: orange
##        AIC      BIC    logLik
##   288.9146 299.3902 -137.4573
##
## Random effects:
##  Formula: ~age | Tree
##  Structure: General positive-definite, Log-Cholesky parametrization
##             StdDev     Corr
## (Intercept) 1.89023628 (Intr)
## age         0.02387393 -0.999
## Residual    0.42008398
##
## Variance function:
##  Structure: Power of variance covariate
##  Formula: ~fitted(.)
##  Parameter estimates:
##     power
## 0.6764976
## Fixed effects:  circumference ~ age
##               Value Std.Error DF  t-value p-value
## (Intercept) 17.064045 2.1014270 29 8.120218       0
## age          0.106924 0.0110542 29 9.672654       0
##  Correlation:
##     (Intr)
## age -0.561
##
## Standardized Within-Group Residuals:
##       Min        Q1        Med        Q3        Max
```

```
## -2.4587098 -0.5736373  0.1834177  0.7107694  1.4487497
##
## Number of Observations: 35
## Number of Groups: 5
```

```r
anova(orange.lme, orange.gls)
```

```
##             Model df    AIC      BIC    logLik   Test  L.Ratio p-value
## orange.lme     1  7 288.9146 299.3902 -137.4573
## orange.gls     2  3 328.1542 332.6438 -161.0771 1 vs 2 47.23961  <.0001
```

```r
orange.gls.1 = gls(circumference ~ age, data = orange, weights = varExp())
orange.gls.2 = gls(circumference ~ age, data = orange, weights = varIdent(form=~1))
orange.gls.3 = gls(circumference ~ age, data = orange, weights = varPower())
```

```r
anova(orange.gls, orange.gls.1)
```

```
##             Model df    AIC      BIC    logLik   Test L.Ratio p-value
## orange.gls     1  3 328.1542 332.6438 -161.0771
## orange.gls.1   2  4 316.3708 322.3569 -154.1854 1 vs 2 13.7834   2e-04
```

```r
anova(orange.gls.1, orange.gls.2)
```

```
##              Model df    AIC      BIC    logLik   Test L.Ratio p-value
## orange.gls.1    1  4 316.3708 322.3569 -154.1854
## orange.gls.2    2  3 328.1542 332.6438 -161.0771 1 vs 2 13.7834   2e-04
```

```r
anova(orange.gls.1, orange.gls.3)
```

```
##              Model df    AIC      BIC    logLik
## orange.gls.1    1  4 316.3708 322.3569 -154.1854
## orange.gls.3    2  4 310.8246 316.8107 -151.4123
```

```r
anova(orange.gls.3, orange.lme)
```

```
##             Model df    AIC      BIC    logLik   Test L.Ratio p-value
## orange.gls.3   1  4 310.8246 316.8107 -151.4123
## orange.lme     2  7 288.9146 299.3902 -137.4573 1 vs 2   27.91  <.0001
```

```r
orange.lme1 = lme(circumference ~ age, random = ~ age | Tree, data = orange,
weights = varExp())
```

```
## Warning in logLik.reStruct(object, conLin): Singular precision matrix in level
## -1, block 1
```

```
orange.lme.1 = lme(circumference ~ age, random = ~ age | Tree, data = orange,
weights = varPower(), correlation = corAR1(form=~1|Tree))
```

```
orange.lme.2 = lme(circumference ~ age, random = ~ age | Tree, data = orange,
weights = varPower(), correlation = corSymm())
```

```
orange.lme.3 = lme(circumference ~ age, random = ~ age | Tree, data = orange,
weights = varPower(), correlation = corCompSymm(form=~1|Tree))
```

```
anova(orange.lme, orange.lme.1)
```

```
##              Model df   AIC     BIC    logLik   Test  L.Ratio  p-value
## orange.lme       1 7 288.9146 299.3902 -137.4573
## orange.lme.1     2 8 290.8085 302.7805 -137.4042 1 vs 2 0.1061433  0.7446
```
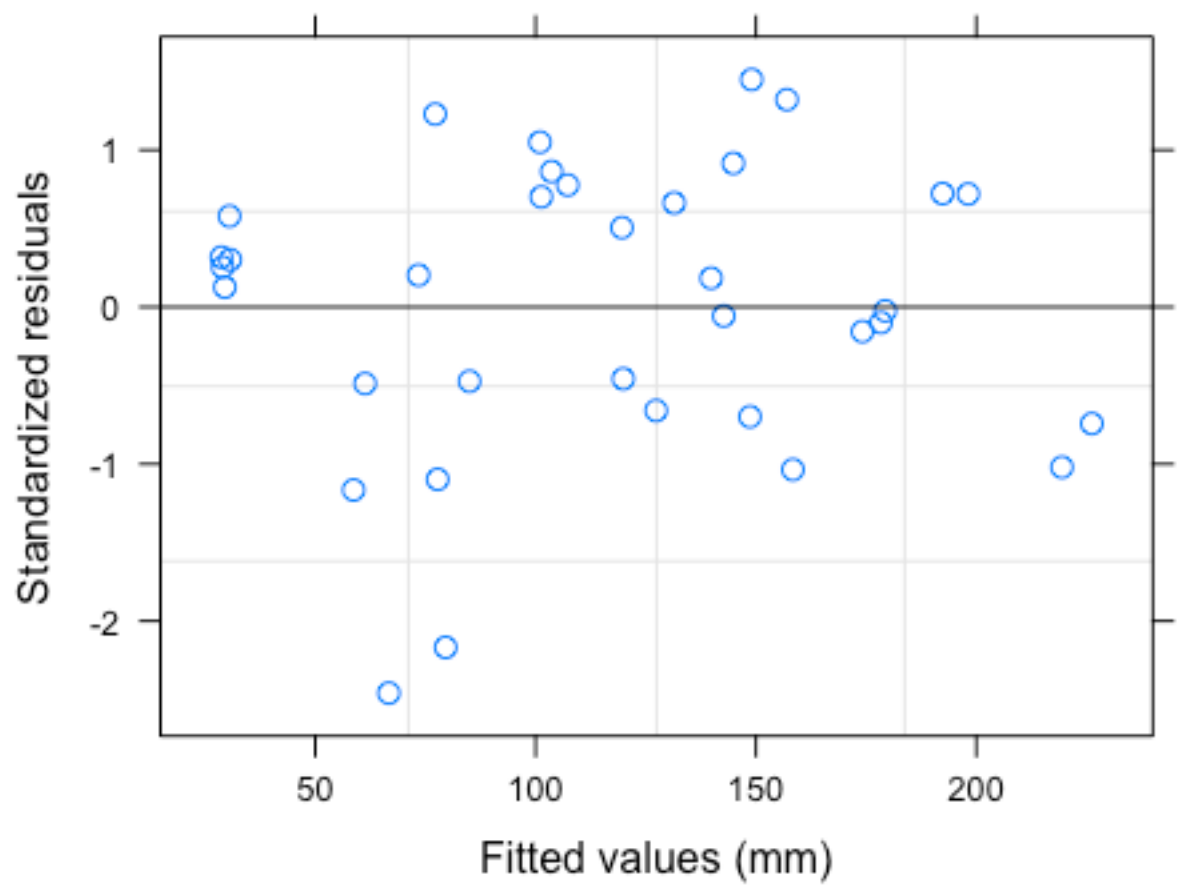
```
anova(orange.lme, orange.lme.2)
```

```
##              Model df   AIC     BIC    logLik   Test  L.Ratio p-value
## orange.lme       1 7 288.9146 299.3902 -137.45731
## orange.lme.2     2 28 216.5078 258.4100  -80.25391 1 vs 2 114.4068  <.0001
```

```
anova(orange.lme, orange.lme.3)
```
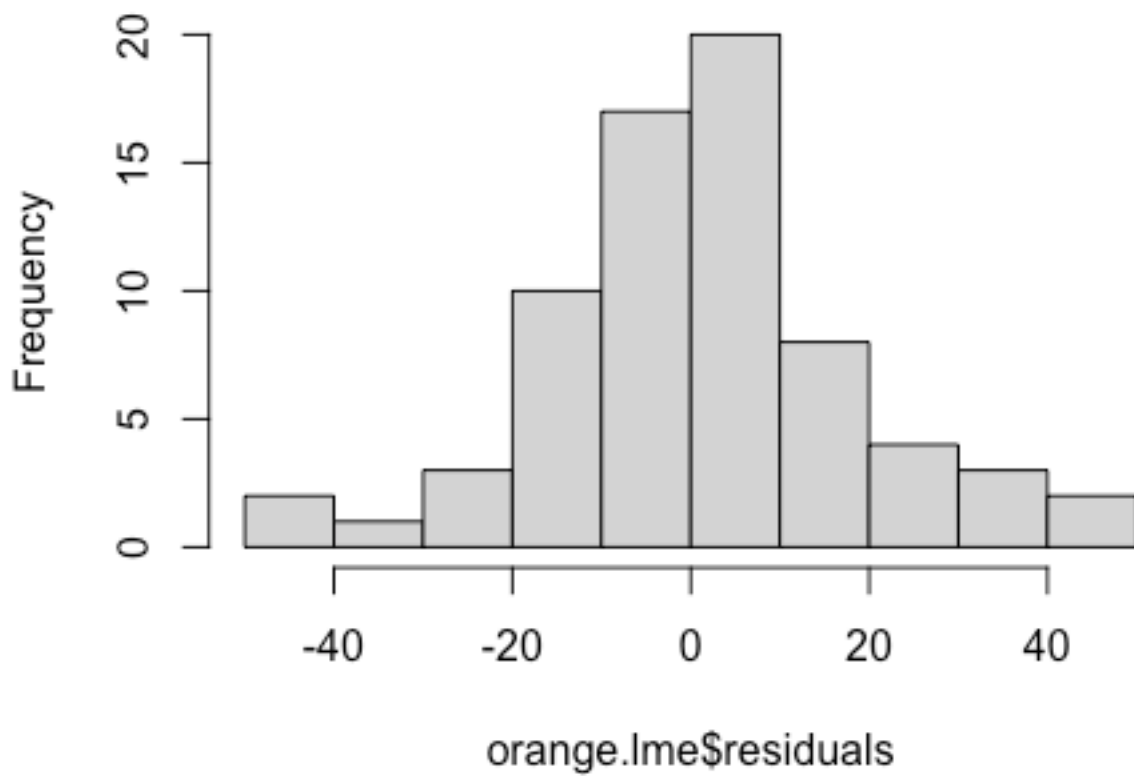
```
##              Model df   AIC     BIC    logLik   Test   L.Ratio p-value
## orange.lme       1 7 288.9146 299.3902 -137.4573
## orange.lme.3     2 8 290.5910 302.5630 -137.2955 1 vs 2 0.3236642  0.5694
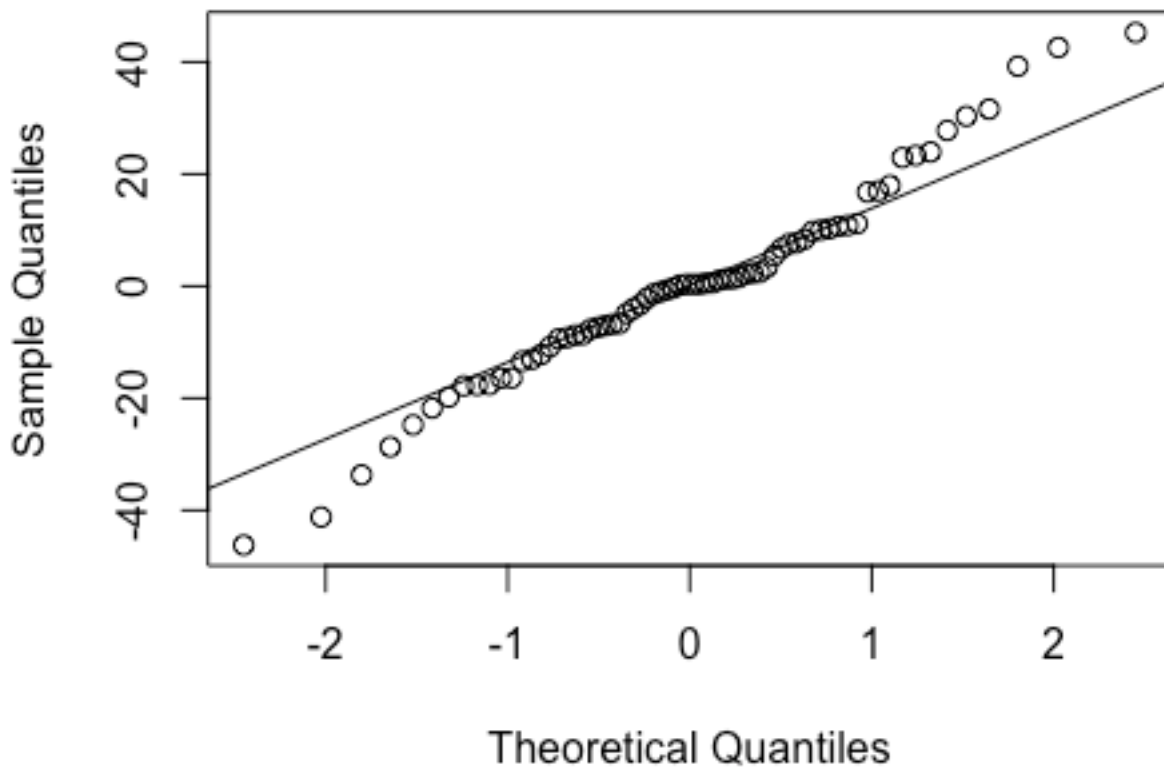```

```
plot(orange.lme)
```

hist(orange.lme$residuals)

Histogram of orange.lme$residuals


```
qqnorm(orange.lme$residuals)
qqline(orange.lme$residuals)
```

Normal Q-Q Plot

summary(orange.lme)

```
## Linear mixed-effects model fit by REML
##   Data: orange
##       AIC      BIC    logLik
##   288.9146 299.3902 -137.4573
##
## Random effects:
##  Formula: ~age | Tree
##  Structure: General positive-definite, Log-Cholesky parametrization
##            StdDev     Corr
## (Intercept) 1.89023628 (Intr)
## age         0.02387393 -0.999
## Residual    0.42008398
##
## Variance function:
##  Structure: Power of variance covariate
##  Formula: ~fitted(.)
```

```
##   Parameter estimates:
##     power
## 0.6764976
## Fixed effects:  circumference ~ age
##               Value Std.Error DF  t-value p-value
## (Intercept) 17.064045 2.1014270 29 8.120218      0
## age          0.106924 0.0110542 29 9.672654      0
##   Correlation:
##     (Intr)
## age -0.561
##
## Standardized Within-Group Residuals:
##      Min        Q1        Med        Q3        Max
## -2.4587098 -0.5736373  0.1834177  0.7107694  1.4487497
##
## Number of Observations: 35
## Number of Groups: 5
```

Project1 Phlebitis

2023-04-02

```r
library(nlme)
library("MASS")

phlebitis = read.table("phlebitis.csv", header=T, sep=",")
phlebitis$Time = as.factor(phlebitis$Time)
phlebitis$Treatment = as.factor(phlebitis$Treatment)
phlebitis$Animal = as.factor(phlebitis$Animal)

summary(phlebitis)
```
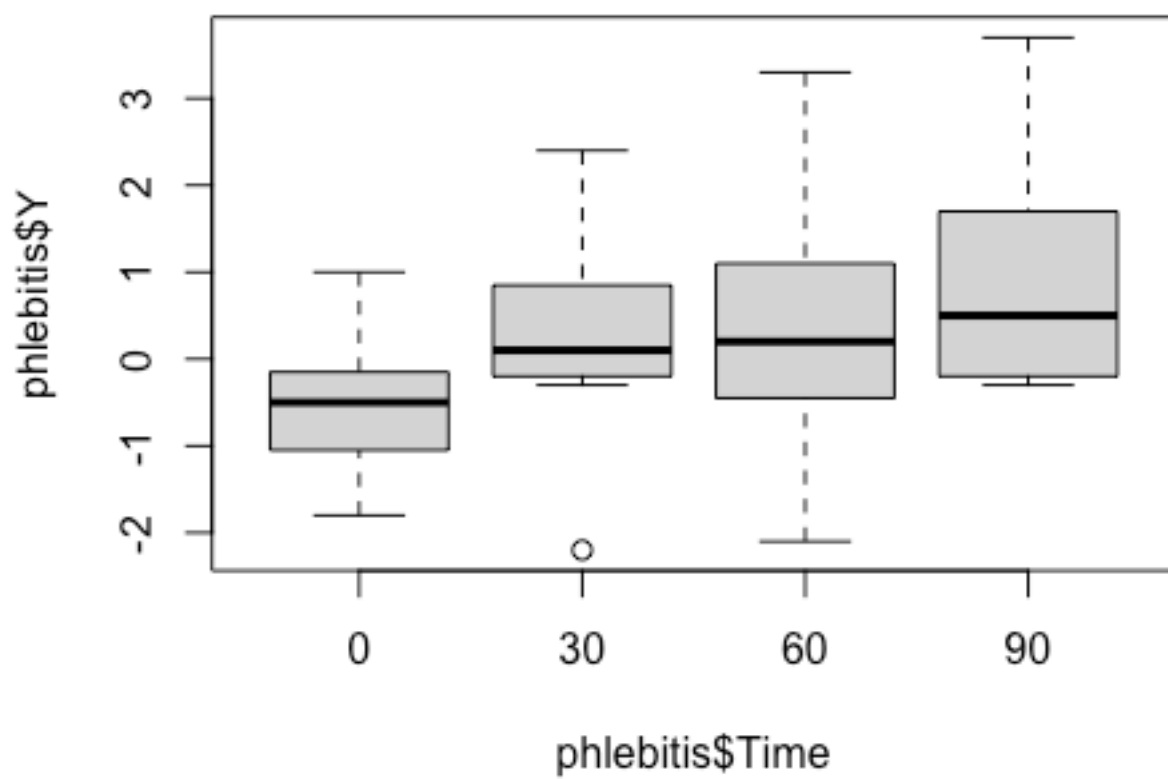
```
##     Animal   Treatment  Time        Y
## 1      : 4   1:20      0 :15   Min.   :-2.2000
## 2      : 4   2:20     30:15   1st Qu.:-0.3000
## 3      : 4   3:20     60:15   Median :-0.0500
## 4      : 4            90:15   Mean   : 0.3167
## 5      : 4                    3rd Qu.: 0.8250
## 6      : 4                    Max.   : 3.7000
## (Other):36
```

```r
boxplot(phlebitis$Y ~ phlebitis$Time)
```

boxplot(phlebitis$Y ~ phlebitis$Treatment)
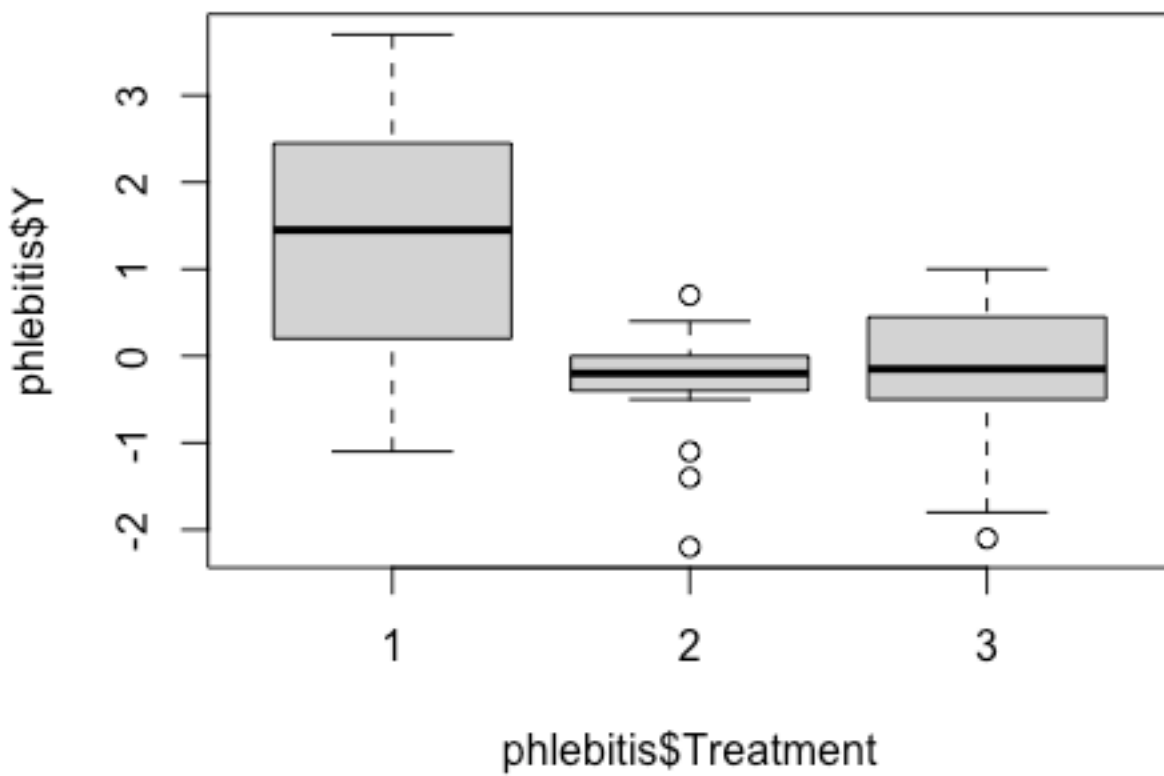
```
phlebitis.lm = lm(Y ~ Time + Treatment + Time:Treatment, data = phlebitis)
summary(phlebitis.lm)
```

```
##
## Call:
## lm(formula = Y ~ Time + Treatment + Time:Treatment, data = phlebitis)
##
## Residuals:
##    Min    1Q Median    3Q   Max
## -1.680 -0.440  0.140  0.405  1.420
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -0.2400     0.3638  -0.660 0.512570
## Time30         1.6200     0.5145   3.149 0.002818 **
## Time60         2.1200     0.5145   4.121 0.000148 ***
## Time90         2.8200     0.5145   5.482 1.54e-06 ***
## Treatment2    -0.3400     0.5145  -0.661 0.511842
```

```
## Treatment3        -0.4400      0.5145  -0.855 0.396651
## Time30:Treatment2  -1.5600      0.7276  -2.144 0.037112 *
## Time60:Treatment2  -1.6000      0.7276  -2.199 0.032718 *
## Time90:Treatment2  -2.2400      0.7276  -3.079 0.003432 **
## Time30:Treatment3  -0.7000      0.7276  -0.962 0.340807
## Time60:Treatment3  -1.8600      0.7276  -2.557 0.013791 *
## Time90:Treatment3  -1.9200      0.7276  -2.639 0.011180 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8134 on 48 degrees of freedom
## Multiple R-squared:  0.6595, Adjusted R-squared:  0.5815
## F-statistic: 8.453 on 11 and 48 DF,  p-value: 5.007e-08
```

phlebitis.lm1 = **stepAIC**(phlebitis.lm)
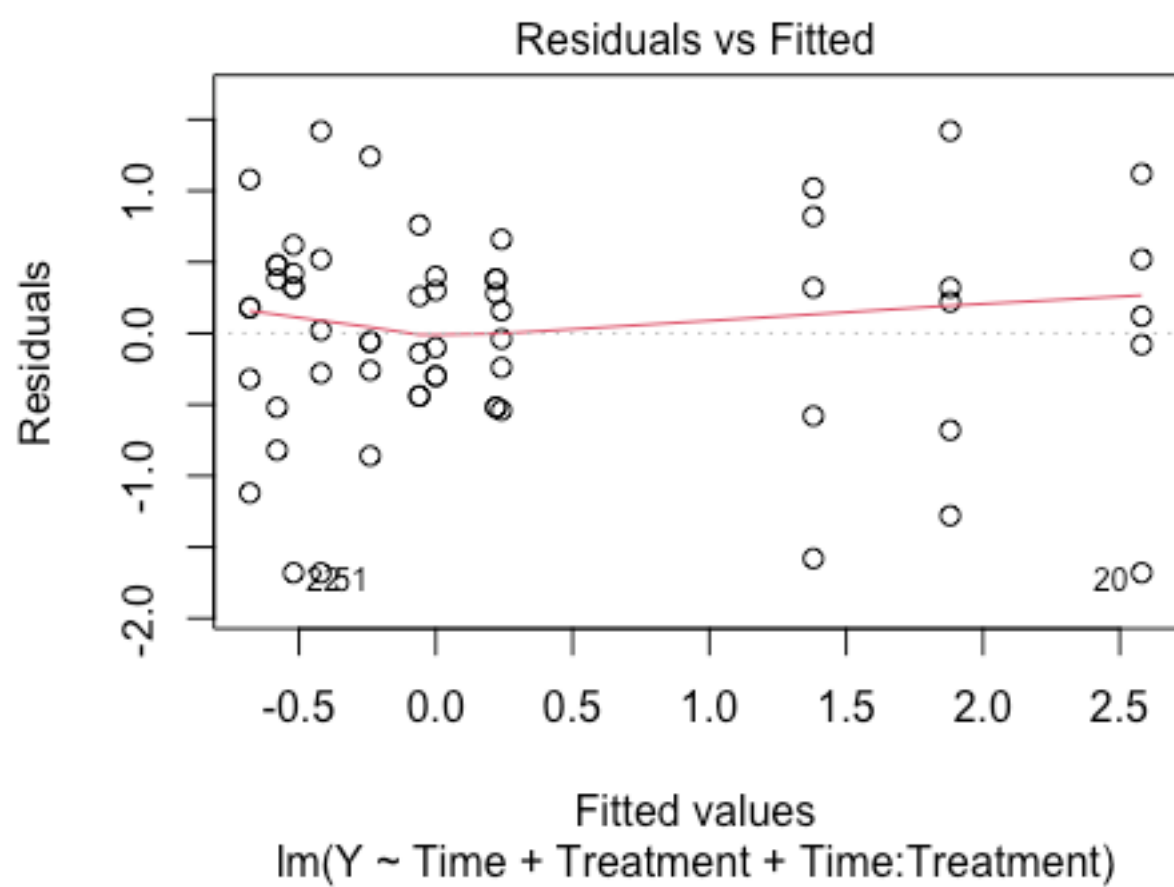
```
## Start:  AIC=-14.17
## Y ~ Time + Treatment + Time:Treatment
##
##                 Df Sum of Sq    RSS      AIC
## <none>                        31.760 -14.1682
## - Time:Treatment  6    10.063 41.823  -9.6544
```

summary(phlebitis.lm1)

```
##
## Call:
## lm(formula = Y ~ Time + Treatment + Time:Treatment, data = phlebitis)
##
## Residuals:
##    Min    1Q Median    3Q    Max
## -1.680 -0.440  0.140  0.405  1.420
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -0.2400     0.3638  -0.660 0.512570
## Time30         1.6200     0.5145   3.149 0.002818 **
## Time60         2.1200     0.5145   4.121 0.000148 ***
## Time90         2.8200     0.5145   5.482 1.54e-06 ***
## Treatment2    -0.3400     0.5145  -0.661 0.511842
## Treatment3    -0.4400     0.5145  -0.855 0.396651
```

```
## Time30:Treatment2  -1.5600     0.7276  -2.144 0.037112 *
## Time60:Treatment2  -1.6000     0.7276  -2.199 0.032718 *
## Time90:Treatment2  -2.2400     0.7276  -3.079 0.003432 **
## Time30:Treatment3  -0.7000     0.7276  -0.962 0.340807
## Time60:Treatment3  -1.8600     0.7276  -2.557 0.013791 *
## Time90:Treatment3  -1.9200     0.7276  -2.639 0.011180 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8134 on 48 degrees of freedom
## Multiple R-squared:  0.6595, Adjusted R-squared:  0.5815
## F-statistic: 8.453 on 11 and 48 DF,  p-value: 5.007e-08

plot(phlebitis.lm1)
```

Residuals vs Fitted

Residuals

Fitted values
lm(Y ~ Time + Treatment + Time:Treatment)

Normal Q-Q

Standardized residuals

Theoretical Quantiles
lm(Y ~ Time + Treatment + Time:Treatment)

Scale-Location

$\sqrt{|\text{Standardized residuals}|}$

Fitted values
lm(Y ~ Time + Treatment + Time:Treatment)

Constant Leverage:
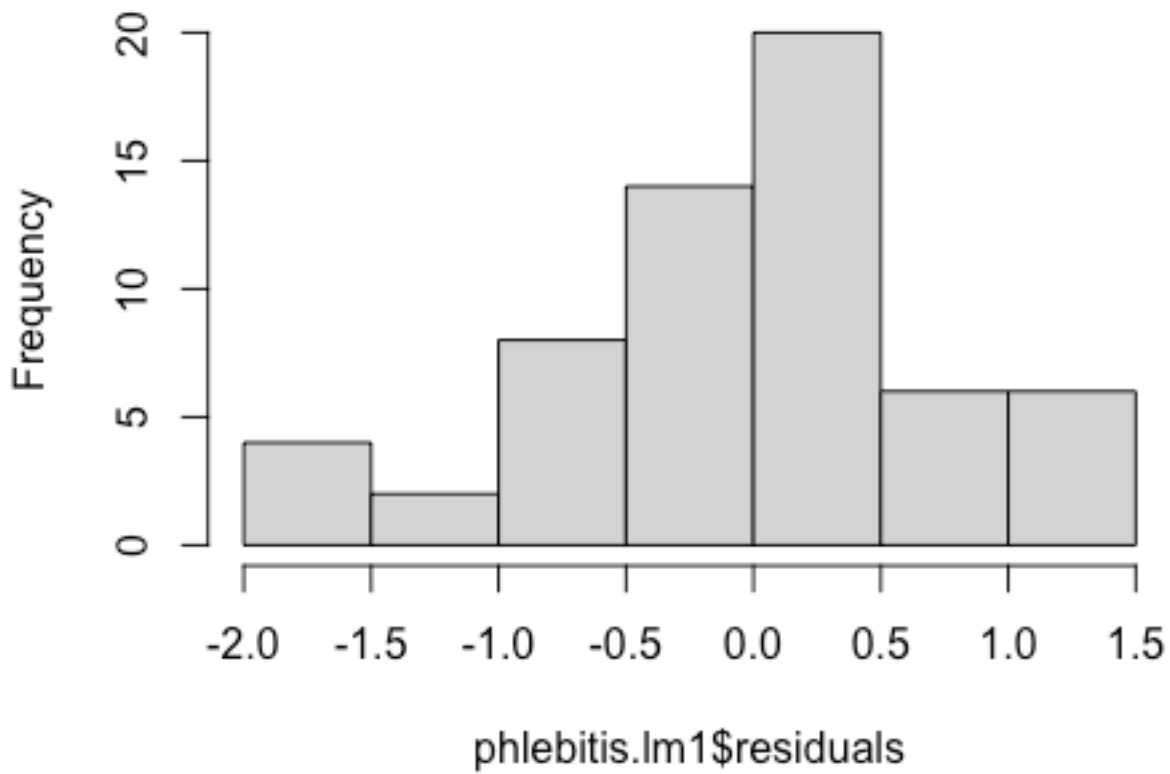Residuals vs Factor Levels
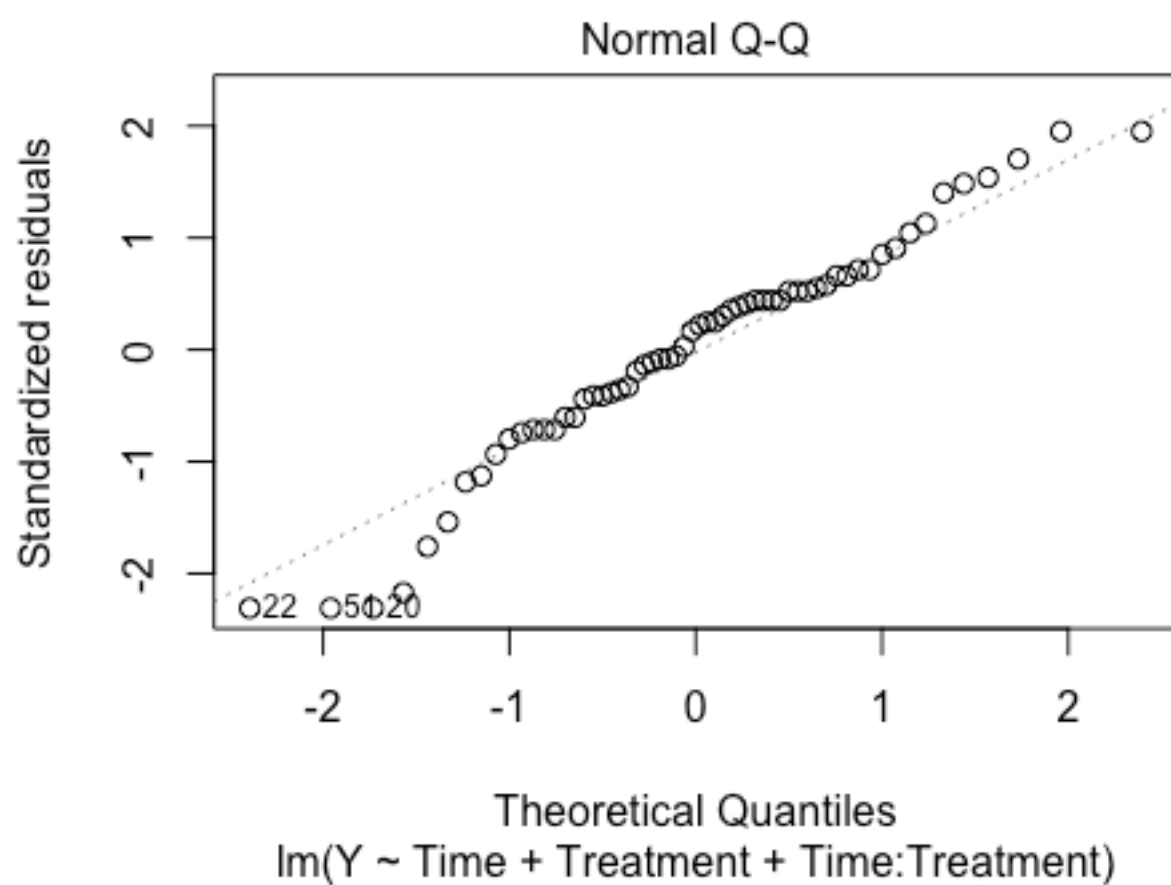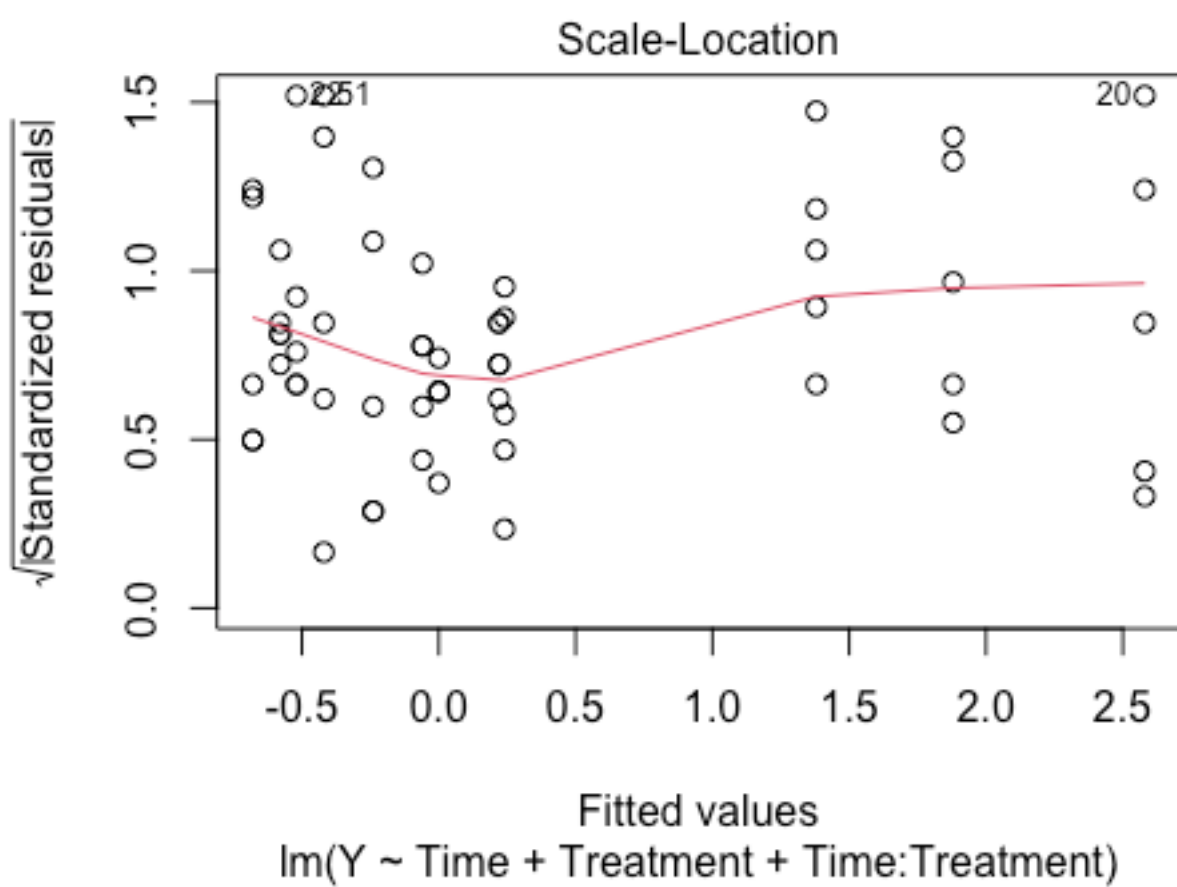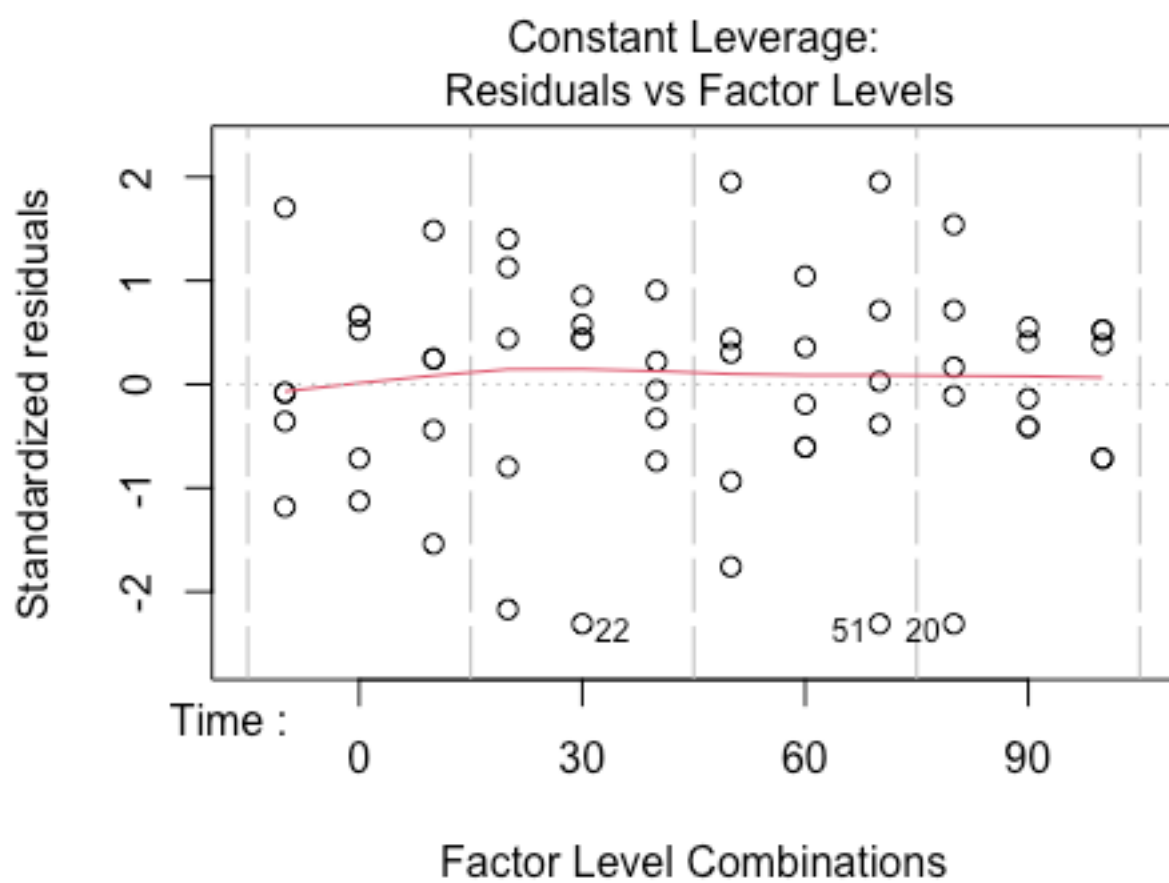
```
hist(phlebitis.lm1$residuals)
```

Histogram of phlebitis.lm1$residuals

phlebitis.lme <- **lme**(Y ~ Time **+** Treatment **+** Time**:**Treatment, data = phlebitis, random = **~1 |** Animal)
summary(phlebitis.lme)

```
## Linear mixed-effects model fit by REML
##   Data: phlebitis
##       AIC    BIC    logLik
##   162.7072 188.904 -67.35359
##
## Random effects:
##  Formula: ~1 | Animal
##         (Intercept) Residual
## StdDev:   0.2887232 0.760464
##
## Fixed effects:  Y ~ Time + Treatment + Time:Treatment
##              Value Std.Error DF   t-value p-value
## (Intercept)  -0.24 0.3637765 36 -0.659746  0.5136
## Time30        1.62 0.4809597 36  3.368266  0.0018
```

```
## Time60             2.12 0.4809597 36  4.407854  0.0001
## Time90             2.82 0.4809597 36  5.863277  0.0000
## Treatment2        -0.34 0.5144576 12 -0.660890  0.5212
## Treatment3        -0.44 0.5144576 12 -0.855270  0.4092
## Time30:Treatment2 -1.56 0.6801797 36 -2.293512  0.0278
## Time60:Treatment2 -1.60 0.6801797 36 -2.352319  0.0242
## Time90:Treatment2 -2.24 0.6801797 36 -3.293247  0.0022
## Time30:Treatment3 -0.70 0.6801797 36 -1.029140  0.3103
## Time60:Treatment3 -1.86 0.6801797 36 -2.734571  0.0096
## Time90:Treatment3 -1.92 0.6801797 36 -2.822783  0.0077
##  Correlation:
##               (Intr) Time30 Time60 Time90 Trtmn2 Trtmn3 T30:T2 T60:T2
## Time30         -0.661
## Time60         -0.661  0.500
## Time90         -0.661  0.500  0.500
## Treatment2     -0.707  0.467  0.467  0.467
## Treatment3     -0.707  0.467  0.467  0.467  0.500
## Time30:Treatment2  0.467 -0.707 -0.354 -0.354 -0.661 -0.331
## Time60:Treatment2  0.467 -0.354 -0.707 -0.354 -0.661 -0.331  0.500
## Time90:Treatment2  0.467 -0.354 -0.354 -0.707 -0.661 -0.331  0.500  0.500
## Time30:Treatment3  0.467 -0.707 -0.354 -0.354 -0.331 -0.661  0.500  0.250
## Time60:Treatment3  0.467 -0.354 -0.707 -0.354 -0.331 -0.661  0.250  0.500
## Time90:Treatment3  0.467 -0.354 -0.354 -0.707 -0.331 -0.661  0.250  0.250
##               T90:T2 T30:T3 T60:T3
## Time30
## Time60
## Time90
## Treatment2
## Treatment3
## Time30:Treatment2
## Time60:Treatment2
## Time90:Treatment2
## Time30:Treatment3  0.250
## Time60:Treatment3  0.250  0.500
## Time90:Treatment3  0.500  0.500  0.500
##
## Standardized Within-Group Residuals:
##      Min        Q1       Med       Q3       Max
## -2.0120020 -0.4931562  0.1115870  0.5572932  1.6701055
##
```

```
## Number of Observations: 60
## Number of Groups: 15
```

phlebitis.gls = **gls**(Y **~** Time **+** Treatment **+** Time**:**Treatment, data = phlebitis)
summary(phlebitis.gls)

```
## Generalized least squares fit by REML
##   Model: Y ~ Time + Treatment + Time:Treatment
##   Data: phlebitis
##        AIC      BIC    logLik
##   161.7077 186.0333 -67.85384
##
## Coefficients:
##                   Value Std.Error   t-value p-value
## (Intercept)       -0.24 0.3637765 -0.659746  0.5126
## Time30             1.62 0.5144576  3.148947  0.0028
## Time60             2.12 0.5144576  4.120845  0.0001
## Time90             2.82 0.5144576  5.481501  0.0000
## Treatment2        -0.34 0.5144576 -0.660890  0.5118
## Treatment3        -0.44 0.5144576 -0.855270  0.3967
## Time30:Treatment2 -1.56 0.7275530 -2.144174  0.0371
## Time60:Treatment2 -1.60 0.7275530 -2.199153  0.0327
## Time90:Treatment2 -2.24 0.7275530 -3.078814  0.0034
## Time30:Treatment3 -0.70 0.7275530 -0.962129  0.3408
## Time60:Treatment3 -1.86 0.7275530 -2.556515  0.0138
## Time90:Treatment3 -1.92 0.7275530 -2.638983  0.0112
##
##  Correlation:
##                   (Intr) Time30 Time60 Time90 Trtmn2 Trtmn3 T30:T2 T60:T2
## Time30            -0.707
## Time60            -0.707  0.500
## Time90            -0.707  0.500  0.500
## Treatment2        -0.707  0.500  0.500  0.500
## Treatment3        -0.707  0.500  0.500  0.500  0.500
## Time30:Treatment2  0.500 -0.707 -0.354 -0.354 -0.707 -0.354
## Time60:Treatment2  0.500 -0.354 -0.707 -0.354 -0.707 -0.354  0.500
## Time90:Treatment2  0.500 -0.354 -0.354 -0.707 -0.707 -0.354  0.500  0.500
## Time30:Treatment3  0.500 -0.707 -0.354 -0.354 -0.354 -0.707  0.500  0.250
## Time60:Treatment3  0.500 -0.354 -0.707 -0.354 -0.354 -0.707  0.250  0.500
## Time90:Treatment3  0.500 -0.354 -0.354 -0.707 -0.354 -0.707  0.250  0.250
##                   T90:T2 T30:T3 T60:T3
```

```
## Time30
## Time60
## Time90
## Treatment2
## Treatment3
## Time30:Treatment2
## Time60:Treatment2
## Time90:Treatment2
## Time30:Treatment3  0.250
## Time60:Treatment3  0.250  0.500
## Time90:Treatment3  0.500  0.500  0.500
##
## Standardized residuals:
##      Min        Q1       Med        Q3       Max
## -2.0653310 -0.5409200  0.1721109  0.4978923  1.7456964
##
## Residual standard error: 0.813429
## Degrees of freedom: 60 total; 48 residual
```

anova(phlebitis.lme, phlebitis.gls)

```
##               Model df    AIC      BIC    logLik  Test  L.Ratio p-value
## phlebitis.lme     1 14 162.7072 188.9040 -67.35359
## phlebitis.gls     2 13 161.7077 186.0333 -67.85384 1 vs 2 1.000496  0.3172
```

phlebitis.lme.1 <- **lme**(Y ~ Time + Treatment + Time:Treatment, data = phlebitis,
random = ~1 | Animal, weights = **varExp**())
phlebitis.lme.3 <- **lme**(Y ~ Time + Treatment + Time:Treatment, data = phlebitis,
random = ~1 | Animal, weights = **varIdent**(form = ~1))

anova(phlebitis.lme.1, phlebitis.lme.3)

```
##               Model df    AIC      BIC    logLik  Test  L.Ratio p-value
## phlebitis.lme.1     1 15 164.3456 192.4136 -67.17281
## phlebitis.lme.3     2 14 162.7072 188.9040 -67.35359 1 vs 2 0.3615492
## 0.5476
```

anova(phlebitis.lme.3, phlebitis.lme)

```
##               Model df    AIC     BIC    logLik
## phlebitis.lme.3     1 14 162.7072 188.904 -67.35359
## phlebitis.lme       2 14 162.7072 188.904 -67.35359
```

```r
phlebitis.gls.1 = gls(Y ~ Time + Treatment + Time:Treatment, data = phlebitis,
weights = varPower())
phlebitis.gls.2 = gls(Y ~ Time + Treatment + Time:Treatment, data = phlebitis,
weights = varIdent(form = ~1))
phlebitis.gls.3 = gls(Y ~ Time + Treatment + Time:Treatment, data = phlebitis,
weights = varExp())

anova(phlebitis.gls.1, phlebitis.gls)
```

```
##               Model df    AIC      BIC    logLik   Test  L.Ratio p-value
## phlebitis.gls.1     1 14 158.8121 185.0089 -65.40605
## phlebitis.gls       2 13 161.7077 186.0333 -67.85384 1 vs 2 4.895563  0.0269
```

```r
anova(phlebitis.gls.2, phlebitis.gls)
```

```
##               Model df    AIC      BIC    logLik
## phlebitis.gls.2     1 13 161.7077 186.0333 -67.85384
## phlebitis.gls       2 13 161.7077 186.0333 -67.85384
```

```r
anova(phlebitis.gls.3, phlebitis.gls)
```

```
##               Model df    AIC      BIC    logLik   Test  L.Ratio p-value
## phlebitis.gls.3     1 14 162.3950 188.5918 -67.19752
## phlebitis.gls       2 13 161.7077 186.0333 -67.85384 1 vs 2 1.312633  0.2519
```

```r
anova(phlebitis.gls, phlebitis.lme.3)
```

```
##               Model df    AIC      BIC    logLik   Test  L.Ratio p-value
## phlebitis.gls       1 13 161.7077 186.0333 -67.85384
## phlebitis.lme.3     2 14 162.7072 188.9040 -67.35359 1 vs 2 1.000496  0.3172
```

```r
phlebitis.lme.0.1 <- lme(Y ~ Time + Treatment + Time:Treatment, data =
phlebitis, random = ~1 | Animal, correlation = corAR1(form=~1|Animal))
phlebitis.lme.0.2 <- lme(Y ~ Time + Treatment + Time:Treatment, data =
phlebitis, random = ~1 | Animal, correlation = corSymm(form=~1|Animal))
phlebitis.lme.0.3 <- lme(Y ~ Time + Treatment + Time:Treatment, data =
phlebitis, random = ~1 | Animal, correlation = corCompSymm(form=~1|
Animal))

anova(phlebitis.lme, phlebitis.lme.0.1)
```

```
##             Model df    AIC      BIC    logLik   Test  L.Ratio p-value
## phlebitis.lme     1 14 162.7072 188.9040 -67.35359
```

```
## phlebitis.lme.0.1     2 15 162.1418 190.2098 -66.07088 1 vs 2 2.565425
0.1092
```

anova(phlebitis.lme, phlebitis.lme.0.2)

```
##              Model df    AIC    BIC    logLik   Test  L.Ratio p-value
## phlebitis.lme        1 14 162.7072 188.904 -67.35359
## phlebitis.lme.0.2    2 20 169.7880 207.212 -64.89401 1 vs 2 4.91916  0.5542
```

anova(phlebitis.lme, phlebitis.lme.0.3)

```
##              Model df    AIC    BIC   logLik  Test    L.Ratio
## phlebitis.lme        1 14 162.7072 188.9040 -67.35359
## phlebitis.lme.0.3    2 15 164.7072 192.7752 -67.35359 1 vs 2 2.842171e-14
##              p-value
## phlebitis.lme
## phlebitis.lme.0.3      1
```

phlebitis.gls.0.1 = **gls**(Y **~** Time **+** Treatment **+** Time**:**Treatment, data = phlebitis,
correlation = **corAR1**(form=**~1|**Animal))
phlebitis.gls.0.2 = **gls**(Y **~** Time **+** Treatment **+** Time**:**Treatment, data = phlebitis,
correlation = **corSymm**(form=**~1|**Animal))
phlebitis.gls.0.3 = **gls**(Y **~** Time **+** Treatment **+** Time**:**Treatment, data = phlebitis,
correlation = **corCompSymm**(form=**~1|**Animal))

anova(phlebitis.gls, phlebitis.gls.0.1)

```
##              Model df    AIC    BIC   logLik  Test  L.Ratio p-value
## phlebitis.gls        1 13 161.7077 186.0333 -67.85384
## phlebitis.gls.0.1    2 14 160.1418 186.3386 -66.07088 1 vs 2 3.565921   0.059
```
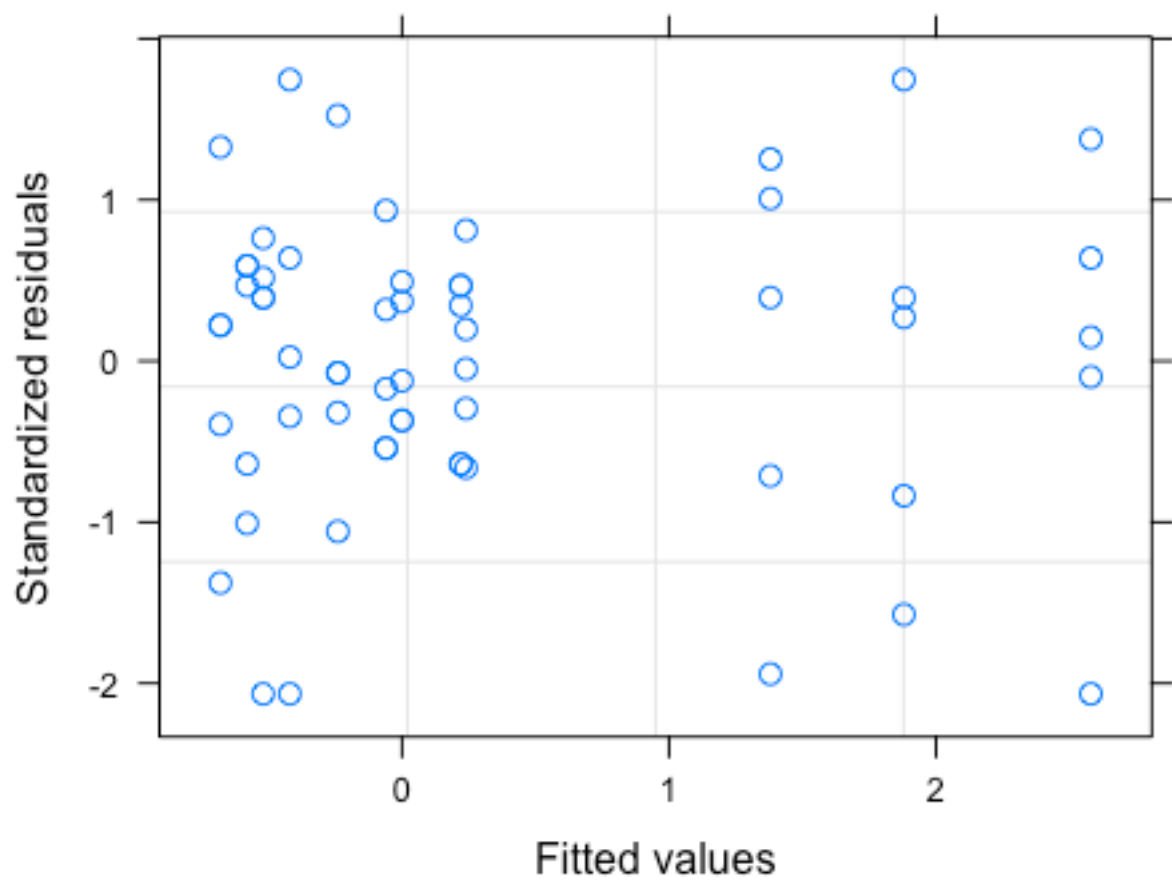
anova(phlebitis.gls, phlebitis.gls.0.2)

```
##              Model df    AIC    BIC   logLik  Test  L.Ratio p-value
## phlebitis.gls        1 13 161.7077 186.0333 -67.85384
## phlebitis.gls.0.2    2 19 167.7880 203.3408 -64.89401 1 vs 2 5.919656  0.4323
```

anova(phlebitis.gls, phlebitis.gls.0.3)
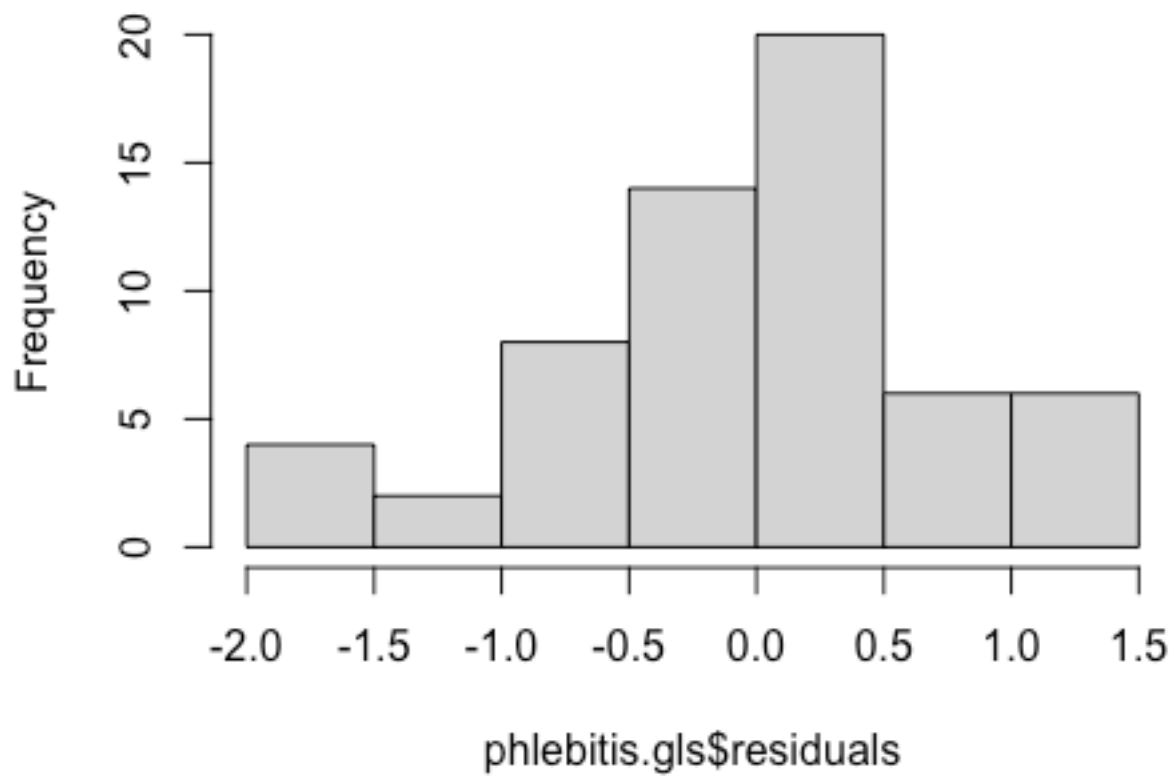
```
##              Model df    AIC    BIC   logLik  Test  L.Ratio p-value
## phlebitis.gls        1 13 161.7077 186.0333 -67.85384
## phlebitis.gls.0.3    2 14 162.7072 188.9040 -67.35359 1 vs 2 1.000496  0.3172
```
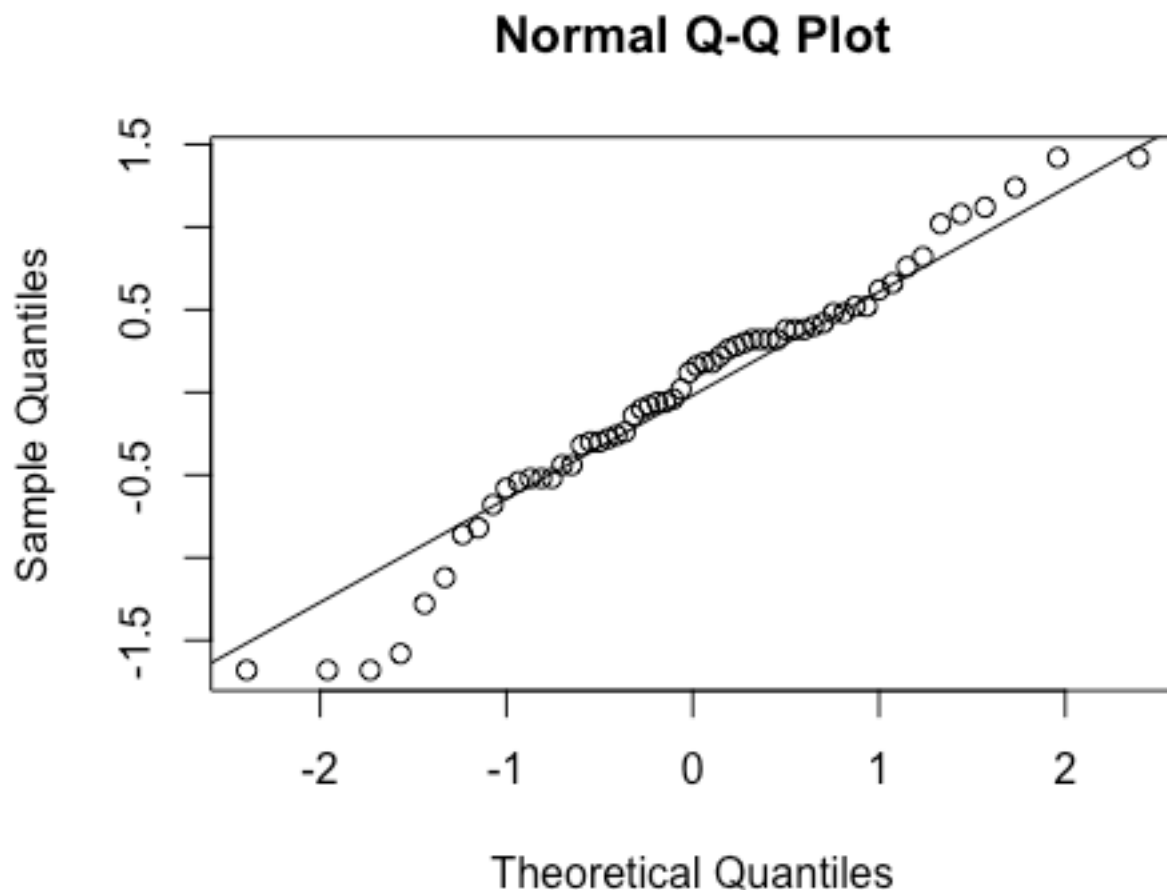
plot(phlebitis.gls)

hist(phlebitis.gls**$**residuals)

Histogram of phlebitis.gls$residuals


```
qqnorm(phlebitis.gls$residuals)
qqline(phlebitis.gls$residuals)
```

Normal Q-Q Plot

summary(phlebitis.gls)

```
## Generalized least squares fit by REML
##   Model: Y ~ Time + Treatment + Time:Treatment
##   Data: phlebitis
##       AIC     BIC    logLik
##   161.7077 186.0333 -67.85384
##
## Coefficients:
##                 Value Std.Error   t-value p-value
## (Intercept)      -0.24 0.3637765 -0.659746  0.5126
## Time30            1.62 0.5144576  3.148947  0.0028
## Time60            2.12 0.5144576  4.120845  0.0001
## Time90            2.82 0.5144576  5.481501  0.0000
## Treatment2       -0.34 0.5144576 -0.660890  0.5118
## Treatment3       -0.44 0.5144576 -0.855270  0.3967
## Time30:Treatment2 -1.56 0.7275530 -2.144174  0.0371
## Time60:Treatment2 -1.60 0.7275530 -2.199153  0.0327
```

```
## Time90:Treatment2 -2.24 0.7275530 -3.078814  0.0034
## Time30:Treatment3 -0.70 0.7275530 -0.962129  0.3408
## Time60:Treatment3 -1.86 0.7275530 -2.556515  0.0138
## Time90:Treatment3 -1.92 0.7275530 -2.638983  0.0112
##
##  Correlation:
##               (Intr) Time30 Time60 Time90 Trtmn2 Trtmn3 T30:T2 T60:T2
## Time30          -0.707
## Time60          -0.707  0.500
## Time90          -0.707  0.500  0.500
## Treatment2       -0.707  0.500  0.500  0.500
## Treatment3       -0.707  0.500  0.500  0.500  0.500
## Time30:Treatment2  0.500 -0.707 -0.354 -0.354 -0.707 -0.354
## Time60:Treatment2  0.500 -0.354 -0.707 -0.354 -0.707 -0.354  0.500
## Time90:Treatment2  0.500 -0.354 -0.354 -0.707 -0.707 -0.354  0.500  0.500
## Time30:Treatment3  0.500 -0.707 -0.354 -0.354 -0.354 -0.707  0.500  0.250
## Time60:Treatment3  0.500 -0.354 -0.707 -0.354 -0.354 -0.707  0.250  0.500
## Time90:Treatment3  0.500 -0.354 -0.354 -0.707 -0.354 -0.707  0.250  0.250
##               T90:T2 T30:T3 T60:T3
## Time30
## Time60
## Time90
## Treatment2
## Treatment3
## Time30:Treatment2
## Time60:Treatment2
## Time90:Treatment2
## Time30:Treatment3  0.250
## Time60:Treatment3  0.250  0.500
## Time90:Treatment3  0.500  0.500  0.500
##
## Standardized residuals:
##     Min       Q1      Med       Q3      Max
## -2.0653310 -0.5409200  0.1721109  0.4978923  1.7456964
##
## Residual standard error: 0.813429
## Degrees of freedom: 60 total; 48 residual
```