

Floral morphology and sexual dimorphism in *Embelia*

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Introduction

The main objective of this study is to test the occurrence of sexual dimorphism (a difference between male and female individuals) on 17 floral characters in *Embelia*. The morphological characters were measured on several specimens (“spec_ID”) for each species and several flowers within each specimen. By definition, some characters have one observation per flower (there is only one pedicel, one ovary per flower), and others have several observations per flower (there are several sepals, several petals and several stamens per flower, and each of them were measured). These variables therefore have an additional grouping level, called “flower_ID”. It is important to control whether the groups have an effect on the variables of interest. A simple t.test or Chi2 test cannot account for these random effects; linear regression models with mixed effects will therefore be used to assess whether there is an effect of gender on each variable of interest, while controlling for the effect of specimens.

The dataframe used in this study is named **flwr**, it contains measurements of floral characters conducted on dissected flowers (3 species, 6 to 8 herbarium specimens examined per species, 3 to 10 flowers examined per herbarium specimen).

For each morphological character, the number of observations and distribution of the data are checked to assess which model can be used, the effect of gender is tested with the relevant method and, finally, the fit of the chosen model is checked (to see whether it accurately explains the variations observed in the variable of interest).

The models used in this study are: - **linear mixed-effect regression model (lmer)** using maximum likelihood to estimate the parameters when the response variable is a continuous quantitative variable with a normal distribution - **generalised linear mixed effect regression model (glmer)** using Laplace approximation to assess the parameters and a Poisson distribution function when the response variable is a discrete quantitative variable (like a count variable with few possible values).

A detailed example of **lmer**, including explanations on the way the results are interpreted, is presented in section 3.1.2 Pedicel length. An example of **glmer** is presented in section 3.2.2 Statistical tests - Sepal number.

The conditions for each test, the choice of the effects included in the models and the arguments used in each function are explained on their first appearance only. The other iterations of these commands and models are stripped of comments, in order to declutter the code.

Libraries used in this code: library(here) #sets the top level of the project file as “here” (to easily set a path to the data files)

```
library(prettyR) #descriptive statistics {describe}
```

```
library(ggplot2) #plots {ggplot}
```

```
library(lme4) #Generalised linear mixed regression models {lmer, glmer}
```

```
library(car) #Plot distribution & extract p-value from lme4 regression models {qqp, Anova}
```

```
library(MASS) #test distribution of variables {fitdistr}
```

```
library(knitr) #to generate the Rmarkdown output
```

```
library(formatR) #to format the Rmarkdown output
```

Custom function used to check the overdispersion of data (for glmm with Laplace approximation):

```
# The following code is from
# https://ase.tufts.edu/gsc/gradresources/guidetomixedmodelsinr/mixed%20model%20guide.html
# This function is used to assess whether the conditions of a
# generalized linear mixed model with a binomial distribution
# using the Laplace approximation are met (i.e. whether the
# data is not overdispersed).
overdisp_fun <- function(model) {
```

```

## number of variance parameters in an n-by-n
## variance-covariance matrix
vpars <- function(m) {
  nrow(m) * (nrow(m) + 1)/2
}
# The next two lines calculate the residual degrees of
# freedom
model.df <- sum(sapply(VarCorr(model), vpars)) + length(fixef(model))
rdf <- nrow(model.frame(model)) - model.df
# extracts the Pearson residuals
rp <- residuals(model, type = "pearson")
Pearson.chisq <- sum(rp^2)
prat <- Pearson.chisq/rdf
# Generates a p-value. If less than 0.05, the data are
# overdispersed.
pval <- pchisq(Pearson.chisq, df = rdf, lower.tail = FALSE)
c(chisq = Pearson.chisq, ratio = prat, rdf = rdf, p = pval)
}

```

1 Dataframe setup

```
flwr <- read.csv(here("fl_msrrmt.csv"))
```

1.1 Variables

```
names(flwr)
```

```

## [1] "species"      "sex"           "spec_ID"
## [4] "flower_ID"    "sepal_nb"      "petal_nb"
## [7] "pedicel_length" "pedicel_width" "ovary_diameter"
## [10] "style_length"  "sepal_length"  "sepal_width"
## [13] "sepal_fusion"  "s_fusion_ratio" "petal_length"
## [16] "petal_width"   "petal_fusion"  "p_fusion_ratio"
## [19] "filament_length" "filament_width" "filament_fusion"
## [22] "fil_fusion_ratio" "anther_length" "anther_width"

```

Check that the variables are properly coded and that there are no accidental values

```
sapply(flwr, class)
```

```

##      species      sex      spec_ID      flower_ID
##      "factor"    "factor"    "factor"    "factor"
##      sepal_nb    petal_nb    pedicel_length    pedicel_width
##      "integer"    "integer"    "numeric"    "numeric"
##      ovary_diameter    style_length    sepal_length    sepal_width
##      "numeric"    "numeric"    "numeric"    "numeric"
##      sepal_fusion    s_fusion_ratio    petal_length    petal_width
##      "numeric"    "numeric"    "numeric"    "numeric"
##      petal_fusion    p_fusion_ratio    filament_length    filament_width
##      "integer"    "numeric"    "factor"    "numeric"
##      filament_fusion    fil_fusion_ratio    anther_length    anther_width
##      "numeric"    "numeric"    "numeric"    "numeric"

```

```
# requires library(prettyR)
describe(Filter(is.numeric, flwr), num.desc = c("valid.n", "min",
  "max", "median", "mean", "sd"))
```

```
## Description of Filter(is.numeric, flwr)
```

```
##
## Numeric
##
```

	valid.n	min	max	median	mean	sd
## sepal_nb	149	4.00	7.00	5.00	4.96	0.46
## petal_nb	149	3.00	6.00	5.00	4.80	0.46
## pedicel_length	144	5.50	53.00	23.00	23.39	10.44
## pedicel_width	149	3.00	9.00	5.50	5.72	1.26
## ovary_diameter	148	2.00	15.00	7.00	6.97	3.52
## style_length	147	0.50	23.00	7.00	7.71	6.94
## sepal_length	725	4.00	15.00	10.00	9.81	1.97
## sepal_width	733	1.00	18.00	8.00	8.39	3.44
## sepal_fusion	735	1.00	6.00	3.00	2.91	0.92
## s_fusion_ratio	725	0.07	0.83	0.30	0.30	0.10
## petal_length	683	15.00	40.00	27.50	26.72	4.53
## petal_width	690	5.00	24.00	12.00	12.13	3.60
## petal_fusion	589	0.00	29.00	0.00	1.90	4.43
## p_fusion_ratio	580	0.00	1.00	0.00	0.07	0.16
## filament_width	693	1.00	6.00	1.50	1.76	0.79
## filament_fusion	687	3.00	19.00	9.00	9.23	3.47
## fil_fusion_ratio	676	0.14	0.55	0.32	0.34	0.09
## anther_length	639	1.50	14.00	6.00	6.90	2.48
## anther_width	639	2.00	10.00	5.00	5.19	1.47

Reformat variables

```
flwr$s_fusion_ratio <- as.numeric(as.character(flwr$s_fusion_ratio))
flwr$filament_length <- as.numeric(as.character(flwr$filament_length))
```

```
## Warning: NAs introduced by coercion
```

Create a new binary variable to describe the fusion of the petals:

```
flwr$petal_fused <- ifelse(flwr$petal_fusion > 0, 1, 0)
head(factor(flwr$petal_fused, labels = c("fused", "free")))
```

```
## [1] <NA> <NA> <NA> <NA> <NA> <NA>
## Levels: fused free
```

1.2 Create distinct dataframes for each species

```
tsjer <- subset(flwr, flwr$species == "tsjeriamcottam")
effusa <- subset(flwr, flwr$species == "effusa")
schimp <- subset(flwr, flwr$species == "schimperi")
```

2 Number of observations

2.1 Number of herbarium specimens examined per species and per gender

In flwr:

```
aggregate(spec_ID ~ sex + species, data = flwr, function(x) length(unique(x)))
```

```
##      sex      species spec_ID
## 1 female      effusa      4
## 2  male      effusa      4
## 3 female    schimperi      3
## 4  male    schimperi      3
## 5 female tsjeriamcottam      3
## 6  male tsjeriamcottam      4
```

2.2 Number of individual flowers examined per species and per gender

```
aggregate(flower_ID ~ sex + species, data = flwr, function(x) length(unique(x)))
```

```
##      sex      species flower_ID
## 1 female      effusa      32
## 2  male      effusa      26
## 3 female    schimperi      20
## 4  male    schimperi      21
## 5 female tsjeriamcottam      25
## 6  male tsjeriamcottam      25
```

2.3 Number of flowers examined on each herbarium specimen

```
aggregate(flower_ID ~ sex + species + spec_ID, data = flwr, function(x) length(unique(x)))
```

```
##      sex      species spec_ID flower_ID
## 1 female tsjeriamcottam   BK1         5
## 2 female tsjeriamcottam   BK2        10
## 3  male tsjeriamcottam   BK3         5
## 4  male tsjeriamcottam   BK4         3
## 5  male tsjeriamcottam   BK5         7
## 6  male tsjeriamcottam    E4        10
## 7 female      effusa    E5         6
## 8  male      effusa   K10         6
## 9  male      effusa   K11         5
## 10 female    schimperi   K20        10
## 11 female    schimperi   K21         7
## 12 female    schimperi  K23b         3
## 13  male      schimperi   K25         5
## 14  male      schimperi   K26        10
## 15  male      schimperi   K28         6
## 16 female      effusa    K5        10
## 17  male      effusa   K51         5
## 18 female      effusa    K6        10
## 19 female tsjeriamcottam  K67        10
## 20 female      effusa    K7         6
## 21  male      effusa    K8        10
```

3 Variability of floral morphology accross species and gender

3.1 Pedicels

3.1.1 Descriptive statistics

Pedicel length

Mean

```
aggregate(pedicel_length ~ sex + species, data = flwr, mean)
```

```
##      sex      species pedicel_length
## 1 female    effusa      21.43750
## 2 male      effusa      26.26923
## 3 female    schimperi    38.06667
## 4 male      schimperi    34.95238
## 5 female tsjeriamcottam    9.46000
## 6 male      tsjeriamcottam    18.30000
```

Variance

```
aggregate(pedicel_length ~ sex + species, data = flwr, var)
```

```
##      sex      species pedicel_length
## 1 female    effusa      6.125000
## 2 male      effusa     20.684615
## 3 female    schimperi    58.209524
## 4 male      schimperi    30.947619
## 5 female tsjeriamcottam    4.623333
## 6 male      tsjeriamcottam    60.416667
```

Standard deviation

```
aggregate(pedicel_length ~ sex + species, data = flwr, sd)
```

```
##      sex      species pedicel_length
## 1 female    effusa      2.474874
## 2 male      effusa      4.548034
## 3 female    schimperi    7.629517
## 4 male      schimperi    5.563058
## 5 female tsjeriamcottam    2.150194
## 6 male      tsjeriamcottam    7.772816
```

Pedicel width Mean

```
aggregate(pedicel_width ~ sex + species, data = flwr, mean)
```

```
##      sex      species pedicel_width
## 1 female    effusa      6.953125
## 2 male      effusa      4.846154
## 3 female    schimperi    5.925000
## 4 male      schimperi    5.738095
## 5 female tsjeriamcottam    5.420000
## 6 male      tsjeriamcottam    5.180000
```

Variance

```
aggregate(pedicel_width ~ sex + species, data = flwr, var)
```

```
##      sex      species pedicel_width
```

```
## 1 female      effusa      1.6670867
## 2  male      effusa      0.8353846
## 3 female      schimperi    0.5335526
## 4  male      schimperi    0.8404762
## 5 female tsjeriamcottam    1.2433333
## 6  male tsjeriamcottam    1.0808333
```

Standard deviation

```
aggregate(pedicel_width ~ sex + species, data = flwr, sd)
```

```
##      sex      species pedicel_width
## 1 female      effusa      1.2911571
## 2  male      effusa      0.9139938
## 3 female      schimperi    0.7304469
## 4  male      schimperi    0.9167749
## 5 female tsjeriamcottam    1.1150486
## 6  male tsjeriamcottam    1.0396313
```

3.1.2 Statistical tests - Pedicel length

Embelia effusa

Number of observations

```
aggregate(pedicel_length ~ sex + species, data = flwr, function(x) length(x))
```

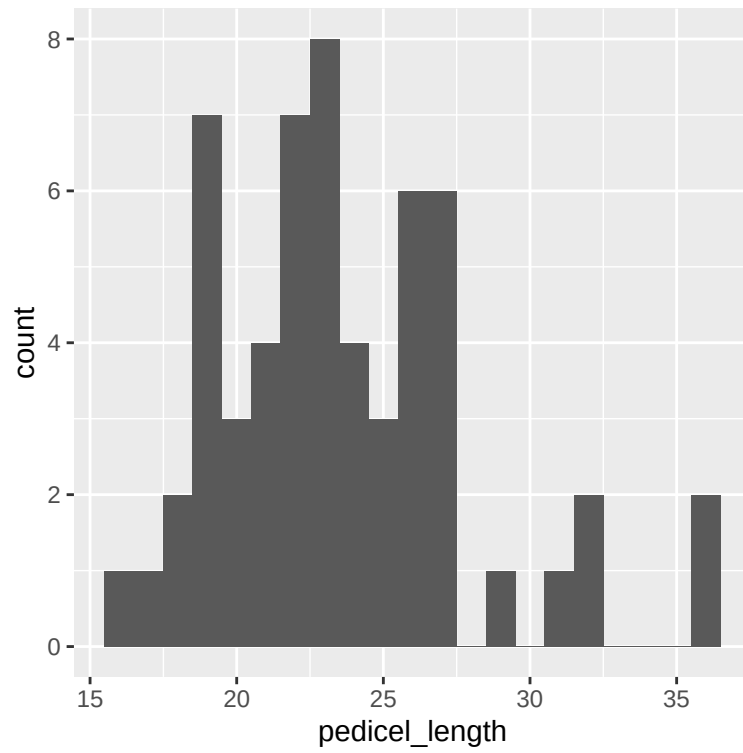
```
##      sex      species pedicel_length
## 1 female      effusa             32
## 2  male      effusa             26
## 3 female      schimperi          15
## 4  male      schimperi          21
## 5 female tsjeriamcottam          25
## 6  male tsjeriamcottam          25
```

The number of observations per group varies between 15 and 32. It is quite low, and the number of observations in male and female groups are not always equal (the data is unbalanced), so the statistical tests have to be chosen and interpreted with caution.

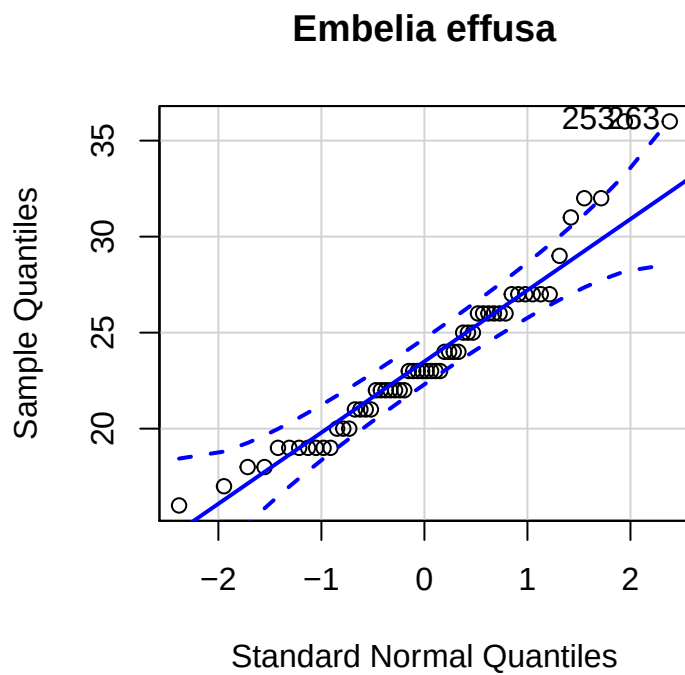
Distribution Pedicel length is a continuous quantitative variable, so its distribution should be normal. It can be checked by plotting the data (the histogram must resemble a Gaussian curve and, in the q-q plot, the sample data points must fit between the two dotted lines representing the 95% confidence interval of the theoretical perfect normal distribution fit).

```
histnormPedL <- ggplot(effusa, aes(pedicel_length))
histnormPedL + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 234 rows containing non-finite values (stat_bin).
```

```
# qqp requires library(car)
qqp(effusa$pedicel_length, "norm", xlab = "Standard Normal Quantiles",
    ylab = "Sample Quantiles", main = "Embelia effusa")
```



```
## [1] 253 263
```

Mixed linear regression model - *Embelia effusa* - pedicel length

In this case, the chosen model is a linear mixed effect regression (`lmer`) because I want to distinguish fixed effects from random effects. The model is built in this way:

```
model<-chosen.model(response.variable ~ explanatory.variable.1 + explanatory.variable.2,
dataframe, options).
```

- The variable of interest (`sex`), of which I want to investigate the effect, is set as a **fixed effect**; the groups that I want to control for (`spec_ID`) are set as **random effects** by using the syntax `(1|random.effect)`. - When there is only one random effect or the random effects are nested (as is the case here), and the data is balanced (the number of observation in each group is similar), the model can use **maximum likelihood** to estimate the parameters (`REML=FALSE`). If not, the model must use **restricted maximum likelihood** (`REML=TRUE`).

Build model

```
# requires library(lme4)
lmPedE <- lmer(pedicel_length ~ sex + (1 | spec_ID), effusa,
              REML = FALSE)
```

Display results

```
summary(lmPedE)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: pedicel_length ~ sex + (1 | spec_ID)
##      Data: effusa
##
##           AIC          BIC    logLik deviance df.resid
##      283.9       292.2   -138.0    275.9        54
##
## Scaled residuals:
##      Min         1Q       Median         3Q        Max
## -1.68190 -0.67517  0.07997  0.54375  2.48443
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   spec_ID  (Intercept)  10.030     3.167
##   Residual                  4.649     2.156
## Number of obs: 58, groups:  spec_ID, 8
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   21.041     1.632   12.897
## sexmale        5.381     2.316    2.324
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.705
```

In the **Random effects** section, in the **Variance** column, we can see how much of the variance observed in the data is explained by “`spec_ID`”. If it had been close to 0, I could have removed `spec_ID` from the model and used a simple linear regression model. But this is not the case here, which means that the specimen on which the pedicel length was recorded has a significant influence on the measurement. In the **Fixed effect** section, the **Estimate** column displays the size of the effect of `sex` on pedicel length: the value in the **Intercept** row represents the average value of pedicel length in the reference level (R automatically takes the first level of a variable, “female” in this case, as a reference). Here, the estimated average length of pedicels in females is “21.04” (which corresponds to 2.104 mm because the length was measured in 0.1 mm). The

value in the **sexmale** row shows the estimated difference between a male and a female. Here, this value is 5.38 (0.538 mm). This means that the model estimates that, on average, the pedicels are 0.538 mm longer in males than in females.

To get a more accurate idea of the size of the effect of sex on pedicel length, we can look at the confidence interval of the effect:

```
confint(lmPedE)

## Computing profile confidence intervals ...
##           2.5 %    97.5 %
## .sig01      1.9470450  5.855077
## .sigma      1.7930452  2.661251
## (Intercept) 17.3909529 24.672163
## sexmale      0.2351851 10.555071
```

By looking at the ***sexmale** row, we can see that the model estimates that the confidence interval is quite wide (0.235 - 10.555). What it means is that there is a 95% probability that the pedicels are 0.024 to 1.06 mm longer in males than in females.

By default, the lme4 package does not provide a p-value in the results of the linear mixed models, because the authors of lme4 do not agree that it is a suitable way to assess the results. If we want an estimate of the significance of the effect of sex on pedicel length, we can do a **Wald-Chi-Squared test**, which will tell us if sex has a significant effect on the model (i.e. if adding it to the model influences the results):

```
# requires library(car)
Anova(lmPedE)

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: pedicel_length
##      Chisq Df Pr(>Chisq)
## sex  5.4005  1    0.02013 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The p-value is below 0.05, which means that, with a 95% confidence, sex does have a significant effect on the length of the pedicels in *Embelia effusa*.

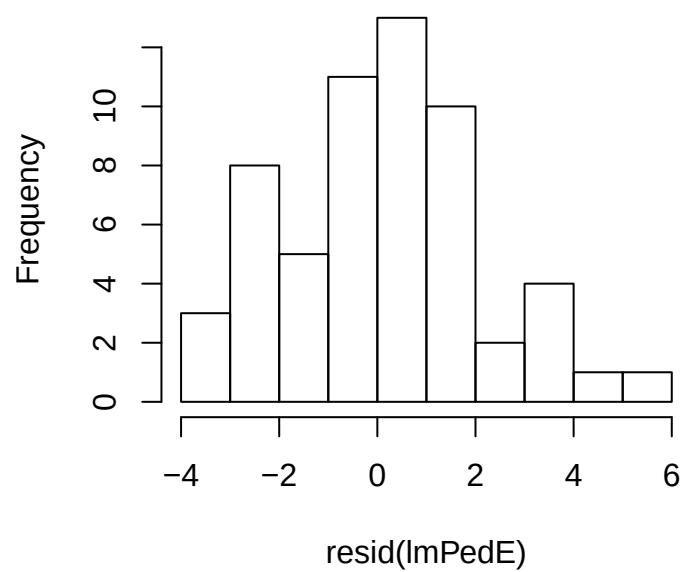
To summarise, the linear mixed effect regression model estimates that sex has a significant effect on the length of the pedicels and that there is a 95% probability that the pedicels are 0.02 to 1 mm longer in males than females, with an average of 0.5 mm longer.

Check normality of residuals

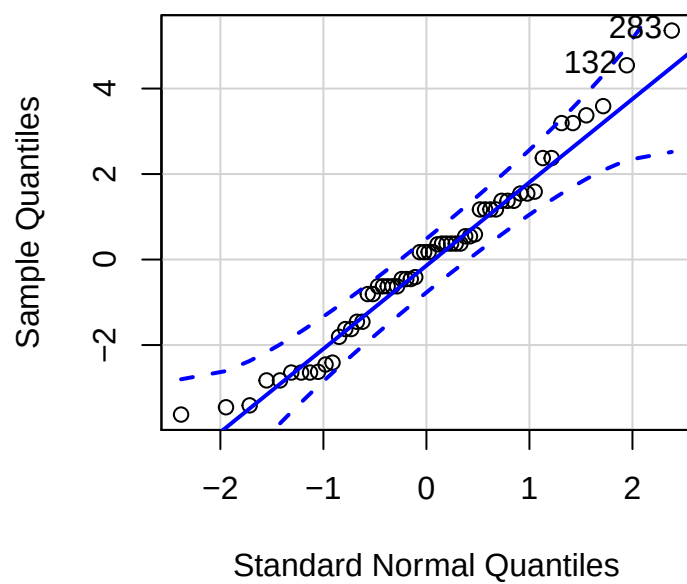
One of the conditions to use a linear regression model is that the residuals must have a normal distribution. We can check this by plotting them (the histogram must resemble a Gaussian curve; the residual points must fit between the two dotted lines representing the 95% confidence interval of the theoretical perfect normal distribution fit)

```
hist(resid(lmPedE))
```

Histogram of resid(lmPedE)



```
qqp(resid(lmPedE), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```



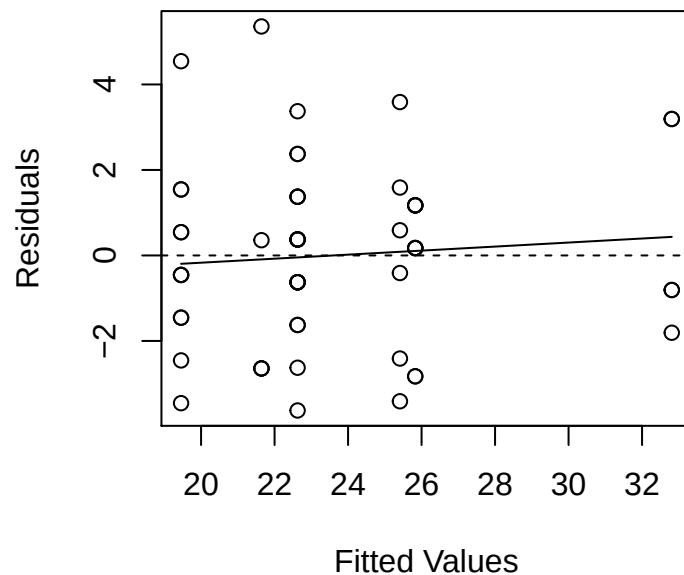
```
## 283 132
## 57 27
```

Check model fit

We can also check whether the model adequately describes the variation in the data by plotting the residuals against a line representing the best-fitting model:

```
plot(fitted(lmPedE), residuals(lmPedE), xlab = "Fitted Values",  
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")  
abline(h = 0, lty = 2)  
lines(smooth.spline(fitted(lmPedE), residuals(lmPedE)))
```

Linear mixed model using maximum likelih



The residuals are not perfectly aligned with the best-fit model line, which means that there are other factors that influence pedicel length, apart from sex and specimen. It is a relatively good fit, however, so I will accept the results of the model but keep in mind that they are imperfect.

Embelia schimperi

Number of observations

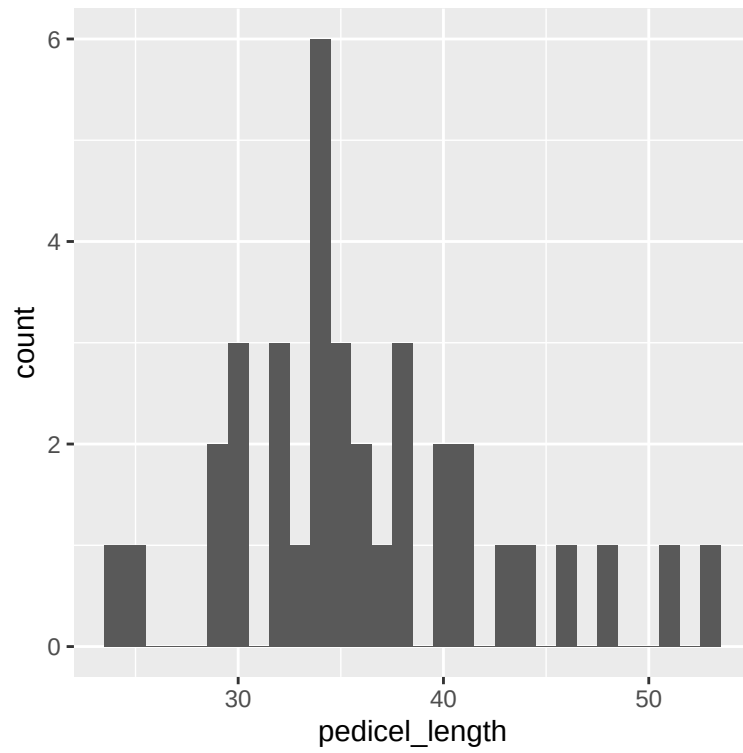
```
aggregate(pedicel_length ~ sex + species, data = schimp, function(x) length(x))
```

```
##      sex  species pedicel_length  
## 1 female schimperi             15  
## 2  male schimperi             21
```

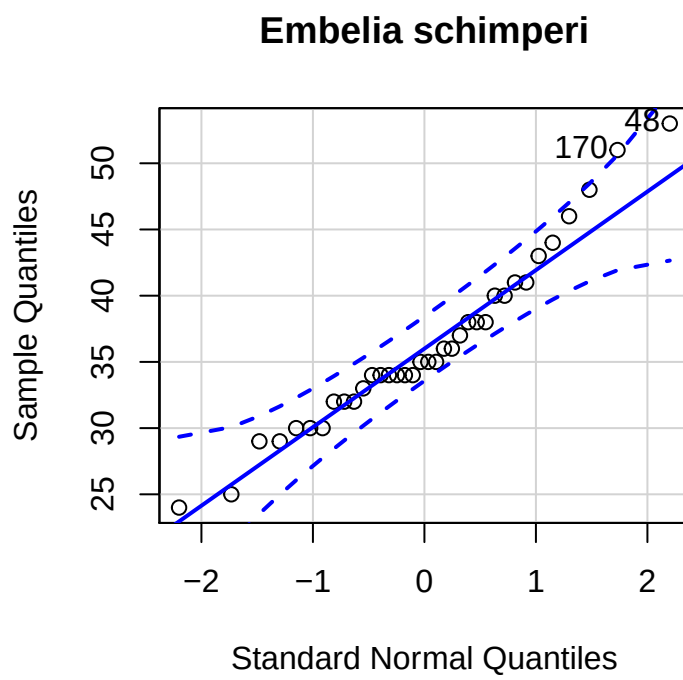
Distribution

```
histnormPedS <- ggplot(schimp, aes(pedicel_length))  
histnormPedS + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",  
  "lightsalmon"))
```

```
## Warning: Removed 158 rows containing non-finite values (stat_bin).
```



```
qqp(schimp$pedicel_length, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia schimperi")
```



```
## [1] 48 170
```

Build model

```
lmPedS <- lmer(pedichel_length ~ sex + (1 | spec_ID), schimp,  
  REML = FALSE)
```

Display results

```
summary(lmPedS)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']  
## Formula: pedichel_length ~ sex + (1 | spec_ID)  
## Data: schimp  
##  
##      AIC      BIC    logLik deviance df.resid  
##  235.6    242.0   -113.8    227.6      32  
##  
## Scaled residuals:  
##      Min       1Q   Median       3Q      Max  
## -1.75709 -0.69338  0.09572  0.46909  2.25589  
##  
## Random effects:  
## Groups Name Variance Std.Dev.  
## spec_ID (Intercept) 13.73  3.705  
## Residual 25.93  5.092  
## Number of obs: 36, groups: spec_ID, 6  
##  
## Fixed effects:  
## Estimate Std. Error t value  
## (Intercept) 38.093 2.580 14.764  
## sexmale -2.776 3.543 -0.784  
##  
## Correlation of Fixed Effects:  
## (Intr)  
## sexmale -0.728
```

```
confint(lmPedS)
```

```
## Computing profile confidence intervals ...  
##      2.5 %    97.5 %  
## .sig01 1.503209 8.279717  
## .sigma 4.038049 6.696882  
## (Intercept) 32.265797 44.027054  
## sexmale -10.966556 5.366592
```

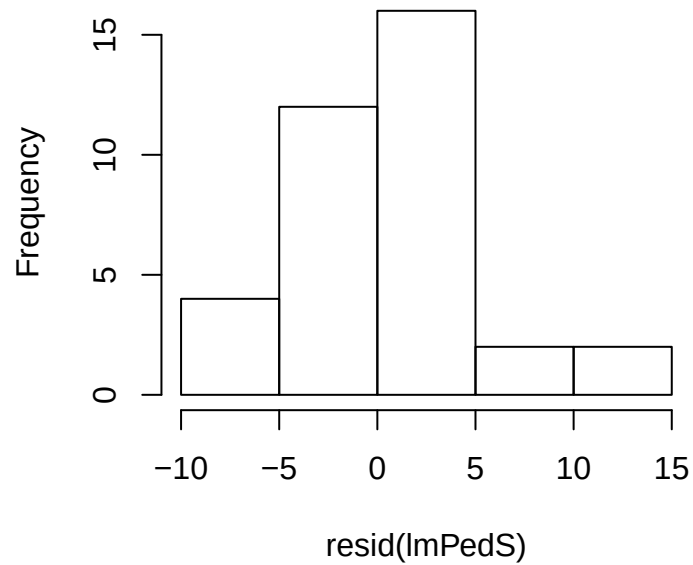
```
Anova(lmPedS)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)  
##  
## Response: pedichel_length  
##      Chisq Df Pr(>Chisq)  
## sex 0.6139 1 0.4333
```

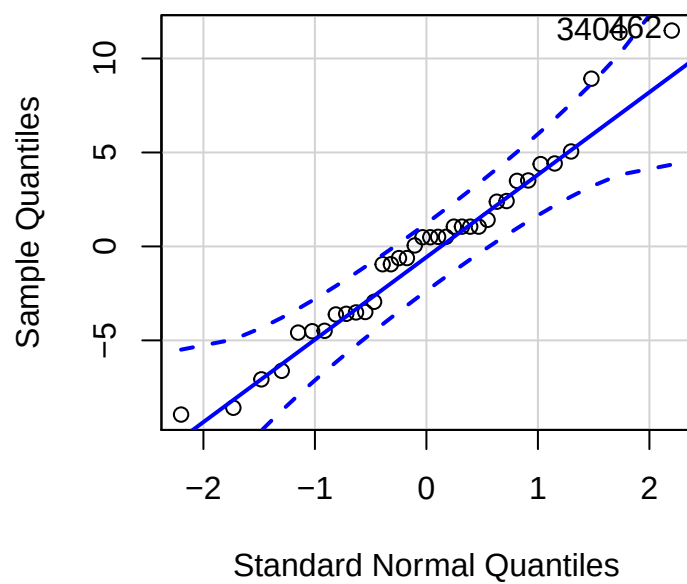
Check normality of residuals

```
hist(resid(lmPedS))
```

Histogram of resid(lmPedS)



```
qqp(resid(lmPedS), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

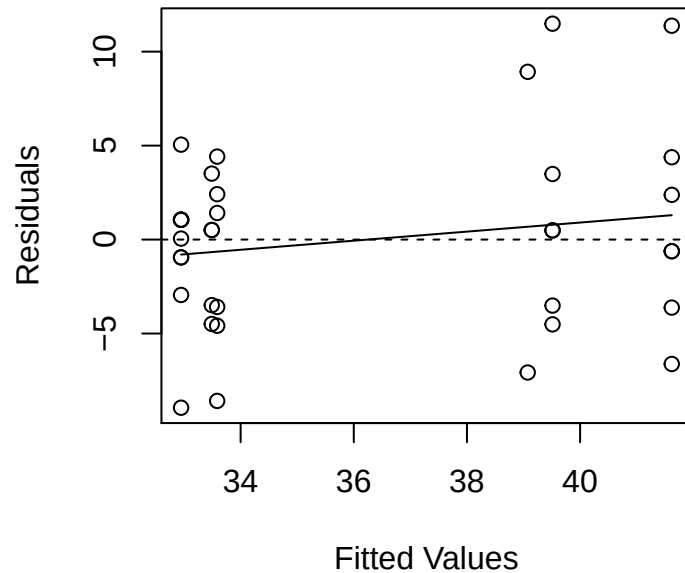


```
## 462 340
## 31 7
```


Check model fit

```
plot(fitted(lmPedS), residuals(lmPedS), xlab = "Fitted Values",  
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")  
abline(h = 0, lty = 2)  
lines(smooth.spline(fitted(lmPedS), residuals(lmPedS)))
```

Linear mixed model using maximum likelih



Embelia tsjeriamcottam

Number of observations

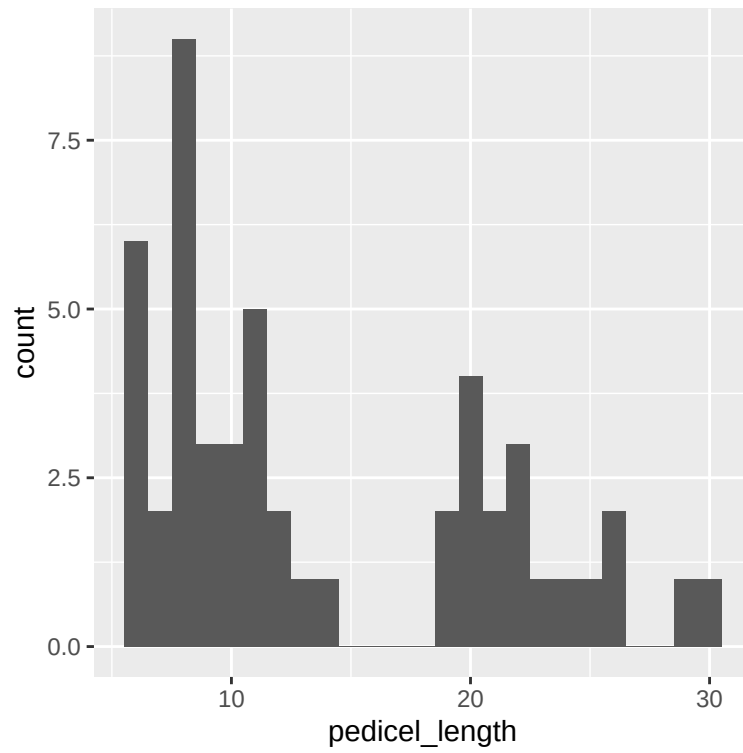
```
aggregate(pedicel_length ~ sex + species, data = tsjer, function(x) length(x))
```

```
##      sex      species pedicel_length  
## 1 female tsjeriamcottam           25  
## 2  male tsjeriamcottam           25
```

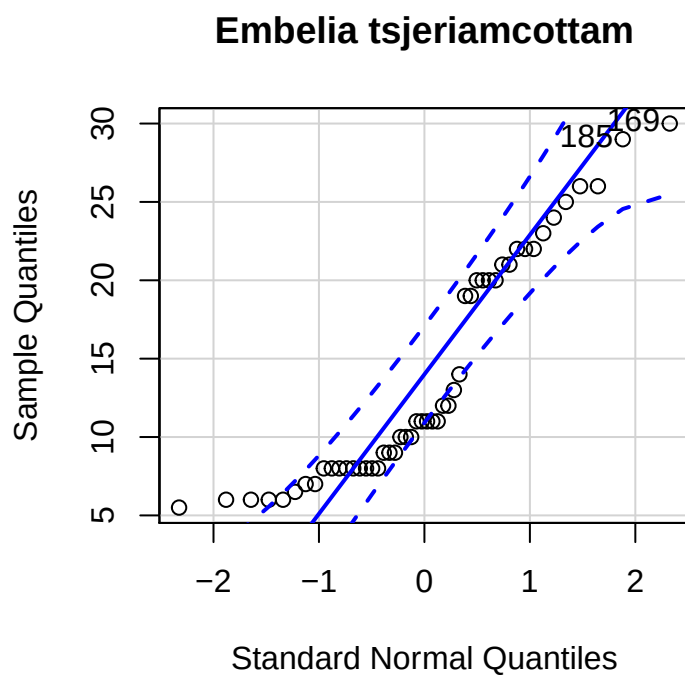
Distribution

```
histnormPedT <- ggplot(tsjer, aes(pedicel_length))  
histnormPedT + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",  
  "lightsalmon"))
```

```
## Warning: Removed 205 rows containing non-finite values (stat_bin).
```



```
qqp(tsjer$pedicel_length, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia tsjeriamcottam")
```



```
## [1] 169 185
```

Build model

```
lmPedT <- lmer(pedicel_length ~ sex + (1 | spec_ID), tsjer, REML = FALSE)
```

Display results

```
summary(lmPedT)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: pedicel_length ~ sex + (1 | spec_ID)
## Data: tsjer
##
##      AIC      BIC    logLik deviance df.resid
##    264.0    271.6   -128.0    256.0      46
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.77543 -0.71457 -0.03321  0.42316  3.03387
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 26.438  5.142
## Residual          6.093  2.468
## Number of obs: 50, groups: spec_ID, 7
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    9.194      3.014    3.051
## sexmale        9.469      3.998    2.368
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.754
```

```
confint(lmPedT)
```

```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01      3.2037091  9.812558
## .sigma      2.0262304  3.098098
## (Intercept) 2.3641311 16.014358
## sexmale     0.4443563 18.531877
```

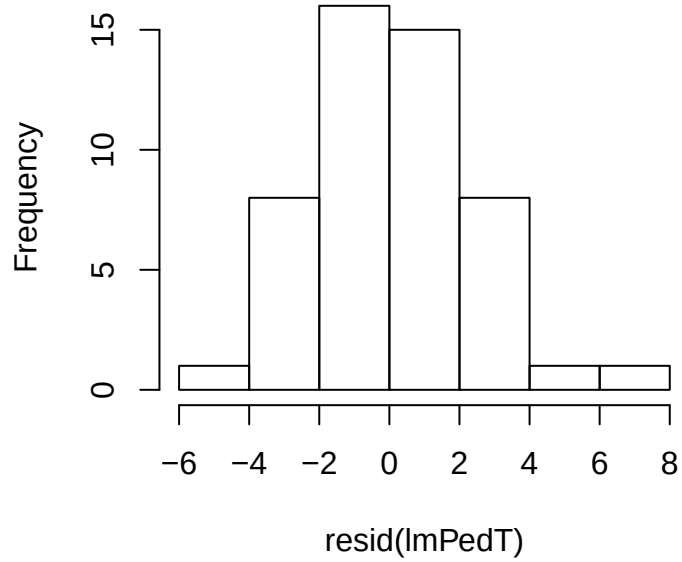
```
Anova(lmPedT)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: pedicel_length
##      Chisq Df Pr(>Chisq)
## sex 5.6087  1  0.01787 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

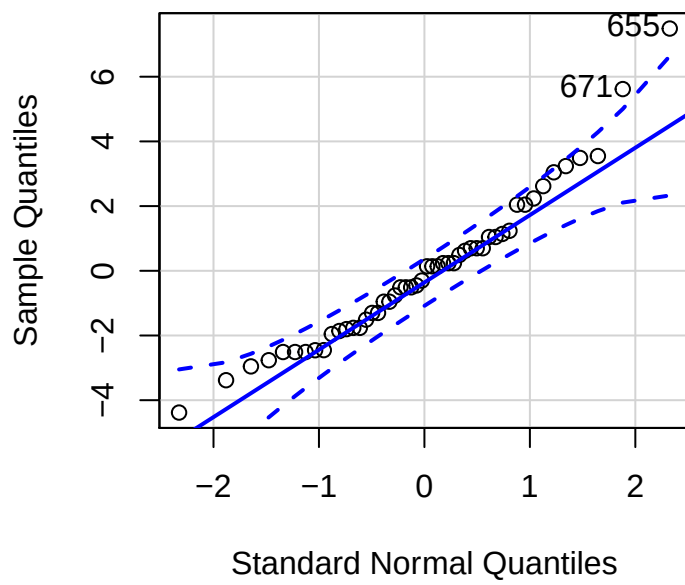
Check normality of residuals

```
hist(resid(lmPedT))
```

Histogram of resid(lmPedT)



```
qqp(resid(lmPedT), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

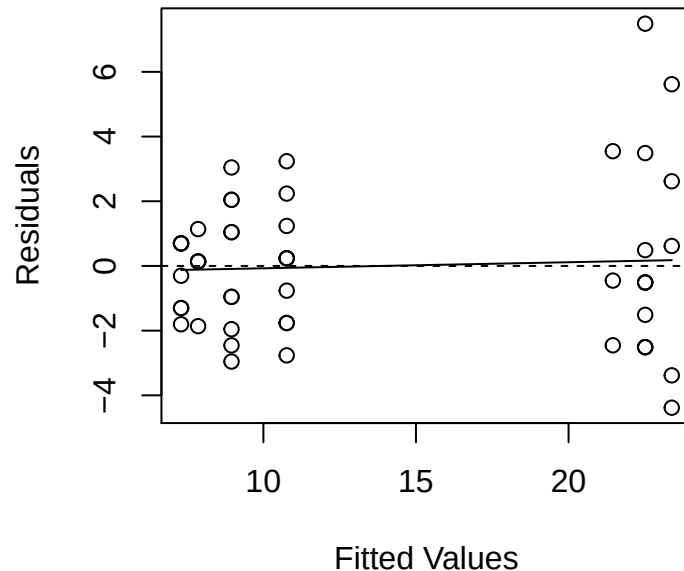


```
## 655 671
## 34 37
```

Check model fit

```
plot(fitted(lmPedT), residuals(lmPedT), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmPedT), residuals(lmPedT)))
```

Linear mixed model using maximum likelih



3.1.3 Statistical tests - Pedicel width

Embelia effusa

Check number of observations

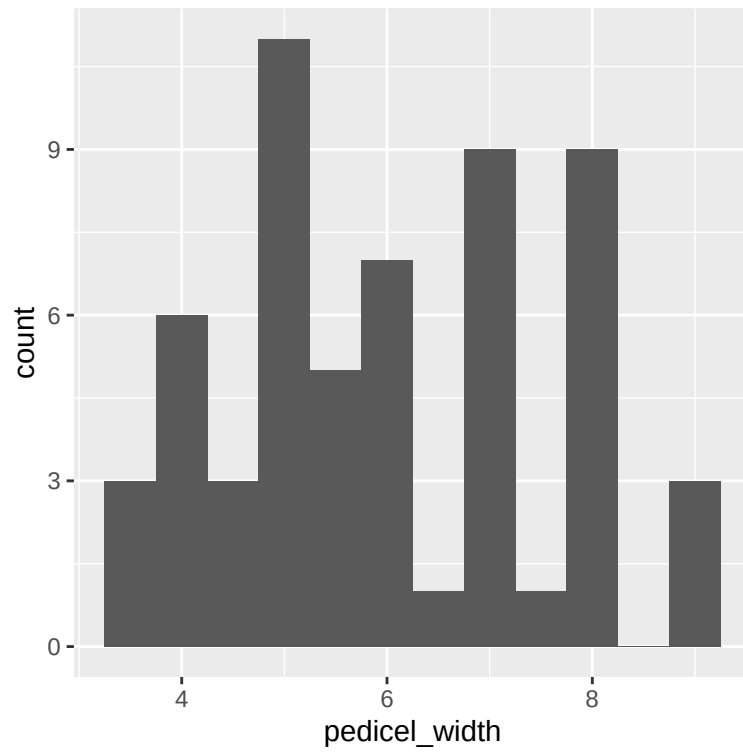
```
aggregate(pedicel_width ~ sex + species, data = flwr, function(x) length(x))
```

```
##      sex      species pedicel_width
## 1 female    effusa      32
## 2 male      effusa      26
## 3 female    schimperi    20
## 4 male      schimperi    21
## 5 female tsjeriamcottam    25
## 6 male      tsjeriamcottam    25
```

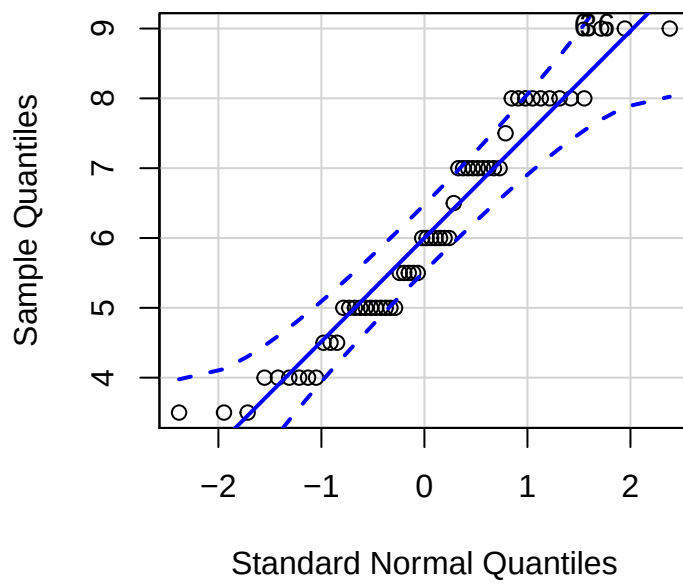
Check distribution

```
histnormPedW <- ggplot(effusa, aes(pedicel_width))
histnormPedW + geom_histogram(binwidth = 0.5) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 234 rows containing non-finite values (stat_bin).
```



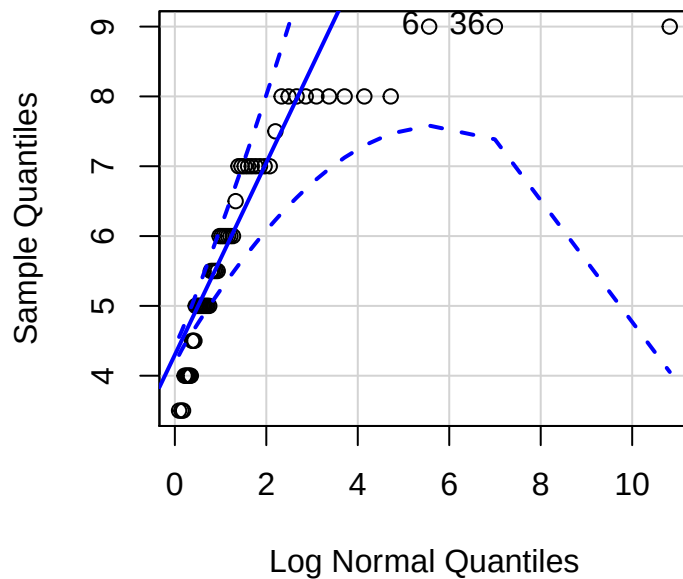
```
qqp(effusa$pedicel_width, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```



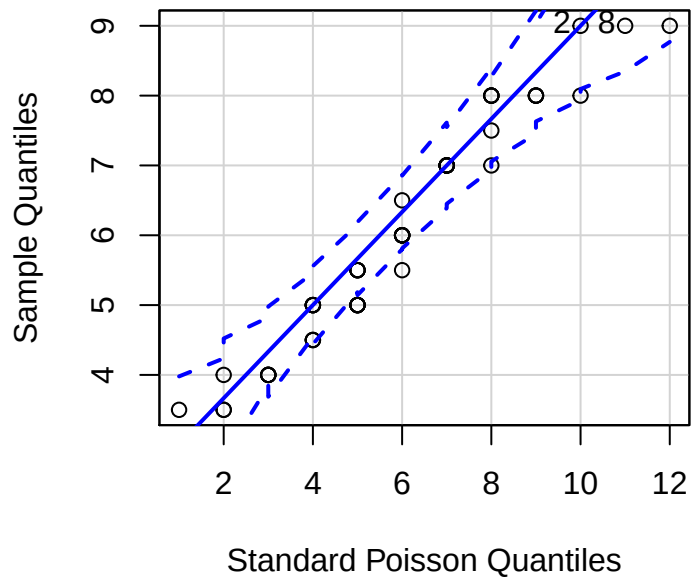
```
## [1] 6 36
```

The pedicel_width data points look more like a “count” value on the graph (maybe because it could only be measured to 0.05 mm, and the range of measurements is limited, so there is a small number of possible values). Its distribution could be closer to a Poisson distribution, I will check several distributions to see which one fits best.

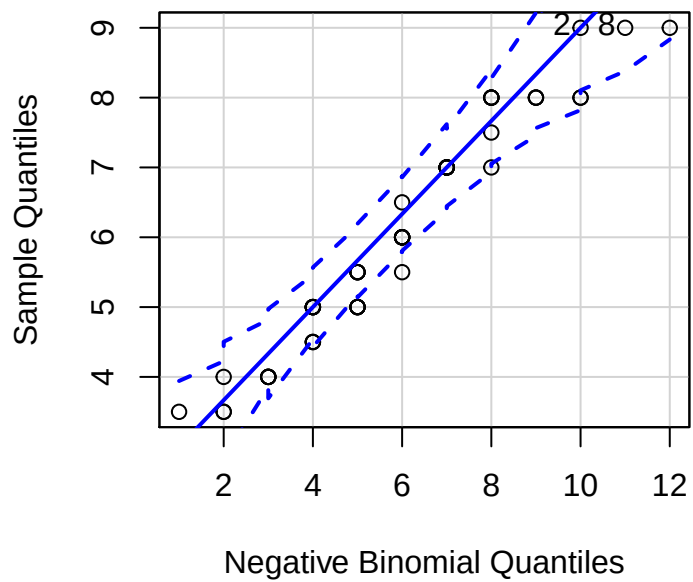
```
# fitdistr requires library(MASS)
qqp(effusa$pedicel_width, "lnorm", xlab = "Log Normal Quantiles",
    ylab = "Sample Quantiles")
```



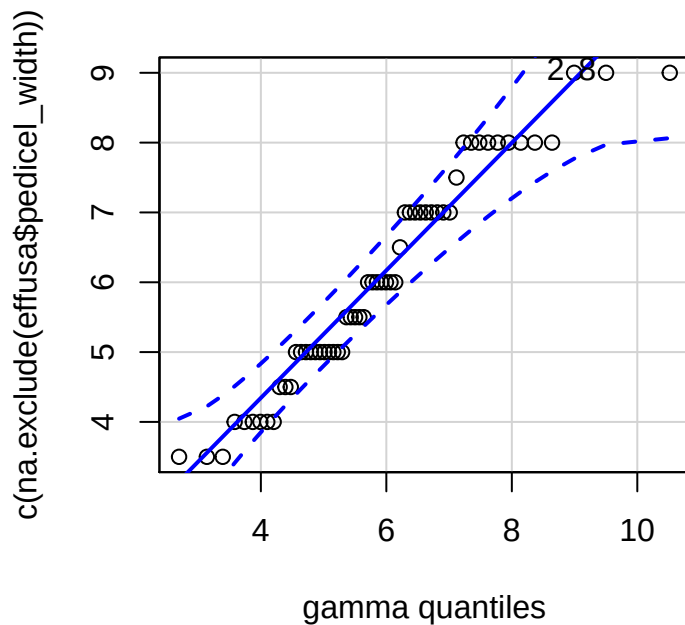
```
## [1] 6 36
poisson <- fitdistr(c(na.exclude(as.integer(effusa$pedicel_width))),
    "Poisson")
# as.integer and na.include are added because a Poisson model
# only takes integers and cannot handle missing values (NAs)
qqp(c(na.exclude(effusa$pedicel_width)), "pois", lambda = poisson$estimate,
    xlab = "Standard Poisson Quantiles", ylab = "Sample Quantiles")
```



```
## [1] 2 8
nbinom <- fitdistr(c(na.exclude(as.integer(effusa$pedicel_width))),
  "Negative Binomial")
qqp(c(na.exclude(effusa$pedicel_width)), "nbinom", size = nbinom$estimate[[1]],
  mu = nbinom$estimate[[2]], xlab = "Negative Binomial Quantiles",
  ylab = "Sample Quantiles")
```

```
## [1] 2 8
gamma <- fitdistr(c(na.exclude(as.integer(effusa$pedicel_width))),
  "gamma")
qqp(c(na.exclude(effusa$pedicel_width)), "gamma", shape = gamma$estimate[[1]],
  rate = gamma$estimate[[2]])
```



```
## [1] 2 8
```

The Poisson distribution fits about as well as a normal distribution.

Build model

```
lmPedwE <- lmer(pedicel_width ~ sex + (1 | spec_ID), effusa,
  REML = FALSE)
```

Display results

```
summary(lmPedwE)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: pedicel_width ~ sex + (1 | spec_ID)
## Data: effusa
##
##      AIC      BIC    logLik deviance df.resid
##    152.1    160.3     -72.0    144.1      54
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.2520 -0.8248 -0.1125  0.5087  2.0129
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 0.6780  0.8234
## Residual          0.5091  0.7135
## Number of obs: 58, groups: spec_ID, 8
##
## Fixed effects:
##              Estimate Std. Error t value
```

```
## (Intercept)    7.0298    0.4317  16.283
## sexmale       -2.2884    0.6140  -3.727
##
## Correlation of Fixed Effects:
##          (Intr)
## sexmale -0.703
```

Confidence interval of the effect

```
confint(lmPedwE)
```

```
## Computing profile confidence intervals ...
```

```
##              2.5 %    97.5 %
## .sig01        0.5023208  1.5280548
## .sigma        0.5937791  0.8795944
## (Intercept)   6.0739379  7.9915512
## sexmale      -3.6566235 -0.9351511
```

Significance of the effect

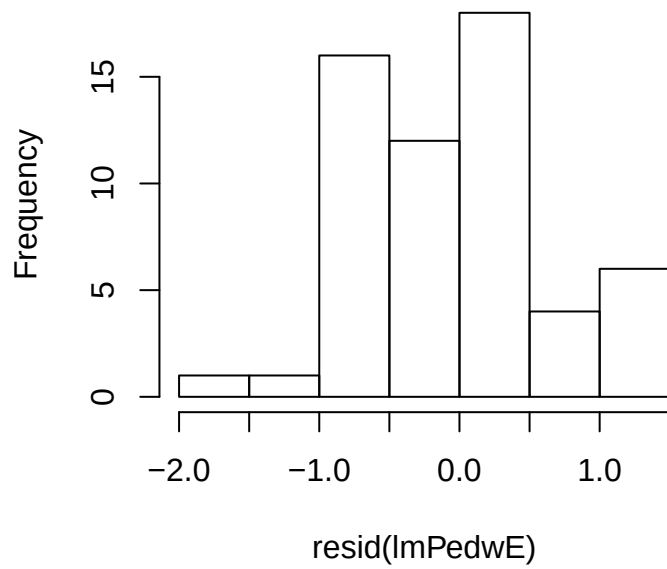
```
Anova(lmPedwE)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: pedicel_width
##      Chisq Df Pr(>Chisq)
## sex 13.892  1  0.0001937 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

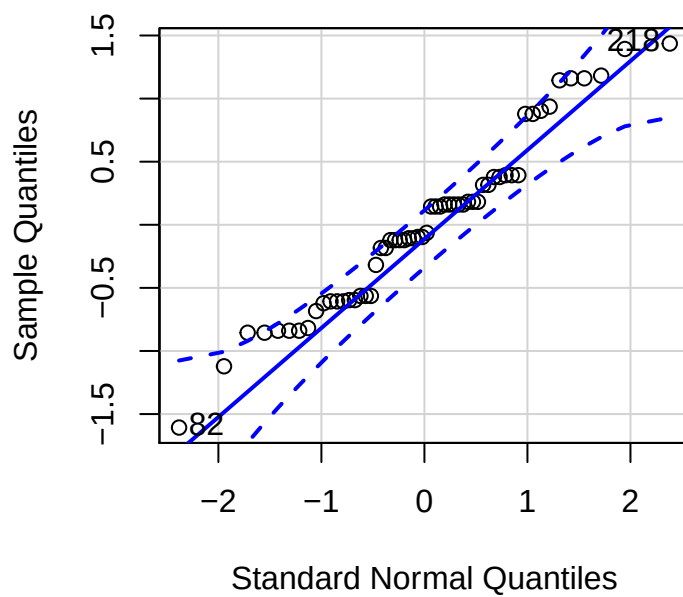
Check residuals

```
hist(resid(lmPedwE))
```

Histogram of resid(lmPedwE)



```
qqp(resid(lmPedwE), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```



```
## 82 218
## 17 44
```

Build Poisson model The distribution of the pedicel width data is not quite normal, which means that a model using maximum likelihood to estimate the parameters may not be appropriate. A **Generalised linear mixed model** using the **Laplace approximation** can handle discrete, non-normal data, as long as there are fewer than 3 random effects (which is the case here).

```
glmPedwE <- glmer(as.integer(pedicel_width) ~ sex + (1 | spec_ID),
  effusa, family = poisson(log))
# The Poisson distribution seemed to be a good fit, so the
# family argument is set as 'poisson'.
```

Display Poisson results

```
summary(glmPedwE)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: as.integer(pedicel_width) ~ sex + (1 | spec_ID)
## Data: effusa
##
##      AIC      BIC    logLik deviance df.resid
##    228.2    234.4   -111.1    222.2      55
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.01000 -0.26375  0.03956  0.33024  1.05124
##
## Random effects:
##  Groups Name      Variance Std.Dev.
## spec_ID (Intercept) 0.003883 0.06232
## Number of obs: 58, groups: spec_ID, 8
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.93242    0.07447  25.950 < 2e-16 ***
## sexmale      -0.39952    0.12253  -3.261  0.00111 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.606
```

Confidence interval of the effect (Poisson)

```
confint(glmPedwE)

## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01        0.0000000 0.2456232
## (Intercept)  1.7597251 2.0985879
## sexmale      -0.6748778 -0.1464718
```

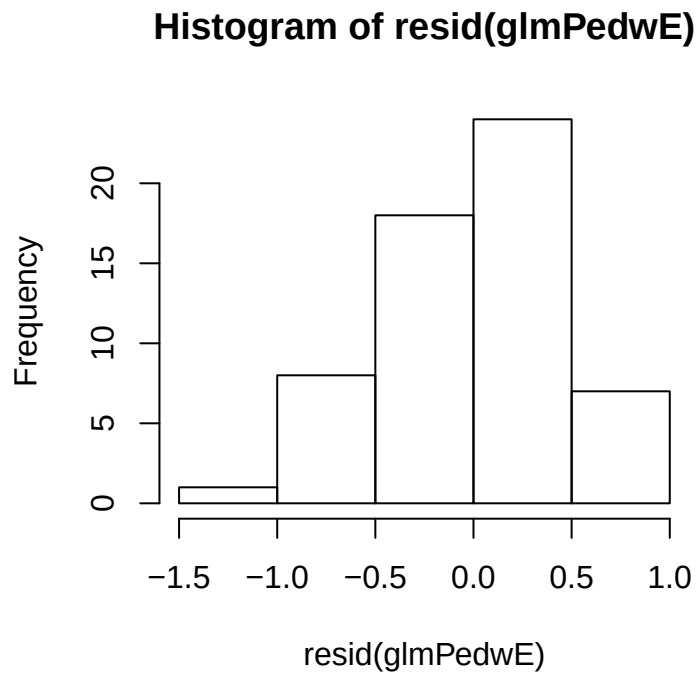
Significance of the effect (Poisson)

```
Anova(glmPedwE)
```

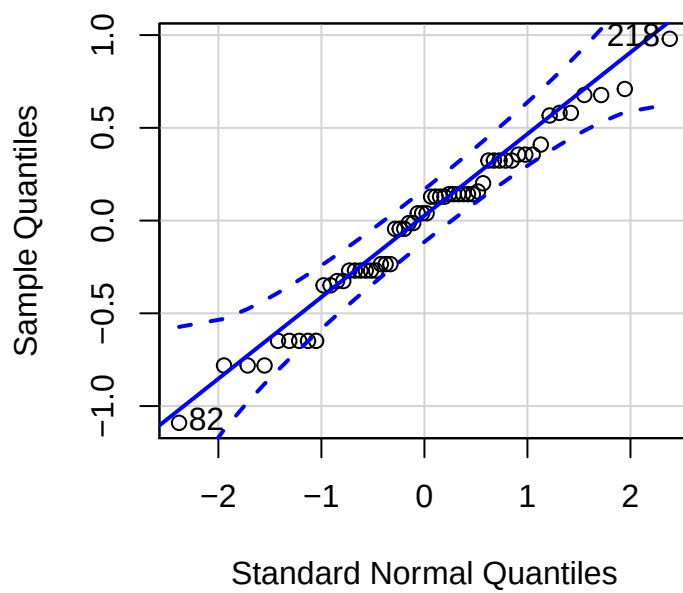
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: as.integer(pedicel_width)
##      Chisq Df Pr(>Chisq)
## sex 10.631  1  0.001112 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Check residuals (Poisson)

```
hist(resid(glmPedwE))
```



```
qqp(resid(glmPedwE), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

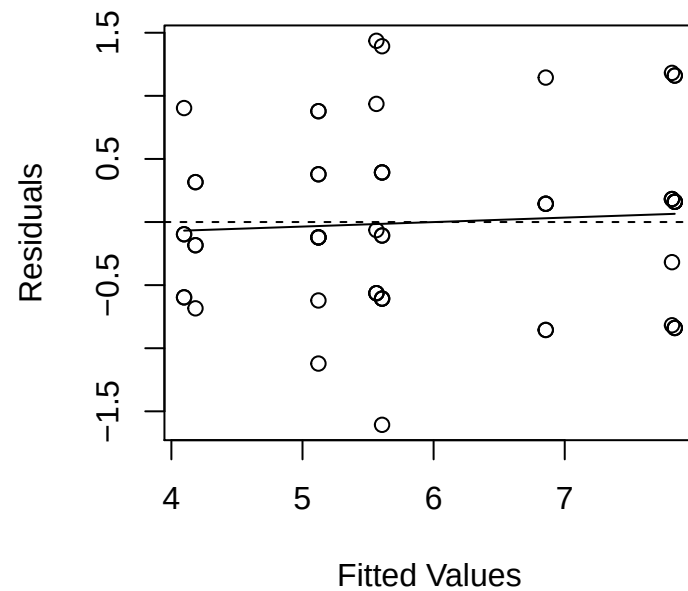


```
## 82 218
## 17 44
```

Check which model has the best fit

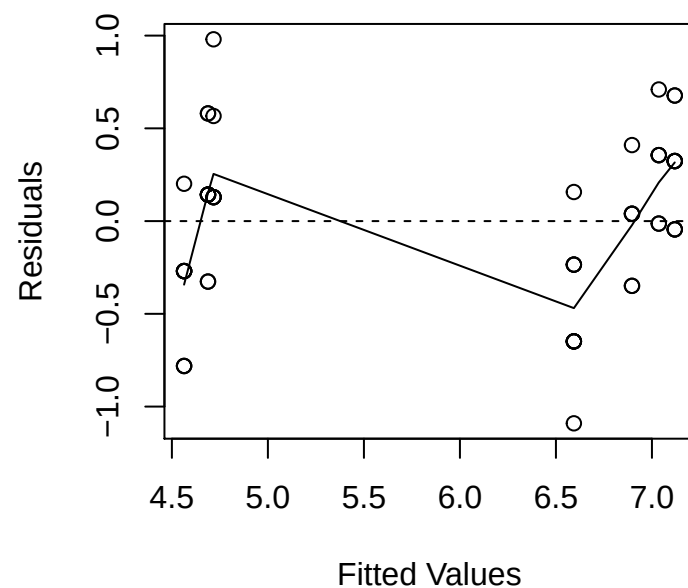
```
plot(fitted(lmPedwE), residuals(lmPedwE), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmPedwE), residuals(lmPedwE)))
```

Linear mixed model using maximum likelihood



```
plot(fitted(glmPedwE), residuals(glmPedwE), xlab = "Fitted Values",
     ylab = "Residuals", main = "Generalised Linear mixed model using Laplace approximation")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(glmPedwE), residuals(glmPedwE)))
```

Generalised Linear mixed model using Laplace approximation



The lmer model has an almost perfect fit, I will keep its results over the glmer-Laplace model

Embelia schimperi

Number of observations

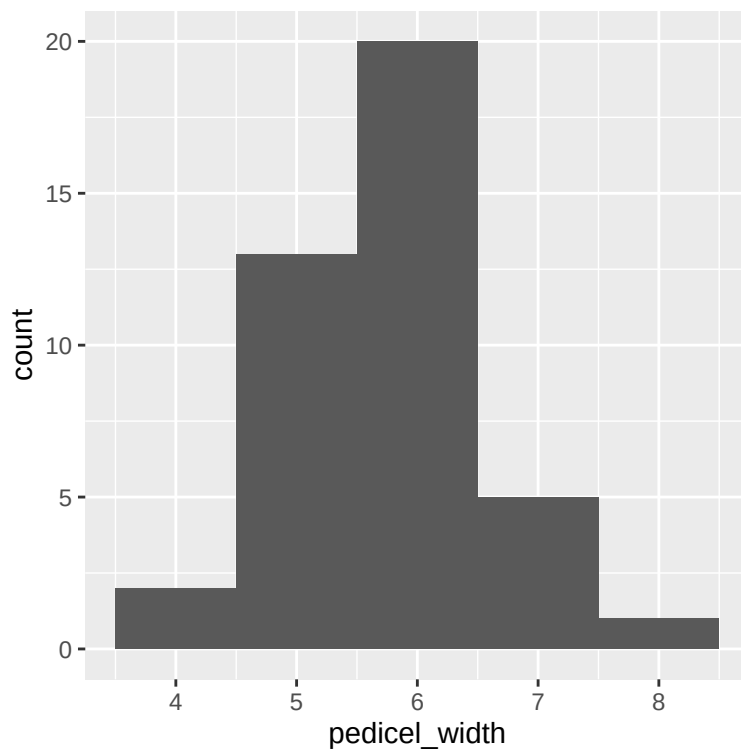
```
aggregate(pedichel_width ~ sex + species, data = schimp, function(x) length(x))
```

```
##      sex  species pedichel_width
## 1 female schimperi             20
## 2  male schimperi             21
```

Distribution

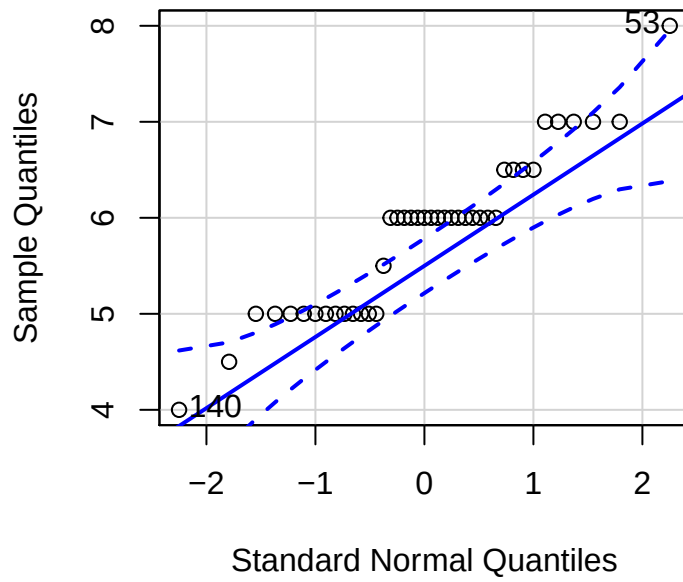
```
histnormPedwS <- ggplot(schimp, aes(pedichel_width))
histnormPedwS + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 153 rows containing non-finite values (stat_bin).
```



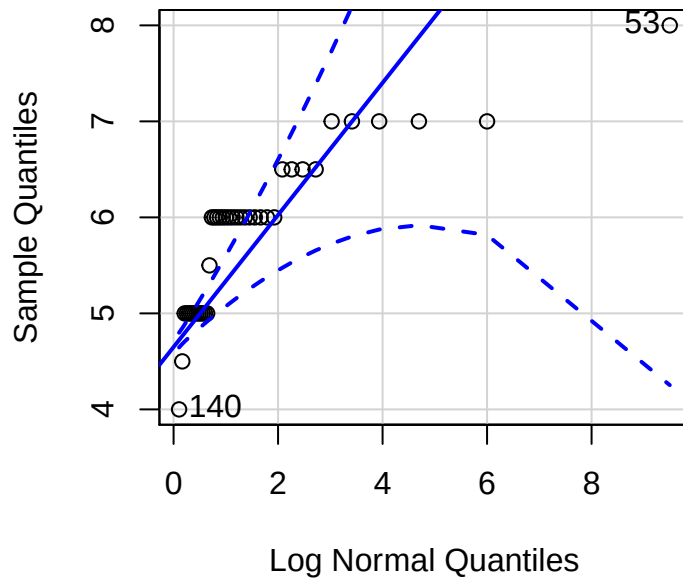
```
qqp(schimp$pedichel_width, "norm", xlab = "Standard Normal Quantiles",
  ylab = "Sample Quantiles", main = "Embelia schimperi")
```

Embelia schimperi



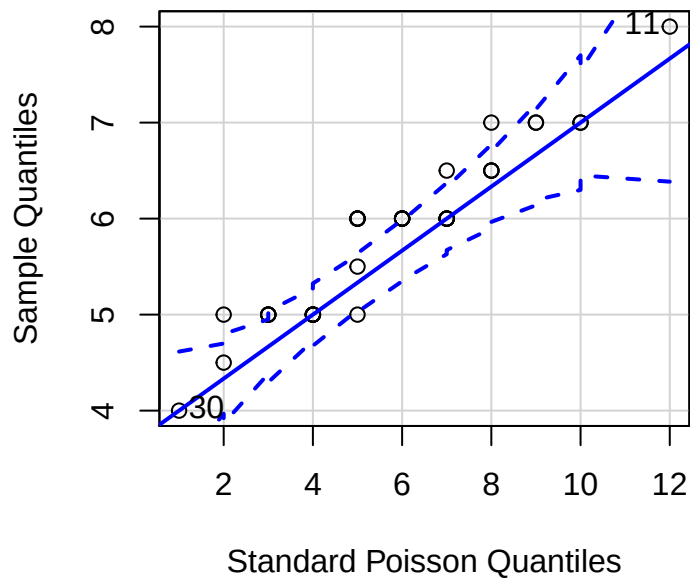
```
## [1] 53 140
```

```
qqp(schimp$pedicel_width, "lnorm", xlab = "Log Normal Quantiles",  
     ylab = "Sample Quantiles")
```



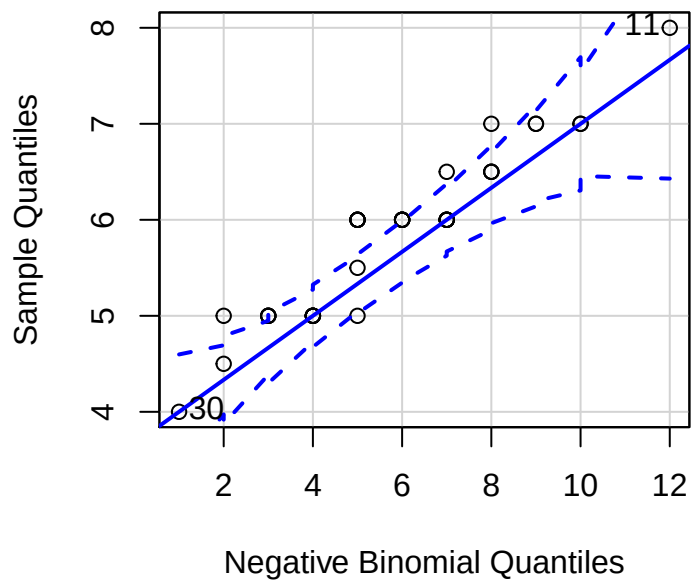
```
## [1] 53 140
```

```
poisson <- fitdistr(c(na.exclude(as.integer(schimp$pedicel_width))),  
  "Poisson")  
# as.integer and na.include are added because a Poisson model  
# only takes integers and cannot handle missing values (NAs)  
qqp(c(na.exclude(schimp$pedicel_width)), "pois", lambda = poisson$estimate,  
  xlab = "Standard Poisson Quantiles", ylab = "Sample Quantiles")
```

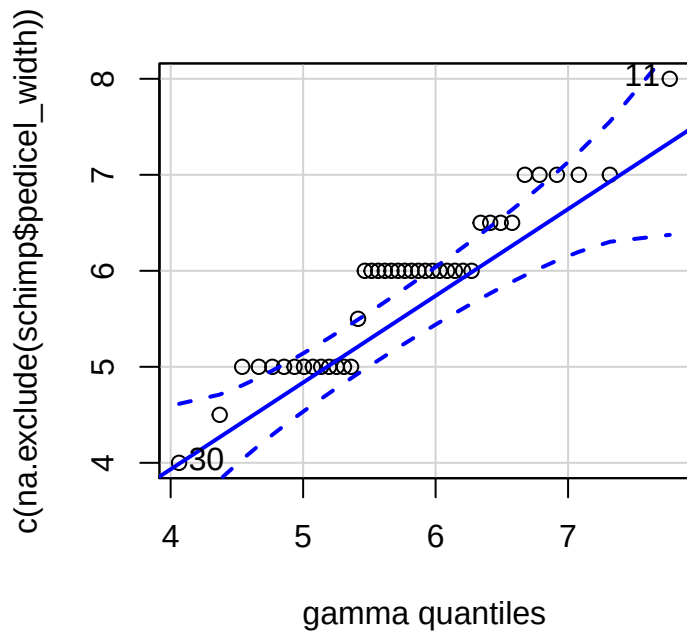


```
## [1] 11 30
```

```
nbinom <- fitdistr(c(na.exclude(as.integer(schimp$pedicel_width))),  
  "Negative Binomial")  
qqp(c(na.exclude(schimp$pedicel_width)), "nbinom", size = nbinom$estimate[[1]],  
  mu = nbinom$estimate[[2]], xlab = "Negative Binomial Quantiles",  
  ylab = "Sample Quantiles")
```



```
## [1] 11 30
gamma <- fitdistr(c(na.exclude(as.integer(schimp$pedicel_width))),
  "gamma")
qqp(c(na.exclude(schimp$pedicel_width)), "gamma", shape = gamma$estimate[[1]],
  rate = gamma$estimate[[2]])
```



```
## [1] 11 30
```

Build model

```
lmPedwS <- lmer(pedicel_width ~ sex + (1 | spec_ID), schimp,
  REML = FALSE)
```

Display results

```
summary(lmPedwS)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: pedicel_width ~ sex + (1 | spec_ID)
## Data: schimp
##
##      AIC      BIC    logLik deviance df.resid
##    99.4    106.3    -45.7    91.4      37
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.9148 -0.4003  0.2006  0.4431  3.1261
##
## Random effects:
##  Groups   Name                Variance Std.Dev.
## spec_ID  (Intercept)  0.2414    0.4914
## Residual                    0.4359    0.6603
## Number of obs: 41, groups:  spec_ID, 6
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  5.96479    0.32639  18.275
```

```
## sexmale      -0.06755    0.45744   -0.148
##
## Correlation of Fixed Effects:
##      (Intr)
## sexmale -0.714

confint(lmPedwS)

## Computing profile confidence intervals ...

##              2.5 %   97.5 %
## .sig01      0.2062272 1.091616
## .sigma      0.5313015 0.851344
## (Intercept) 5.2165388 6.728099
## sexmale     -1.1180532 1.007729

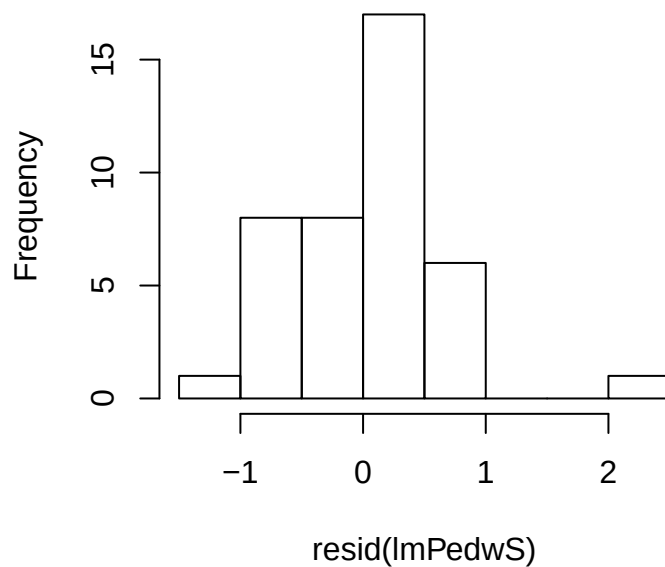
Anova(lmPedwS)

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: pedicel_width
##      Chisq Df Pr(>Chisq)
## sex  0.0218  1    0.8826

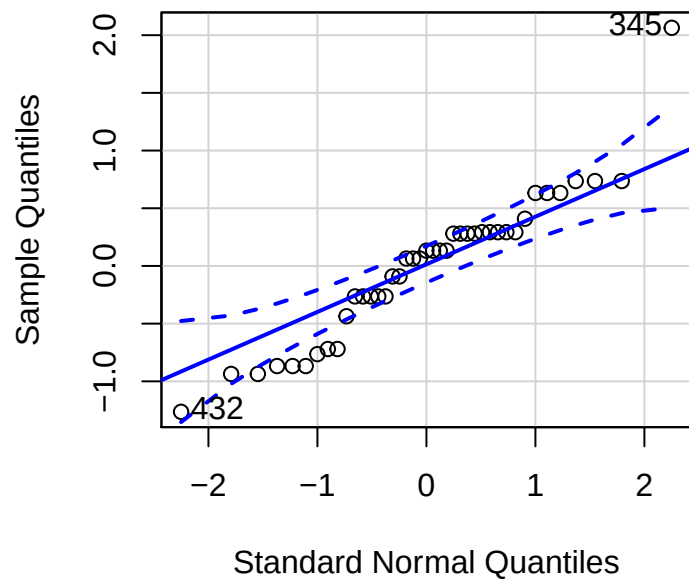
Check normality of residuals

hist(resid(lmPedwS))
```

Histogram of resid(lmPedwS)



```
qqp(resid(lmPedwS), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

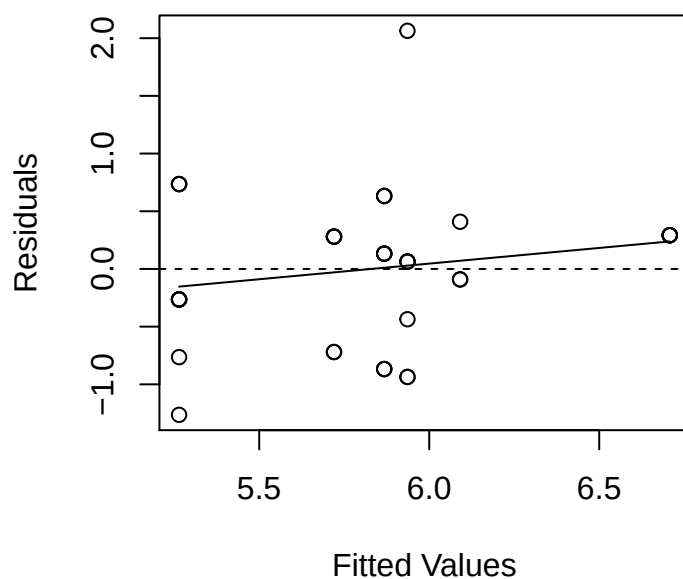


```
## 345 432
## 11 30
```

Check model fit

```
plot(fitted(lmPedwS), residuals(lmPedwS), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmPedwS), residuals(lmPedwS)))
```

Linear mixed model using maximum likelih



Embelia tsjeriamcottam

Number of observations

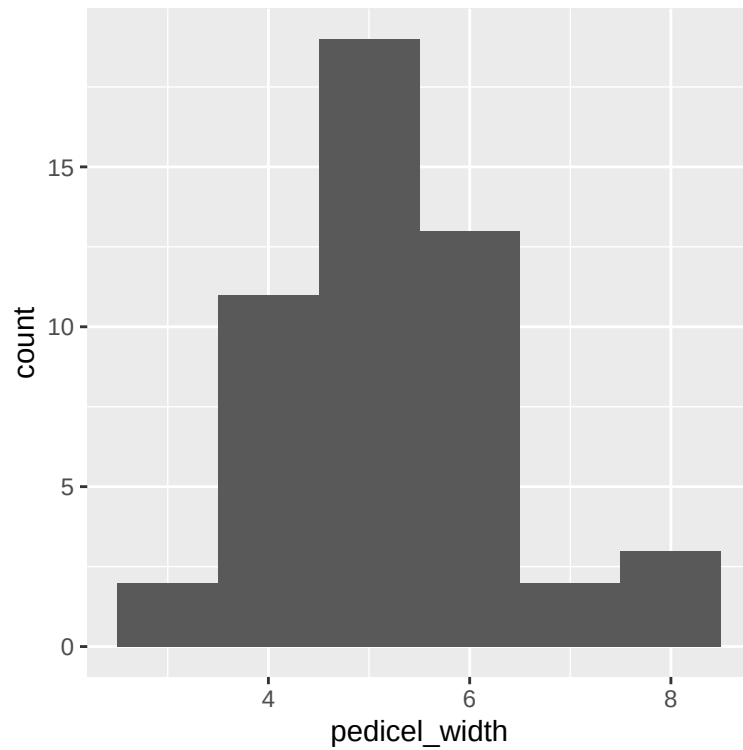
```
aggregate(pedicle_width ~ sex + species, data = tsjer, function(x) length(x))
```

```
##      sex      species pedicle_width
## 1 female tsjeriamcottam           25
## 2  male tsjeriamcottam           25
```

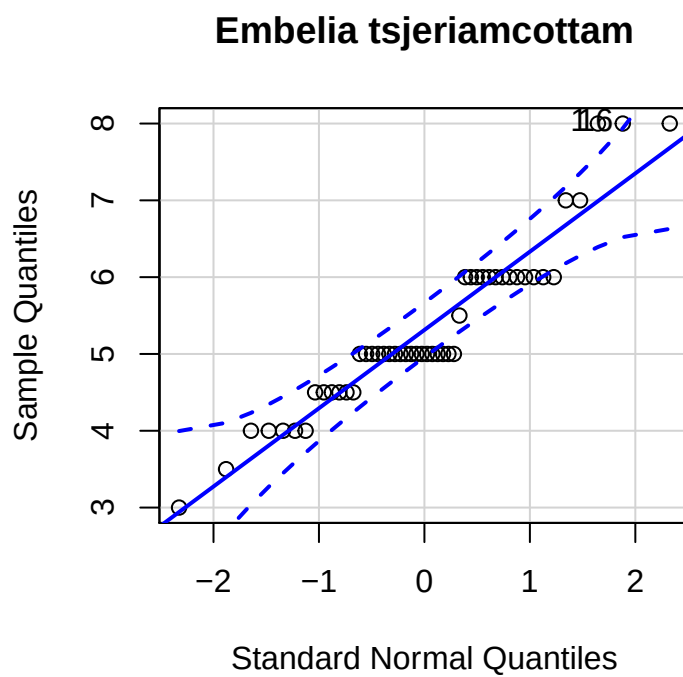
Distribution

```
histnormPedwS <- ggplot(tsjer, aes(pedicle_width))
histnormPedwS + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 205 rows containing non-finite values (stat_bin).
```

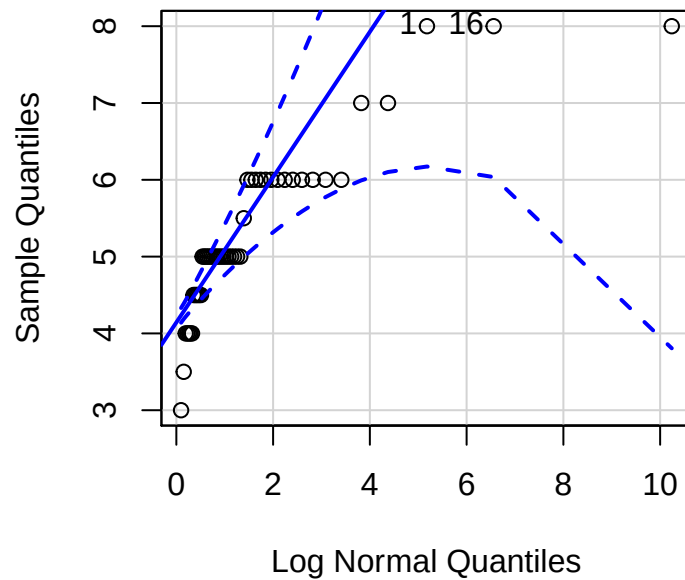



```
qqp(tsjer$pedicel_width, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia tsjeriamcottam")
```



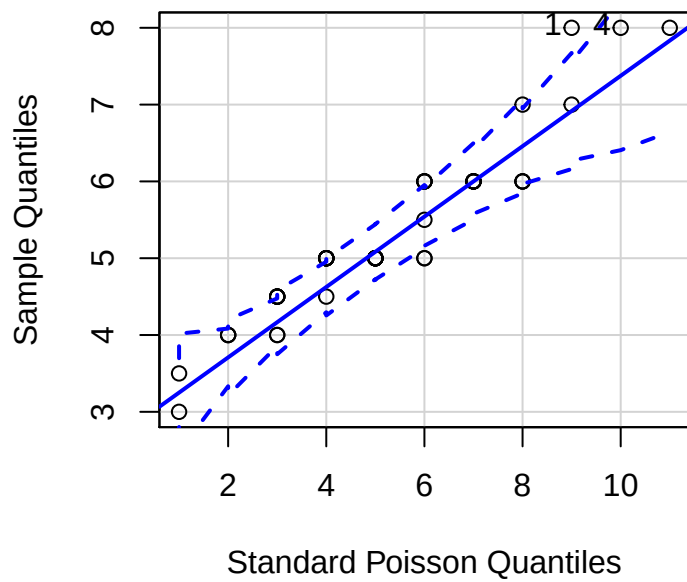
```
## [1] 1 16
```

```
qqp(tsjer$pedicel_width, "lnorm", xlab = "Log Normal Quantiles",
    ylab = "Sample Quantiles")
```

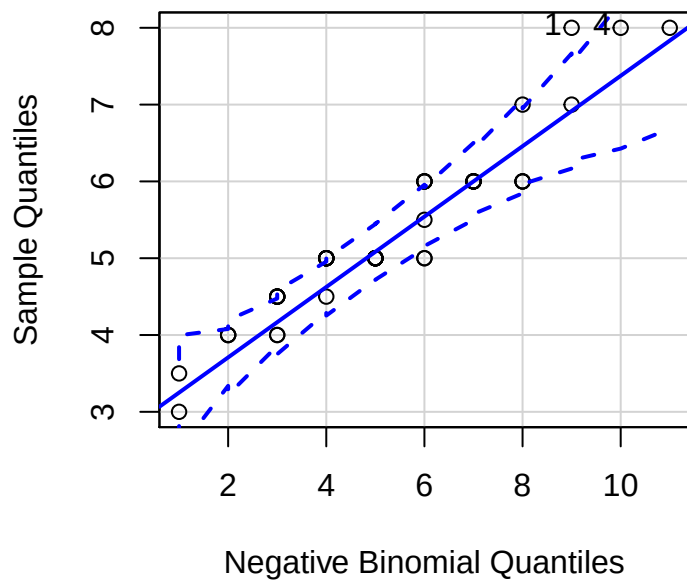


```
## [1] 1 16
```

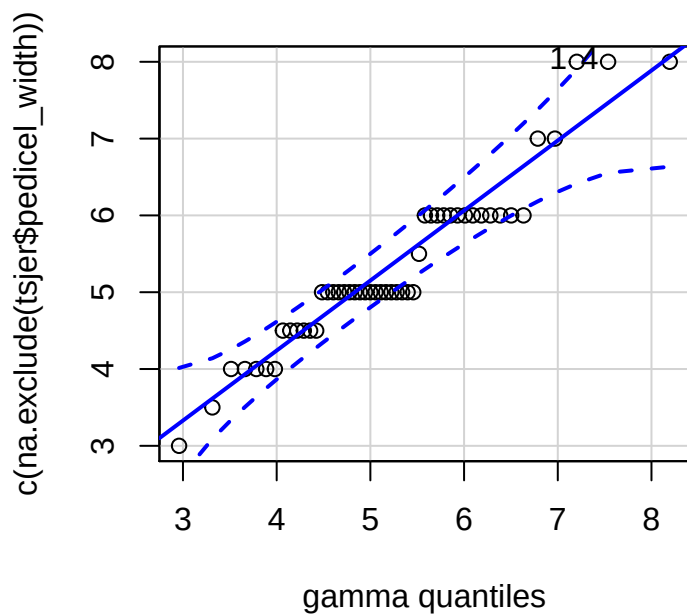
```
poisson <- fitdistr(c(na.exclude(as.integer(tsjer$pedicel_width))),
    "Poisson")
qqp(c(na.exclude(tsjer$pedicel_width)), "pois", lambda = poisson$estimate,
    xlab = "Standard Poisson Quantiles", ylab = "Sample Quantiles")
```



```
## [1] 1 4
nbinom <- fitdistr(c(na.exclude(as.integer(tsjer$pedicel_width))),
  "Negative Binomial")
qqp(c(na.exclude(tsjer$pedicel_width)), "nbinom", size = nbinom$estimate[[1]],
  mu = nbinom$estimate[[2]], xlab = "Negative Binomial Quantiles",
  ylab = "Sample Quantiles")
```



```
## [1] 1 4
gamma <- fitdistr(c(na.exclude(as.integer(tsjer$pedicel_width))),
  "gamma")
qqp(c(na.exclude(tsjer$pedicel_width)), "gamma", shape = gamma$estimate[[1]],
  rate = gamma$estimate[[2]])
```



```
## [1] 1 4
```

Build model

```
lmPedwT <- lmer(pedicel_width ~ sex + (1 | spec_ID), tsjer, REML = FALSE)
```

Display results

```
summary(lmPedwT)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: pedicel_width ~ sex + (1 | spec_ID)
## Data: tsjer
##
##      AIC      BIC    logLik deviance df.resid
##    148.6    156.3     -70.3    140.6      46
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.42360 -0.84888 -0.04519  0.23885  2.44847
##
## Random effects:
##  Groups   Name      Variance Std.Dev.
## spec_ID  (Intercept) 0.3171   0.5631
## Residual                0.8141   0.9023
## Number of obs: 50, groups: spec_ID, 7
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   5.3943    0.3752  14.376
## sexmale      -0.4184    0.5070  -0.825
```

```
##
## Correlation of Fixed Effects:
##      (Intr)
## sexmale -0.740

confint(lmPedwT)

## Computing profile confidence intervals ...

##           2.5 %    97.5 %
## .sig01      0.2113121 1.2230941
## .sigma      0.7401384 1.1332996
## (Intercept) 4.5242159 6.2547347
## sexmale     -1.6167128 0.7032889

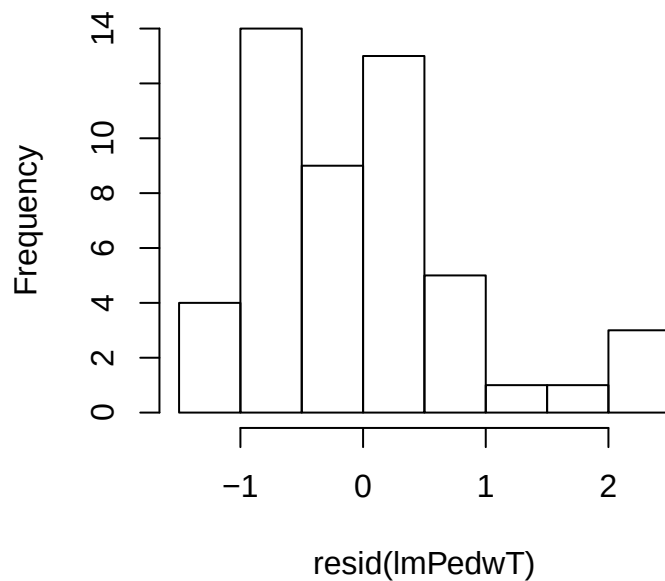
Anova(lmPedwT)

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: pedicel_width
##      Chisq Df Pr(>Chisq)
## sex 0.681  1    0.4092

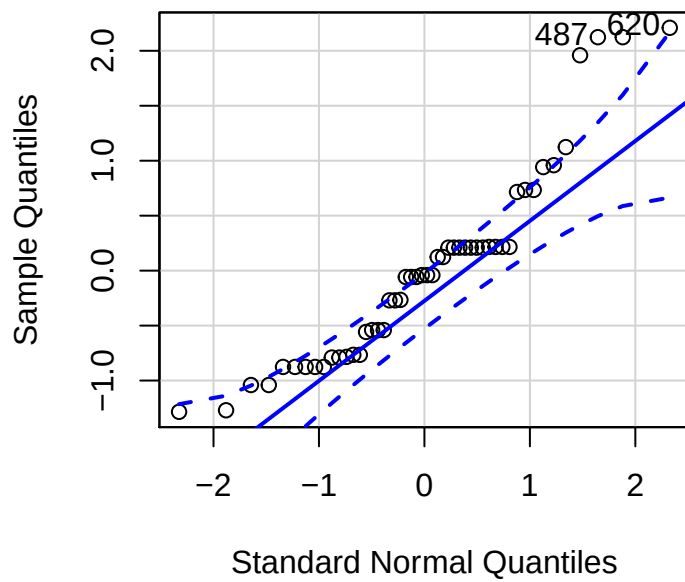
Check normality of residuals

hist(resid(lmPedwT))
```

Histogram of resid(lmPedwT)



```
qqp(resid(lmPedwT), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

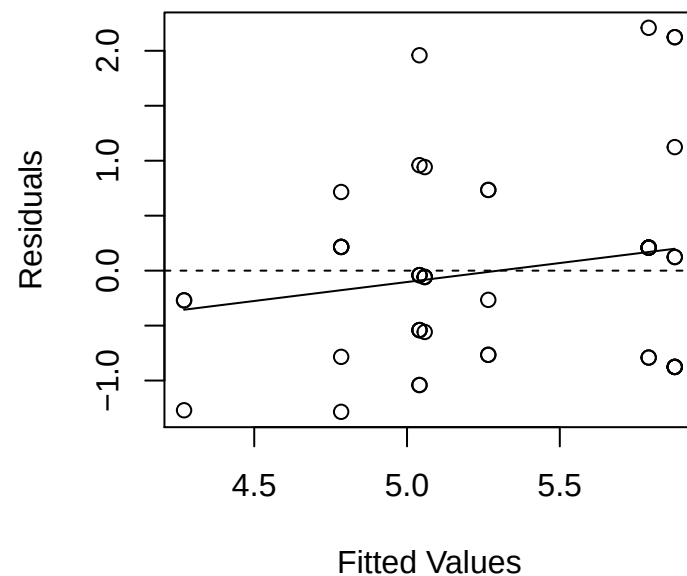


```
## 620 487
## 28 1
```

Check model fit

```
plot(fitted(lmPedwT), residuals(lmPedwT), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmPedwT), residuals(lmPedwT)))
```

Linear mixed model using maximum likelihood



3.2 Sepals

3.2.1 Descriptive statistics

Sepal number

Mean

```
aggregate(sepal_nb ~ sex + species, data = flwr, mean)
```

```
##      sex      species sepal_nb
## 1 female      effusa 5.031250
## 2  male      effusa 5.000000
## 3 female    schimperi 4.650000
## 4  male    schimperi 4.761905
## 5 female tsjeriamcottam 4.920000
## 6  male tsjeriamcottam 5.280000
```

Variance

```
aggregate(sepal_nb ~ sex + species, data = flwr, var)
```

```
##      sex      species sepal_nb
## 1 female      effusa 0.03125000
## 2  male      effusa 0.00000000
## 3 female    schimperi 0.45000000
## 4  male    schimperi 0.39047619
## 5 female tsjeriamcottam 0.07666667
## 6  male tsjeriamcottam 0.29333333
```

Standard deviation


```
aggregate(sepal_nb ~ sex + species, data = flwr, sd)
```

```
##      sex      species sepal_nb
## 1 female      effusa 0.1767767
## 2  male      effusa 0.0000000
## 3 female    schimperi 0.6708204
## 4  male    schimperi 0.6248809
## 5 female tsjeriamcottam 0.2768875
## 6  male tsjeriamcottam 0.5416026
```

Sepal length

Mean

```
aggregate(sepal_length ~ sex + species, data = flwr, mean)
```

```
##      sex      species sepal_length
## 1 female      effusa    9.779503
## 2  male      effusa    8.484496
## 3 female    schimperi   10.054348
## 4  male    schimperi    9.373737
## 5 female tsjeriamcottam    9.762712
## 6  male tsjeriamcottam   11.416667
```

Variance

```
aggregate(sepal_length ~ sex + species, data = flwr, var)
```

```
##      sex      species sepal_length
## 1 female      effusa    1.215140
## 2  male      effusa    2.327883
## 3 female    schimperi    4.029981
## 4  male    schimperi    3.073181
## 5 female tsjeriamcottam    3.515863
## 6  male tsjeriamcottam    5.379000
```

Standard deviation

```
aggregate(sepal_length ~ sex + species, data = flwr, sd)
```

```
##      sex      species sepal_length
## 1 female      effusa    1.102334
## 2  male      effusa    1.525740
## 3 female    schimperi    2.007481
## 4  male    schimperi    1.753049
## 5 female tsjeriamcottam    1.875063
## 6  male tsjeriamcottam    2.319267
```

Sepal width

Mean

```
aggregate(sepal_width ~ sex + species, data = flwr, mean)
```

```
##      sex      species sepal_width
## 1 female      effusa  13.077640
## 2  male      effusa  10.151163
## 3 female    schimperi   7.565217
## 4  male    schimperi   7.385000
## 5 female tsjeriamcottam   4.971311
## 6  male tsjeriamcottam   5.368217
```

Variance

```
aggregate(sepal_width ~ sex + species, data = flwr, var)
```

```
##      sex      species sepal_width
## 1 female      effusa    4.548622
## 2  male      effusa    4.096112
## 3 female    schimperi    2.204491
## 4  male    schimperi    2.640682
## 5 female tsjeriamcottam    0.567352
## 6  male tsjeriamcottam    1.318435
```

Standard deviation

```
aggregate(sepal_width ~ sex + species, data = flwr, sd)
```

```
##      sex      species sepal_width
## 1 female      effusa    2.1327498
## 2  male      effusa    2.0238854
## 3 female    schimperi    1.4847529
## 4  male    schimperi    1.6250175
## 5 female tsjeriamcottam    0.7532277
## 6  male tsjeriamcottam    1.1482313
```

Sepal fusion

Mean

```
aggregate(s_fusion_ratio ~ sex + species, data = flwr, mean)
```

```
##      sex      species s_fusion_ratio
## 1 female      effusa      0.2786335
## 2  male      effusa      0.3552713
## 3 female    schimperi      0.3055435
## 4  male    schimperi      0.3031313
## 5 female tsjeriamcottam      0.2777966
## 6  male tsjeriamcottam      0.3020635
```

Variance

```
aggregate(s_fusion_ratio ~ sex + species, data = flwr, var)
```

```
##      sex      species s_fusion_ratio
## 1 female      effusa    0.008119371
## 2  male      effusa    0.009611059
## 3 female    schimperi    0.013427174
## 4  male    schimperi    0.015027850
## 5 female tsjeriamcottam    0.006947240
## 6  male tsjeriamcottam    0.008813308
```

Standard deviation

```
aggregate(s_fusion_ratio ~ sex + species, data = flwr, sd)
```

```
##      sex      species s_fusion_ratio
## 1 female      effusa    0.09010755
## 2  male      effusa    0.09803601
## 3 female    schimperi    0.11587568
## 4  male    schimperi    0.12258813
## 5 female tsjeriamcottam    0.08335011
## 6  male tsjeriamcottam    0.09387922
```

3.2.2 Statistical tests - Sepal number

Embelia effusa

Check number of observations

```
aggregate(sepal_nb ~ sex + species, data = effusa, function(x) length(x))
```

```
##      sex species sepal_nb
## 1 female  effusa      32
## 2  male   effusa      26
```

Check distribution

The number of sepals is a discrete count variable. A glmer using Laplace approximation and a Poisson distribution is therefore used.

Build model

```
glmSnbE <- glmer(sepal_nb ~ sex + (1 | spec_ID), effusa, family = poisson(log))
```

```
## boundary (singular) fit: see ?isSingular
```

Display results

```
summary(glmSnbE)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: sepal_nb ~ sex + (1 | spec_ID)
## Data: effusa
##
##      AIC      BIC    logLik deviance df.resid
##    208.2    214.4   -101.1    202.2      55
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.01393 -0.01393 -0.01393  0.00000  0.43189
##
## Random effects:
## Groups Name          Variance Std.Dev.
## spec_ID (Intercept) 0          0
## Number of obs: 58, groups: spec_ID, 8
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.615668   0.078811  20.501  <2e-16 ***
## sexmale      -0.006231   0.117913  -0.053   0.958
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.668
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Confidence interval of the effect

```
confint(glmSnbE)
```

```
## Computing profile confidence intervals ...
```

```
##           2.5 %    97.5 %  
## .sig01      0.0000000 0.1315886  
## (Intercept) 1.4571170 1.7662660  
## sexmale     -0.2385434 0.2240741
```

Check overdispersion The condition to use a generalised mixed effect linear regression model with Laplace approximation is that the data must not be overdispersed (the combined residuals must not be much larger than the residual degrees of freedom). I am using a method and code provided by Julia Pelowski to check whether the data is overdispersed. If the p-value generated by the `overdisp` function is <0.05 , then the data is overdispersed. This can be fixed by adding an additional random effect with one level per observation to the model.

```
overdisp_fun(glmSnbE)
```

```
##      chisq      ratio      rdf      p  
## 0.192546584 0.003500847 55.000000000 1.000000000
```

The data is not overdispersed, the model can be used.

Check model fit

```
# plot(fitted(glmSnbE), residuals(glmSnbE), xlab = 'Fitted  
# Values', ylab = 'Residuals', main='Generalised linear mixed  
# model using Laplace approximation') abline(h = 0, lty = 2)  
# lines(smooth.spline(fitted(glmSnbE), residuals(glmSnbE)))
```

There aren't enough levels to sepal number to calculate fitted values.

Embelia schimperi

Check number of observations

```
aggregate(sepal_nb ~ sex + species, data = schimp, function(x) length(x))
```

```
##      sex  species sepal_nb  
## 1 female schimperi      20  
## 2  male schimperi      21
```

Check distribution

The number of sepals is a discrete count variable. A glmer using Laplace approximation and a Poisson distribution is therefore used.

Build model

```
glmSnbS <- glmer(sepal_nb ~ sex + (1 | spec_ID), schimp, family = poisson(log))
```

```
## boundary (singular) fit: see ?isSingular
```

Display results

```
summary(glmSnbS)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: poisson ( log )  
## Formula: sepal_nb ~ sex + (1 | spec_ID)  
## Data: schimp
```

```
##
##      AIC      BIC   logLik deviance df.resid
##    149.4    154.6   -71.7   143.4      38
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.3492 -0.3014  0.1091  0.1623  0.6260
##
## Random effects:
##  Groups Name      Variance Std.Dev.
## spec_ID (Intercept) 0          0
## Number of obs: 41, groups: spec_ID, 6
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.53687    0.10370  14.821  <2e-16 ***
## sexmale      0.02378    0.14406   0.165    0.869
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## sexmale -0.720
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Confidence interval of the effect

```
confint(glmSnbS)
```

```
## Computing profile confidence intervals ...
##              2.5 %    97.5 %
## .sig01        0.0000000 0.1974696
## (Intercept)  1.3245014 1.7332295
## sexmale     -0.2585634 0.3078187
```

Check overdispersion

```
overdisp_fun(glmSnbS)
```

```
##      chisq      ratio      rdf      p
##  3.47870968  0.09154499 38.00000000  1.00000000
```

Check model fit

```
# plot(fitted(glmSnbS), residuals(glmSnbS), xlab = 'Fitted
# Values', ylab = 'Residuals', main='Generalised linear mixed
# model using Laplace approximation') abline(h = 0, lty = 2)
# lines(smooth.spline(fitted(glmSnbS), residuals(glmSnbS)))
```

Embelia tsjeriamcottam

Check number of observations

```
aggregate(sepal_nb ~ sex + species, data = tsjer, function(x) length(x))
```

```
##      sex      species sepal_nb
## 1 female tsjeriamcottam      25
```

```
## 2   male tsjeriamcottam      25
```

Check distribution

The number of sepals is a discrete count variable. A glmer using Laplace approximation and a Poisson distribution is therefore used.

Build model

```
glmSnbT <- glmer(sepal_nb ~ sex + (1 | spec_ID), tsjer, family = poisson(log))
```

```
## boundary (singular) fit: see ?isSingular
```

Display results

```
summary(glmSnbT)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##   Family: poisson ( log )
## Formula: sepal_nb ~ sex + (1 | spec_ID)
##   Data: tsjer
##
##           AIC          BIC    logLik deviance df.resid
##       182.5       188.2     -88.2   176.5      47
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.41477 -0.12185  0.03607  0.03607  0.74853
##
## Random effects:
##   Groups Name            Variance Std.Dev.
##   spec_ID (Intercept) 0          0
## Number of obs: 50, groups:  spec_ID, 7
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.59331    0.09017  17.671  <2e-16 ***
## sexmale      0.07062    0.12532   0.563    0.573
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr)
## sexmale -0.719
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Confidence interval of the effect

```
confint(glmSnbT)
```

```
## Computing profile confidence intervals ...
##
##           2.5 %    97.5 %
## .sig01      0.0000000 0.1483012
## (Intercept)  1.4111462 1.7648561
## sexmale     -0.1748841 0.3170434
```

Check overdispersion

```
overdisp_fun(glmSnbT)
```

```
##      chisq      ratio      rdf      p
## 1.7073171 0.0363259 47.0000000 1.0000000
```

Check model fit

```
# plot(fitted(glmSnbT), residuals(glmSnbT), xlab = 'Fitted
# Values', ylab = 'Residuals', main='Generalised linear mixed
# model using Laplace approximation') abline(h = 0, lty = 2)
# lines(smooth.spline(fitted(glmSnbT), residuals(glmSnbT)))
```

glm tests

Note: Since the variance due to specimen ID was =0 in all tests, we could remove this random variable and replace the model by a simple generalised regression model (without mixed-effects), and obtain exactly the same results:

```
SnbE <- glm(sepal_nb ~ sex, effusa, family = "poisson")
summary(SnbE)
```

```
##
## Call:
## glm(formula = sepal_nb ~ sex, family = "poisson", data = effusa)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.01395 -0.01395 -0.01395  0.00000  0.41904
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.615668   0.078811  20.501  <2e-16 ***
## sexmale      -0.006231   0.117913  -0.053   0.958
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 0.18441  on 57  degrees of freedom
## Residual deviance: 0.18162  on 56  degrees of freedom
##      (234 observations deleted due to missingness)
## AIC: 206.23
##
## Number of Fisher Scoring iterations: 3
```

```
exp(coefficients(SnbE)) #to extract the coefficients (A Poisson regression models the log of the expected
```

```
## (Intercept)      sexmale
##  5.0312500    0.9937888
```

```
SnbS <- glm(sepal_nb ~ sex, schimp, family = "poisson")
summary(SnbS)
```

```
##
## Call:
## glm(formula = sepal_nb ~ sex, family = "poisson", data = schimp)
##
```

```
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.3591  -0.3089   0.1082   0.1603   0.5989
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.53687    0.10370  14.821  <2e-16 ***
## sexmale      0.02378    0.14406   0.165   0.869
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 3.4725  on 40  degrees of freedom
## Residual deviance: 3.4452  on 39  degrees of freedom
## (153 observations deleted due to missingness)
## AIC: 147.42
##
## Number of Fisher Scoring iterations: 4
```

```
exp(coefficients(SnbS))
```

```
## (Intercept)      sexmale
##      4.650000      1.024066
```

```
SnbT <- glm(sepal_nb ~ sex, tsjer, family = "poisson")
summary(SnbT)
```

```
##
## Call:
## glm(formula = sepal_nb ~ sex, family = "poisson", data = tsjer)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.42882  -0.12296   0.03597   0.03597   0.71258
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.59331    0.09017  17.671  <2e-16 ***
## sexmale      0.07062    0.12532   0.563   0.573
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 1.9803  on 49  degrees of freedom
## Residual deviance: 1.6626  on 48  degrees of freedom
## (205 observations deleted due to missingness)
## AIC: 180.47
##
## Number of Fisher Scoring iterations: 4
```

```
exp(coefficients(SnbT))
```

```
## (Intercept)      sexmale
##      4.920000      1.073171
```


3.2.3 Statistical tests - Sepal length

Embelia effusa

Number of observations

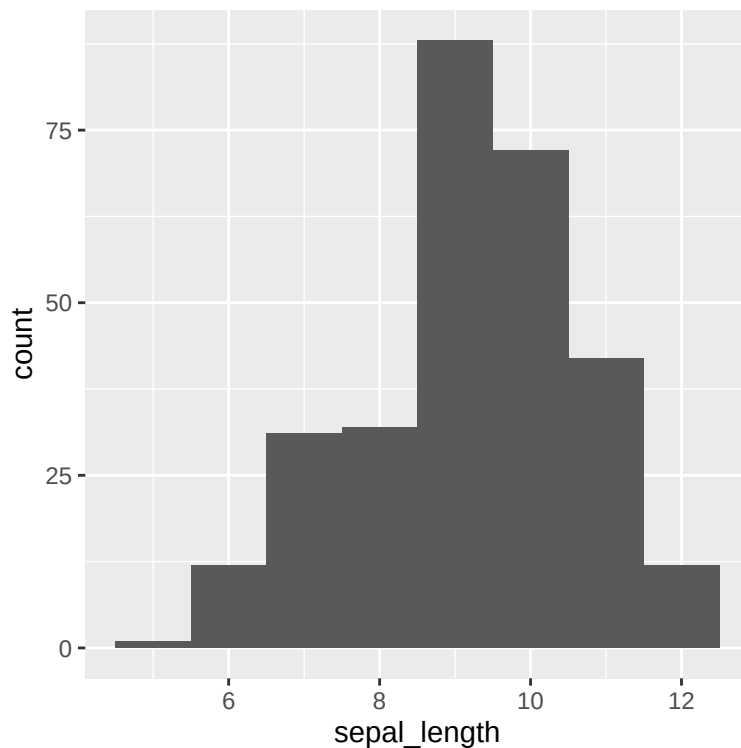
```
aggregate(sepal_length ~ sex + species, data = effusa, function(x) length(x))
```

```
##      sex species sepal_length
## 1 female  effusa          161
## 2  male   effusa          129
```

Distribution

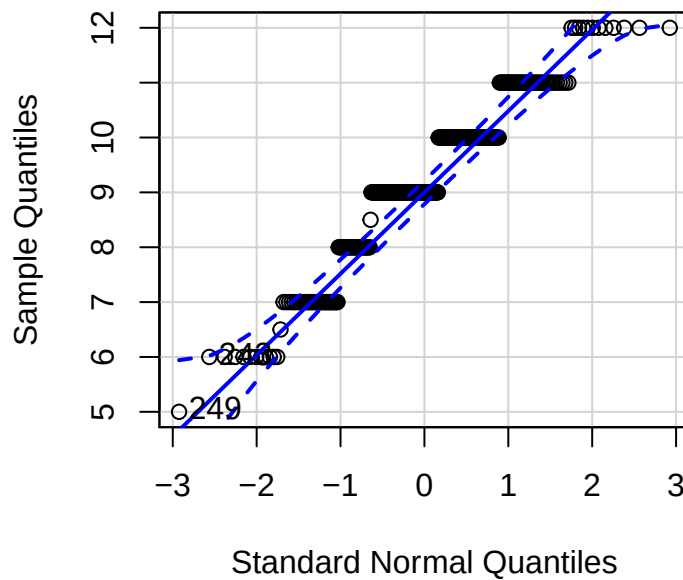
```
histnormSE <- ggplot(effusa, aes(sepal_length))
histnormSE + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 2 rows containing non-finite values (stat_bin).
```



```
qqp(effusa$sepal_length, "norm", xlab = "Standard Normal Quantiles",
  ylab = "Sample Quantiles", main = "Embelia effusa")
```

Embelia effusa



```
## [1] 249 243
```

Build model

```
lmSlE <- lmer(sepal_length ~ sex + (1 | spec_ID), effusa, REML = FALSE)
```

Display results

```
summary(lmSlE)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: sepal_length ~ sex + (1 | spec_ID)
## Data: effusa
##
##      AIC      BIC    logLik deviance df.resid
##    814.8    829.4   -403.4    806.8     286
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.82967 -0.65317 -0.06732  0.66382  2.57865
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## spec_ID  (Intercept)  0.9338     0.9663
## Residual                    0.8547     0.9245
## Number of obs: 290, groups:  spec_ID, 8
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   9.7221     0.4890  19.883
## sexmale      -1.5062     0.6926  -2.175
```

```
##
## Correlation of Fixed Effects:
##      (Intr)
## sexmale -0.706

confint(lmSlE)

## Computing profile confidence intervals ...

##           2.5 %      97.5 %
## .sig01      0.6215757  1.75175148
## .sigma      0.8531457  1.00638832
## (Intercept) 8.6347751 10.80839723
## sexmale     -3.0468808  0.03007421

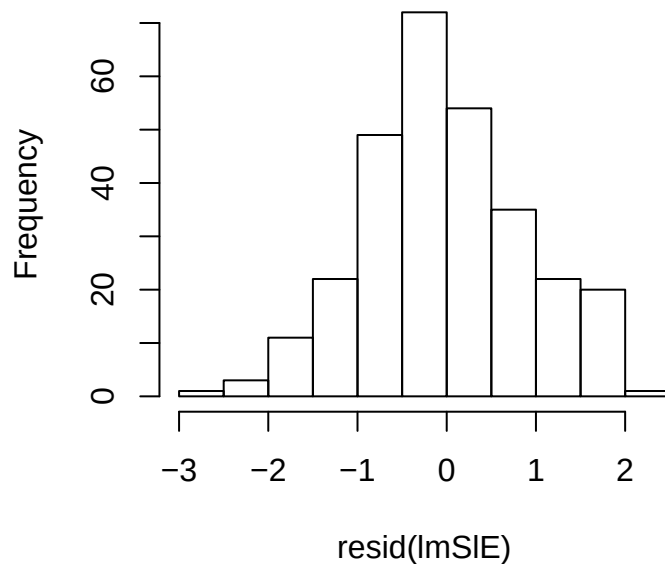
Anova(lmSlE)

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sepal_length
##      Chisq Df Pr(>Chisq)
## sex  4.7295  1    0.02965 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

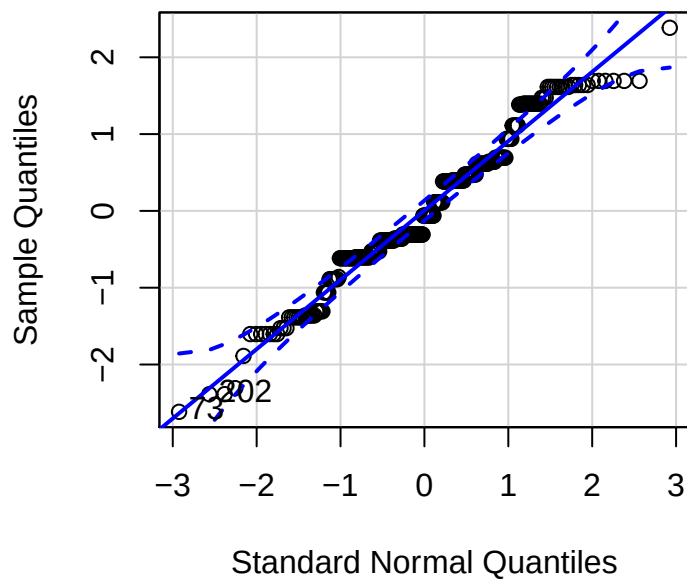
Check normality of residuals

hist(resid(lmSlE))
```

Histogram of resid(lmSlE)



```
qqp(resid(lmSlE), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

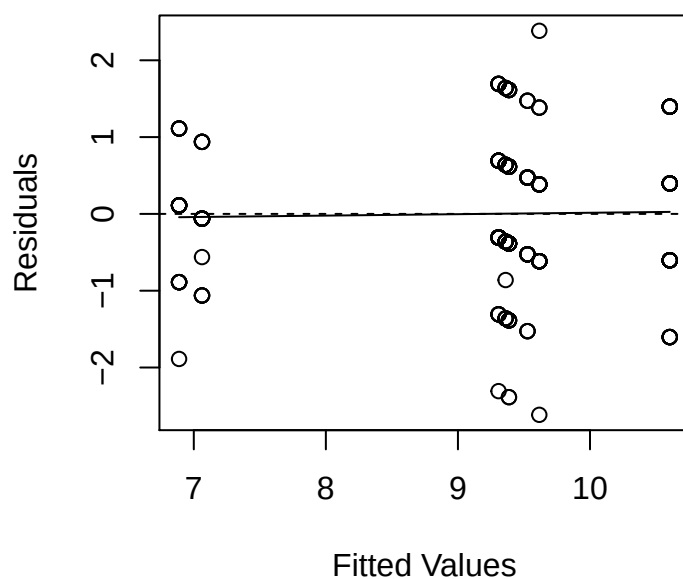


```
## 73 202
## 73 200
```

Check model fit

```
plot(fitted(lmS1E), residuals(lmS1E), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmS1E), residuals(lmS1E)))
```

Linear mixed model using maximum likelihood



Embelia schimperi

Number of observations

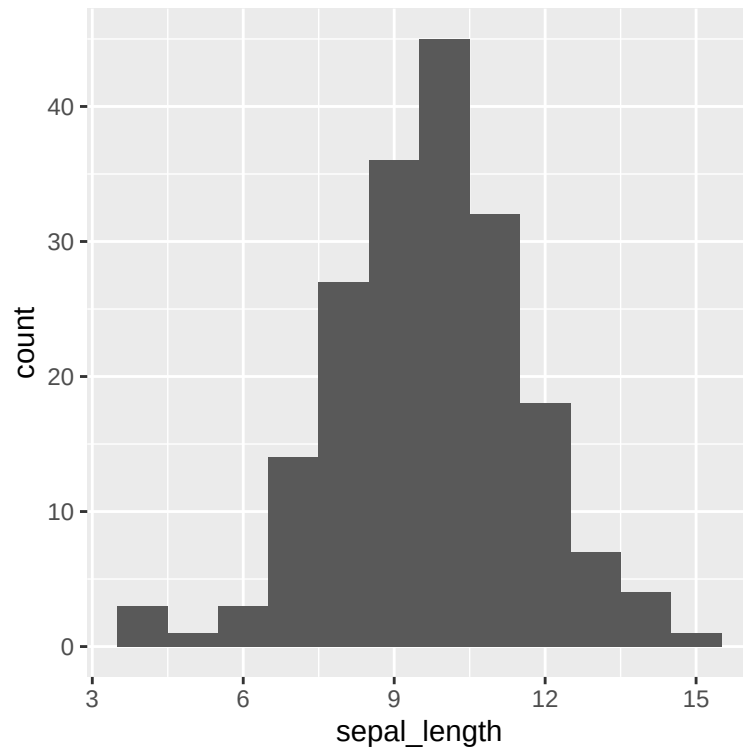
```
aggregate(sepal_length ~ sex + species, data = schimp, function(x) length(x))
```

```
##      sex  species sepal_length
## 1 female schimperi           92
## 2  male schimperi           99
```

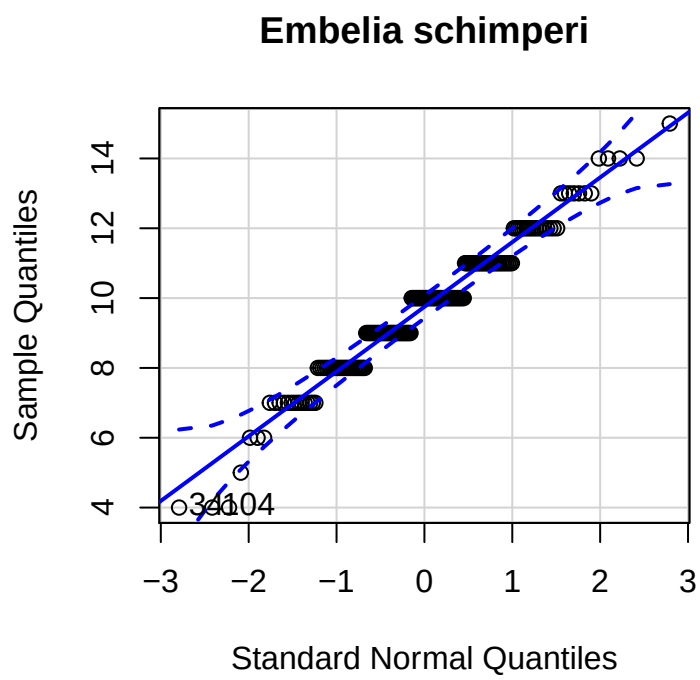
Distribution

```
histnormSS <- ggplot(schimp, aes(sepal_length))
histnormSS + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 3 rows containing non-finite values (stat_bin).
```



```
qqp(schimp$sepal_length, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia schimperi")
```



```
## [1] 34 104
```

Build model

```
lmSSL <- lmer(sepal_length ~ sex + (1 | spec_ID), schimp, REML = FALSE)
```

Display results

```
summary(lmSSL)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: sepal_length ~ sex + (1 | spec_ID)
## Data: schimp
##
##      AIC      BIC    logLik deviance df.resid
##    729.6    742.6   -360.8    721.6      187
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.5543 -0.4790  0.0074  0.6591  2.7793
##
## Random effects:
## Groups   Name      Variance Std.Dev.
## spec_ID (Intercept) 1.079    1.039
## Residual              2.355    1.535
## Number of obs: 191, groups: spec_ID, 6
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   9.8074    0.6272  15.636
## sexmale      -0.1531    0.8830  -0.173
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.710
```

```
confint(lmSSL)
```

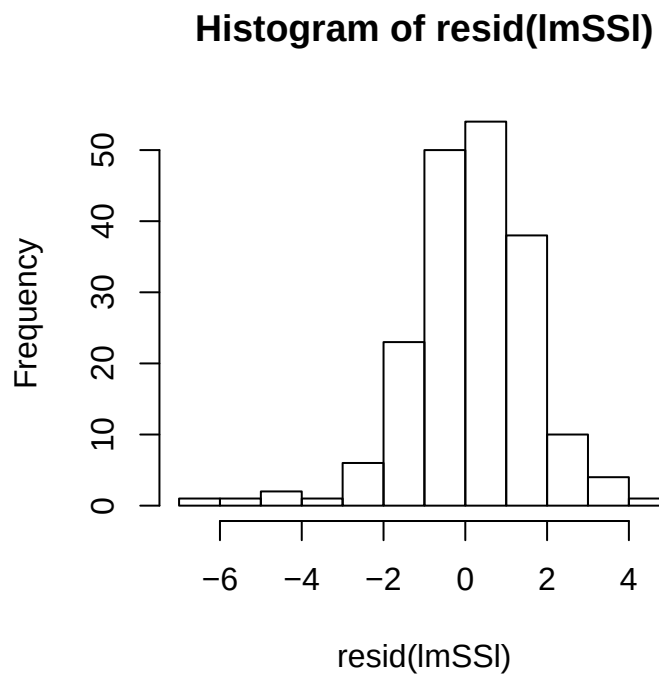
```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01      0.6095158 2.135535
## .sigma      1.3905649 1.705119
## (Intercept) 8.3574467 11.252099
## sexmale     -2.1840961 1.899015
```

```
Anova(lmSSL)
```

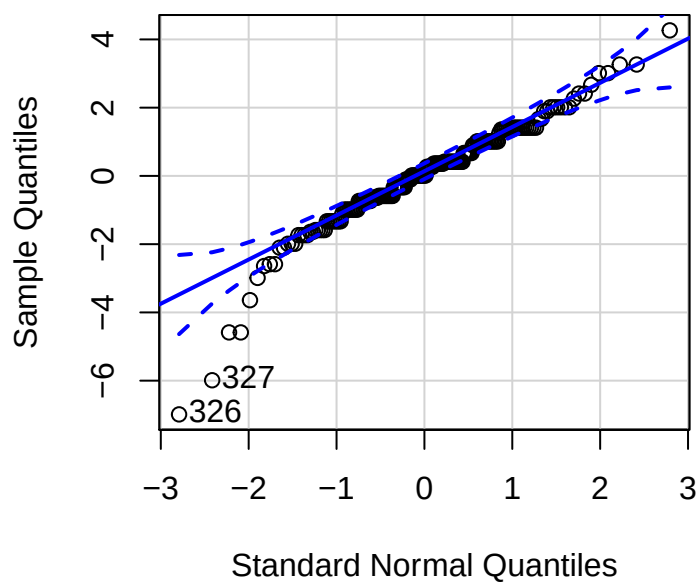
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sepal_length
##      Chisq Df Pr(>Chisq)
## sex 0.0301  1    0.8623
```

Check normality of residuals

```
hist(resid(lmSSL))
```



```
qqp(resid(lmSSL), "norm", xlab = "Standard Normal Quantiles",  
     ylab = "Sample Quantiles")
```

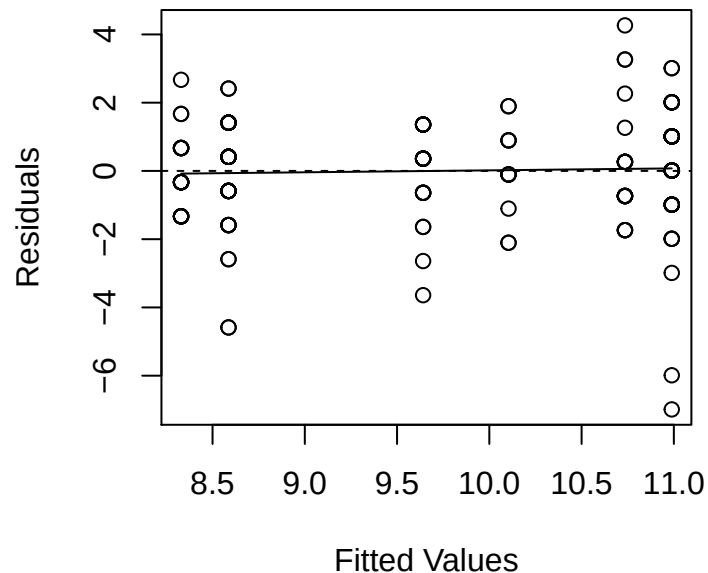



```
## 326 327
## 34 35
```

Check model fit

```
plot(fitted(lmSSL), residuals(lmSSL), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmSSL), residuals(lmSSL)))
```

Linear mixed model using maximum likelih



Embelia tsjeriamcottam

Number of observations

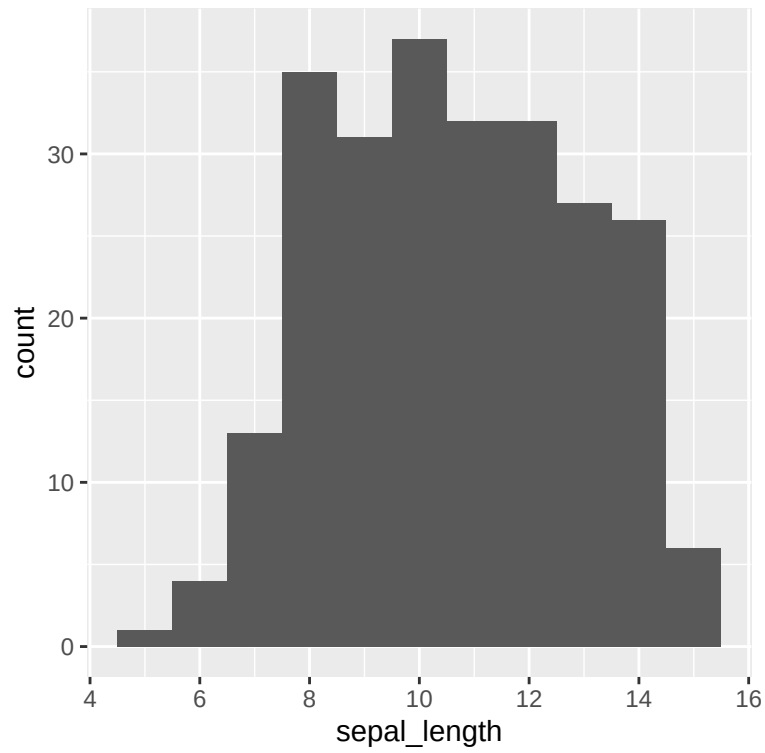
```
aggregate(sepal_length ~ sex + species, data = tsjer, function(x) length(x))
```

```
##      sex      species sepal_length
## 1 female tsjeriamcottam         118
## 2  male tsjeriamcottam         126
```

Distribution

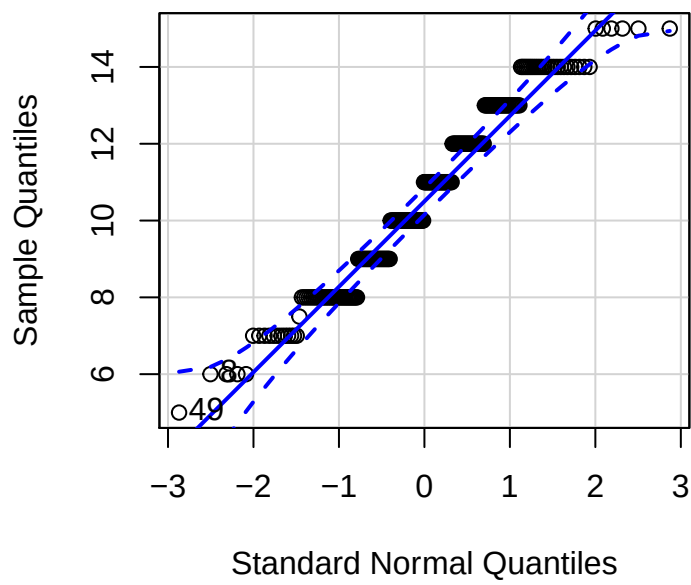
```
histnormST <- ggplot(tsjer, aes(sepal_length))
histnormST + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
"lightsalmon"))
```

```
## Warning: Removed 11 rows containing non-finite values (stat_bin).
```



```
qqp(tsjer$sepal_length, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia tsjeriamcottam")
```

Embelia tsjeriamcottam



```
## [1] 49 8
```

Build model

```
lmST <- lmer(sepal_length ~ sex + (1 | spec_ID), tsjer, REML = FALSE)
```

Display results

```
summary(lmST)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: sepal_length ~ sex + (1 | spec_ID)
## Data: tsjer
##
##      AIC      BIC    logLik deviance df.resid
##    874.3    888.3   -433.1    866.3      240
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.1759 -0.5564  0.0295  0.7440  3.2251
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 2.637  1.624
## Residual 1.826  1.351
## Number of obs: 244, groups: spec_ID, 7
##
## Fixed effects:
## Estimate Std. Error t value
## (Intercept) 9.4687 0.9465 10.004
## sexmale 1.6742 1.2542 1.335
##
## Correlation of Fixed Effects:
## (Intr)
## sexmale -0.755
```

```
confint(lmST)
```

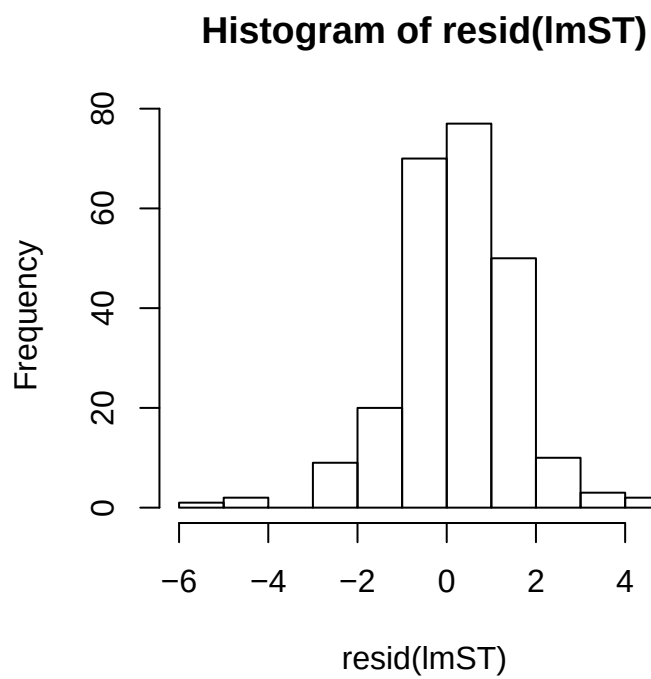
```
## Computing profile confidence intervals ...
##      2.5 %    97.5 %
## .sig01 1.023379 3.082622
## .sigma 1.238097 1.482561
## (Intercept) 7.323697 11.607681
## sexmale -1.161015 4.511665
```

```
Anova(lmST)
```

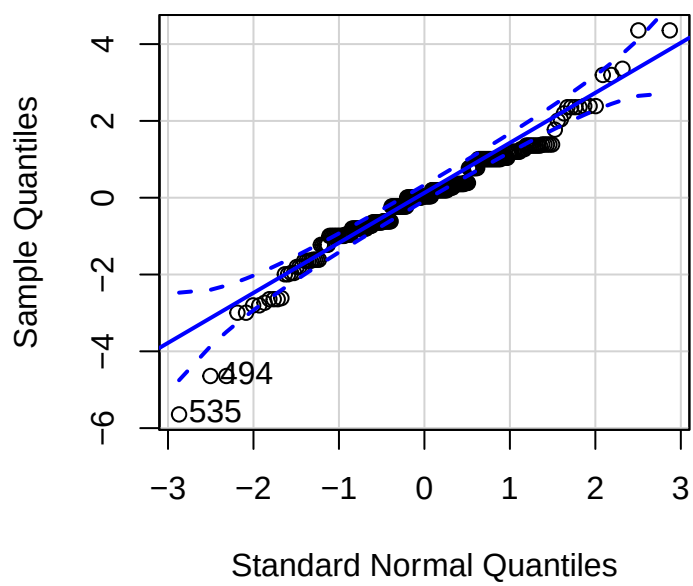
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sepal_length
##      Chisq Df Pr(>Chisq)
## sex 1.7819 1 0.1819
```

Check normality of residuals

```
hist(resid(lmST))
```



```
qqp(resid(lmST), "norm", xlab = "Standard Normal Quantiles",  
     ylab = "Sample Quantiles")
```

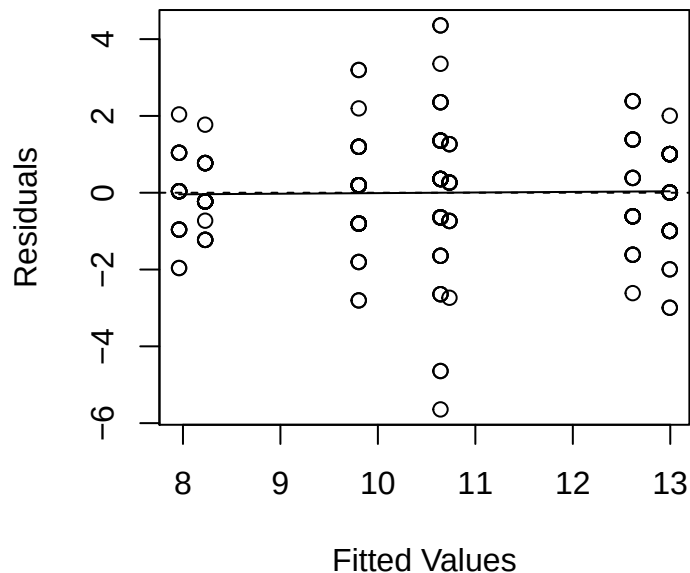


```
## 535 494
## 47 8
```

Check model fit

```
plot(fitted(lmST), residuals(lmST), xlab = "Fitted Values", ylab = "Residuals",
     main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmST), residuals(lmST)))
```

Linear mixed model using maximum likelih



3.2.4 Statistical tests - Sepal width

Embelia effusa

Number of observations

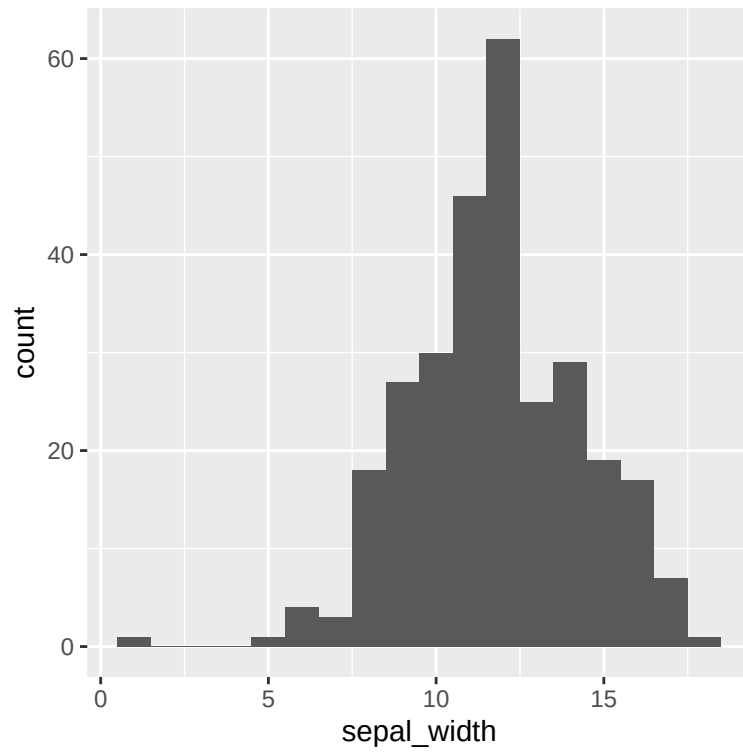
```
aggregate(sepal_width ~ sex + species, data = effusa, function(x) length(x))
```

```
##      sex species sepal_width
## 1 female  effusa         161
## 2  male   effusa         129
```

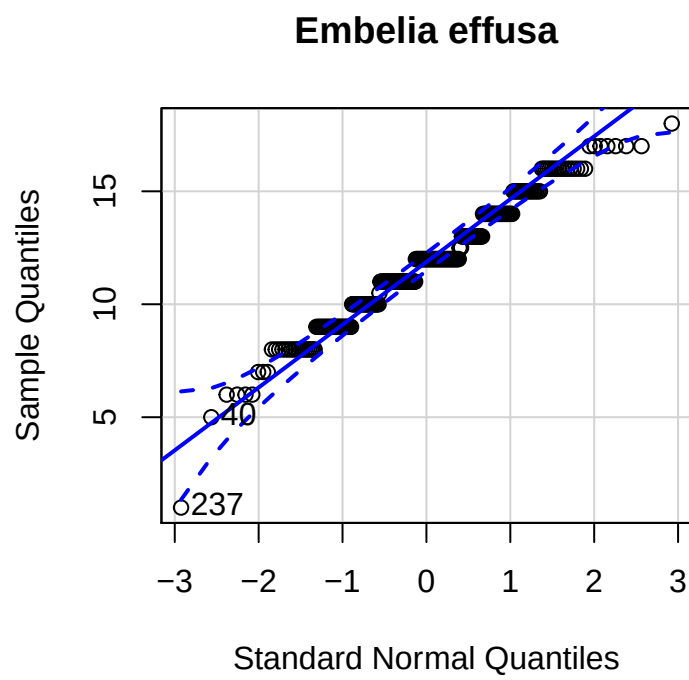
Distribution

```
histnormSwE <- ggplot(effusa, aes(sepal_width))
histnormSwE + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 2 rows containing non-finite values (stat_bin).
```



```
qqp(effusa$sepal_width, "norm", xlab = "Standard Normal Quantiles",
    ylab = "Sample Quantiles", main = "Embelia effusa")
```



```
## [1] 237 40
```

Build model

```
lmSwE <- lmer(sepal_width ~ sex + (1 | spec_ID), effusa, REML = FALSE)
```

Display results

```
summary(lmSwE)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: sepal_width ~ sex + (1 | spec_ID)
## Data: effusa
##
##      AIC      BIC    logLik deviance df.resid
##  1133.6   1148.3   -562.8   1125.6      286
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -5.9779 -0.5619  0.0576  0.6771  3.0413
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 1.604  1.266
## Residual          2.606  1.614
## Number of obs: 290, groups: spec_ID, 8
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  13.0991    0.6466  20.259
## sexmale      -3.1516    0.9169  -3.437
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.705
```

```
confint(lmSwE)
```

```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01      0.8056494  2.307977
## .sigma      1.4896314  1.757158
## (Intercept) 11.6629354 14.535769
## sexmale     -5.1903455 -1.120662
```

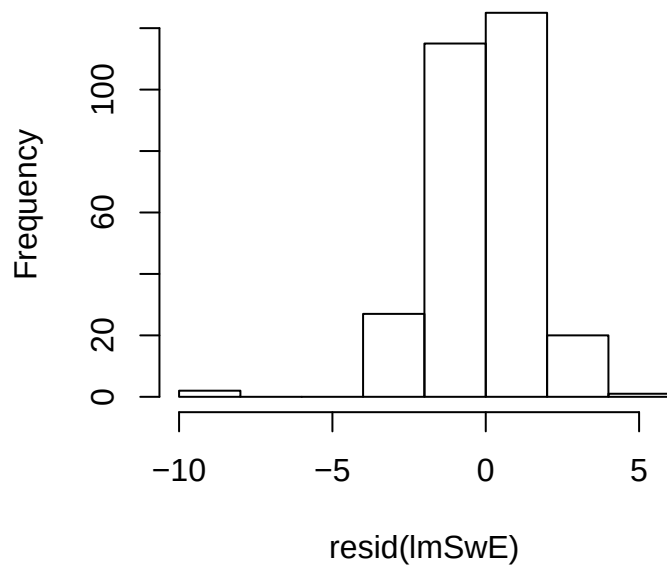
```
Anova(lmSwE)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sepal_width
##      Chisq Df Pr(>Chisq)
## sex  11.816  1  0.0005874 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

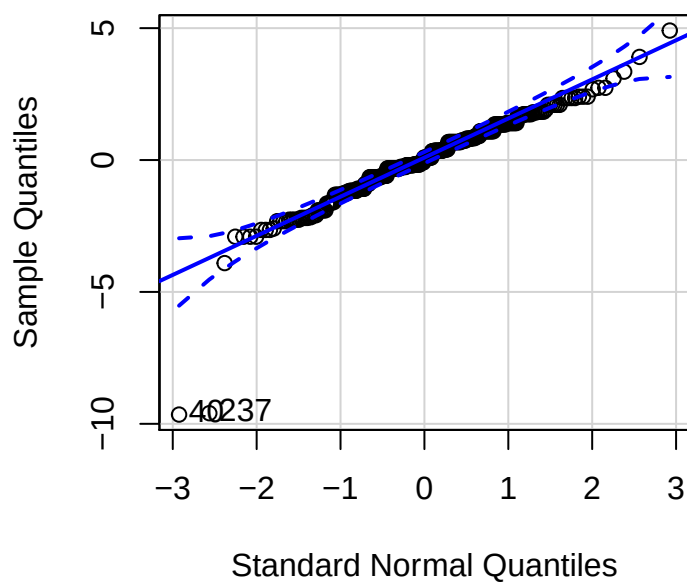
Check normality of residuals

```
hist(resid(lmSwE))
```

Histogram of resid(lmSwE)



```
qqp(resid(lmSwE), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

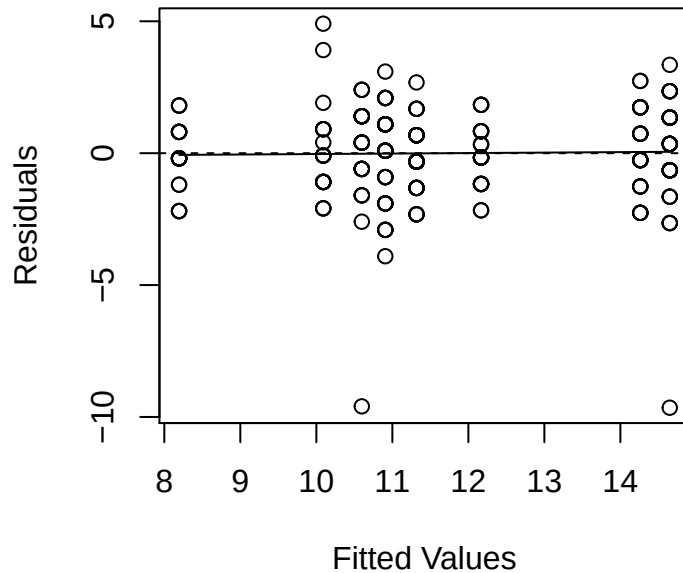


```
## 40 237
## 40 235
```


Check model fit

```
plot(fitted(lmSwE), residuals(lmSwE), xlab = "Fitted Values",  
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")  
abline(h = 0, lty = 2)  
lines(smooth.spline(fitted(lmSwE), residuals(lmSwE)))
```

Linear mixed model using maximum likelih



Embelia schimperi

Number of observations

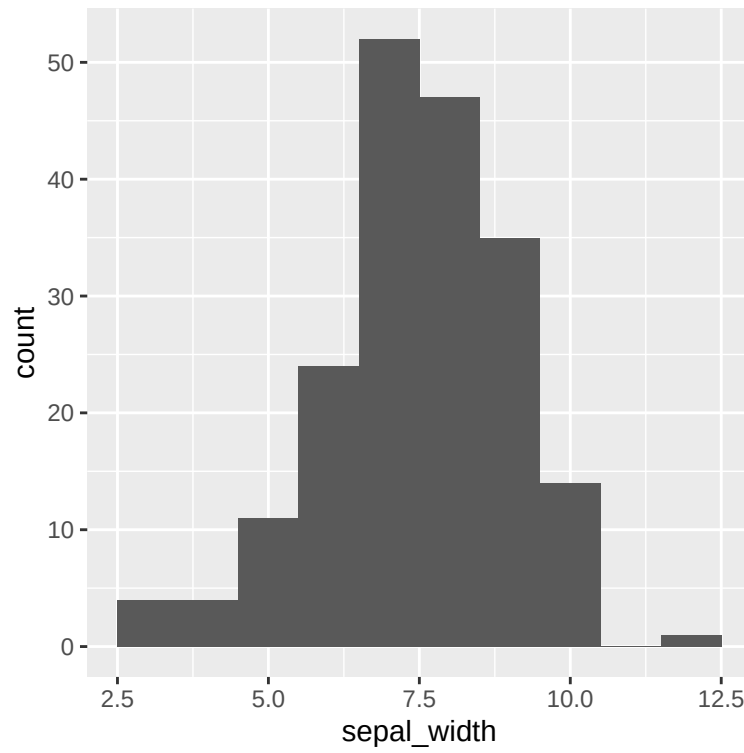
```
aggregate(sepal_width ~ sex + species, data = schimp, function(x) length(x))
```

```
##      sex  species sepal_width  
## 1 female schimperi          92  
## 2  male schimperi         100
```

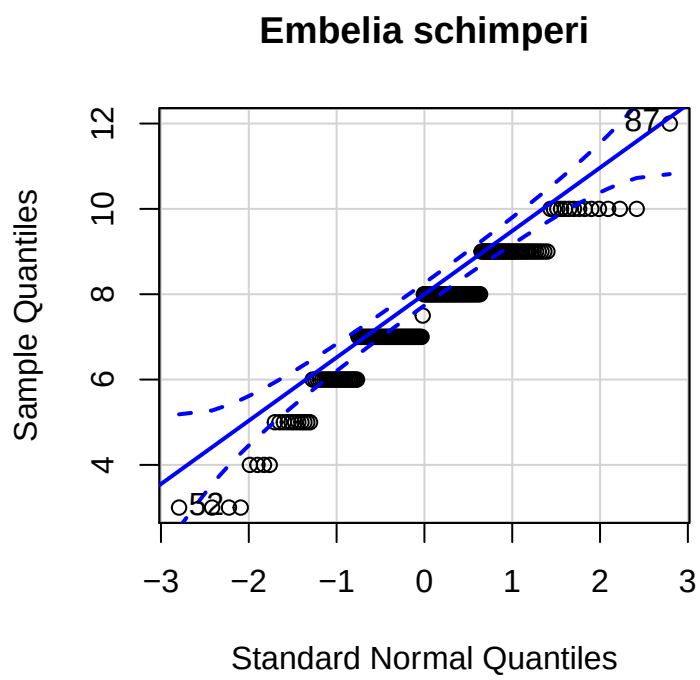
Distribution

```
histnormSwS <- ggplot(schimp, aes(sepal_width))  
histnormSwS + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",  
  "lightsalmon"))
```

```
## Warning: Removed 2 rows containing non-finite values (stat_bin).
```



```
qqp(schimp$sepal_width, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia schimperi")
```



```
## [1] 87 52
```

Build model

```
lmSwS <- lmer(sepal_width ~ sex + (1 | spec_ID), schimp, REML = FALSE)
```

Display results

```
summary(lmSwS)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: sepal_width ~ sex + (1 | spec_ID)
## Data: schimp
##
##      AIC      BIC    logLik deviance df.resid
##    693.2    706.2   -342.6   685.2     188
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.3162 -0.6095  0.1089  0.4500  2.4370
##
## Random effects:
## Groups   Name      Variance Std.Dev.
## spec_ID (Intercept) 0.5437   0.7374
## Residual              1.9378   1.3920
## Number of obs: 192, groups: spec_ID, 6
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   7.7374    0.4567  16.941
## sexmale      -0.1104    0.6412  -0.172
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.712
```

```
confint(lmSwS)
```

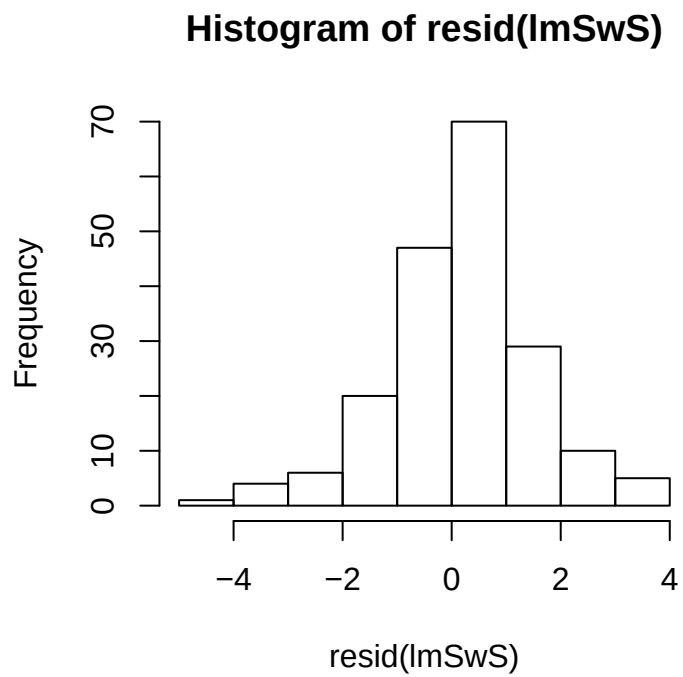
```
## Computing profile confidence intervals ...
##
##              2.5 %   97.5 %
## .sig01      0.4008052 1.560733
## .sigma      1.2616669 1.546504
## (Intercept) 6.6973463 8.818310
## sexmale     -1.6130476 1.373632
```

```
Anova(lmSwS)
```

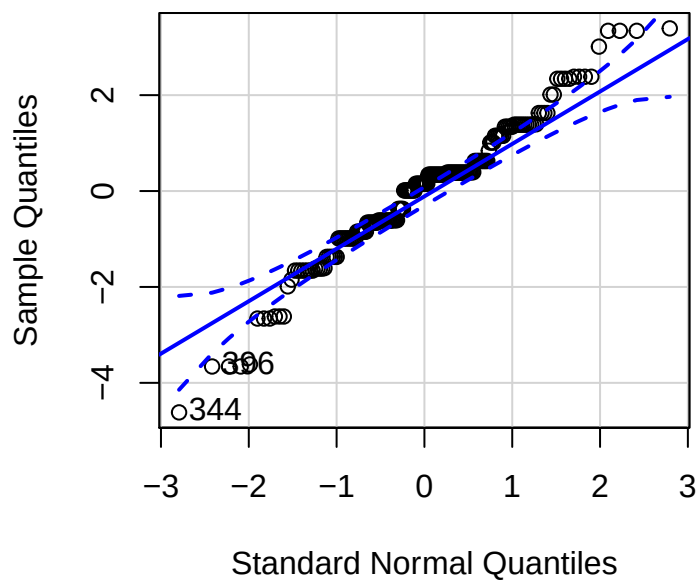
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sepal_width
##      Chisq Df Pr(>Chisq)
## sex 0.0296  1    0.8633
```

Check normality of residuals

```
hist(resid(lmSwS))
```



```
qqp(resid(lmSwS), "norm", xlab = "Standard Normal Quantiles",  
    ylab = "Sample Quantiles")
```

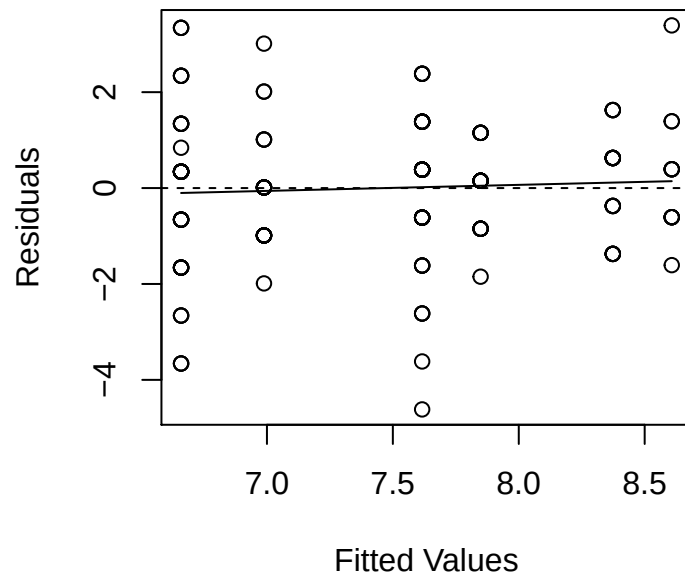


```
## 344 396
## 51 102
```

Check model fit

```
plot(fitted(lmSwS), residuals(lmSwS), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmSwS), residuals(lmSwS)))
```

Linear mixed model using maximum likelih



Embelia tsjeriamcottam

Number of observations

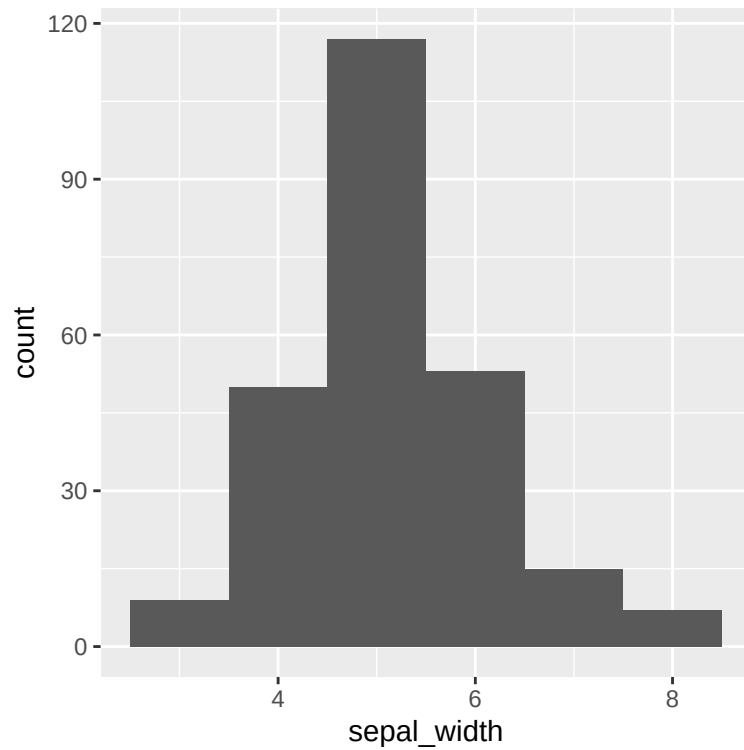
```
aggregate(sepal_width ~ sex + species, data = tsjer, function(x) length(x))
```

```
##      sex      species sepal_width
## 1 female tsjeriamcottam      122
## 2  male tsjeriamcottam      129
```

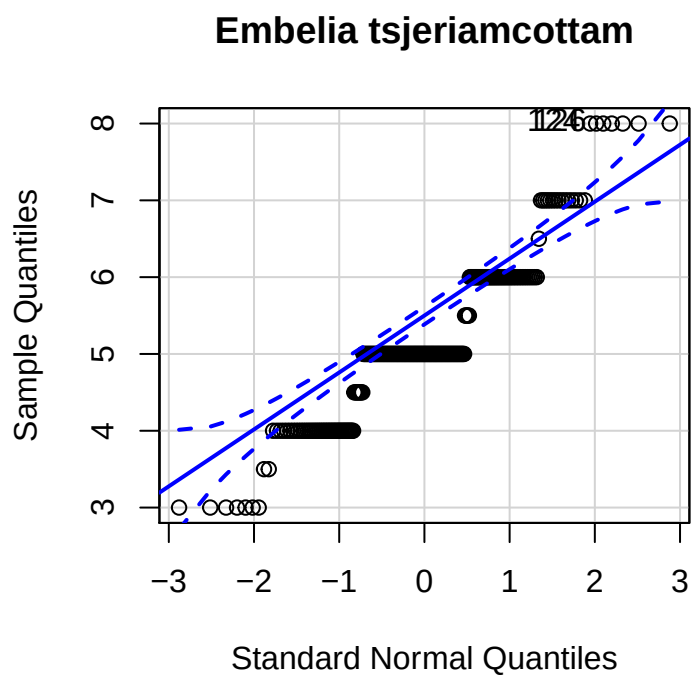
Distribution

```
histnormSwT <- ggplot(tsjer, aes(sepal_width))
histnormSwT + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 4 rows containing non-finite values (stat_bin).
```



```
qqp(tsjer$sepal_width, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia tsjeriamcottam")
```



```
## [1] 124 126
```

Build model

```
lmSwT <- lmer(sepal_width ~ sex + (1 | spec_ID), tsjer, REML = FALSE)
```

Display results

```
summary(lmSwT)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: sepal_width ~ sex + (1 | spec_ID)
## Data: tsjer
##
##      AIC      BIC    logLik deviance df.resid
##    675.9    690.0   -333.9    667.9      247
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.78497 -0.53166 -0.04727  0.46320  2.84830
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## spec_ID (Intercept)  0.1923    0.4385
## Residual                0.7878    0.8876
## Number of obs: 251, groups: spec_ID, 7
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   5.0395     0.2667  18.894
## sexmale        0.2923     0.3560   0.821
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.749
```

```
confint(lmSwT)
```

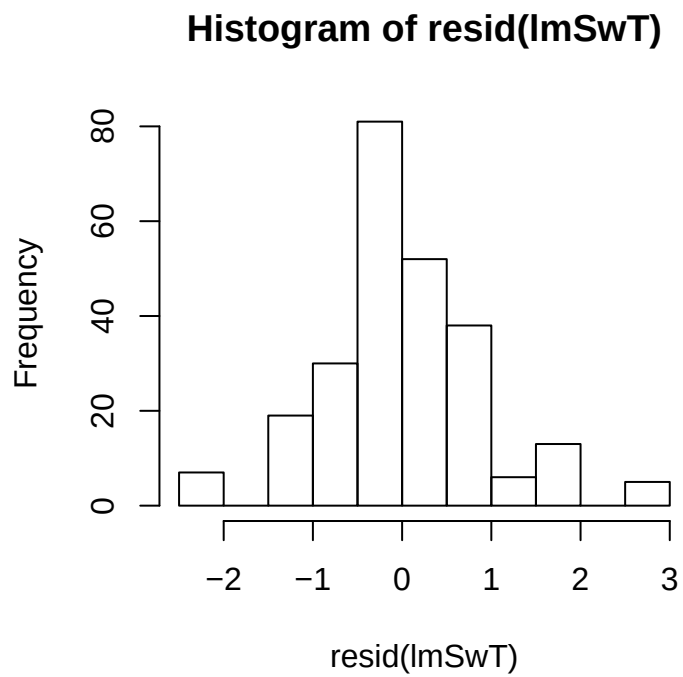
```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01        0.2481338 0.8708113
## .sigma        0.8142722 0.9725992
## (Intercept)   4.4349851 5.6519830
## sexmale      -0.5249734 1.0935069
```

```
Anova(lmSwT)
```

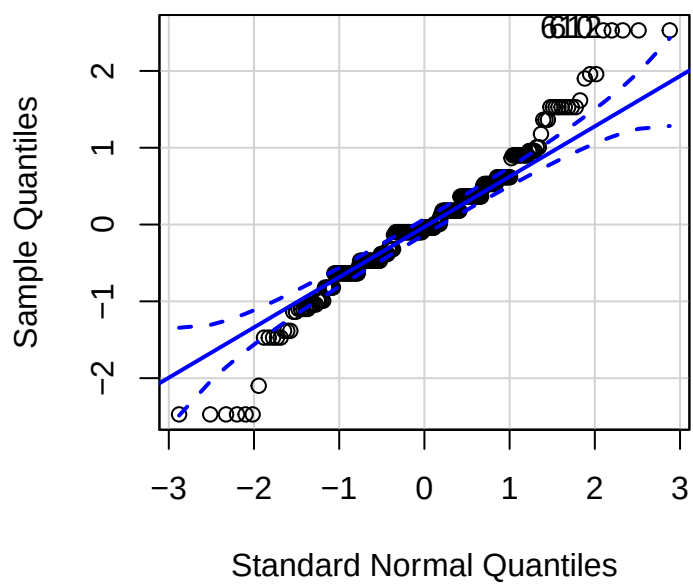
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sepal_width
##      Chisq Df Pr(>Chisq)
## sex  0.674  1    0.4117
```

Check normality of residuals

```
hist(resid(lmSwT))
```



```
qqp(resid(lmSwT), "norm", xlab = "Standard Normal Quantiles",  
     ylab = "Sample Quantiles")
```

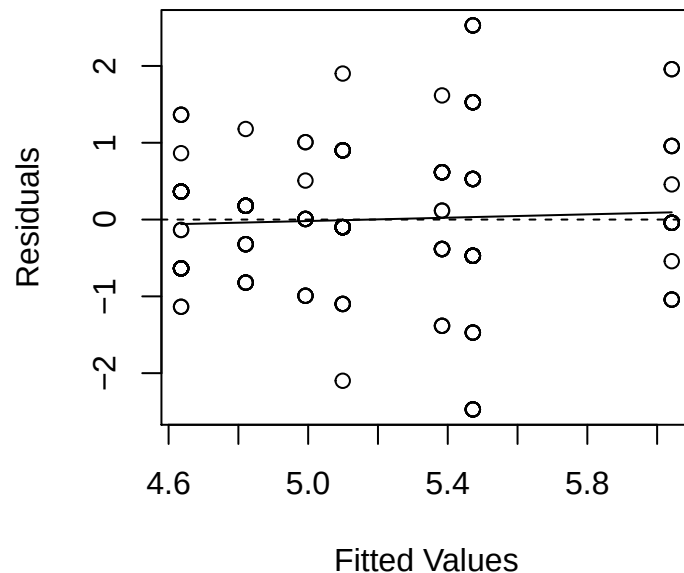



```
## 610 612
## 123 125
```

Check model fit

```
plot(fitted(lmSwT), residuals(lmSwT), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmSwT), residuals(lmSwT)))
```

Linear mixed model using maximum likelih



3.2.5 Statistical tests - Relative length of the fusion of the sepals

Embelia effusa

Number of observations

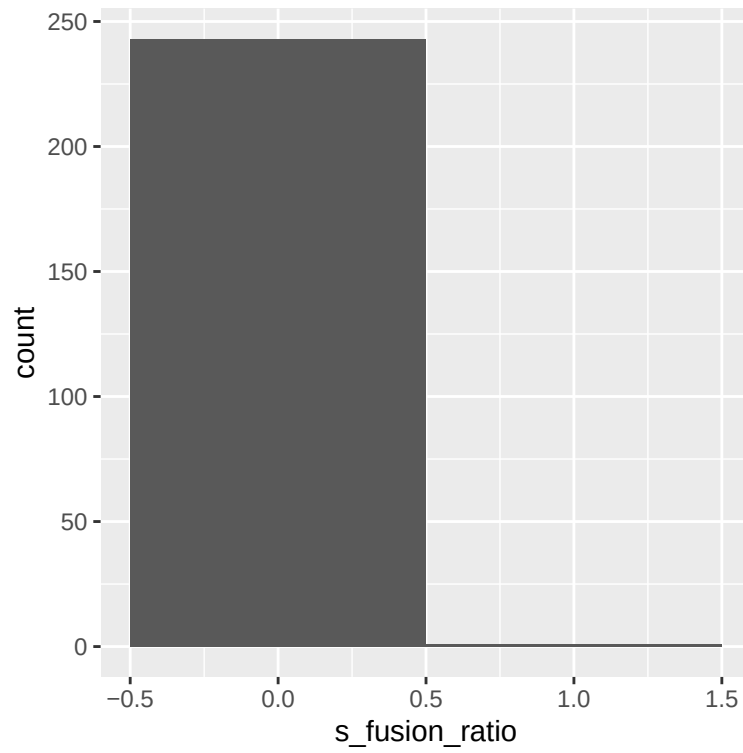
```
aggregate(s_fusion_ratio ~ sex + species, data = effusa, function(x) length(x))
```

```
##      sex species s_fusion_ratio
## 1 female  effusa           161
## 2  male   effusa           129
```

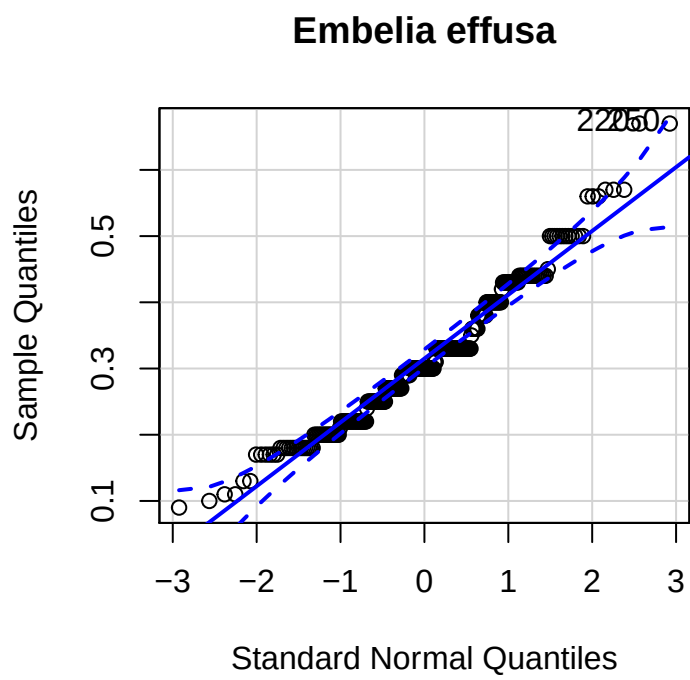
Distribution

```
histnormSfE <- ggplot(tsjer, aes(s_fusion_ratio))
histnormSfE + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 11 rows containing non-finite values (stat_bin).
```



```
qqp(effusa$s_fusion_ratio, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia effusa")
```



```
## [1] 220 250
```

Build model

```
lmSfE <- lmer(s_fusion_ratio ~ sex + (1 | spec_ID), effusa, REML = FALSE)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =  
## control$checkConv, : Model failed to converge with max|grad| = 0.00409401  
## (tol = 0.002, component 1)
```

Display results

```
summary(lmSfE)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']  
## Formula: s_fusion_ratio ~ sex + (1 | spec_ID)  
## Data: effusa  
##  
##      AIC      BIC    logLik deviance df.resid  
##   -601.3   -586.6     304.6   -609.3      286  
##  
## Scaled residuals:  
##      Min       1Q   Median       3Q      Max  
## -1.8256 -0.7243 -0.0706  0.4369  3.3125  
##  
## Random effects:  
## Groups Name Variance Std.Dev.  
## spec_ID (Intercept) 0.002190 0.04680  
## Residual 0.006682 0.08174  
## Number of obs: 290, groups: spec_ID, 8  
##  
## Fixed effects:  
## Estimate Std. Error t value  
## (Intercept) 0.27560 0.02432 11.333  
## sexmale 0.08783 0.03456 2.541  
##  
## Correlation of Fixed Effects:  
## (Intr)  
## sexmale -0.704  
## convergence code: 0  
## Model failed to converge with max|grad| = 0.00409401 (tol = 0.002, component 1)
```

```
confint(lmSfE)
```

```
## Computing profile confidence intervals ...
```

```
##           2.5 %    97.5 %  
## .sig01 0.02870540 0.08660441  
## .sigma 0.07543480 0.08898483  
## (Intercept) 0.22140028 0.32959018  
## sexmale 0.01140712 0.16487779
```

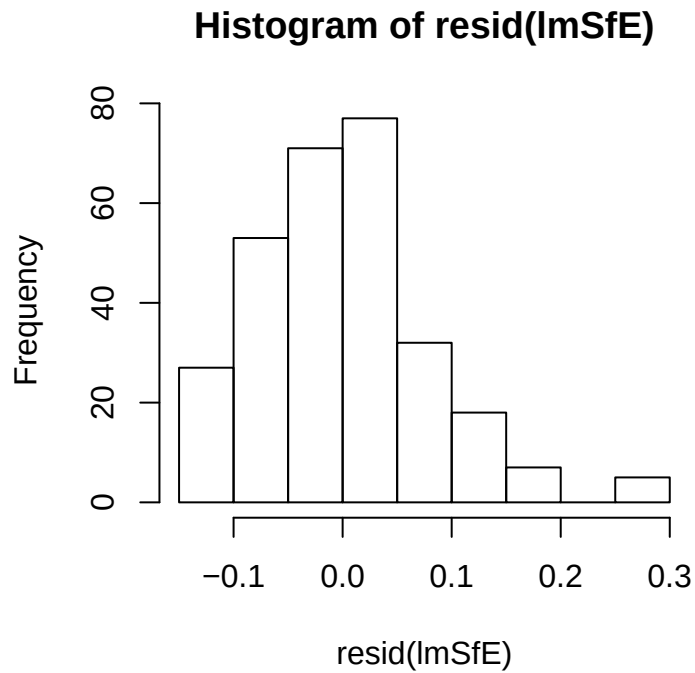
```
Anova(lmSfE)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)  
##  
## Response: s_fusion_ratio  
##      Chisq Df Pr(>Chisq)  
## sex 6.4577 1 0.01105 *  
## ---
```

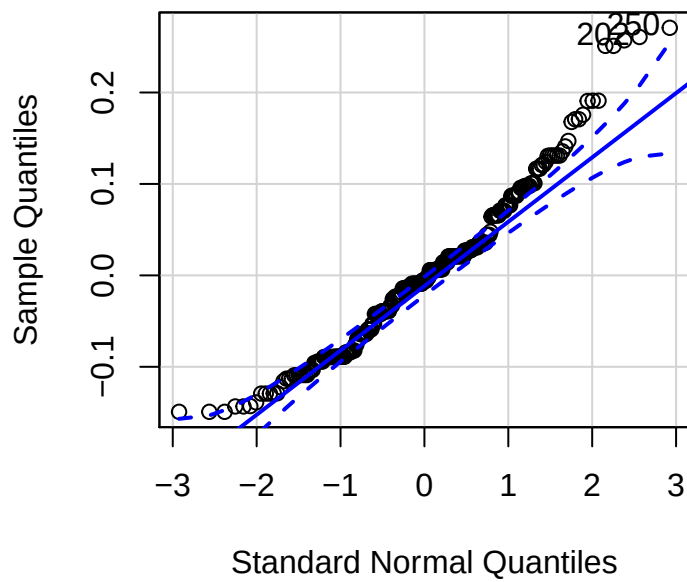
```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Check normality of residuals

```
hist(resid(lmSfE))
```



```
qqp(resid(lmSfE), "norm", xlab = "Standard Normal Quantiles",  
     ylab = "Sample Quantiles")
```

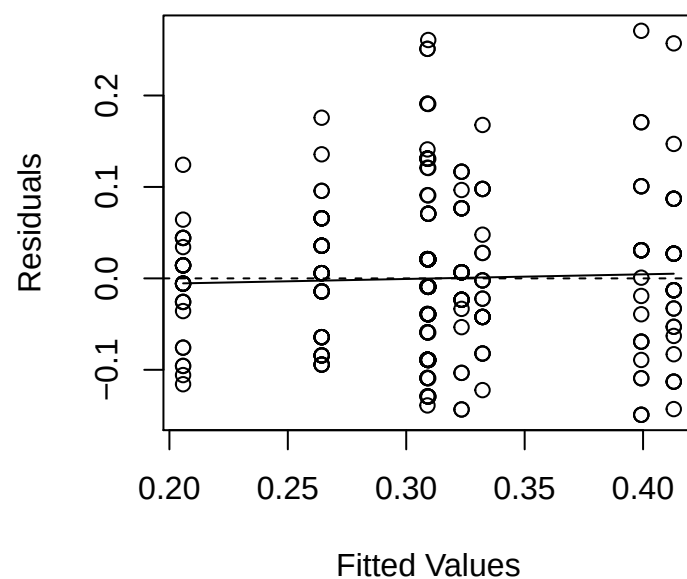


```
## 250 202
## 248 200
```

Check model fit

```
plot(fitted(lmSfE), residuals(lmSfE), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmSfE), residuals(lmSfE)))
```

Linear mixed model using maximum likelih



Embelia schimperi

Number of observations

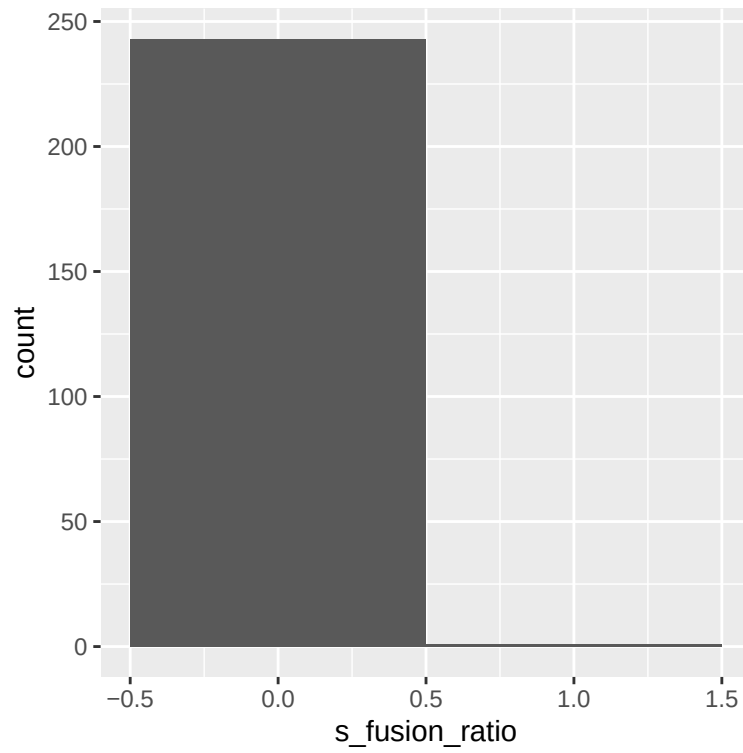
```
aggregate(s_fusion_ratio ~ sex + species, data = schimp, function(x) length(x))
```

```
##      sex  species s_fusion_ratio
## 1 female schimperi           92
## 2  male schimperi           99
```

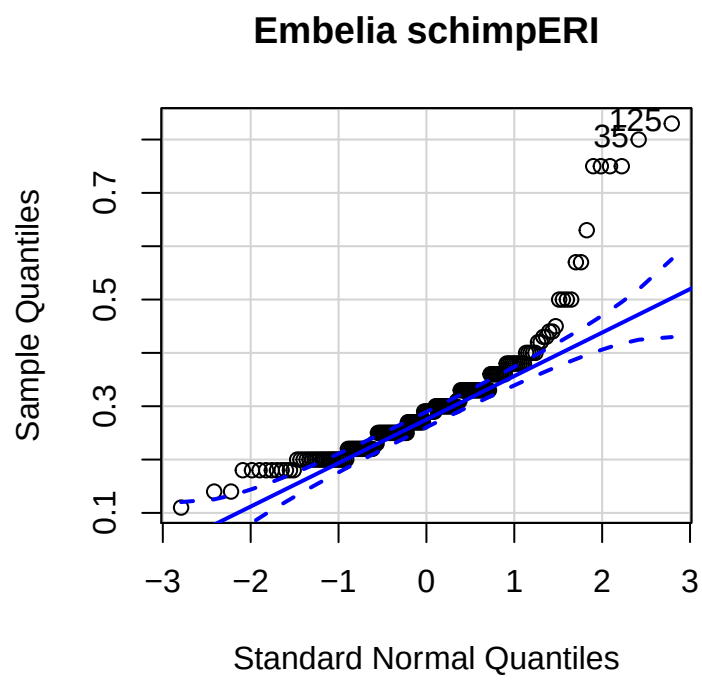
Distribution

```
histnormSfS <- ggplot(tsjer, aes(s_fusion_ratio))
histnormSfS + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 11 rows containing non-finite values (stat_bin).
```



```
qqp(schimp$s_fusion_ratio, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia schimpERI")
```



```
## [1] 125 35
```

Build model

```
lmSfS <- lmer(s_fusion_ratio ~ sex + (1 | spec_ID), schimp, REML = FALSE)
```

Display results

```
summary(lmSfS)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: s_fusion_ratio ~ sex + (1 | spec_ID)
## Data: schimp
##
##      AIC      BIC    logLik deviance df.resid
##   -266.2   -253.2    137.1   -274.2      187
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.5590 -0.6002 -0.1623  0.2968  4.3637
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## spec_ID (Intercept) 0.0005213 0.02283
## Residual              0.0136018 0.11663
## Number of obs: 191, groups: spec_ID, 6
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  0.302218   0.018570  16.275
## sexmale      -0.005524   0.025798  -0.214
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.720
```

```
confint(lmSfS)
```

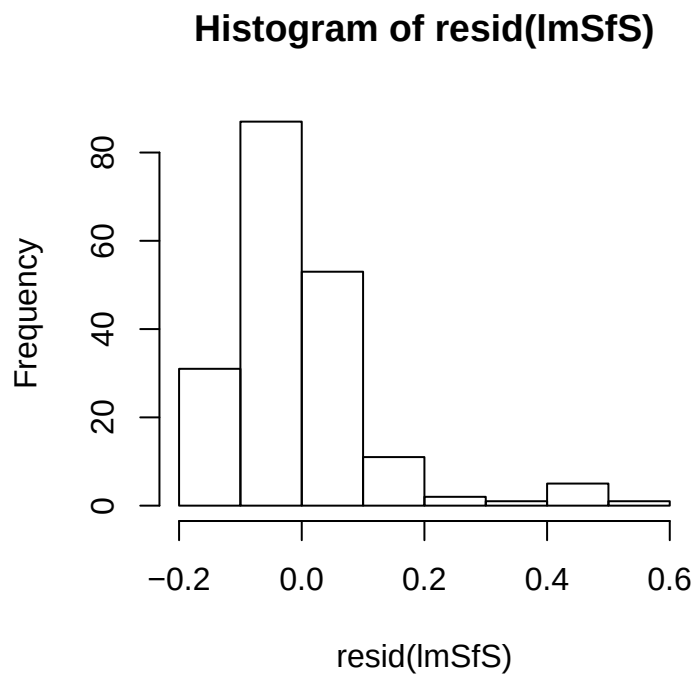
```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01         0.00000000 0.05879425
## .sigma         0.10569258 0.12958524
## (Intercept)    0.25823991 0.34392262
## sexmale        -0.06643756 0.05315478
```

```
Anova(lmSfS)
```

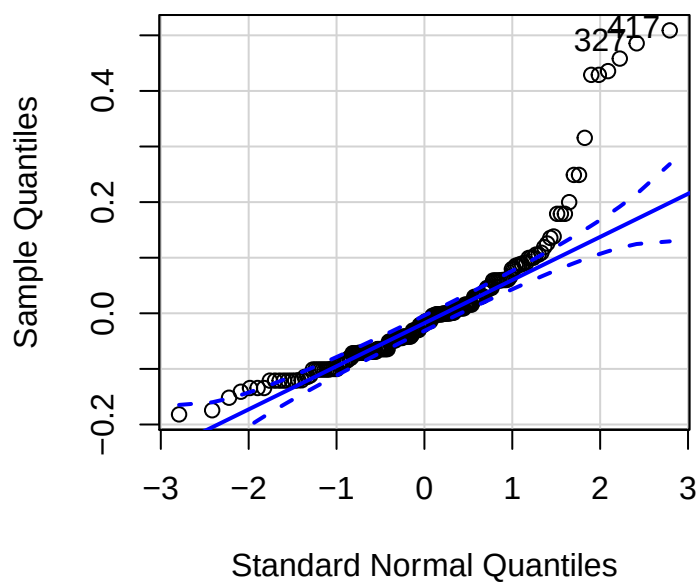
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: s_fusion_ratio
##      Chisq Df Pr(>Chisq)
## sex  0.0459  1    0.8304
```

Check normality of residuals


```
hist(resid(lmSfS))
```



```
qqp(resid(lmSfS), "norm", xlab = "Standard Normal Quantiles",  
     ylab = "Sample Quantiles")
```

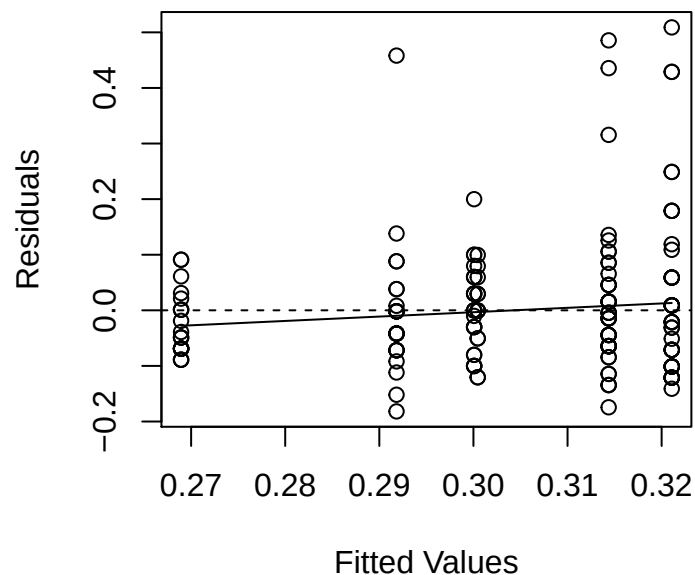


```
## 417 327
## 123 35
```

Check model fit

```
plot(fitted(lmSfS), residuals(lmSfS), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmSfS), residuals(lmSfS)))
```

Linear mixed model using maximum likelih



Embelia tsjeriamcottam

Number of observations

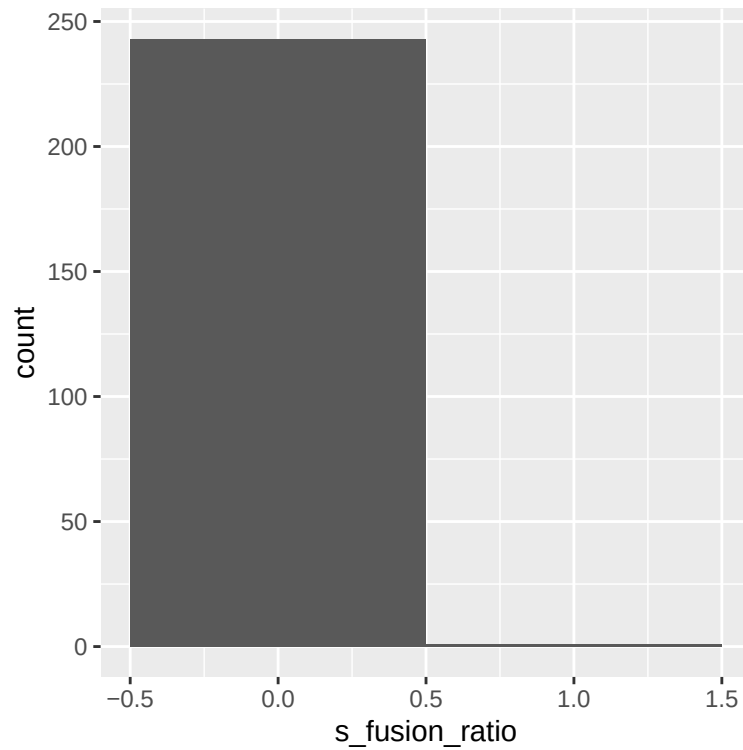
```
aggregate(s_fusion_ratio ~ sex + species, data = tsjer, function(x) length(x))
```

```
##      sex      species s_fusion_ratio
## 1 female tsjeriamcottam          118
## 2  male tsjeriamcottam          126
```

Distribution

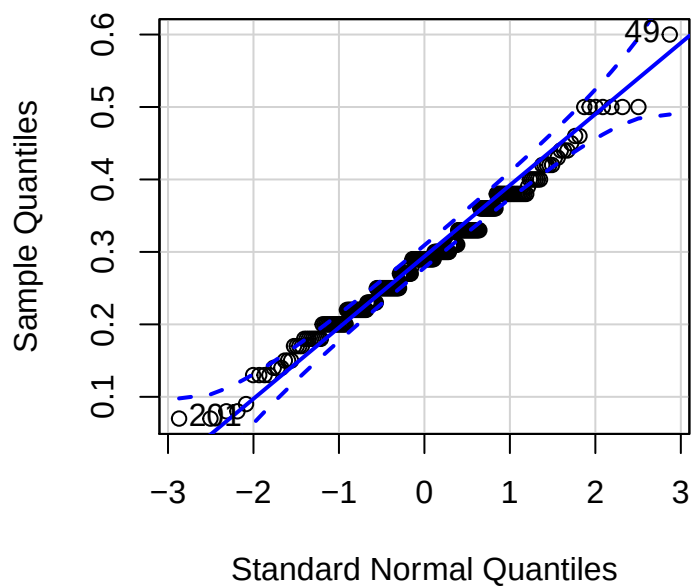
```
histnormSfT <- ggplot(tsjer, aes(s_fusion_ratio))
histnormSfT + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 11 rows containing non-finite values (stat_bin).
```



```
qqp(tsjer$s_fusion_ratio, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia tsjeriamcottam")
```

Embelia tsjeriamcottam



```
## [1] 49 201
```

Build model

```
lmSfT <- lmer(s_fusion_ratio ~ sex + (1 | spec_ID), tsjer, REML = FALSE)
```

Display results

```
summary(lmSfT)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: s_fusion_ratio ~ sex + (1 | spec_ID)
## Data: tsjer
##
##      AIC      BIC    logLik deviance df.resid
##   -559.0   -545.0     283.5   -567.0      240
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.5584 -0.5179 -0.2308  0.6089  3.9140
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## spec_ID  (Intercept)  0.002856  0.05344
## Residual                    0.005273  0.07262
## Number of obs: 244, groups: spec_ID, 7
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  0.27877    0.03164    8.81
## sexmale      0.01471    0.04203    0.35
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.753
```

```
confint(lmSfT)
```

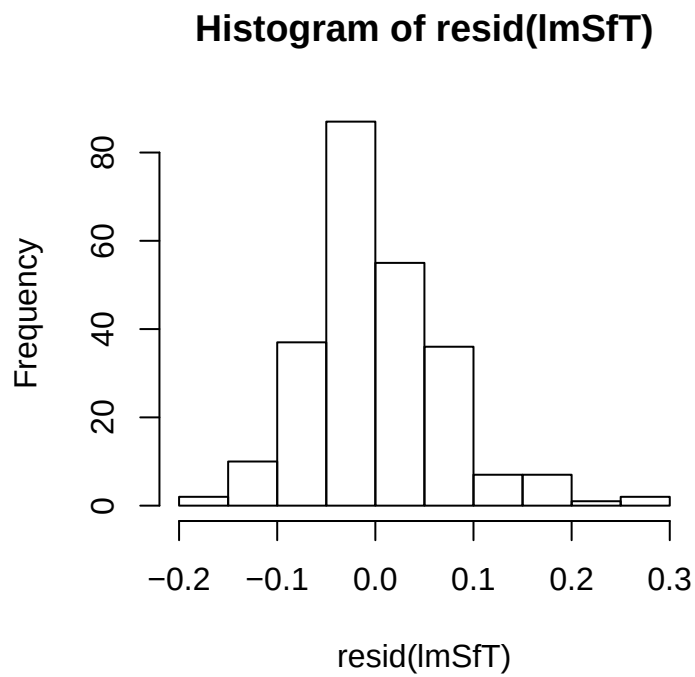
```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01      0.03263172 0.10294384
## .sigma      0.06653915 0.07967826
## (Intercept) 0.20705899 0.35053995
## sexmale     -0.08056165 0.10971328
```

```
Anova(lmSfT)
```

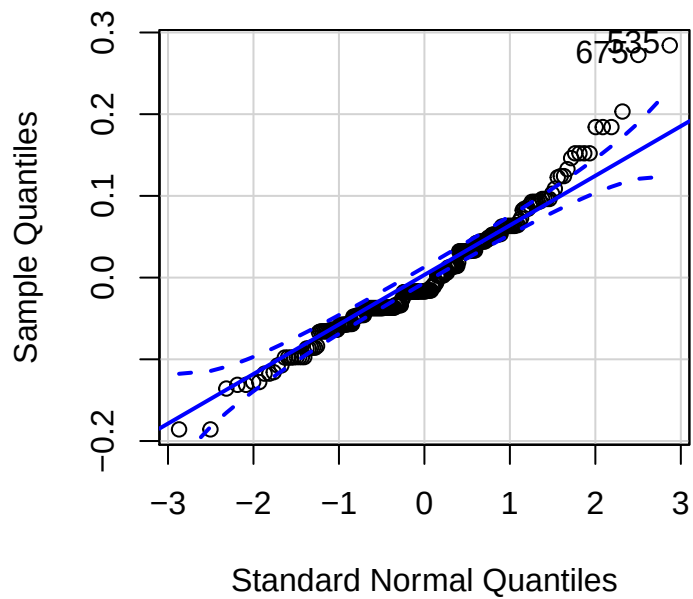
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: s_fusion_ratio
##      Chisq Df Pr(>Chisq)
## sex  0.1225  1    0.7264
```

Check normality of residuals

```
hist(resid(lmSfT))
```



```
qqp(resid(lmSfT), "norm", xlab = "Standard Normal Quantiles",  
     ylab = "Sample Quantiles")
```

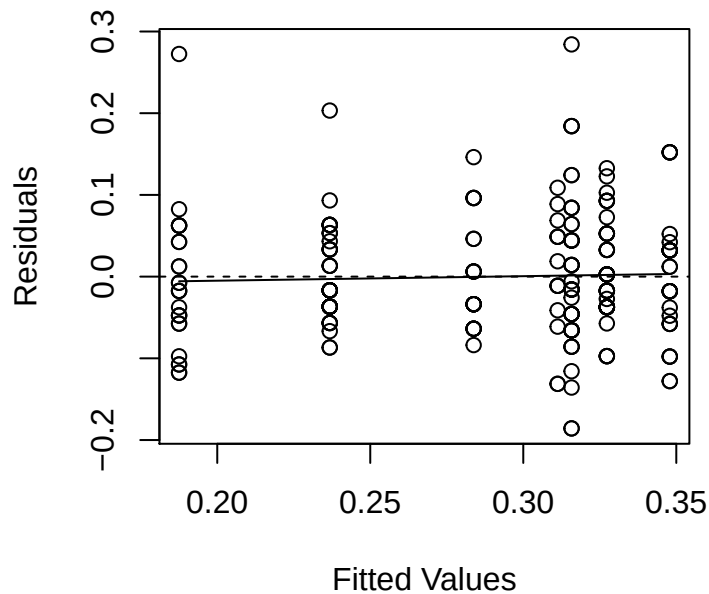


```
## 535 675
## 47 181
```

Check model fit

```
plot(fitted(lmSfT), residuals(lmSfT), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmSfT), residuals(lmSfT)))
```

Linear mixed model using maximum likelih



3.3 Petals

3.3.1 Descriptive statistics

Petal number

Mean

```
aggregate(petal_nb ~ sex + species, data = flwr, mean)
```

```
##      sex      species petal_nb
## 1 female      effusa 5.031250
## 2  male      effusa 5.000000
## 3 female  schimperi 4.500000
## 4  male  schimperi 4.238095
## 5 female tsjeriamcottam 4.760000
## 6  male tsjeriamcottam 5.040000
```

Variance

```
aggregate(petal_nb ~ sex + species, data = flwr, var)
```

```
##      sex      species petal_nb
## 1 female      effusa 0.0312500
```

```
## 2   male      effusa 0.0000000
## 3 female     schimperi 0.2631579
## 4   male      schimperi 0.2904762
## 5 female tsjeriamcottam 0.1900000
## 6   male tsjeriamcottam 0.1233333
```

Standard deviation

```
aggregate(petal_nb ~ sex + species, data = flwr, sd)
```

```
##      sex      species petal_nb
## 1 female      effusa 0.1767767
## 2   male      effusa 0.0000000
## 3 female     schimperi 0.5129892
## 4   male     schimperi 0.5389584
## 5 female tsjeriamcottam 0.4358899
## 6   male tsjeriamcottam 0.3511885
```

Petal length

Mean

```
aggregate(petal_length ~ sex + species, data = flwr, mean)
```

```
##      sex      species petal_length
## 1 female      effusa      30.43624
## 2   male      effusa      27.60465
## 3 female     schimperi      25.68675
## 4   male     schimperi      29.83133
## 5 female tsjeriamcottam      21.04701
## 6   male tsjeriamcottam      25.25410
```

Variance

```
aggregate(petal_length ~ sex + species, data = flwr, var)
```

```
##      sex      species petal_length
## 1 female      effusa      7.234083
## 2   male      effusa      4.311228
## 3 female     schimperi      3.120188
## 4   male     schimperi      7.068763
## 5 female tsjeriamcottam      7.051650
## 6   male tsjeriamcottam     29.959694
```

Standard deviation

```
aggregate(petal_length ~ sex + species, data = flwr, sd)
```

```
##      sex      species petal_length
## 1 female      effusa      2.689625
## 2   male      effusa      2.076350
## 3 female     schimperi      1.766405
## 4   male     schimperi      2.658715
## 5 female tsjeriamcottam      2.655494
## 6   male tsjeriamcottam      5.473545
```

Petal width

Mean

```
aggregate(petal_width ~ sex + species, data = flwr, mean)
```

```
##      sex      species petal_width
## 1 female      effusa  15.743506
## 2  male      effusa  11.846154
## 3 female    schimperi  14.126506
## 4  male    schimperi  14.597561
## 5 female tsjeriamcottam  8.423729
## 6  male tsjeriamcottam  8.463415
```

Variance

```
aggregate(petal_width ~ sex + species, data = flwr, var)
```

```
##      sex      species petal_width
## 1 female      effusa   6.775284
## 2  male      effusa   2.073047
## 3 female    schimperi   5.755143
## 4  male    schimperi   6.910117
## 5 female tsjeriamcottam  1.203535
## 6  male tsjeriamcottam  2.844962
```

Standard deviation

```
aggregate(petal_width ~ sex + species, data = flwr, sd)
```

```
##      sex      species petal_width
## 1 female      effusa   2.602938
## 2  male      effusa   1.439808
## 3 female    schimperi   2.398988
## 4  male    schimperi   2.628710
## 5 female tsjeriamcottam  1.097057
## 6  male tsjeriamcottam  1.686702
```

Petal fusion length

Mean

```
aggregate(p_fusion_ratio ~ sex + species, data = flwr, mean)
```

```
##      sex      species p_fusion_ratio
## 1 female      effusa   0.04650000
## 2  male      effusa   0.09450000
## 3 female    schimperi   0.05182927
## 4  male    schimperi   0.01662651
## 5 female tsjeriamcottam  0.04888889
## 6  male tsjeriamcottam  0.15745763
```

Variance

```
aggregate(p_fusion_ratio ~ sex + species, data = flwr, var)
```

```
##      sex      species p_fusion_ratio
## 1 female      effusa   0.011519949
## 2  male      effusa   0.018103544
## 3 female    schimperi   0.019266983
## 4  male    schimperi   0.006622627
## 5 female tsjeriamcottam  0.012972031
## 6  male tsjeriamcottam  0.068983225
```

Standard deviation


```
aggregate(p_fusion_ratio ~ sex + species, data = flwr, sd)
```

```
##      sex      species p_fusion_ratio
## 1 female      effusa    0.10733103
## 2  male      effusa    0.13454941
## 3 female    schimperi    0.13880556
## 4  male      schimperi    0.08137953
## 5 female tsjeriamcottam    0.11389482
## 6  male tsjeriamcottam    0.26264658
```

Petal fused or free

```
aggregate(petal_fused ~ species, data = flwr, mean)
```

```
##      species petal_fused
## 1      effusa  0.2445652
## 2    schimperi  0.1017964
## 3 tsjeriamcottam  0.2815126
```

```
aggregate(petal_fused ~ sex + species, data = flwr, mean)
```

```
##      sex      species petal_fused
## 1 female      effusa  0.16346154
## 2  male      effusa  0.35000000
## 3 female    schimperi  0.15662651
## 4  male      schimperi  0.04761905
## 5 female tsjeriamcottam  0.17796610
## 6  male tsjeriamcottam  0.38333333
```

```
aggregate(petal_fused ~ species + spec_ID, data = flwr, mean)
```

```
##      species spec_ID petal_fused
## 1 tsjeriamcottam BK1  0.08000000
## 2 tsjeriamcottam BK2  0.19565217
## 3 tsjeriamcottam BK3  0.00000000
## 4 tsjeriamcottam BK4  0.00000000
## 5 tsjeriamcottam BK5  0.35294118
## 6 tsjeriamcottam E4  0.65384615
## 7      effusa     E5  0.10714286
## 8      effusa    K10  0.60000000
## 9      effusa    K11  0.08000000
## 10     schimperi    K20  0.27659574
## 11     schimperi    K21  0.00000000
## 12     schimperi K23b  0.00000000
## 13     schimperi    K25  0.00000000
## 14     schimperi    K26  0.07500000
## 15     schimperi    K28  0.04761905
## 16      effusa     K5  0.06521739
## 17      effusa    K51  0.32000000
## 18 tsjeriamcottam K67  0.21276596
## 19      effusa     K7  0.36666667
```

```
aggregate(petal_fused ~ species + flower_ID, data = flwr, mean)
```

```
##      species flower_ID petal_fused
## 1      effusa    EF11  0.2000000
## 2      effusa    EF12  0.4000000
```

## 3	effusa	EF13	0.2000000
## 4	effusa	EF14	0.2000000
## 5	effusa	EF15	0.6000000
## 6	effusa	EF16	0.6000000
## 7	effusa	EF17	0.2000000
## 8	effusa	EF18	0.0000000
## 9	effusa	EF19	0.2000000
## 10	effusa	EF20	0.2000000
## 11	effusa	EF21	0.0000000
## 12	effusa	EF22	0.0000000
## 13	effusa	EF23	0.0000000
## 14	effusa	EF24	0.0000000
## 15	effusa	EF25	0.0000000
## 16	effusa	EF26	0.0000000
## 17	effusa	EF27	0.0000000
## 18	effusa	EF28	0.2000000
## 19	effusa	EF29	0.3333333
## 20	effusa	EF30	0.0000000
## 21	effusa	EF31	0.0000000
## 22	effusa	EF32	0.0000000
## 23	effusa	EM11	0.4000000
## 24	effusa	EM12	0.6000000
## 25	effusa	EM13	0.6000000
## 26	effusa	EM14	1.0000000
## 27	effusa	EM15	1.0000000
## 28	effusa	EM16	0.0000000
## 29	effusa	EM17	0.0000000
## 30	effusa	EM18	0.2000000
## 31	effusa	EM19	0.2000000
## 32	effusa	EM20	0.0000000
## 33	effusa	EM21	0.0000000
## 34	effusa	EM23	0.2000000
## 35	effusa	EM24	0.4000000
## 36	effusa	EM25	0.6000000
## 37	effusa	EM26	0.2000000
## 38	effusa	EM27	0.2000000
## 39	schimperi	SF1	0.4000000
## 40	schimperi	SF10	0.6666667
## 41	schimperi	SF11	0.0000000
## 42	schimperi	SF12	0.0000000
## 43	schimperi	SF13	0.0000000
## 44	schimperi	SF14	0.0000000
## 45	schimperi	SF15	0.0000000
## 46	schimperi	SF16	0.0000000
## 47	schimperi	SF17	0.0000000
## 48	schimperi	SF18	0.0000000
## 49	schimperi	SF19	0.0000000
## 50	schimperi	SF2	0.4000000
## 51	schimperi	SF20	0.0000000
## 52	schimperi	SF3	0.0000000
## 53	schimperi	SF4	0.2000000
## 54	schimperi	SF5	0.0000000
## 55	schimperi	SF6	0.0000000
## 56	schimperi	SF7	0.6000000

## 57	schimperi	SF8	0.0000000
## 58	schimperi	SF9	0.6000000
## 59	schimperi	SM1	0.0000000
## 60	schimperi	SM10	0.0000000
## 61	schimperi	SM11	0.0000000
## 62	schimperi	SM12	0.0000000
## 63	schimperi	SM13	0.0000000
## 64	schimperi	SM14	0.0000000
## 65	schimperi	SM15	0.0000000
## 66	schimperi	SM16	0.0000000
## 67	schimperi	SM17	0.0000000
## 68	schimperi	SM18	0.2500000
## 69	schimperi	SM19	0.0000000
## 70	schimperi	SM2	0.2500000
## 71	schimperi	SM20	0.0000000
## 72	schimperi	SM21	0.0000000
## 73	schimperi	SM3	0.0000000
## 74	schimperi	SM4	0.0000000
## 75	schimperi	SM5	0.0000000
## 76	schimperi	SM6	0.2000000
## 77	schimperi	SM7	0.0000000
## 78	schimperi	SM8	0.0000000
## 79	schimperi	SM9	0.2500000
## 80	tsjeriamcottam	TF1	0.0000000
## 81	tsjeriamcottam	TF10	0.5000000
## 82	tsjeriamcottam	TF11	0.0000000
## 83	tsjeriamcottam	TF12	0.2000000
## 84	tsjeriamcottam	TF13	0.2000000
## 85	tsjeriamcottam	TF14	0.0000000
## 86	tsjeriamcottam	TF15	0.0000000
## 87	tsjeriamcottam	TF16	0.4000000
## 88	tsjeriamcottam	TF17	0.2000000
## 89	tsjeriamcottam	TF18	0.4000000
## 90	tsjeriamcottam	TF19	0.0000000
## 91	tsjeriamcottam	TF2	0.4000000
## 92	tsjeriamcottam	TF20	0.4000000
## 93	tsjeriamcottam	TF21	0.0000000
## 94	tsjeriamcottam	TF22	0.0000000
## 95	tsjeriamcottam	TF23	0.0000000
## 96	tsjeriamcottam	TF24	0.0000000
## 97	tsjeriamcottam	TF25	0.4000000
## 98	tsjeriamcottam	TF3	0.4000000
## 99	tsjeriamcottam	TF4	0.0000000
## 100	tsjeriamcottam	TF5	0.2000000
## 101	tsjeriamcottam	TF6	0.0000000
## 102	tsjeriamcottam	TF7	0.2000000
## 103	tsjeriamcottam	TF8	0.0000000
## 104	tsjeriamcottam	TF9	0.4000000
## 105	tsjeriamcottam	TM1	0.4000000
## 106	tsjeriamcottam	TM10	1.0000000
## 107	tsjeriamcottam	TM11	0.0000000
## 108	tsjeriamcottam	TM12	0.0000000
## 109	tsjeriamcottam	TM13	0.0000000
## 110	tsjeriamcottam	TM14	0.0000000

```
## 111 tsjeriamcottam      TM15  0.0000000
## 112 tsjeriamcottam      TM16  0.0000000
## 113 tsjeriamcottam      TM17  0.0000000
## 114 tsjeriamcottam      TM19  0.4000000
## 115 tsjeriamcottam       TM2  1.0000000
## 116 tsjeriamcottam      TM20  0.4000000
## 117 tsjeriamcottam      TM21  0.4000000
## 118 tsjeriamcottam      TM22  0.2000000
## 119 tsjeriamcottam      TM23  0.6000000
## 120 tsjeriamcottam      TM24  0.2500000
## 121 tsjeriamcottam      TM25  0.2000000
## 122 tsjeriamcottam       TM3  0.1666667
## 123 tsjeriamcottam       TM4  0.6000000
## 124 tsjeriamcottam       TM5  0.8000000
## 125 tsjeriamcottam       TM6  0.4000000
## 126 tsjeriamcottam       TM7  0.0000000
## 127 tsjeriamcottam       TM8  1.0000000
## 128 tsjeriamcottam       TM9  1.0000000
```

Variance

```
aggregate(petal_fused ~ sex + species, data = flwr, var)
```

```
##      sex      species petal_fused
## 1 female      effusa  0.13806945
## 2  male      effusa  0.23037975
## 3 female    schimperi  0.13370555
## 4  male    schimperi  0.04589788
## 5 female tsjeriamcottam  0.14754455
## 6  male tsjeriamcottam  0.23837535
```

Standard deviation

```
aggregate(petal_fused ~ sex + species, data = flwr, sd)
```

```
##      sex      species petal_fused
## 1 female      effusa  0.3715770
## 2  male      effusa  0.4799789
## 3 female    schimperi  0.3656577
## 4  male    schimperi  0.2142379
## 5 female tsjeriamcottam  0.3841153
## 6  male tsjeriamcottam  0.4882370
```

3.3.2 Statistical tests - Petal number

Embelia effusa

Check number of observations

```
aggregate(petal_nb ~ sex + species, data = effusa, function(x) length(x))
```

```
##      sex species petal_nb
## 1 female  effusa      32
## 2  male  effusa      26
```

Check distribution

The number of petals is a discrete count variable. A glmer using Laplace approximation and a Poisson distribution is therefore used.

Build model

```
glmPnbE <- glmer(petal_nb ~ sex + (1 | spec_ID), effusa, family = poisson(log))
```

```
## boundary (singular) fit: see ?isSingular
```

Display results

```
summary(glmPnbE)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: petal_nb ~ sex + (1 | spec_ID)
## Data: effusa
##
##          AIC      BIC   logLik deviance df.resid
##    208.2    214.4  -101.1    202.2     55
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.01393 -0.01393 -0.01393  0.00000  0.43189
##
## Random effects:
## Groups Name          Variance Std.Dev.
## spec_ID (Intercept) 0          0
## Number of obs: 58, groups: spec_ID, 8
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.615668   0.078811  20.501  <2e-16 ***
## sexmale     -0.006231   0.117913  -0.053   0.958
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr)
## sexmale -0.668
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Confidence interval of the effect

```
confint(glmPnbE)
```

```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01         0.0000000 0.1315886
## (Intercept)    1.4571170 1.7662660
## sexmale       -0.2385434 0.2240741
```

Check overdispersion

The condition to use a generalised mixed effect linear regression model with Laplace approximation is that the data must not be overdispersed (the combined residuals must not be much larger than the residual degrees of freedom). I am using a method and code provided by Julia Pelowski to check whether the data is overdispersed. If the p-value generated by the `overdisp` function is <0.05 , then the data is overdispersed. This can be fixed by adding an additional random effect with one level per observation to the model.

```
overdisp_fun(glmPnbE)
```

```
##           chisq          ratio          rdf          p
## 0.192546584 0.003500847 55.000000000 1.000000000
```

The data is not overdispersed, the model can be used.

Check model fit

```
# plot(fitted(glmPnbE), residuals(glmPnbE), xlab = 'Fitted
# Values', ylab = 'Residuals', main='Generalised linear mixed
# model using Laplace approximation') abline(h = 0, lty = 2)
# lines(smooth.spline(fitted(glmPnbE), residuals(glmPnbE)))
```

Embelia schimperi

Check number of observations

```
aggregate(petal_nb ~ sex + species, data = schimp, function(x) length(x))
```

```
##      sex  species petal_nb
## 1 female schimperi      20
## 2  male schimperi      21
```

Check distribution

The number of petals is a discrete count variable.

Build model

```
glmPnbS <- glmer(petal_nb ~ sex + (1 | spec_ID), schimp, family = poisson(log))
```

```
## boundary (singular) fit: see ?isSingular
```

Display results

```
summary(glmPnbS)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: petal_nb ~ sex + (1 | spec_ID)
## Data: schimp
##
##      AIC      BIC    logLik deviance df.resid
##   145.5   150.7    -69.8   139.5      38
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.6014 -0.2357 -0.1157  0.2357  0.3701
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 0      0
## Number of obs: 41, groups: spec_ID, 6
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.50408    0.10541  14.269  <2e-16 ***
## sexmale     -0.05996    0.14949  -0.401    0.688
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## sexmale -0.705
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Confidence interval of the effect

```
confint(glmPnbS)
```

```
## Computing profile confidence intervals ...
##              2.5 %    97.5 %
## .sig01        0.0000000 0.1873093
## (Intercept)   1.2903456 1.7035593
## sexmale      -0.3536412 0.2331496
```

Check overdispersion

```
overdisp_fun(glmPnbS)
```

```
##      chisq      ratio      rdf      p
## 2.4818976 0.0653131 38.0000000 1.0000000
```

Check model fit

```
# plot(fitted(glmPnbS), residuals(glmPnbS), xlab = 'Fitted
# Values', ylab = 'Residuals', main='Generalised linear mixed
# model using Laplace approximation') abline(h = 0, lty = 2)
# lines(smooth.spline(fitted(glmPnbS), residuals(glmPnbS)))
```

Embelia tsjeriamcottam

Check number of observations

```
aggregate(petal_nb ~ sex + species, data = tsjer, function(x) length(x))
```

```
##      sex      species petal_nb
## 1 female tsjeriamcottam      25
## 2  male tsjeriamcottam      25
```

Check distribution

The number of petals is a discrete count variable.

Build model

```
glmPnbT <- glmer(petal_nb ~ sex + (1 | spec_ID), tsjer, family = poisson(log))
```

```
## boundary (singular) fit: see ?isSingular
```

Display results

```
summary(glmPnbT)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: petal_nb ~ sex + (1 | spec_ID)
## Data: tsjer
```

```
##
##      AIC      BIC   logLik deviance df.resid
##    180.5    186.2   -87.2   174.5      47
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.46325 -0.01782 -0.01782  0.11000  0.42762
##
## Random effects:
##  Groups Name      Variance Std.Dev.
## spec_ID (Intercept) 0          0
## Number of obs: 50, groups: spec_ID, 7
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.56025    0.09167  17.020  <2e-16 ***
## sexmale      0.05716    0.12783   0.447   0.655
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## sexmale -0.717
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Confidence interval of the effect

```
confint(glmPnbT)
```

```
## Computing profile confidence intervals ...
##              2.5 %    97.5 %
## .sig01        0.0000000 0.1488724
## (Intercept)  1.3749582 1.7345606
## sexmale      -0.1934447 0.3084493
```

Check overdispersion

```
overdisp_fun(glmPnbT)
```

```
##      chisq      ratio      rdf      p
##  1.5452848  0.0328784 47.0000000  1.0000000
```

Check model fit

```
# plot(fitted(glmPnbT), residuals(glmPnbT), xlab = 'Fitted
# Values', ylab = 'Residuals', main='Generalised linear mixed
# model using Laplace approximation') abline(h = 0, lty = 2)
# lines(smooth.spline(fitted(glmPnbT), residuals(glmPnbT)))
```

3.3.3 Statistical tests - Petal length

Embelia effusa

Number of observations

```
aggregate(petal_length ~ sex + species, data = effusa, function(x) length(x))
```

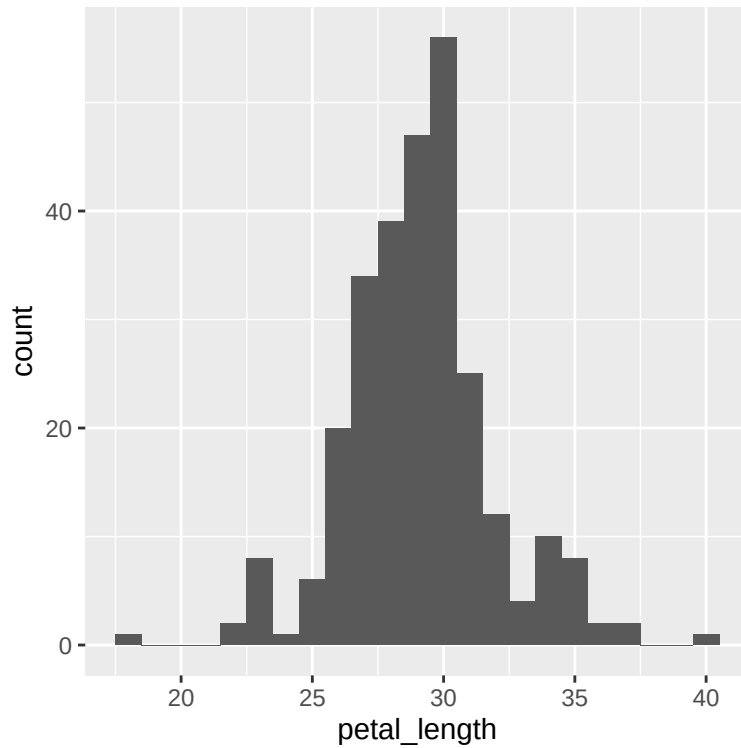


```
##      sex species petal_length
## 1 female  effusa           149
## 2  male   effusa           129
```

Distribution

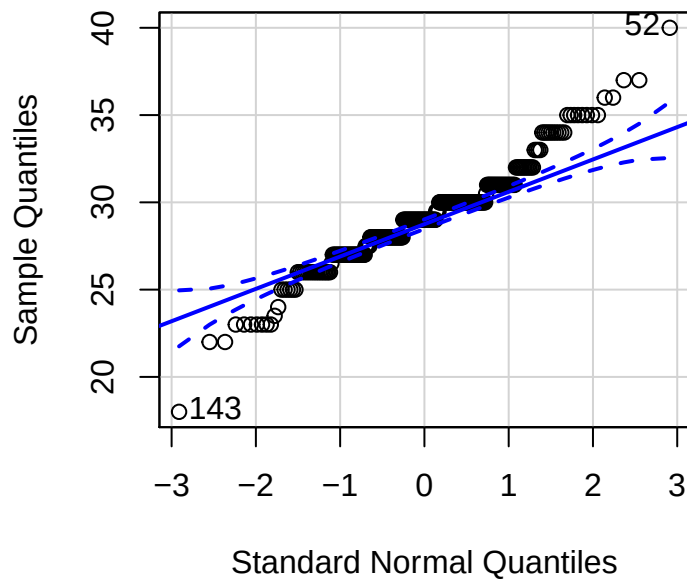
```
histnormPE <- ggplot(effusa, aes(petal_length))
histnormPE + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 14 rows containing non-finite values (stat_bin).
```



```
qqp(effusa$petal_length, "norm", xlab = "Standard Normal Quantiles",
  ylab = "Sample Quantiles", main = "Embelia effusa")
```

Embelia effusa



```
## [1] 143 52
```

Build model

```
lmPlE <- lmer(petal_length ~ sex + (1 | spec_ID), effusa, REML = FALSE)
```

Display results

```
summary(lmPlE)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: petal_length ~ sex + (1 | spec_ID)
## Data: effusa
##
##      AIC      BIC    logLik deviance df.resid
## 1100.3   1114.8   -546.2   1092.3     274
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -6.5815 -0.6272 -0.0703  0.5170  3.5401
##
## Random effects:
## Groups   Name      Variance Std.Dev.
## spec_ID (Intercept) 3.746    1.936
## Residual                2.664    1.632
## Number of obs: 278, groups: spec_ID, 8
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept) 30.5977    0.9777  31.297
## sexmale     -3.2595    1.3837  -2.356
```

```
##
## Correlation of Fixed Effects:
##      (Intr)
## sexmale -0.707

confint(lmPlE)

## Computing profile confidence intervals ...

##           2.5 %      97.5 %
## .sig01      1.248856  3.5031405
## .sigma      1.503733  1.7803040
## (Intercept) 28.426138 32.7712344
## sexmale     -6.336638 -0.1887226

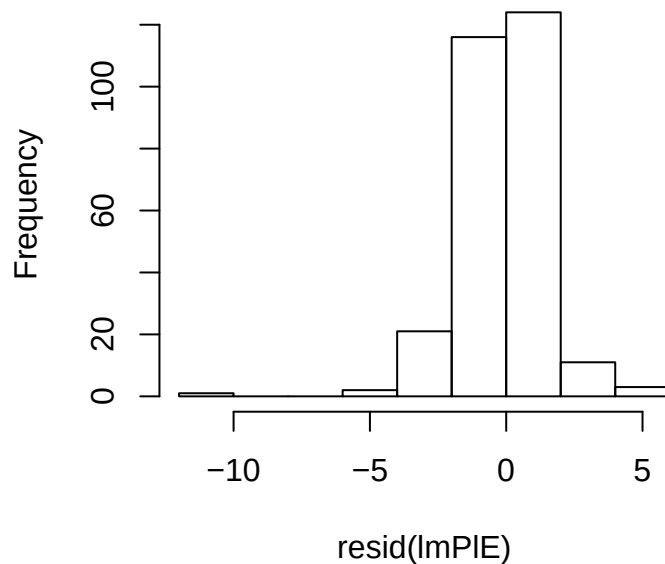
Anova(lmPlE)

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: petal_length
##      Chisq Df Pr(>Chisq)
## sex  5.5491  1    0.01849 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

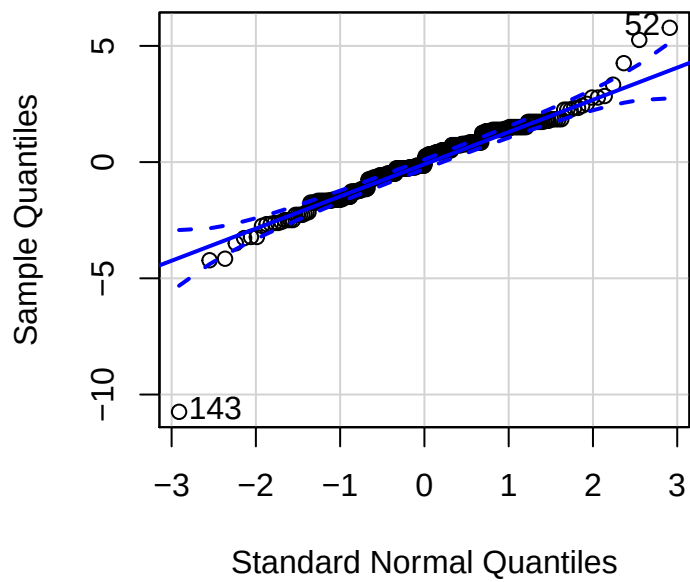
Check normality of residuals

hist(resid(lmPlE))
```

Histogram of resid(lmPlE)



```
qqp(resid(lmPlE), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

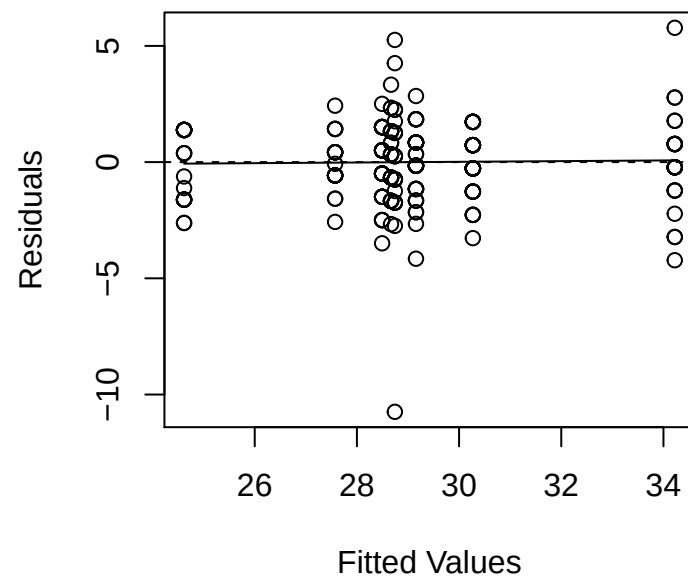


```
## 143 52
## 133 51
```

Check model fit

```
plot(fitted(lmP1E), residuals(lmP1E), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmP1E), residuals(lmP1E)))
```

Linear mixed model using maximum likelih



Embelia schimperi

Number of observations

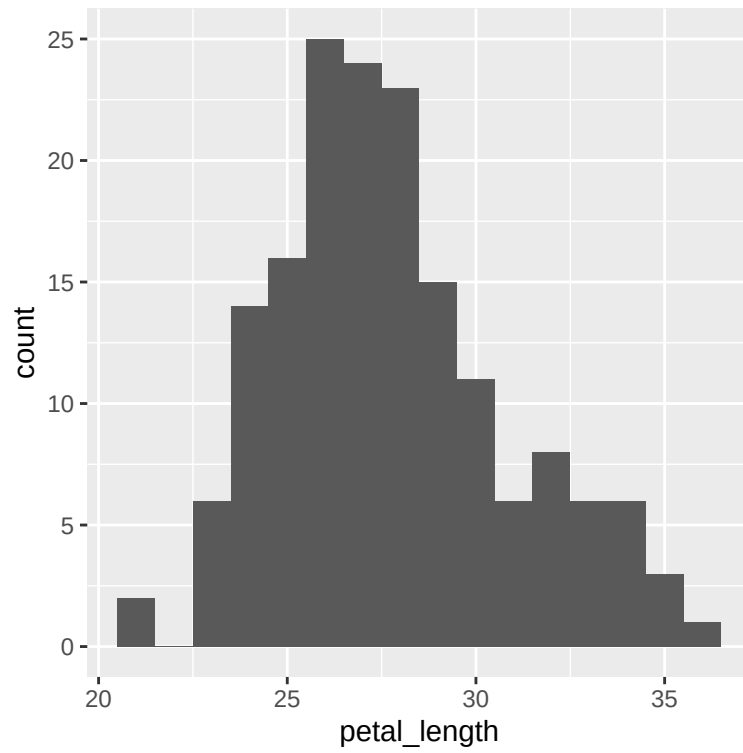
```
aggregate(petal_length ~ sex + species, data = schimp, function(x) length(x))
```

```
##      sex  species petal_length
## 1 female schimperi           83
## 2  male schimperi           83
```

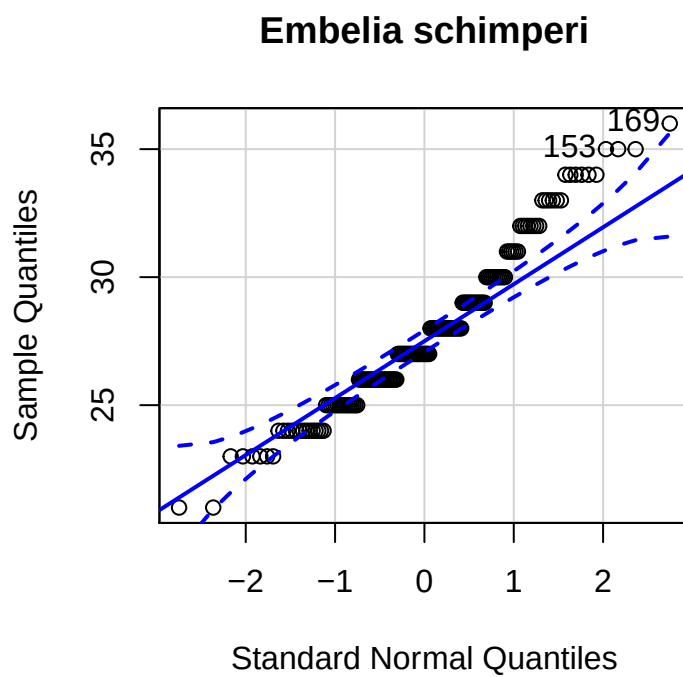
Distribution

```
histnormPS <- ggplot(schimp, aes(petal_length))
histnormPS + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 28 rows containing non-finite values (stat_bin).
```



```
qqp(schimp$petal_length, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia schimperi")
```



```
## [1] 169 153
```

Build model

```
lmSP1 <- lmer(petal_length ~ sex + (1 | spec_ID), schimp, REML = FALSE)
```

Display results

```
summary(lmSP1)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: petal_length ~ sex + (1 | spec_ID)
## Data: schimp
##
##      AIC      BIC    logLik deviance df.resid
##    648.8    661.3   -320.4    640.8     162
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.1259 -0.7035 -0.0648  0.5739  2.4901
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 3.125  1.768
## Residual          2.451  1.566
## Number of obs: 166, groups: spec_ID, 6
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  26.210     1.042  25.165
## sexmale      3.784     1.469   2.575
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.709
```

```
confint(lmSP1)
```

```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01      1.0655069  3.593024
## .sigma      1.4085512  1.754157
## (Intercept) 23.8078416 28.635180
## sexmale      0.3650072  7.182124
```

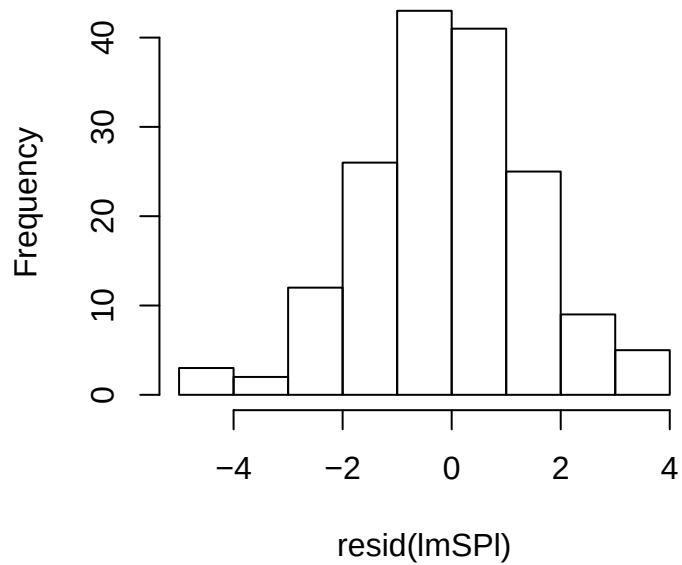
```
Anova(lmSP1)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: petal_length
##      Chisq Df Pr(>Chisq)
## sex 6.6328  1  0.01001 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

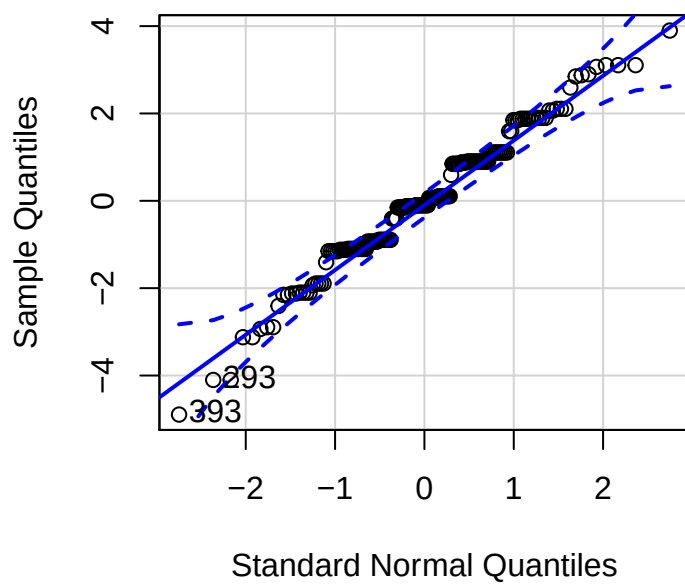
Check normality of residuals

```
hist(resid(lmSP1))
```

Histogram of resid(lmSPI)



```
qqp(resid(lmSPI), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

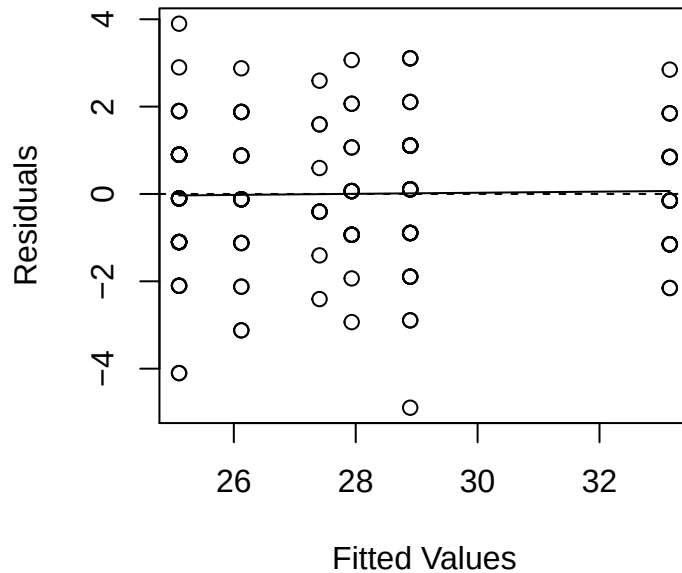


```
## 393 293
## 89 1
```


Check model fit

```
plot(fitted(lmSP1), residuals(lmSP1), xlab = "Fitted Values",  
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")  
abline(h = 0, lty = 2)  
lines(smooth.spline(fitted(lmSP1), residuals(lmSP1)))
```

Linear mixed model using maximum likelih



Embelia tsjeriamcottam

Number of observations

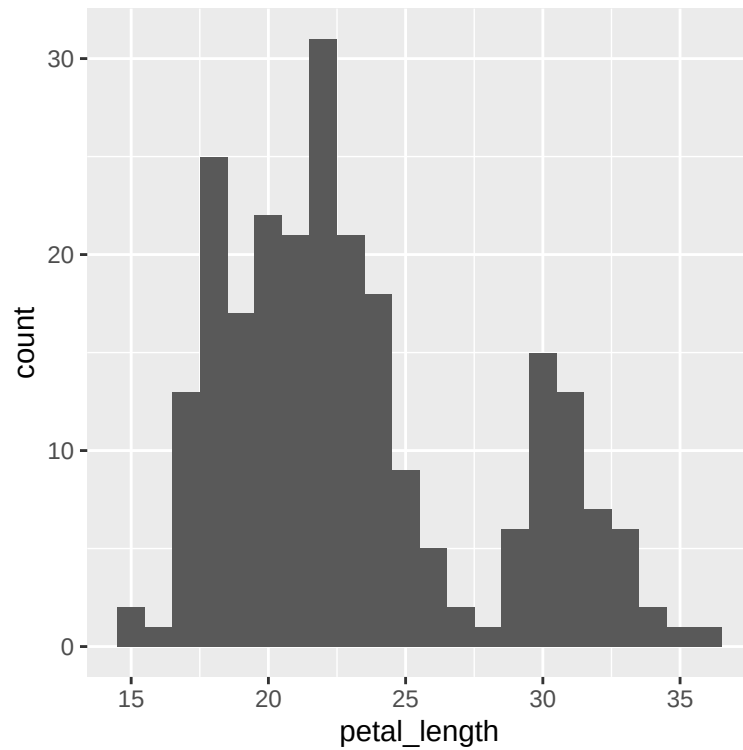
```
aggregate(petal_length ~ sex + species, data = tsjer, function(x) length(x))
```

```
##      sex      species petal_length  
## 1 female tsjeriamcottam      117  
## 2  male tsjeriamcottam      122
```

Distribution

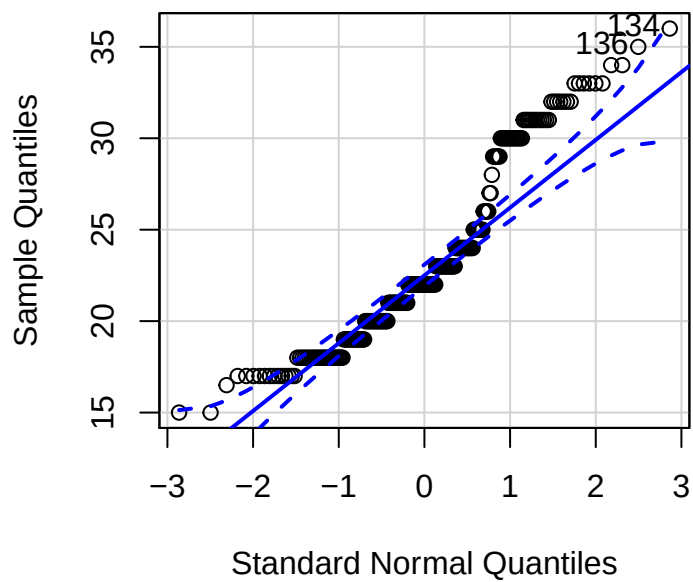
```
histnormPT <- ggplot(tsjer, aes(petal_length))  
histnormPT + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",  
  "lightsalmon"))
```

```
## Warning: Removed 16 rows containing non-finite values (stat_bin).
```



```
qqp(tsjer$petal_length, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia tsjeriamcottam")
```

Embelia tsjeriamcottam



```
## [1] 134 136
```

Build model

```
lmPT <- lmer(petal_length ~ sex + (1 | spec_ID), tsjer, REML = FALSE)
```

Display results

```
summary(lmPT)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: petal_length ~ sex + (1 | spec_ID)
## Data: tsjer
##
##      AIC      BIC    logLik deviance df.resid
##    890.0    903.9   -441.0    882.0      235
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.7158 -0.7010  0.0057  0.6657  3.4922
##
## Random effects:
## Groups   Name      Variance Std.Dev.
## spec_ID (Intercept) 14.104   3.756
## Residual              2.003   1.415
## Number of obs: 239, groups: spec_ID, 7
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   20.462     2.173   9.419
## sexmale        3.649     2.875   1.269
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.756
```

```
confint(lmPT)
```

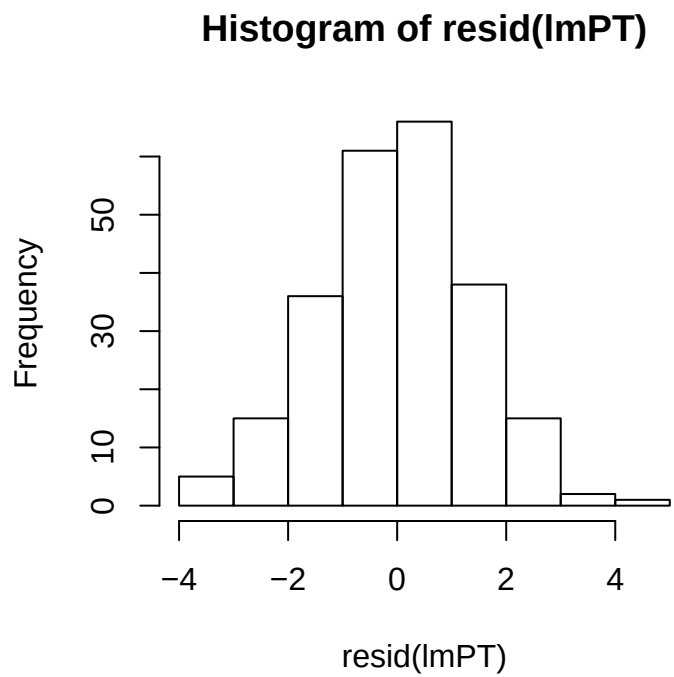
```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01      2.397155  7.086013
## .sigma      1.295545  1.554368
## (Intercept) 15.546487 25.375707
## sexmale     -2.853703 10.152409
```

```
Anova(lmPT)
```

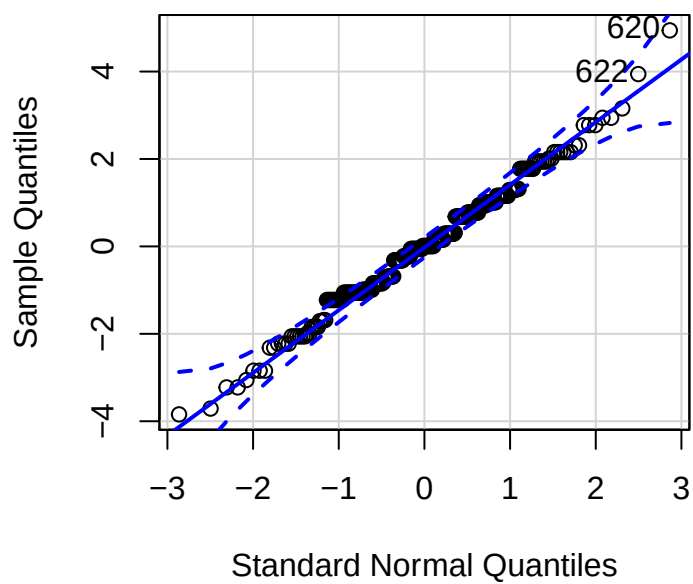
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: petal_length
##      Chisq Df Pr(>Chisq)
## sex 1.6109  1    0.2044
```

Check normality of residuals

```
hist(resid(lmPT))
```



```
qqp(resid(lmPT), "norm", xlab = "Standard Normal Quantiles",  
     ylab = "Sample Quantiles")
```

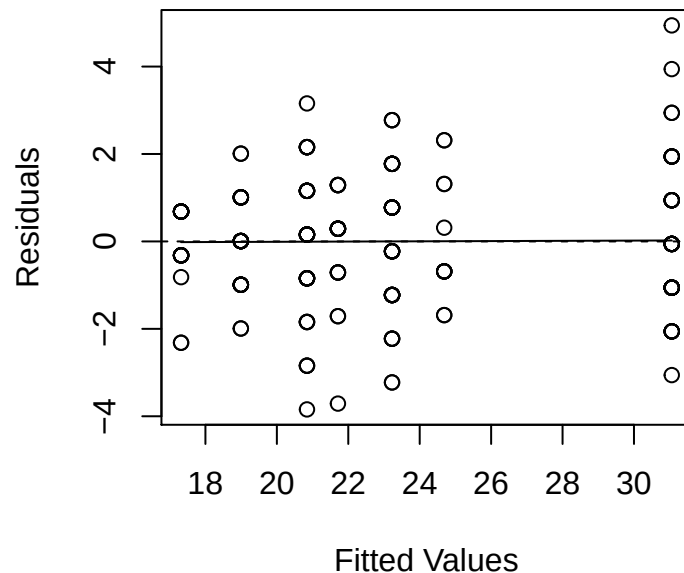


```
## 620 622
## 128 130
```

Check model fit

```
plot(fitted(lmPT), residuals(lmPT), xlab = "Fitted Values", ylab = "Residuals",
     main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmPT), residuals(lmPT)))
```

Linear mixed model using maximum likelih



3.3.4 Statistical tests - Petal width

Embelia effusa

Number of observations

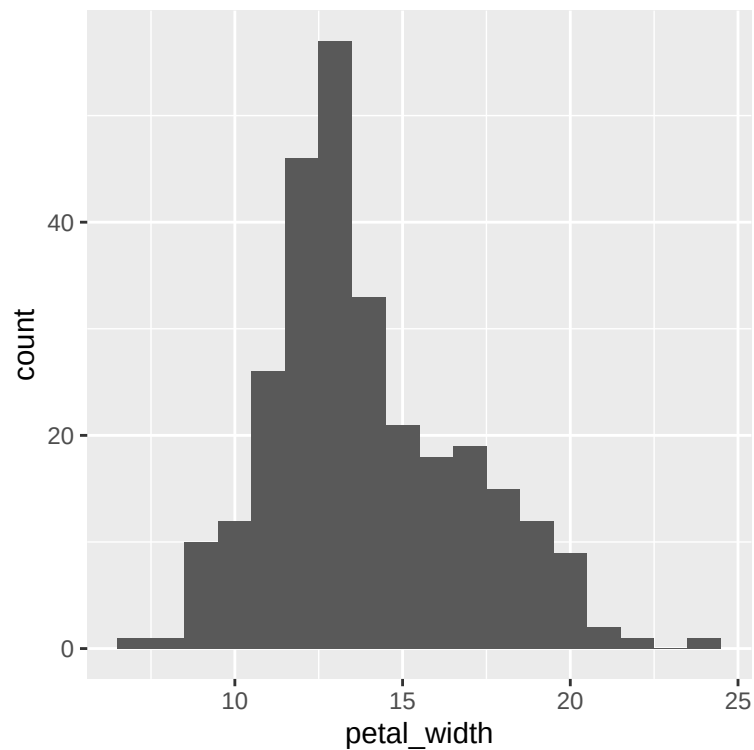
```
aggregate(petal_width ~ sex + species, data = effusa, function(x) length(x))
```

```
##      sex species petal_width
## 1 female  effusa         154
## 2  male   effusa         130
```

Distribution

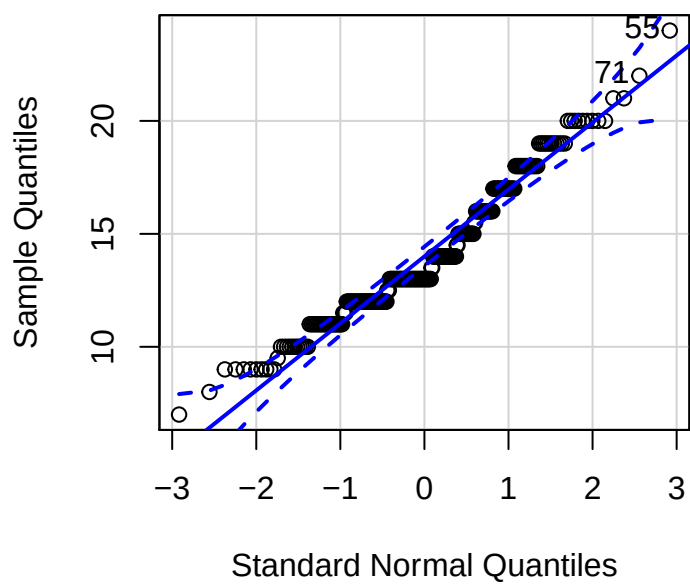
```
histnormPwE <- ggplot(effusa, aes(petal_width))
histnormPwE + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 8 rows containing non-finite values (stat_bin).
```



```
qqp(effusa$petal_width, "norm", xlab = "Standard Normal Quantiles",
    ylab = "Sample Quantiles", main = "Embelia effusa")
```

Embelia effusa



```
## [1] 55 71
```

Build model

```
lmPwE <- lmer(petal_width ~ sex + (1 | spec_ID), effusa, REML = FALSE)
```

Display results

```
summary(lmPwE)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: petal_width ~ sex + (1 | spec_ID)
## Data: effusa
##
##      AIC      BIC    logLik deviance df.resid
##  1081.8   1096.4   -536.9   1073.8     280
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.6671 -0.5890  0.0670  0.5808  3.5598
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 2.300  1.516
## Residual          2.324  1.524
## Number of obs: 284, groups: spec_ID, 8
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  15.8051    0.7687  20.560
## sexmale      -4.0629    1.0887  -3.732
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.706
```

```
confint(lmPwE)
```

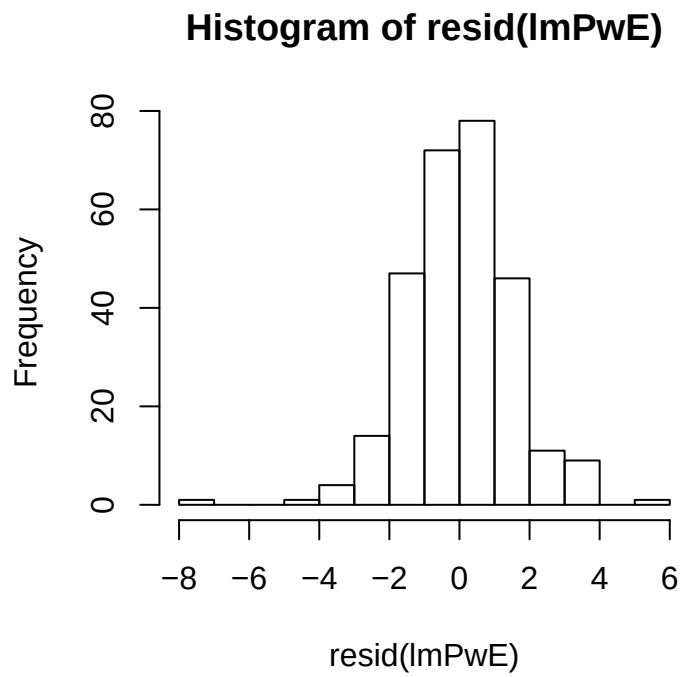
```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01      0.9747735  2.749954
## .sigma      1.4055766  1.660997
## (Intercept) 14.0979625 17.513579
## sexmale     -6.4819623 -1.647411
```

```
Anova(lmPwE)
```

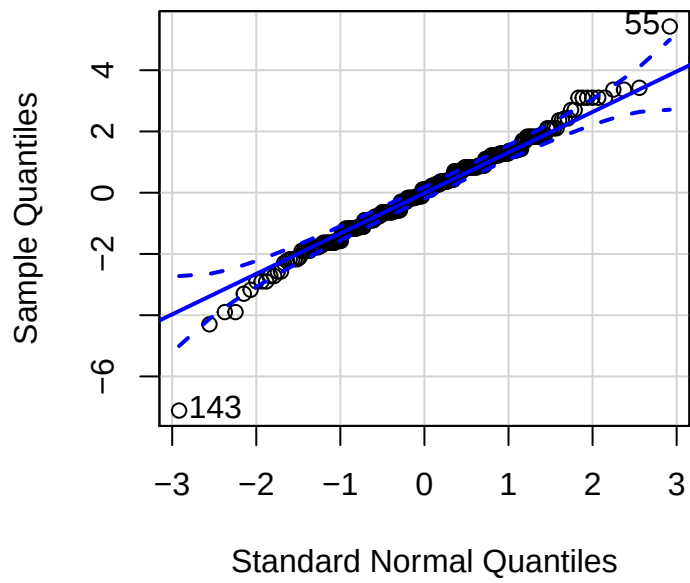
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: petal_width
##      Chisq Df Pr(>Chisq)
## sex 13.927  1  0.00019 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Check normality of residuals

```
hist(resid(lmPwE))
```



```
qqp(resid(lmPwE), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

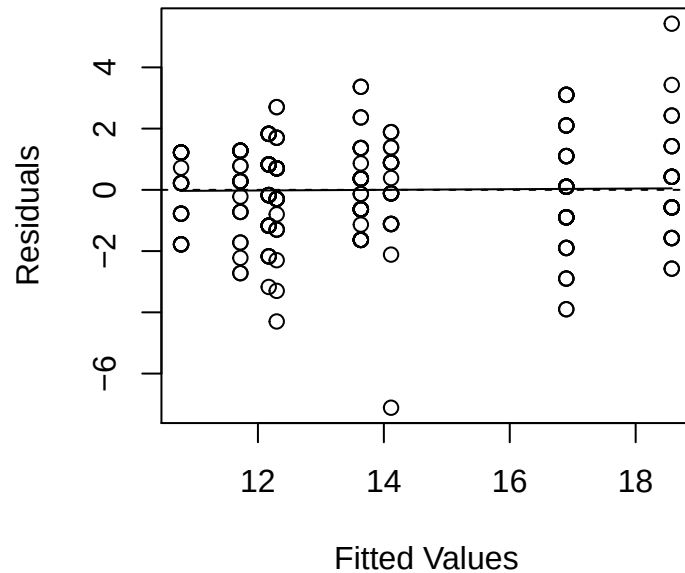


```
## 143 55
## 136 55
```


Check model fit

```
plot(fitted(lmPwE), residuals(lmPwE), xlab = "Fitted Values",  
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")  
abline(h = 0, lty = 2)  
lines(smooth.spline(fitted(lmPwE), residuals(lmPwE)))
```

Linear mixed model using maximum likelih



Embelia schimperi

Number of observations

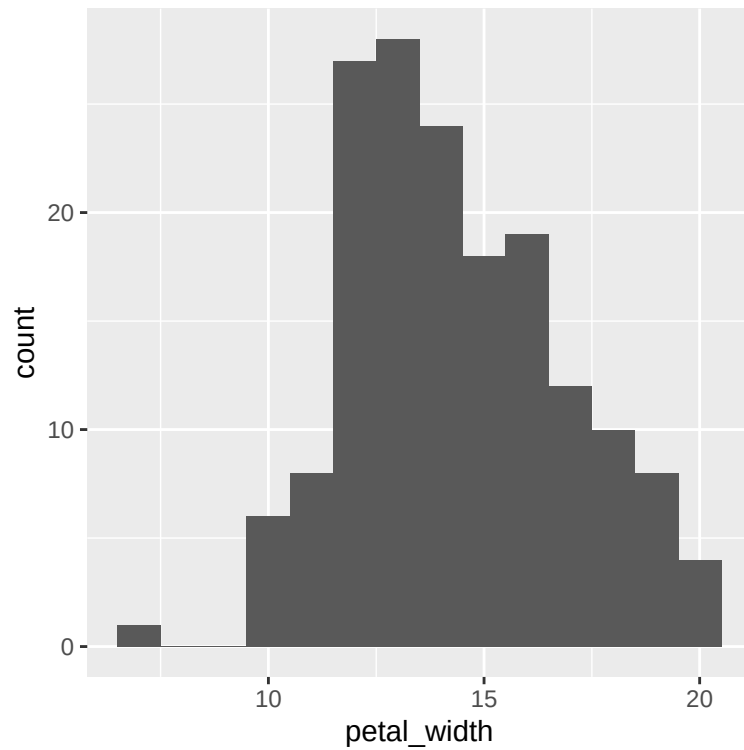
```
aggregate(petal_width ~ sex + species, data = schimp, function(x) length(x))
```

```
##      sex  species petal_width  
## 1 female schimperi          83  
## 2  male schimperi          82
```

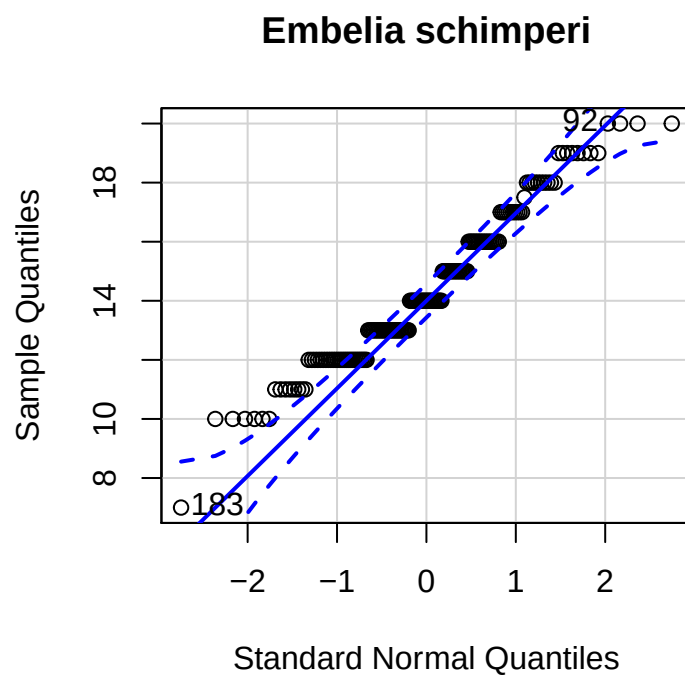
Distribution

```
histnormPwS <- ggplot(schimp, aes(petal_width))  
histnormPwS + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",  
  "lightsalmon"))
```

```
## Warning: Removed 29 rows containing non-finite values (stat_bin).
```



```
qqp(schimp$petal_width, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia schimperi")
```



```
## [1] 183 92
```

Build model

```
lmPwS <- lmer(petal_width ~ sex + (1 | spec_ID), schimp, REML = FALSE)
```

Display results

```
summary(lmPwS)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: petal_width ~ sex + (1 | spec_ID)
## Data: schimp
##
##      AIC      BIC    logLik deviance df.resid
##    684.1    696.5   -338.1    676.1      161
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.9907 -0.6136 -0.0465  0.5207  3.8238
##
## Random effects:
## Groups   Name      Variance Std.Dev.
## spec_ID (Intercept) 3.864    1.966
## Residual              3.109    1.763
## Number of obs: 165, groups: spec_ID, 6
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  15.2435    1.1586  13.157
## sexmale      -0.3485    1.6347  -0.213
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.709
```

```
confint(lmPwS)
```

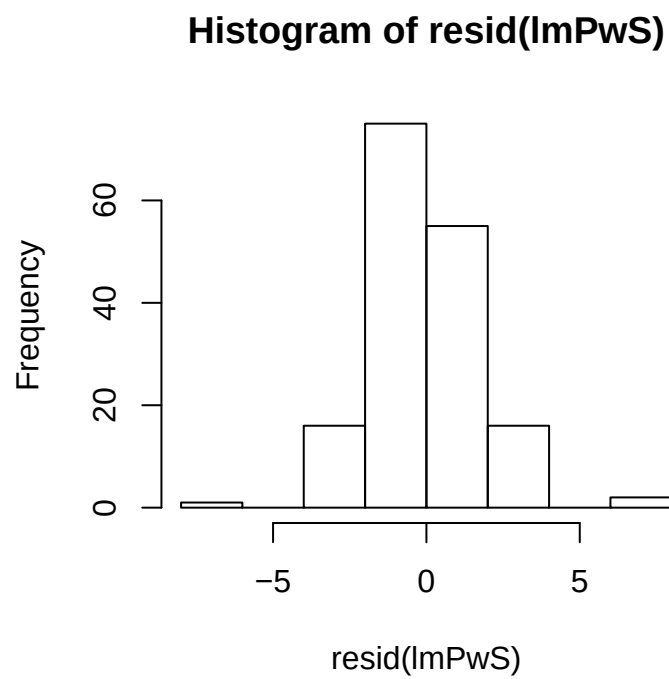
```
## Computing profile confidence intervals ...
##              2.5 %    97.5 %
## .sig01      1.179020  4.004467
## .sigma      1.585784  1.976317
## (Intercept) 12.580578 17.957327
## sexmale     -4.168009  3.425967
```

```
Anova(lmPwS)
```

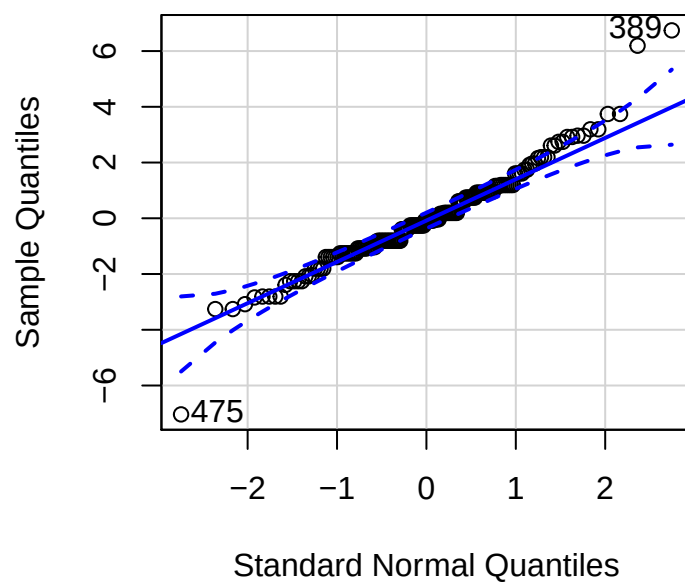
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: petal_width
##      Chisq Df Pr(>Chisq)
## sex  0.0454  1    0.8312
```

Check normality of residuals

```
hist(resid(lmPwS))
```



```
qqp(resid(lmPwS), "norm", xlab = "Standard Normal Quantiles",  
    ylab = "Sample Quantiles")
```

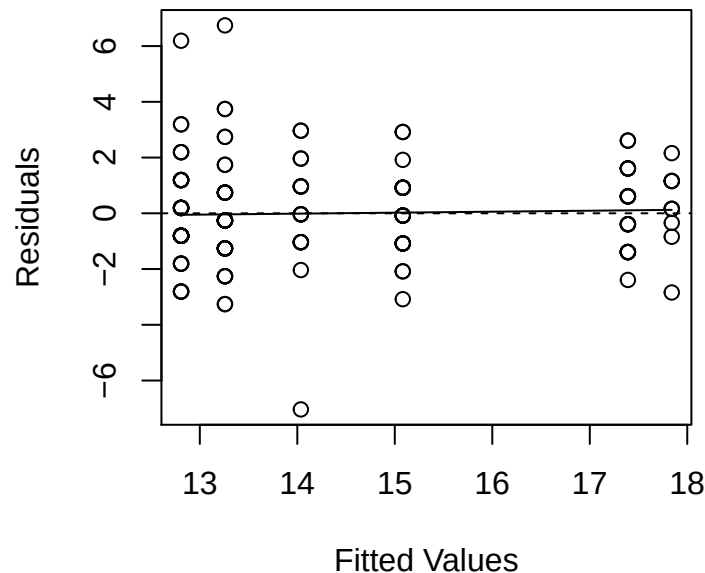


```
## 475 389
## 155 86
```

Check model fit

```
plot(fitted(lmPwS), residuals(lmPwS), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmPwS), residuals(lmPwS)))
```

Linear mixed model using maximum likelih



Embelia tsjeriamcottam

Number of observations

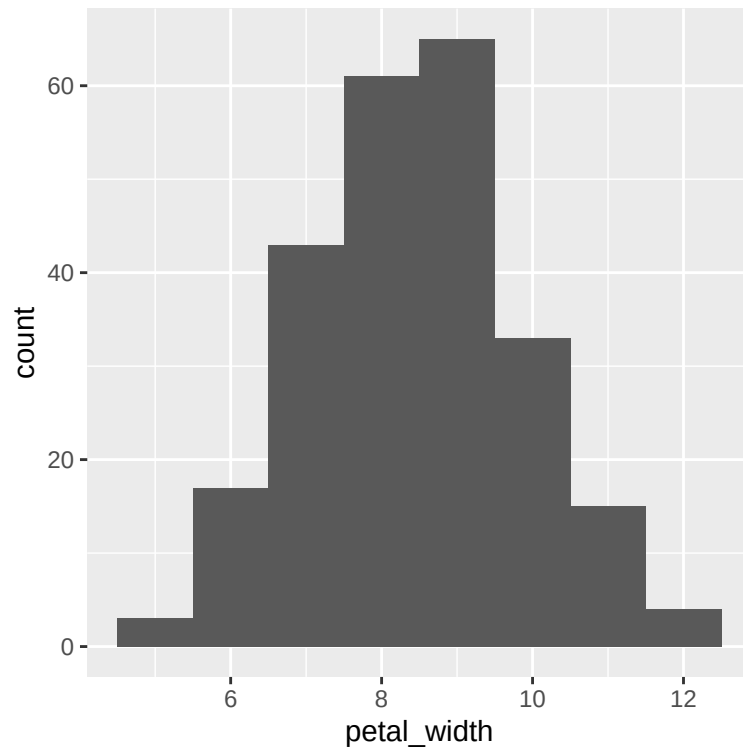
```
aggregate(petal_width ~ sex + species, data = tsjer, function(x) length(x))
```

```
##      sex      species petal_width
## 1 female tsjeriamcottam      118
## 2  male tsjeriamcottam      123
```

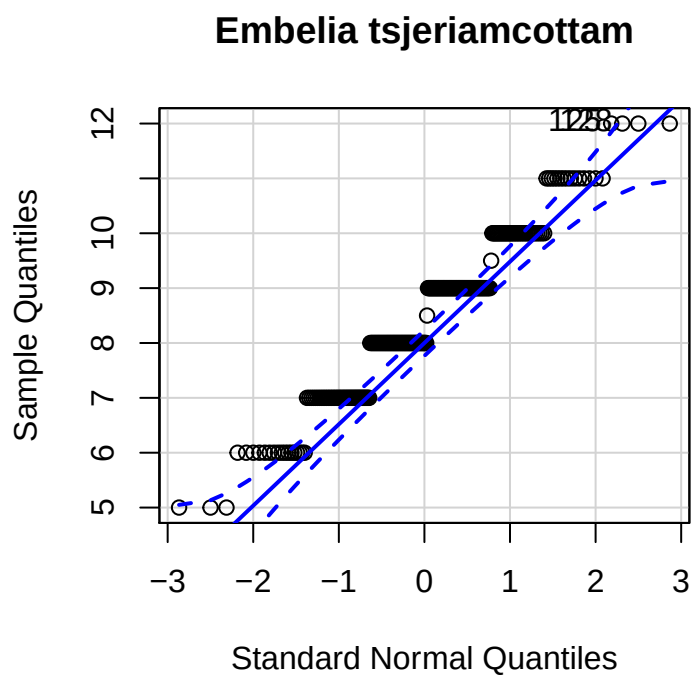
Distribution

```
histnormPwT <- ggplot(tsjer, aes(petal_width))
histnormPwT + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 14 rows containing non-finite values (stat_bin).
```



```
qqp(tsjer$petal_width, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia tsjeriamcottam")
```



```
## [1] 125 128
```

Build model

```
lmPwT <- lmer(petal_width ~ sex + (1 | spec_ID), tsjer, REML = FALSE)
```

Display results

```
summary(lmPwT)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: petal_width ~ sex + (1 | spec_ID)
## Data: tsjer
##
##      AIC      BIC    logLik deviance df.resid
##    747.7    761.6   -369.8    739.7     237
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.6024 -0.5911  0.1715  0.3445  2.6279
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## spec_ID  (Intercept)  0.777      0.8815
## Residual                    1.151      1.0730
## Number of obs: 241, groups: spec_ID, 7
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   8.3769    0.5192  16.133
## sexmale      -0.1061    0.6895  -0.154
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.753
```

```
confint(lmPwT)
```

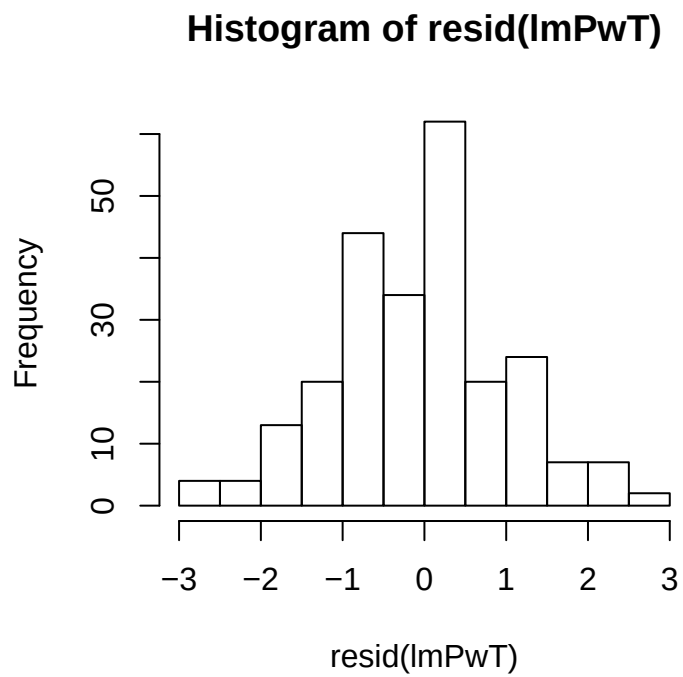
```
## Computing profile confidence intervals ...
##
##              2.5 %   97.5 %
## .sig01         0.5477301 1.684707
## .sigma         0.9827168 1.178060
## (Intercept)    7.2014610 9.550326
## sexmale       -1.6649666 1.449395
```

```
Anova(lmPwT)
```

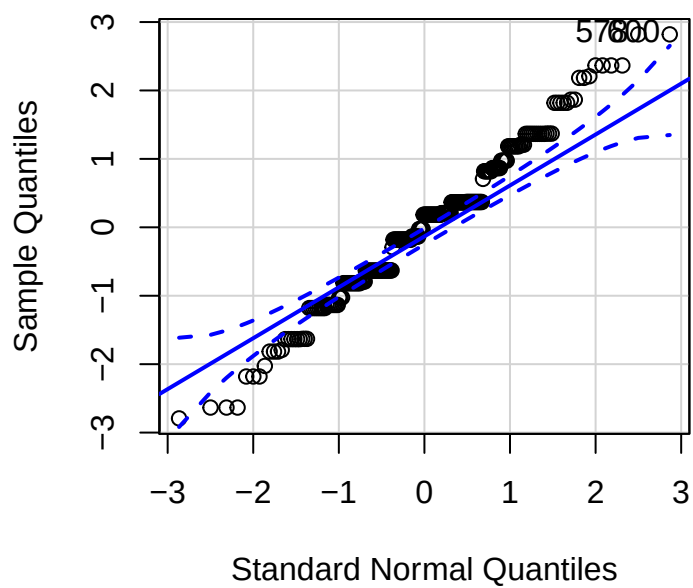
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: petal_width
##      Chisq Df Pr(>Chisq)
## sex  0.0237  1    0.8777
```

Check normality of residuals

```
hist(resid(lmPwT))
```



```
qqp(resid(lmPwT), "norm", xlab = "Standard Normal Quantiles",  
    ylab = "Sample Quantiles")
```

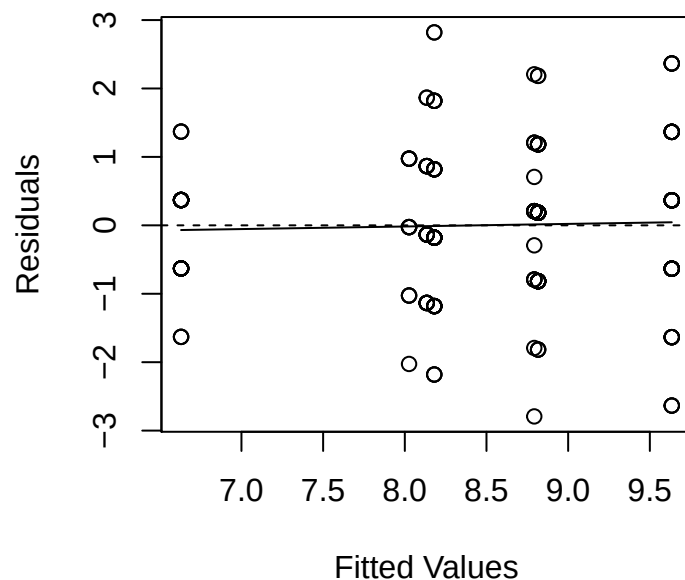



```
## 578 600
## 90 110
```

Check model fit

```
plot(fitted(lmPwT), residuals(lmPwT), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmPwT), residuals(lmPwT)))
```

Linear mixed model using maximum likelih



3.3.5 Statistical tests - Relative length of the fusion of the petals

Embelia effusa

Number of observations

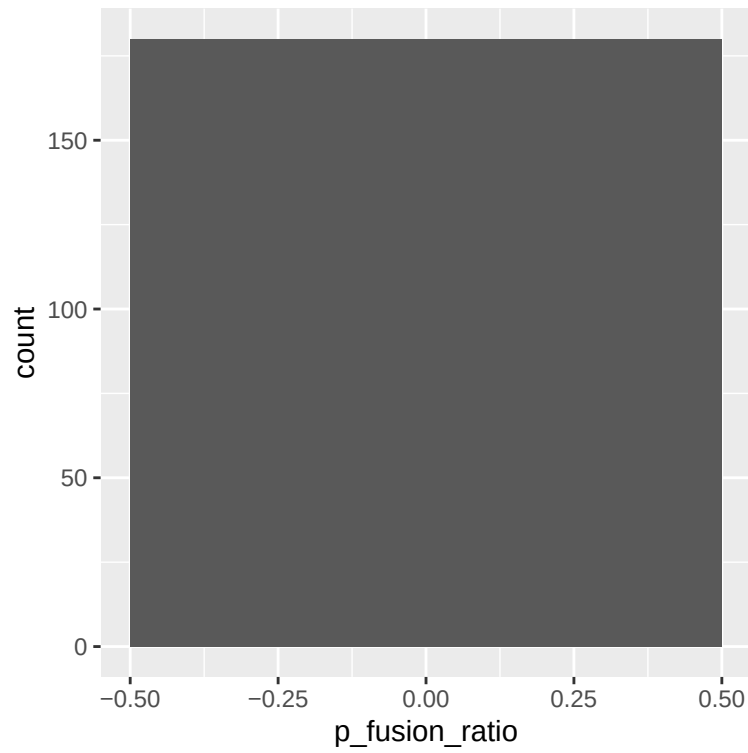
```
aggregate(p_fusion_ratio ~ sex + species, data = effusa, function(x) length(x))
```

```
##      sex species p_fusion_ratio
## 1 female  effusa             100
## 2  male   effusa              80
```

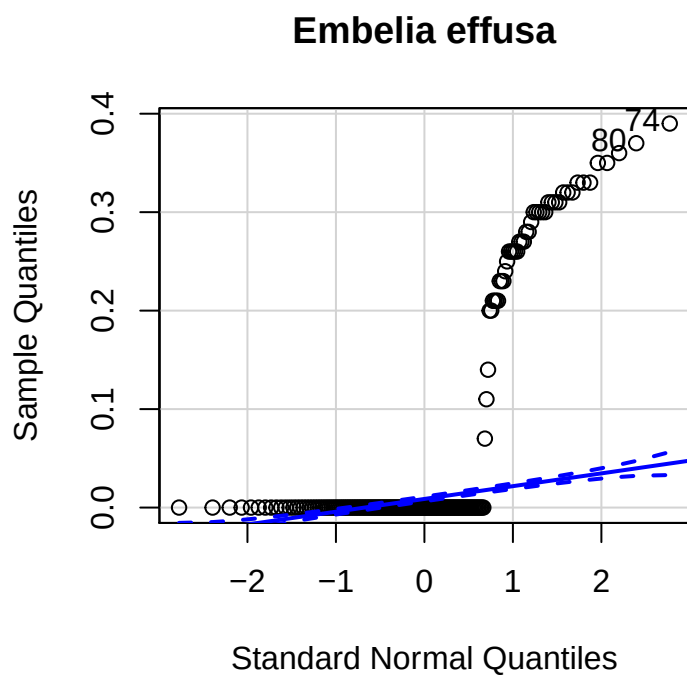
Distribution

```
histnormPfE <- ggplot(effusa, aes(p_fusion_ratio))
histnormPfE + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 112 rows containing non-finite values (stat_bin).
```



```
qqp(effusa$p_fusion_ratio, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia effusa")
```



```
## [1] 74 80
```

Build model

```
lmPfE <- lmer(p_fusion_ratio ~ sex + (1 | spec_ID), effusa, REML = FALSE)
```

Display results

```
summary(lmPfE)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: p_fusion_ratio ~ sex + (1 | spec_ID)
## Data: effusa
##
##      AIC      BIC    logLik deviance df.resid
##   -261.5   -248.7    134.8   -269.5      176
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.3189 -0.8575 -0.2685 -0.1666  2.7664
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## spec_ID  (Intercept)  0.002009  0.04482
## Residual                    0.012356  0.11116
## Number of obs: 180, groups: spec_ID, 6
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  0.05047    0.02827   1.785
## sexmale      0.04056    0.04030   1.006
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.701
```

```
confint(lmPfE)
```

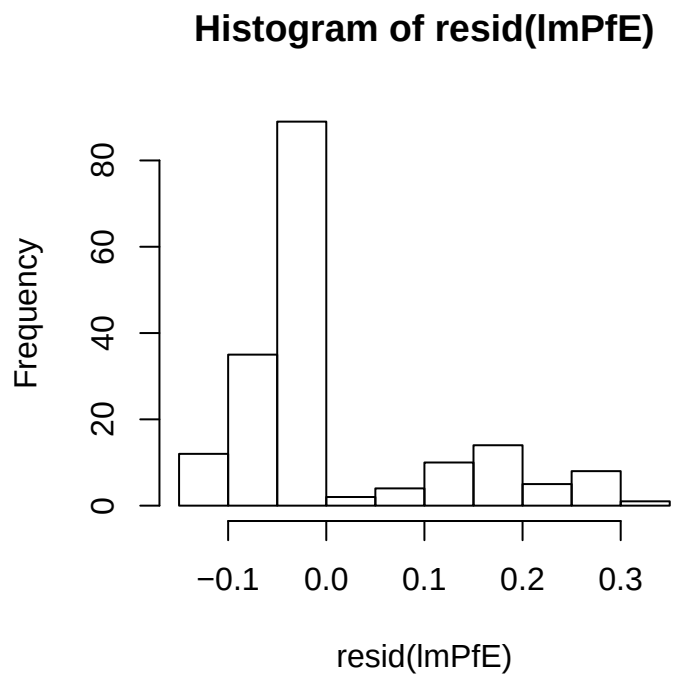
```
## Computing profile confidence intervals ...
##
##              2.5 %      97.5 %
## .sig01         0.02239199 0.09696263
## .sigma         0.10042647 0.12394595
## (Intercept) -0.01516215 0.11666292
## sexmale      -0.05368234 0.13351762
```

```
Anova(lmPfE)
```

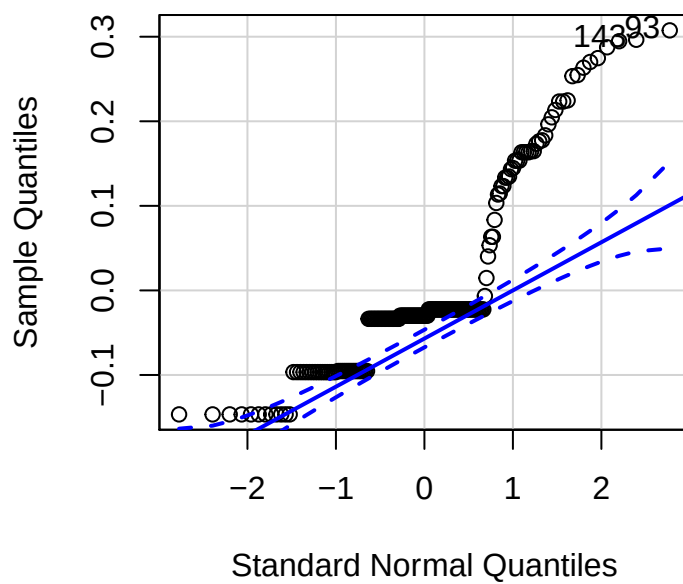
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: p_fusion_ratio
##      Chisq Df Pr(>Chisq)
## sex  1.0126  1    0.3143
```

Check normality of residuals

```
hist(resid(lmPfE))
```



```
qqp(resid(lmPfE), "norm", xlab = "Standard Normal Quantiles",  
     ylab = "Sample Quantiles")
```

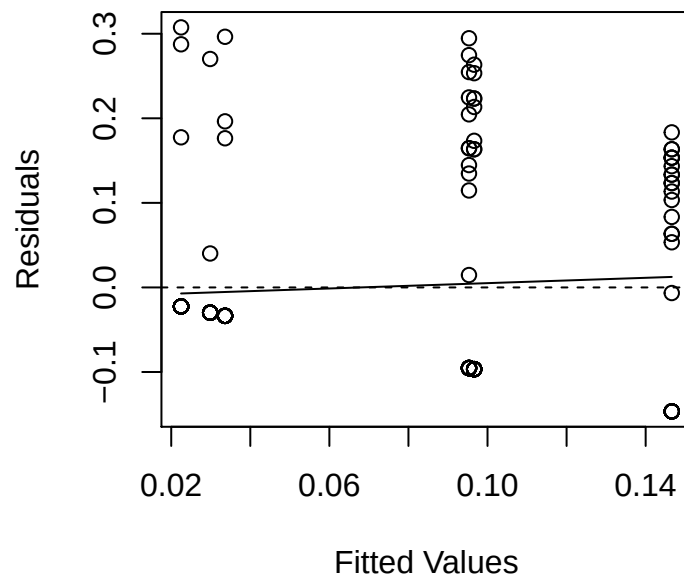


```
## 93 143
## 41 84
```

Check model fit

```
plot(fitted(lmPfE), residuals(lmPfE), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmPfE), residuals(lmPfE)))
```

Linear mixed model using maximum likelih



Embelia schimperi

Number of observations

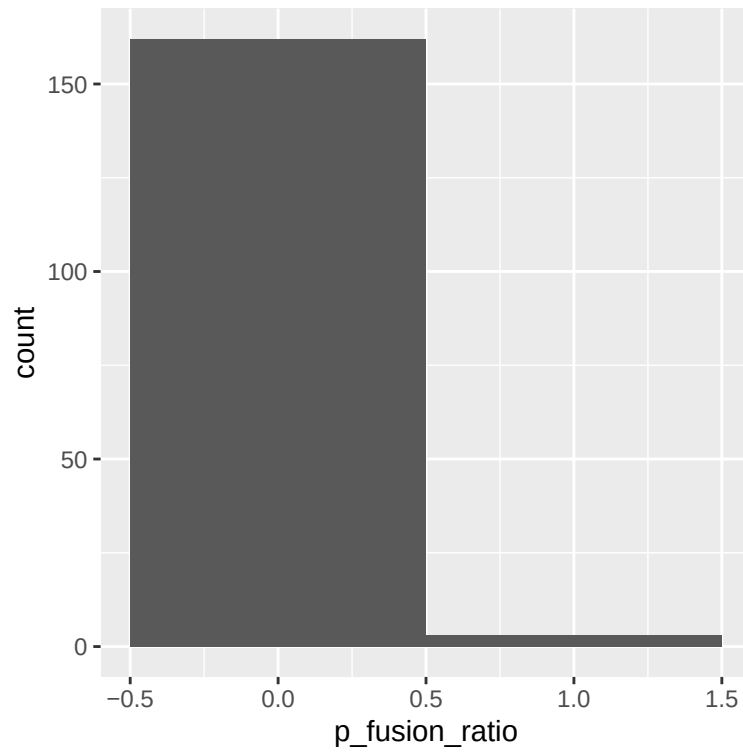
```
aggregate(p_fusion_ratio ~ sex + species, data = schimp, function(x) length(x))
```

```
##      sex  species p_fusion_ratio
## 1 female schimperi           82
## 2  male schimperi           83
```

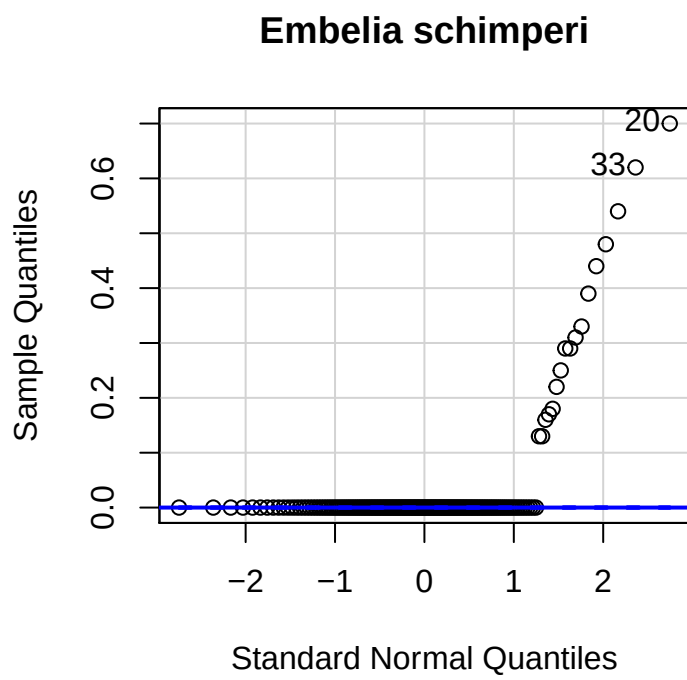
Distribution

```
histnormPfS <- ggplot(schimp, aes(p_fusion_ratio))
histnormPfS + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 29 rows containing non-finite values (stat_bin).
```



```
qqp(schimp$p_fusion_ratio, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia schimperi")
```



```
## [1] 20 33
```

Build model

```
lmPfS <- lmer(p_fusion_ratio ~ sex + (1 | spec_ID), schimp, REML = FALSE)
```

Display results

```
summary(lmPfS)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: p_fusion_ratio ~ sex + (1 | spec_ID)
## Data: schimp
##
##      AIC      BIC    logLik deviance df.resid
##   -247.0   -234.6    127.5   -255.0      161
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.6871 -0.2385 -0.1670 -0.1580  5.6749
##
## Random effects:
## Groups   Name      Variance Std.Dev.
## spec_ID (Intercept) 0.0006228 0.02496
## Residual              0.0121063 0.11003
## Number of obs: 165, groups: spec_ID, 6
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  0.03974    0.01967   2.020
## sexmale     -0.02414    0.02733  -0.883
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.720
```

```
confint(lmPfS)
```

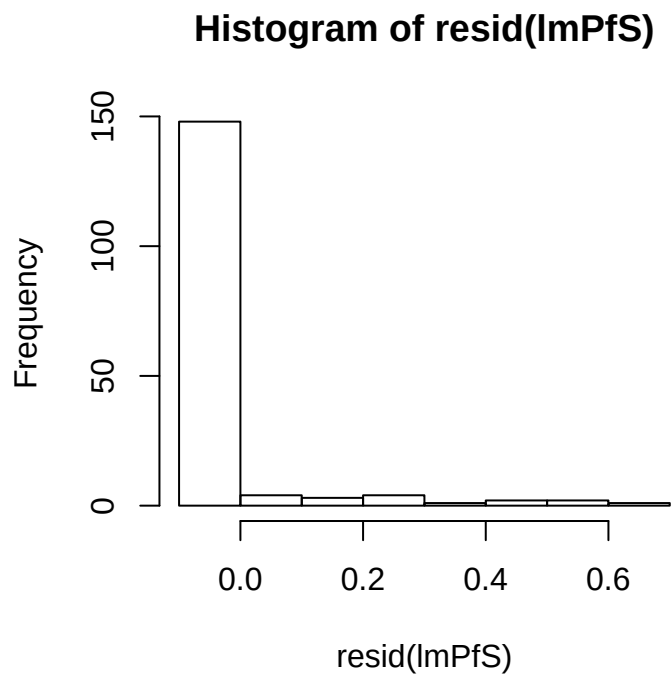
```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01         0.000000000 0.06169480
## .sigma         0.098984775 0.12328622
## (Intercept) -0.009665408 0.08104163
## sexmale     -0.083301505 0.04269978
```

```
Anova(lmPfS)
```

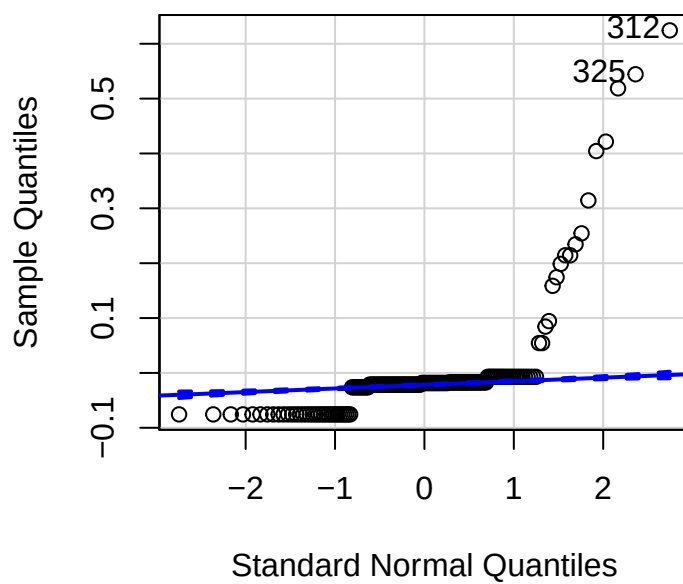
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: p_fusion_ratio
##      Chisq Df Pr(>Chisq)
## sex  0.7799  1    0.3772
```

Check normality of residuals

```
hist(resid(lmPfS))
```



```
qqp(resid(lmPfS), "norm", xlab = "Standard Normal Quantiles",  
     ylab = "Sample Quantiles")
```

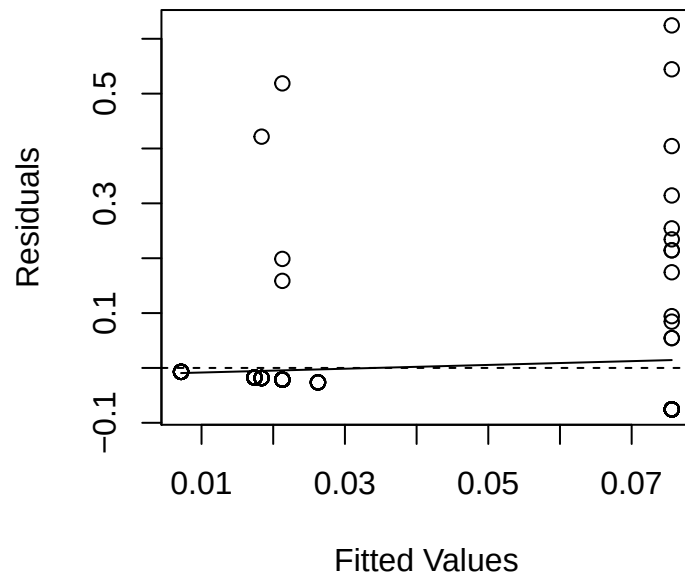



```
## 312 325
## 19 31
```

Check model fit

```
plot(fitted(lmPfS), residuals(lmPfS), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmPfS), residuals(lmPfS)))
```

Linear mixed model using maximum likelih



Embelia tsjeriamcottam

Number of observations

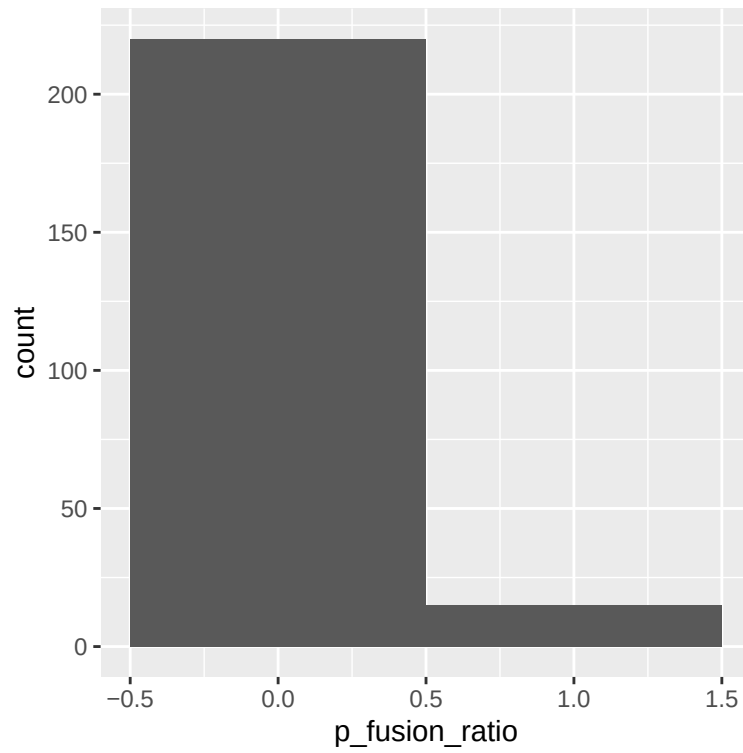
```
aggregate(p_fusion_ratio ~ sex + species, data = tsjer, function(x) length(x))
```

```
##      sex      species p_fusion_ratio
## 1 female tsjeriamcottam          117
## 2  male tsjeriamcottam          118
```

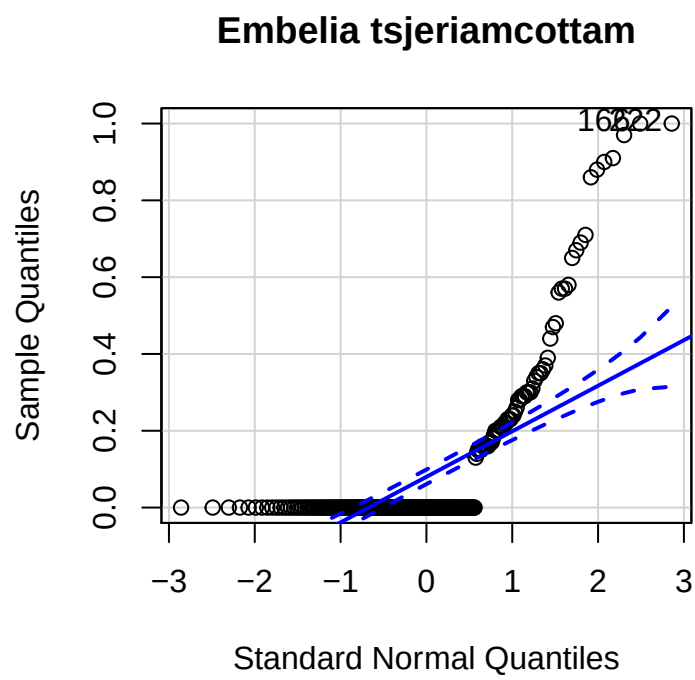
Distribution

```
histnormPfT <- ggplot(tsjer, aes(p_fusion_ratio))
histnormPfT + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 20 rows containing non-finite values (stat_bin).
```



```
qqp(tsjer$p_fusion_ratio, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia tsjeriamcottam")
```



```
## [1] 166 222
```

Build model

```
lmPfT <- lmer(p_fusion_ratio ~ sex + (1 | spec_ID), tsjer, REML = FALSE)
```

Display results

```
summary(lmPfT)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: p_fusion_ratio ~ sex + (1 | spec_ID)
## Data: tsjer
##
##      AIC      BIC    logLik deviance df.resid
##    -94.3    -80.4     51.1  -102.3     231
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.2866 -0.3068 -0.2601 -0.1376  4.5197
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## spec_ID  (Intercept)  0.005359  0.07321
## Residual                    0.036008  0.18976
## Number of obs: 235, groups: spec_ID, 7
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  0.04627    0.04600   1.006
## sexmale      0.06922    0.06215   1.114
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.740
```

```
confint(lmPfT)
```

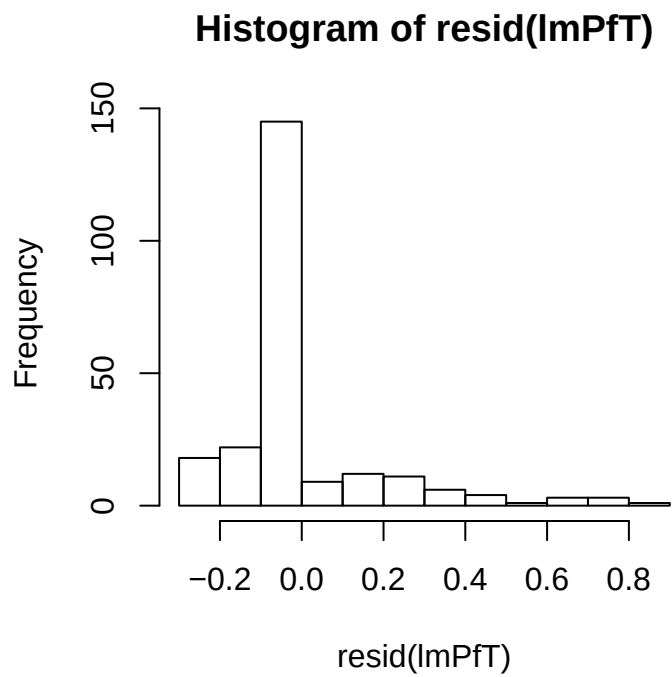
```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01      0.03742459 0.1508409
## .sigma      0.17358491 0.2086089
## (Intercept) -0.05964128 0.1516434
## sexmale     -0.07762281 0.2058808
```

```
Anova(lmPfT)
```

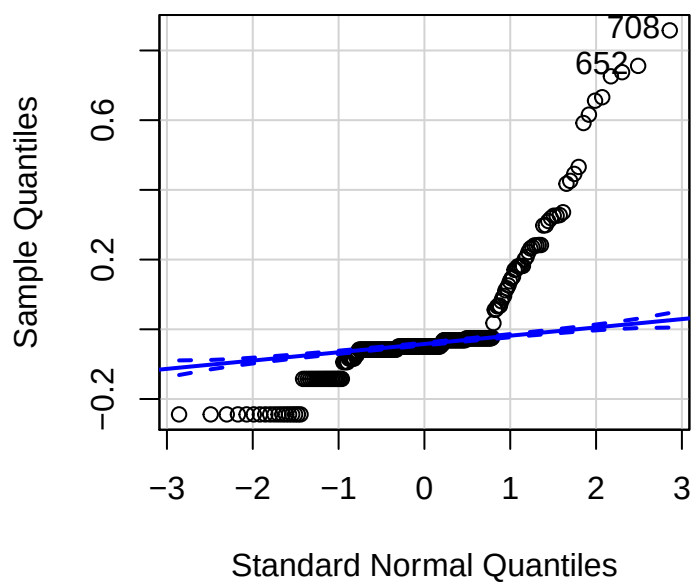
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: p_fusion_ratio
##      Chisq Df Pr(>Chisq)
## sex  1.2405  1    0.2654
```

Check normality of residuals

```
hist(resid(lmPfT))
```



```
qqp(resid(lmPfT), "norm", xlab = "Standard Normal Quantiles",  
     ylab = "Sample Quantiles")
```

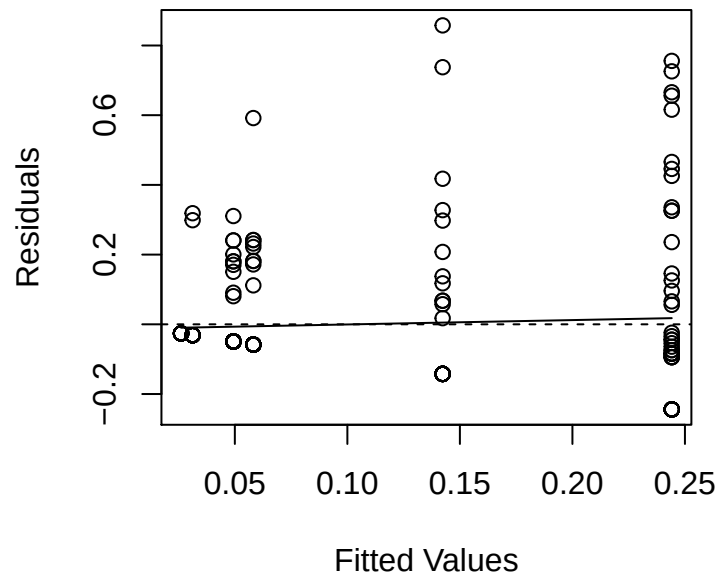


```
## 708 652
## 203 156
```

Check model fit

```
plot(fitted(lmPfT), residuals(lmPfT), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmPfT), residuals(lmPfT)))
```

Linear mixed model using maximum likelih



3.3.6 Statistical tests - Petals fused or free

Number of observations

```
aggregate(petal_fused ~ sex + species, data = flwr, function(x) length(x))
```

```
##      sex      species petal_fused
## 1 female      effusa          104
## 2  male      effusa           80
## 3 female    schimperi           83
## 4  male    schimperi           84
## 5 female tsjeriamcottam        118
## 6  male tsjeriamcottam        120
```

Distribution Petal fused is a binary variable, a glmer with binomial distribution and Laplace approximation is therefore used.

Build model

```
lmPfused <- glmer(petal_fused ~ sex + (1 | species) + (1 | spec_ID),
                  flwr, family = "binomial")
```

Display results

```
summary(lmPfused)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: petal_fused ~ sex + (1 | species) + (1 | spec_ID)
## Data: flwr
##
##      AIC      BIC   logLik deviance df.resid
##    535.8    553.3   -263.9    527.8     585
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.3068 -0.5085 -0.2933 -0.1620  3.8872
##
## Random effects:
## Groups Name          Variance Std.Dev.
## spec_ID (Intercept) 1.927     1.3883
## species (Intercept) 0.141     0.3756
## Number of obs: 589, groups:  spec_ID, 19; species, 3
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -2.1380     0.5667  -3.773 0.000161 ***
## sexmale       0.2270     0.7157   0.317 0.751090
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.643
```

```
confint(lmPfused)
```

```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01      0.8693581  2.3654283
## .sig02      0.0000000  2.2184731
## (Intercept) -3.6437726 -0.8458986
## sexmale     -1.3978024  1.7419425
```

Check overdispersion

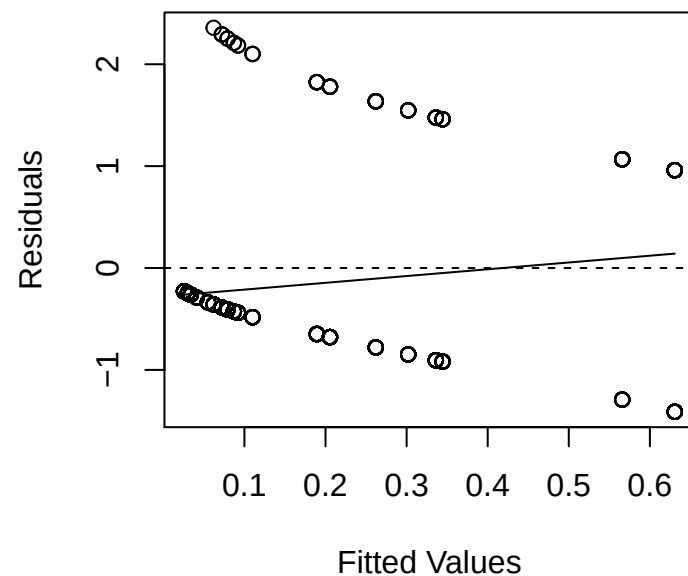
```
overdisp_fun(lmPfused)
```

```
##      chisq      ratio      rdf      p
## 488.0629121  0.8342956 585.0000000 0.9985953
```

Check model fit

```
plot(fitted(lmPfused), residuals(lmPfused), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmPfused), residuals(lmPfused)))
```

Linear mixed model using maximum likelihood



3.4 Filaments

3.4.1 Descriptive statistics

Filament length

Mean

```
aggregate(filament_length ~ sex + species, data = flwr, mean)
```

##	sex	species	filament_length
## 1	female	effusa	5.884868
## 2	male	effusa	9.307087
## 3	female	schimperi	6.120482
## 4	male	schimperi	15.333333
## 5	female	tsjeriamcottam	1.517857
## 6	male	tsjeriamcottam	7.483051

Variance

```
aggregate(filament_length ~ sex + species, data = flwr, var)
```

##	sex	species	filament_length
## 1	female	effusa	3.2333457
## 2	male	effusa	4.3732033
## 3	female	schimperi	1.9365266
## 4	male	schimperi	27.5502008
## 5	female	tsjeriamcottam	0.2699485
## 6	male	tsjeriamcottam	8.5424453

Standard deviation

```
aggregate(filament_length ~ sex + species, data = flwr, sd)
```

```
##      sex      species filament_length
## 1 female    effusa      1.7981506
## 2  male    effusa      2.0912205
## 3 female  schimperi      1.3915914
## 4  male    schimperi      5.2488285
## 5 female tsjeriamcottam      0.5195657
## 6  male    tsjeriamcottam      2.9227462
```

Filament width

Mean

```
aggregate(filament_width ~ sex + species, data = flwr, mean)
```

```
##      sex      species filament_width
## 1 female    effusa      1.408497
## 2  male    effusa      1.853846
## 3 female  schimperi      2.500000
## 4  male    schimperi      3.053571
## 5 female tsjeriamcottam      1.008475
## 6  male    tsjeriamcottam      1.407258
```

Variance

```
aggregate(filament_width ~ sex + species, data = flwr, var)
```

```
##      sex      species filament_width
## 1 female    effusa      0.188940488
## 2  male    effusa      0.071496720
## 3 female  schimperi      0.566265060
## 4  male    schimperi      0.451914802
## 5 female tsjeriamcottam      0.008474576
## 6  male    tsjeriamcottam      0.147833071
```

Standard deviation

```
aggregate(filament_width ~ sex + species, data = flwr, sd)
```

```
##      sex      species filament_width
## 1 female    effusa      0.43467285
## 2  male    effusa      0.26738871
## 3 female  schimperi      0.75250585
## 4  male    schimperi      0.67224609
## 5 female tsjeriamcottam      0.09205746
## 6  male    tsjeriamcottam      0.38449066
```

Filament fusion

Mean

```
aggregate(fil_fusion_ratio ~ sex + species, data = flwr, mean)
```

```
##      sex      species fil_fusion_ratio
## 1 female    effusa      0.4210135
## 2  male    effusa      0.4334109
## 3 female  schimperi      0.3101205
## 4  male    schimperi      0.2953659
## 5 female tsjeriamcottam      0.2343590
## 6  male    tsjeriamcottam      0.2722222
```


Variance

```
aggregate(fil_fusion_ratio ~ sex + species, data = flwr, var)
```

```
##      sex      species fil_fusion_ratio
## 1 female    effusa    0.0027955644
## 2 male     effusa    0.0019679627
## 3 female   schimperi  0.0061963268
## 4 male     schimperi  0.0028967781
## 5 female tsjeriamcottam 0.0008230769
## 6 male tsjeriamcottam  0.0016519157
```

Standard deviation

```
aggregate(fil_fusion_ratio ~ sex + species, data = flwr, sd)
```

```
##      sex      species fil_fusion_ratio
## 1 female    effusa    0.05287310
## 2 male     effusa    0.04436173
## 3 female   schimperi  0.07871675
## 4 male     schimperi  0.05382172
## 5 female tsjeriamcottam 0.02868932
## 6 male tsjeriamcottam  0.04064377
```

3.4.2 Statistical tests - Filament length

Embelia effusa

Number of observations

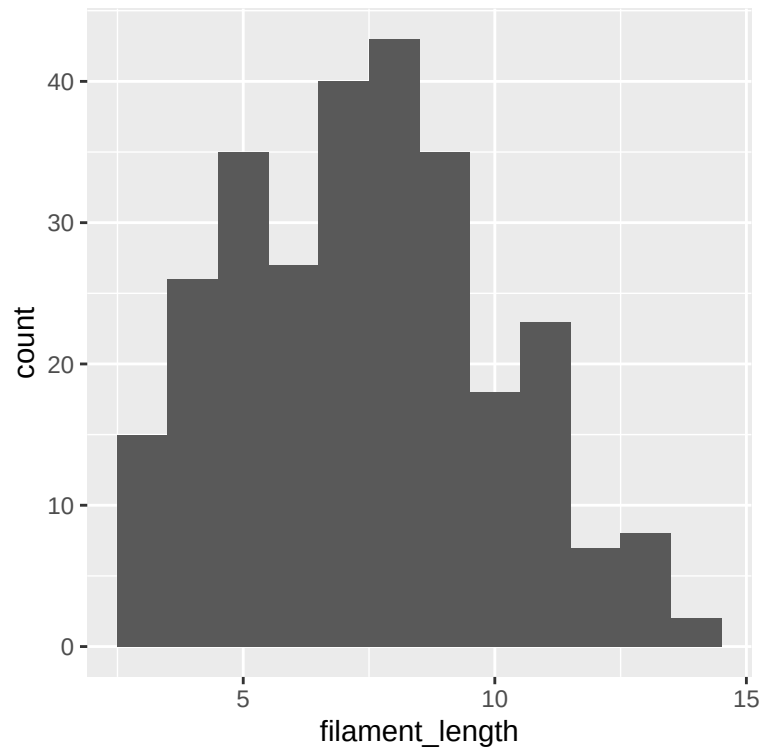
```
aggregate(filament_length ~ sex + species, data = effusa, function(x) length(x))
```

```
##      sex species filament_length
## 1 female  effusa             152
## 2 male   effusa             127
```

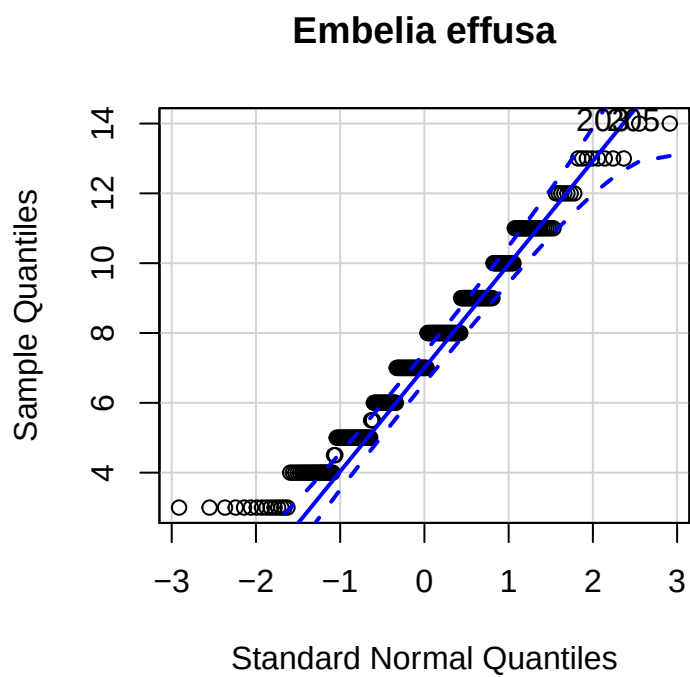
Distribution

```
histnormFlE <- ggplot(effusa, aes(filament_length))
histnormFlE + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 13 rows containing non-finite values (stat_bin).
```

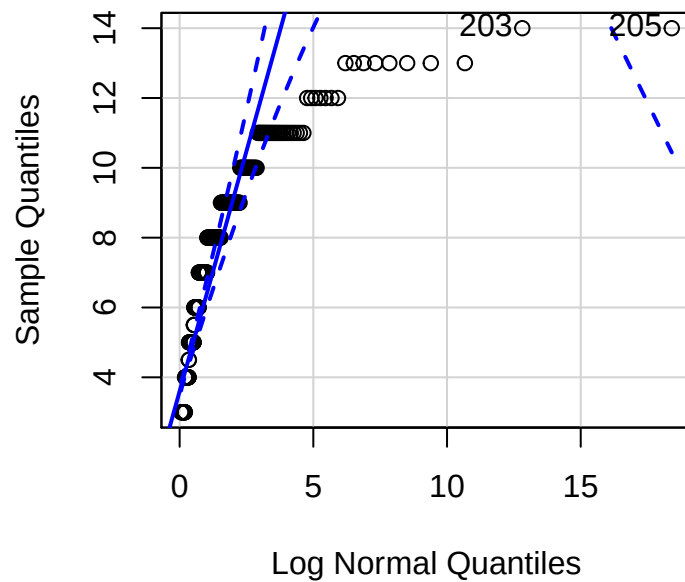


```
qqp(effusa$filament_length, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia effusa")
```



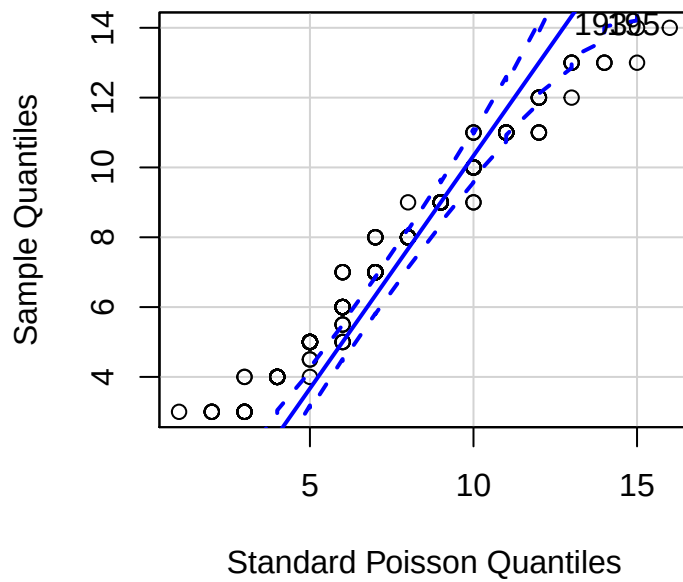
```
## [1] 203 205
```

```
qqp(effusa$filament_length, "lnorm", xlab = "Log Normal Quantiles",
    ylab = "Sample Quantiles")
```

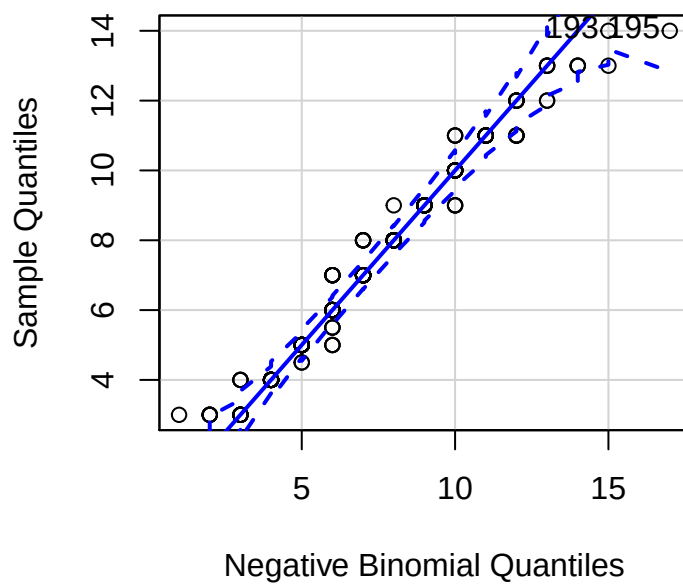


```
## [1] 203 205
```

```
poisson <- fitdistr(c(na.exclude(as.integer(effusa$filament_length))),
    "Poisson")
qqp(c(na.exclude(effusa$filament_length)), "pois", lambda = poisson$estimate,
    xlab = "Standard Poisson Quantiles", ylab = "Sample Quantiles")
```



```
## [1] 193 195
nbinom <- fitdistr(c(na.exclude(as.integer(effusa$filament_length))),
  "Negative Binomial")
qqp(c(na.exclude(effusa$filament_length)), "nbinom", size = nbinom$estimate[[1]],
  mu = nbinom$estimate[[2]], xlab = "Negative Binomial Quantiles",
  ylab = "Sample Quantiles")
```



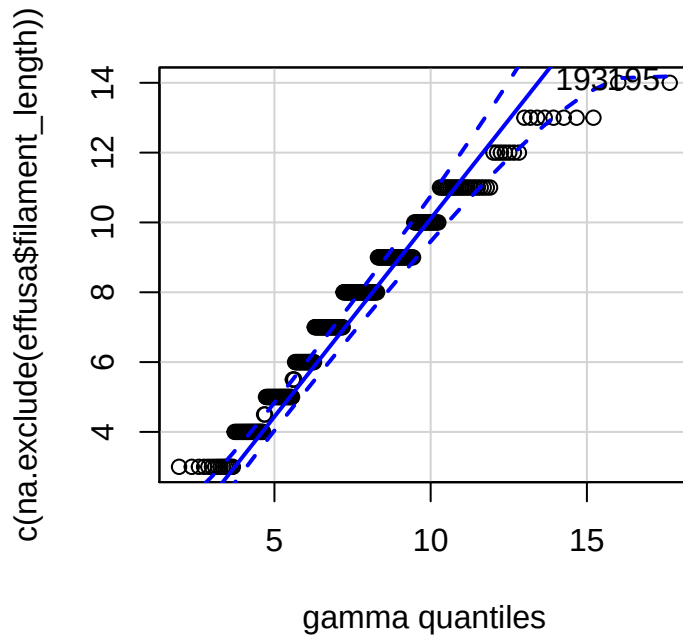
```
## [1] 193 195
```

```
gamma <- fitdistr(c(na.exclude(as.integer(effusa$filament_length))),
  "gamma")
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
qqp(c(na.exclude(effusa$filament_length)), "gamma", shape = gamma$estimate[[1]],
  rate = gamma$estimate[[2]])
```



```
## [1] 193 195
```

Build model

```
lmFlE <- lmer(filament_length ~ sex + (1 | spec_ID), effusa,
  REML = FALSE)
```

Display results

```
summary(lmFlE)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: filament_length ~ sex + (1 | spec_ID)
## Data: effusa
##
##      AIC      BIC   logLik deviance df.resid
##  1086.4   1101.0   -539.2   1078.4     275
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.2122 -0.6549  0.0323  0.5591  2.5191
##
## Random effects:
## Groups   Name      Variance Std.Dev.
## spec_ID (Intercept) 1.053    1.026
## Residual                2.587    1.609
## Number of obs: 279, groups: spec_ID, 8
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   5.8895    0.5306  11.099
```

```
## sexmale      3.1946      0.7530      4.243
##
## Correlation of Fixed Effects:
##      (Intr)
## sexmale -0.705
```

```
confint(lmFlE)
```

```
## Computing profile confidence intervals ...
```

```
##           2.5 %   97.5 %
## .sig01      0.6420847 1.885184
## .sigma      1.4820551 1.754004
## (Intercept) 4.7115484 7.067988
## sexmale     1.5190456 4.858708
```

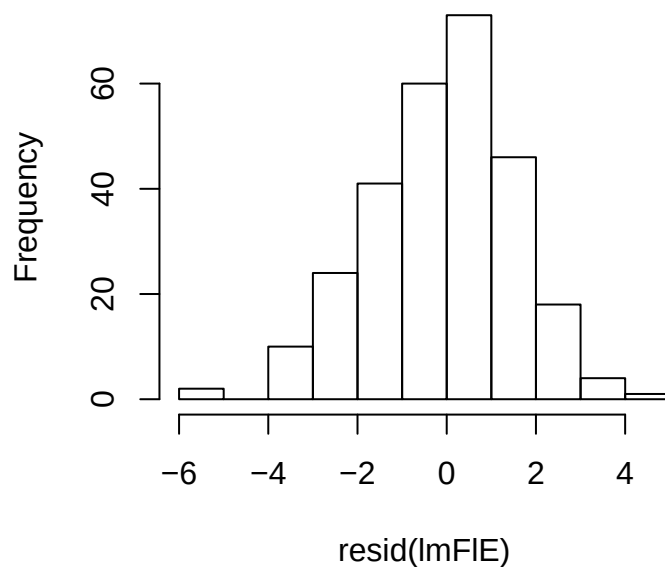
```
Anova(lmFlE)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: filament_length
##      Chisq Df Pr(>Chisq)
## sex      18  1 2.209e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

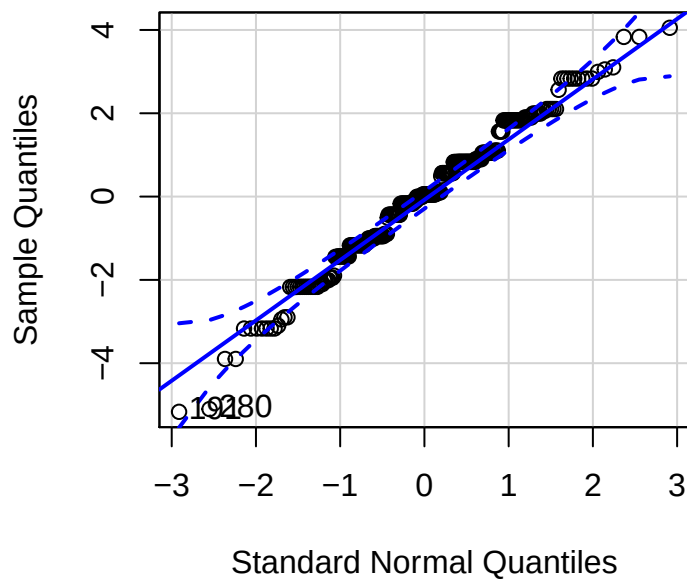
Check normality of residuals

```
hist(resid(lmFlE))
```

Histogram of resid(lmFlE)



```
qqp(resid(lmFlE), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

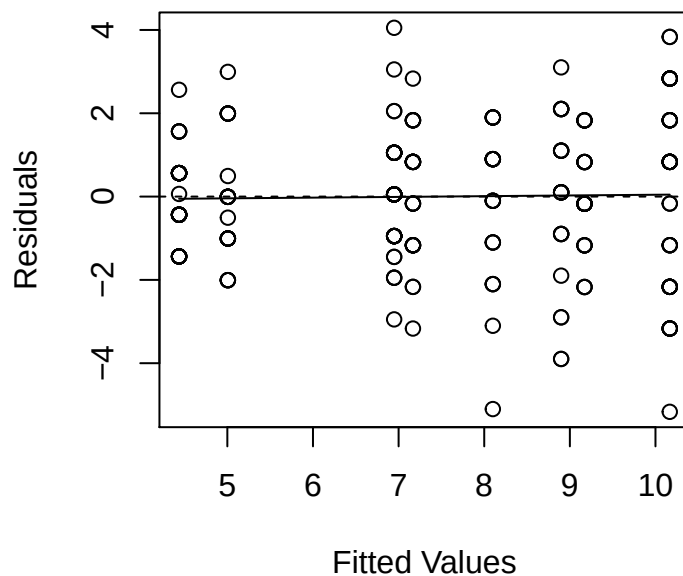


```
## 191 280
## 181 268
```

Check model fit

```
plot(fitted(lmF1E), residuals(lmF1E), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmF1E), residuals(lmF1E)))
```


Linear mixed model using maximum likelih



Embelia schimperi

Number of observations

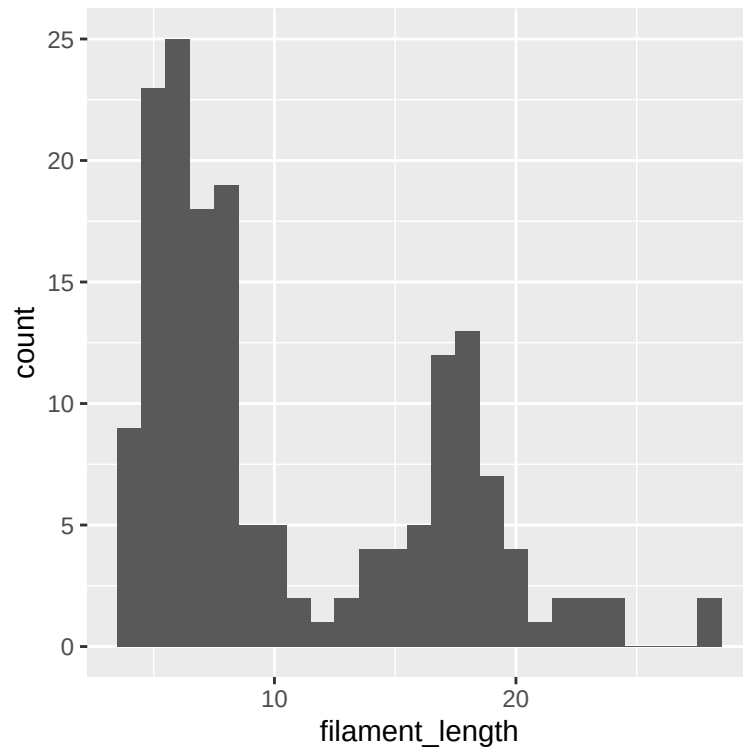
```
aggregate(filament_length ~ sex + species, data = schimp, function(x) length(x))
```

```
##      sex  species filament_length
## 1 female schimperi             83
## 2  male schimperi             84
```

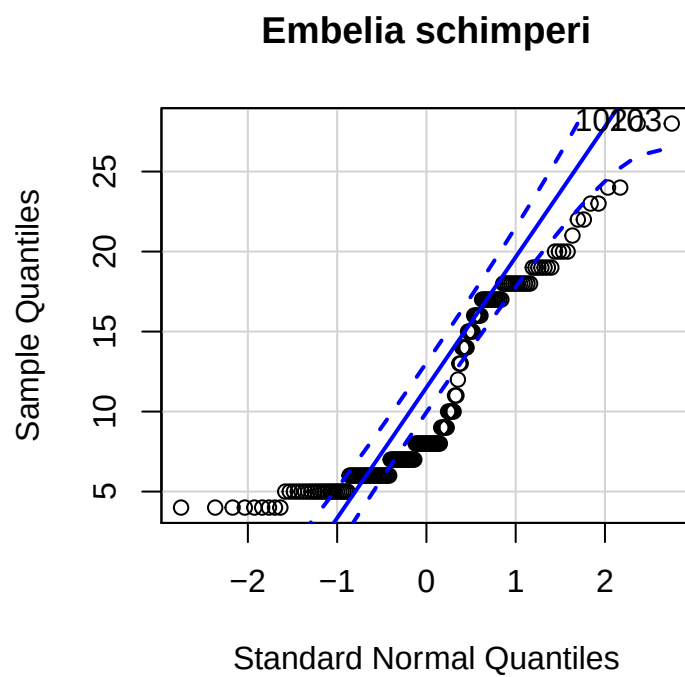
Distribution

```
histnormFLE <- ggplot(schimp, aes(filament_length))
histnormFLE + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 27 rows containing non-finite values (stat_bin).
```

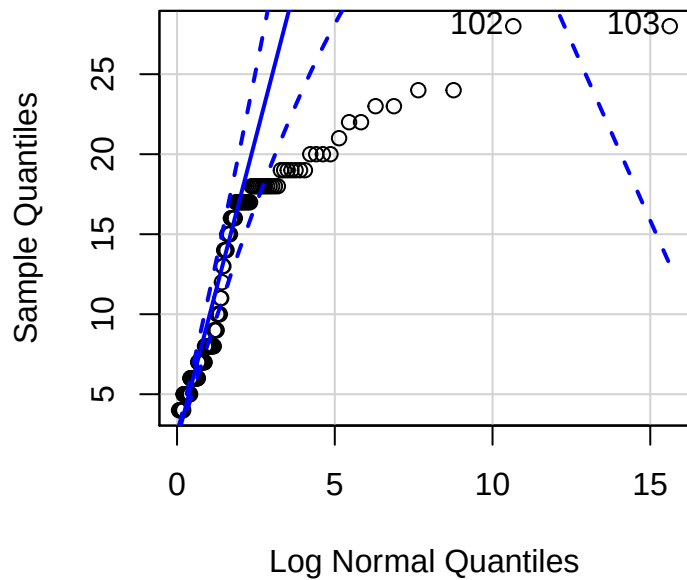


```
qqp(schimp$filament_length, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia schimperi")
```



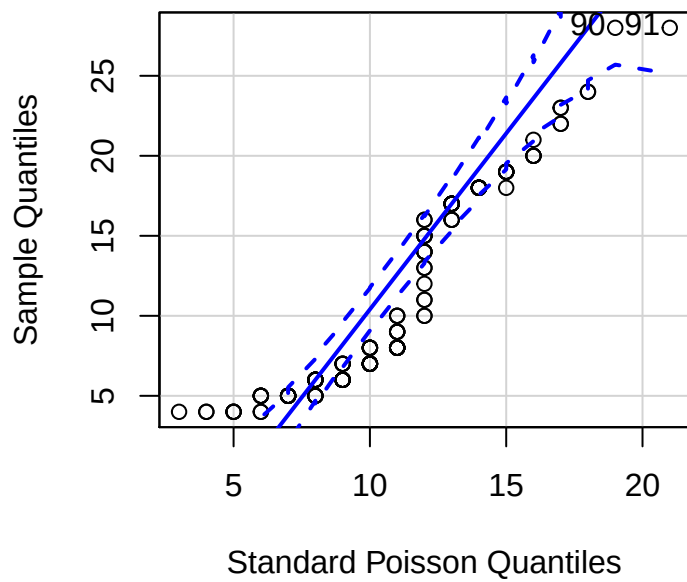
```
## [1] 102 103
```

```
qqp(schimp$filament_length, "lnorm", xlab = "Log Normal Quantiles",
    ylab = "Sample Quantiles")
```

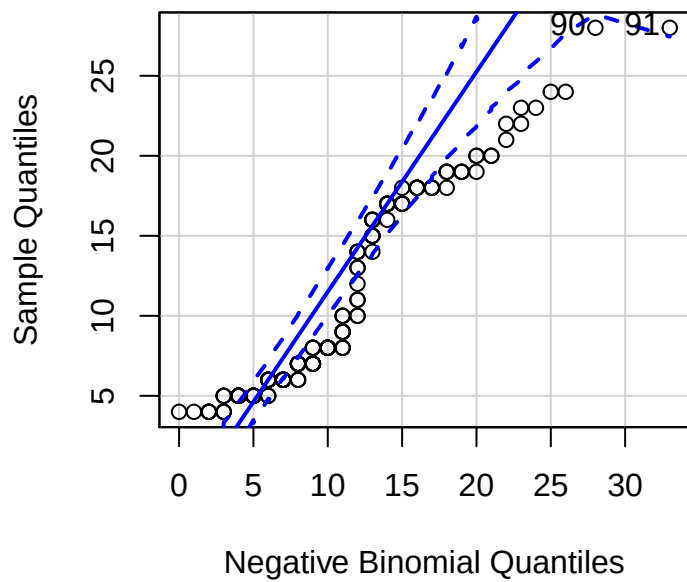


```
## [1] 102 103
```

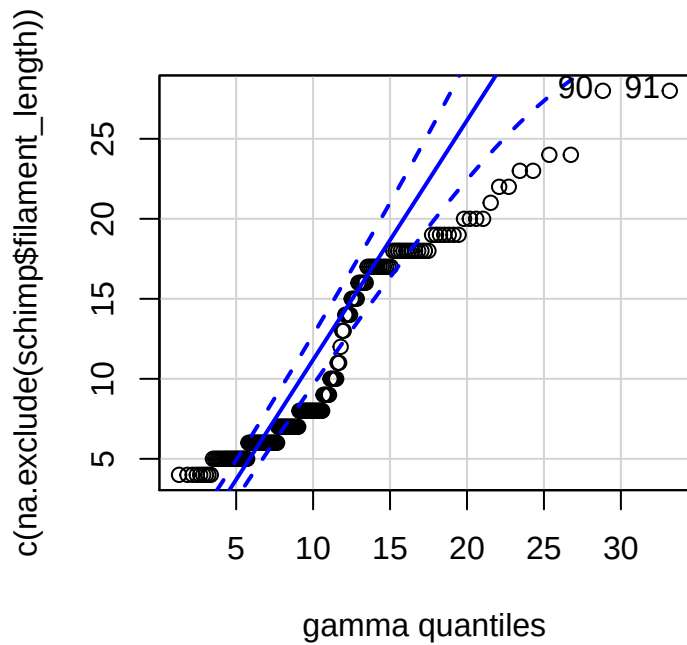
```
poisson <- fitdistr(c(na.exclude(as.integer(schimp$filament_length))),
    "Poisson")
qqp(c(na.exclude(schimp$filament_length)), "pois", lambda = poisson$estimate,
    xlab = "Standard Poisson Quantiles", ylab = "Sample Quantiles")
```



```
## [1] 90 91
nbinom <- fitdistr(c(na.exclude(as.integer(schimp$filament_length))),
  "Negative Binomial")
qqp(c(na.exclude(schimp$filament_length)), "nbinom", size = nbinom$estimate[[1]],
  mu = nbinom$estimate[[2]], xlab = "Negative Binomial Quantiles",
  ylab = "Sample Quantiles")
```



```
## [1] 90 91
gamma <- fitdistr(c(na.exclude(as.integer(schimp$filament_length))),
  "gamma")
qqp(c(na.exclude(schimp$filament_length)), "gamma", shape = gamma$estimate[[1]],
  rate = gamma$estimate[[2]])
```



```
## [1] 90 91
```

Build model

```
lmFls <- lmer(filament_length ~ sex + (1 | spec_ID), schimp,
  REML = FALSE)
```

Display results

```
summary(lmFls)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: filament_length ~ sex + (1 | spec_ID)
## Data: schimp
##
##      AIC      BIC    logLik deviance df.resid
##  799.3    811.8   -395.6    791.3     163
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.2272 -0.5120 -0.0882  0.3986  4.0508
##
## Random effects:
##  Groups   Name      Variance Std.Dev.
## spec_ID  (Intercept) 10.176   3.190
## Residual                5.837   2.416
## Number of obs: 167, groups:  spec_ID, 6
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    6.179     1.870    3.305
```

```
## sexmale      8.090      2.639      3.066
##
## Correlation of Fixed Effects:
##      (Intr)
## sexmale -0.708
```

```
confint(lmFlS)
```

```
## Computing profile confidence intervals ...
```

```
##           2.5 %    97.5 %
## .sig01      1.941412  6.455953
## .sigma      2.174395  2.706012
## (Intercept) 1.850310 10.513346
## sexmale      1.957082 14.195843
```

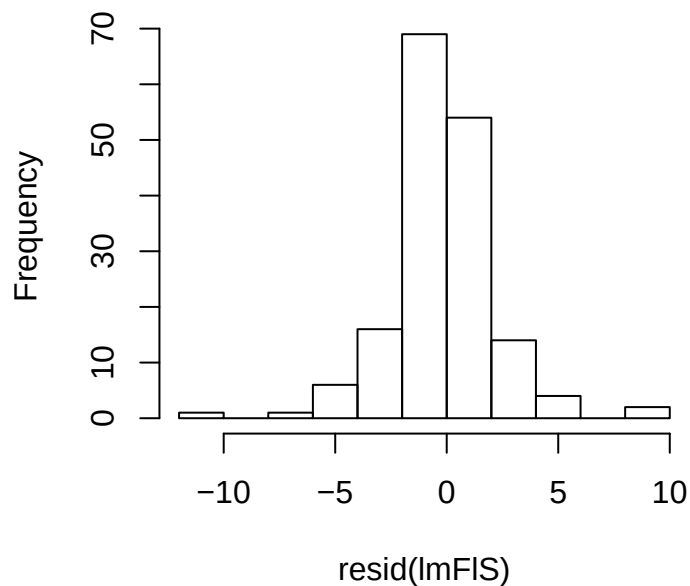
```
Anova(lmFlS)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: filament_length
##      Chisq Df Pr(>Chisq)
## sex  9.3991  1  0.002171 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

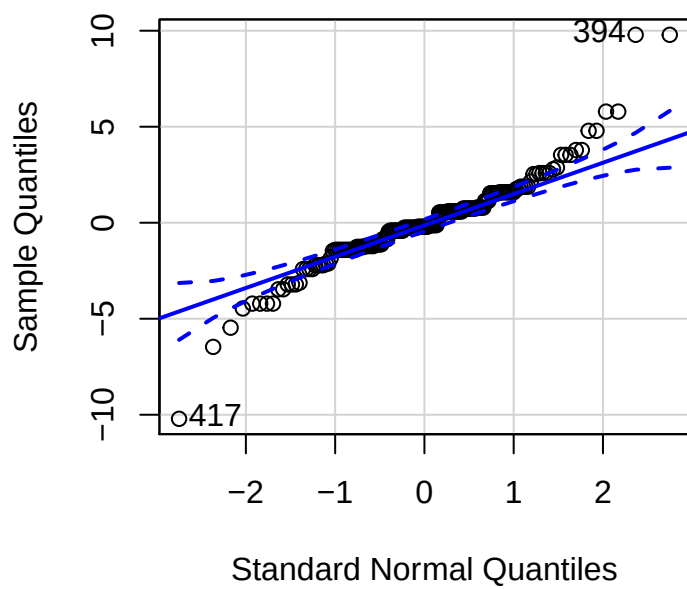
Check normality of residuals

```
hist(resid(lmFlS))
```

Histogram of resid(lmFlS)



```
qqp(resid(lmFlS), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

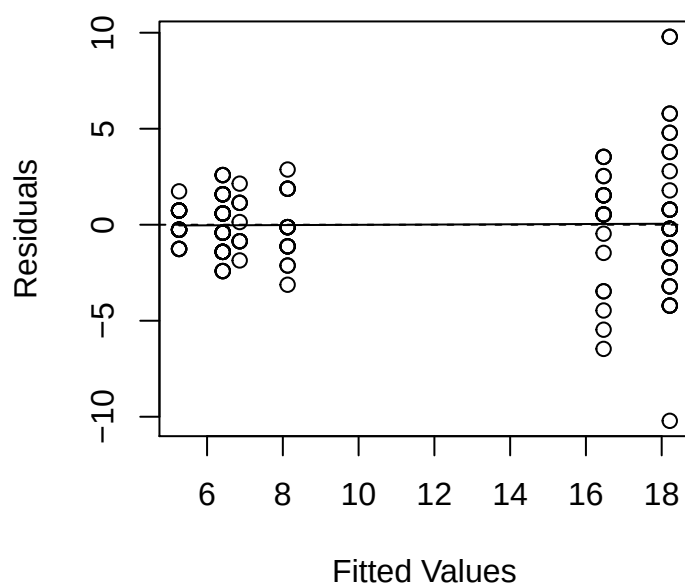


```
## 417 394
## 108 90
```

Check model fit

```
plot(fitted(lmF1S), residuals(lmF1S), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmF1S), residuals(lmF1S)))
```


Linear mixed model using maximum likelih



Embelia tsjeriamcottam

Number of observations

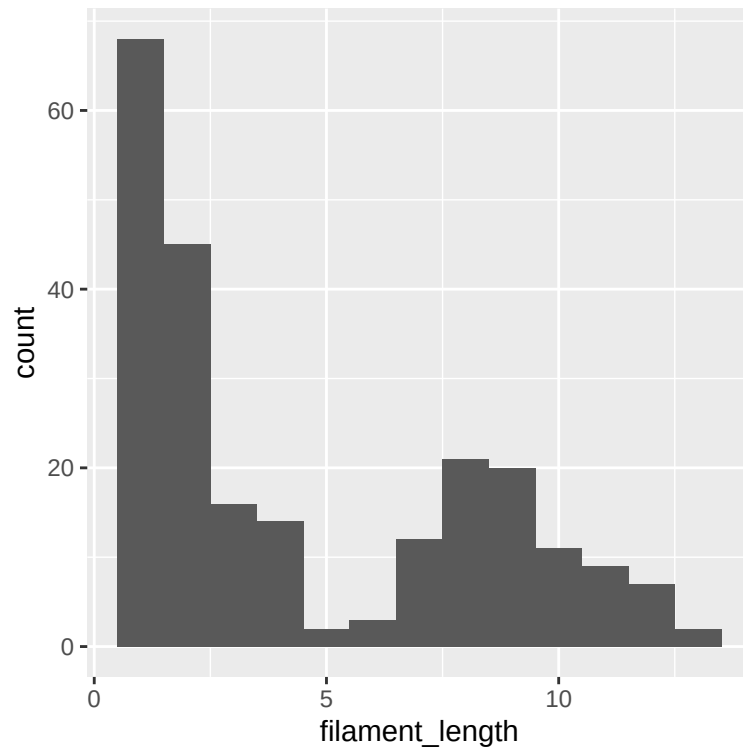
```
aggregate(filament_length ~ sex + species, data = tsjer, function(x) length(x))
```

```
##      sex      species filament_length
## 1 female tsjeriamcottam           112
## 2  male tsjeriamcottam           118
```

Distribution

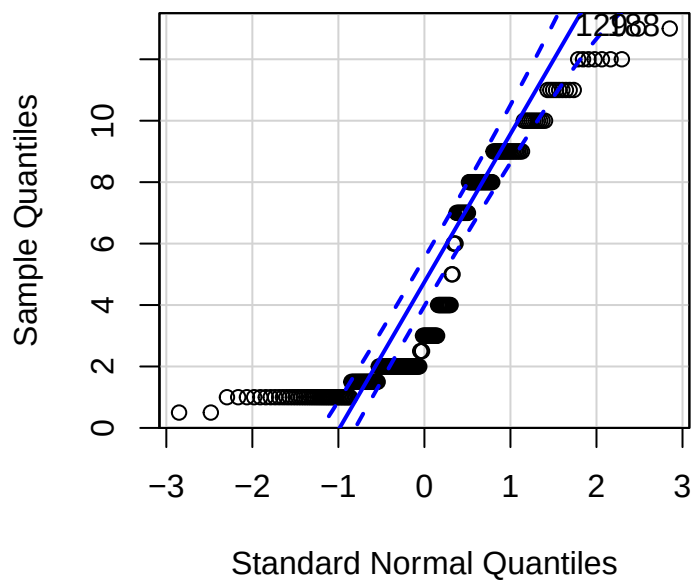
```
histnormFLE <- ggplot(tsjer, aes(filament_length))
histnormFLE + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 25 rows containing non-finite values (stat_bin).
```



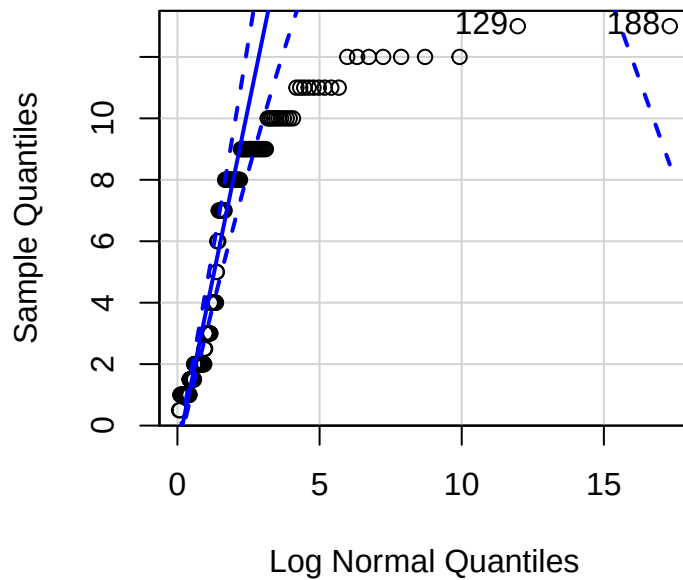
```
qqp(tsjer$filament_length, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia tsjeriamcottam")
```

Embelia tsjeriamcottam



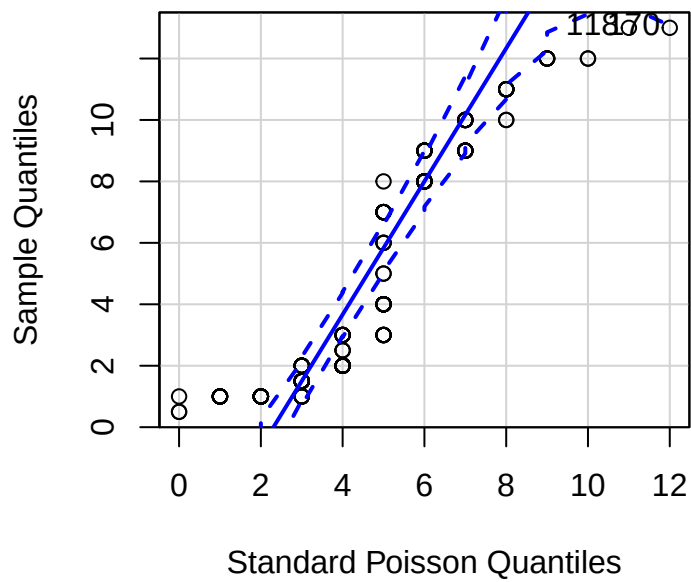
```
## [1] 129 188
```

```
qqp(tsjer$filament_length, "lnorm", xlab = "Log Normal Quantiles",
    ylab = "Sample Quantiles")
```

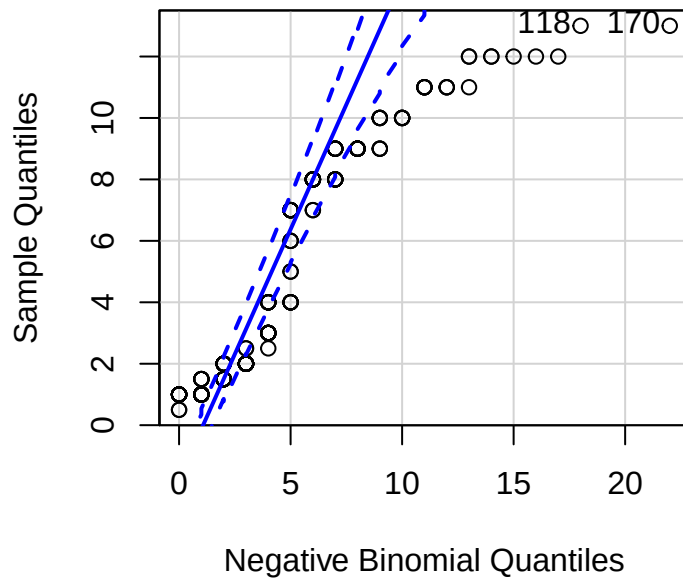


```
## [1] 129 188
```

```
poisson <- fitdistr(c(na.exclude(as.integer(tsjer$filament_length))),
    "Poisson")
qqp(c(na.exclude(tsjer$filament_length)), "pois", lambda = poisson$estimate,
    xlab = "Standard Poisson Quantiles", ylab = "Sample Quantiles")
```



```
## [1] 118 170
nbinom <- fitdistr(c(na.exclude(as.integer(tsjer$filament_length))),
  "Negative Binomial")
qqp(c(na.exclude(tsjer$filament_length)), "nbinom", size = nbinom$estimate[[1]],
  mu = nbinom$estimate[[2]], xlab = "Negative Binomial Quantiles",
  ylab = "Sample Quantiles")
```



```
## [1] 118 170
```

```
# gamma <-
# fitdistr(c(na.exclude(as.integer(tsjer$filament_length))),
# 'gamma') qqp(c(na.exclude(tsjer$filament_length)), 'gamma',
# shape = gamma$estimate[[1]], rate = gamma$estimate[[2]])
```

Build model

```
lmFlT <- lmer(filament_length ~ sex + (1 | spec_ID), tsjer, REML = FALSE)
```

Display results

```
summary(lmFlT)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: filament_length ~ sex + (1 | spec_ID)
## Data: tsjer
##
##      AIC      BIC    logLik deviance df.resid
##  699.3    713.1   -345.7    691.3     226
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.1032 -0.4834 -0.0933  0.4930  4.1926
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 3.655  1.912
## Residual 1.026  1.013
## Number of obs: 230, groups: spec_ID, 7
```

```
##
## Fixed effects:
##           Estimate Std. Error t value
## (Intercept)   1.603      1.108   1.446
## sexmale       6.012      1.467   4.097
##
## Correlation of Fixed Effects:
##           (Intr)
## sexmale -0.755

confint(lmFlT)

## Computing profile confidence intervals ...

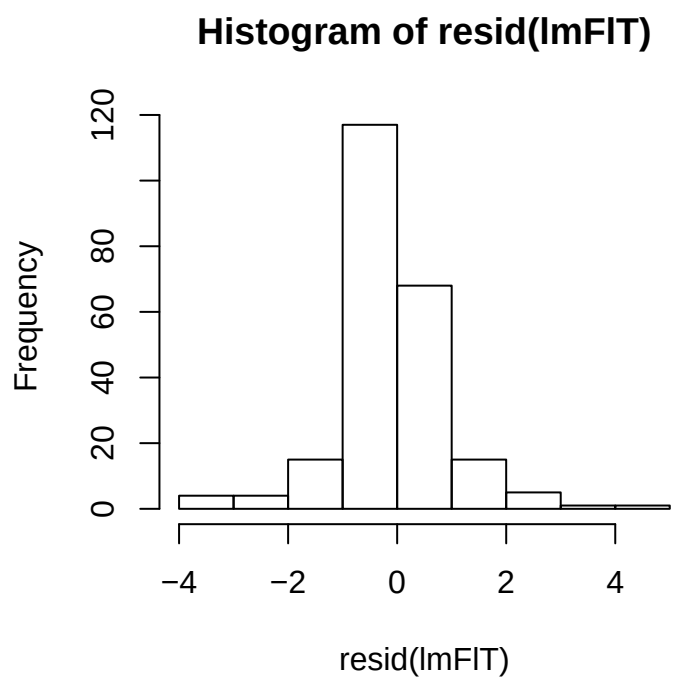
##           2.5 %   97.5 %
## .sig01      1.2152009 3.614706
## .sigma      0.9256396 1.114622
## (Intercept) -0.9046033 4.111084
## sexmale      2.6935057 9.332183

Anova(lmFlT)

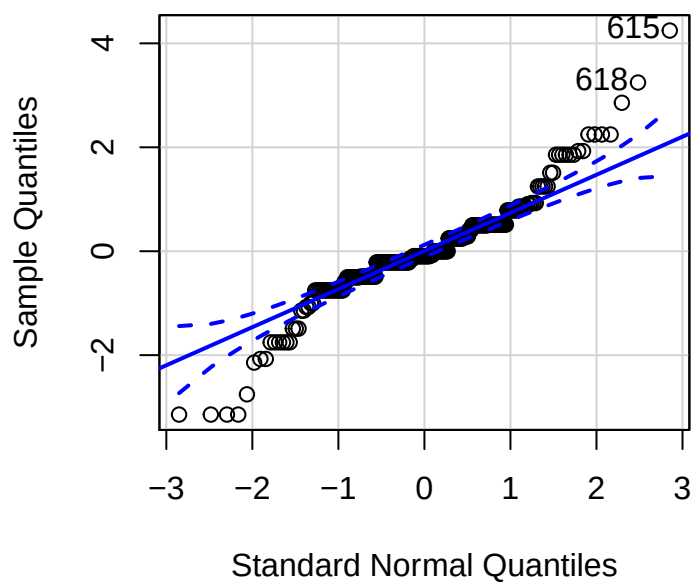
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: filament_length
##      Chisq Df Pr(>Chisq)
## sex 16.785  1 4.187e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Check normality of residuals

hist(resid(lmFlT))
```



```
qqp(resid(lmFIT), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

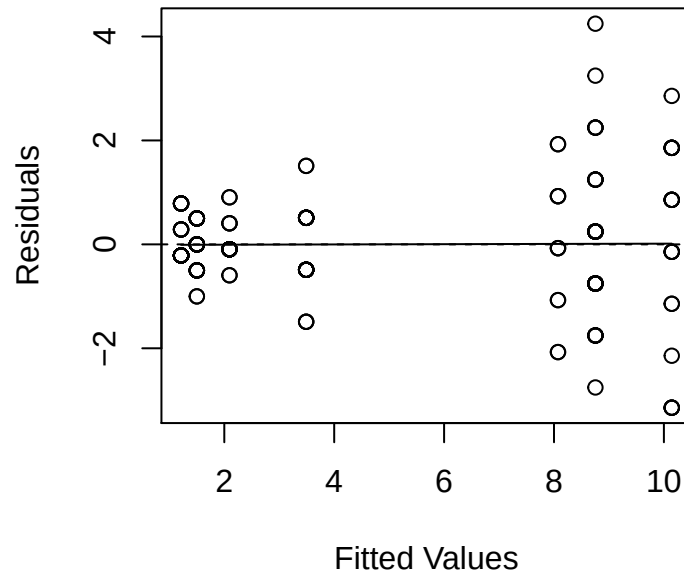


```
## 615 618
## 118 121
```

Check model fit

```
plot(fitted(lmFlT), residuals(lmFlT), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmFlT), residuals(lmFlT)))
```

Linear mixed model using maximum likelih



3.4.3 Statistical tests - Filament width

Number of observations

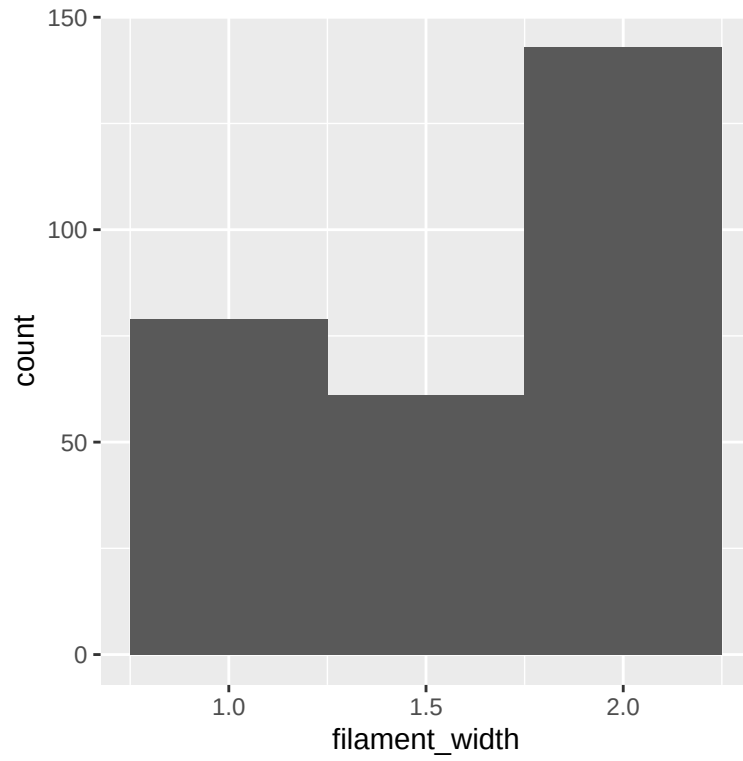
```
aggregate(filament_width ~ sex + species, data = flwr, function(x) length(x))
```

```
##      sex      species filament_width
## 1 female    effusa          153
## 2 male     effusa          130
## 3 female   schimperi          84
## 4 male     schimperi          84
## 5 female tsjeriamcottam        118
## 6 male     tsjeriamcottam        124
```

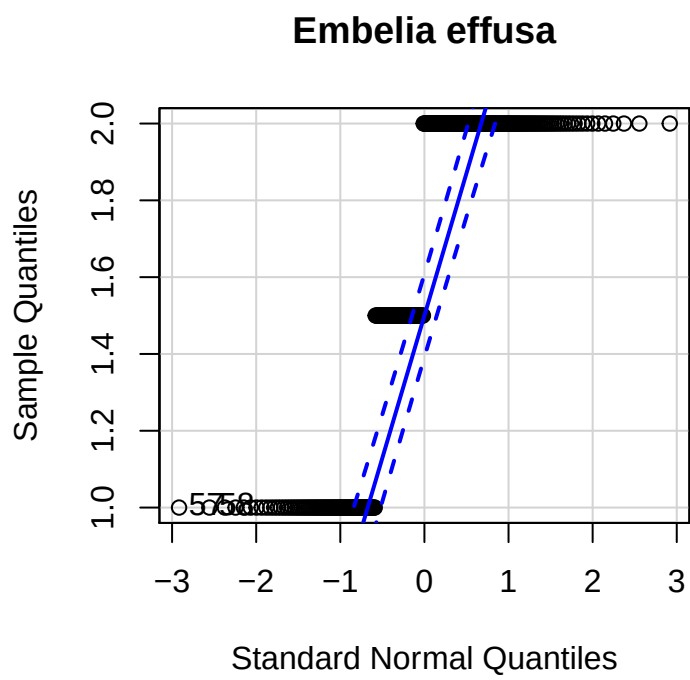
Distribution

```
histnormFwE <- ggplot(effusa, aes(filament_width))
histnormFwE + geom_histogram(binwidth = 0.5) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 9 rows containing non-finite values (stat_bin).
```

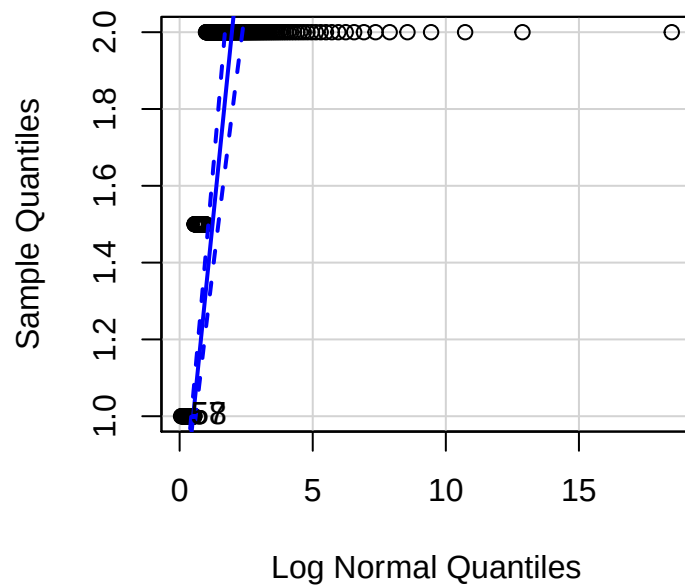



```
qqp(effusa$filament_width, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia effusa")
```



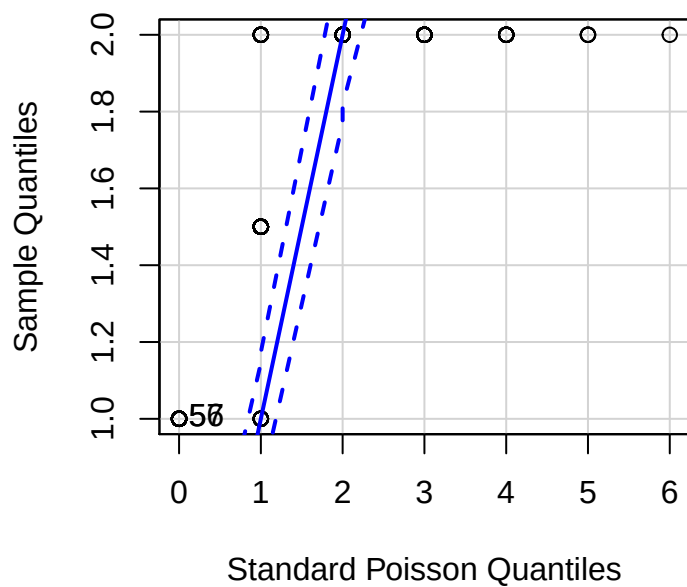
```
## [1] 57 58
```

```
qqp(effusa$filament_width, "lnorm", xlab = "Log Normal Quantiles",
    ylab = "Sample Quantiles")
```



```
## [1] 57 58
```

```
poisson <- fitdistr(c(na.exclude(as.integer(effusa$filament_width))),
    "Poisson")
qqp(c(na.exclude(effusa$filament_width)), "pois", lambda = poisson$estimate,
    xlab = "Standard Poisson Quantiles", ylab = "Sample Quantiles")
```

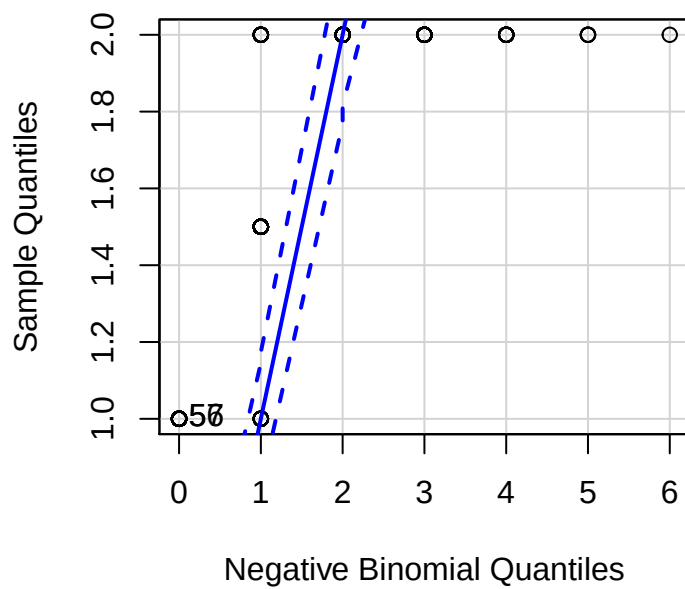


```
## [1] 56 57
```

```
nbinom <- fitdistr(c(na.exclude(as.integer(effusa$filament_width))),  
  "Negative Binomial")
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
qqp(c(na.exclude(effusa$filament_width)), "nbinom", size = nbinom$estimate[[1]],  
  mu = nbinom$estimate[[2]], xlab = "Negative Binomial Quantiles",  
  ylab = "Sample Quantiles")
```



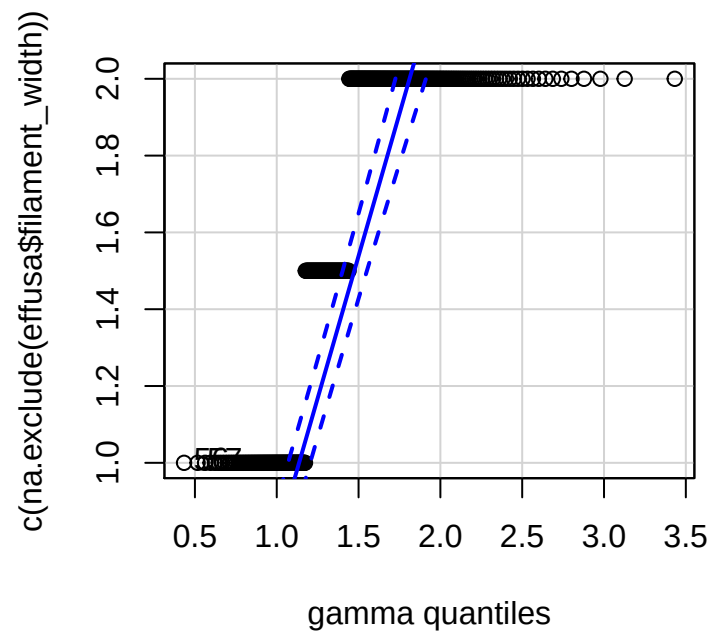
```
## [1] 56 57
```

```
gamma <- fitdistr(c(na.exclude(as.integer(effusa$filament_width))),  
  "gamma")
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

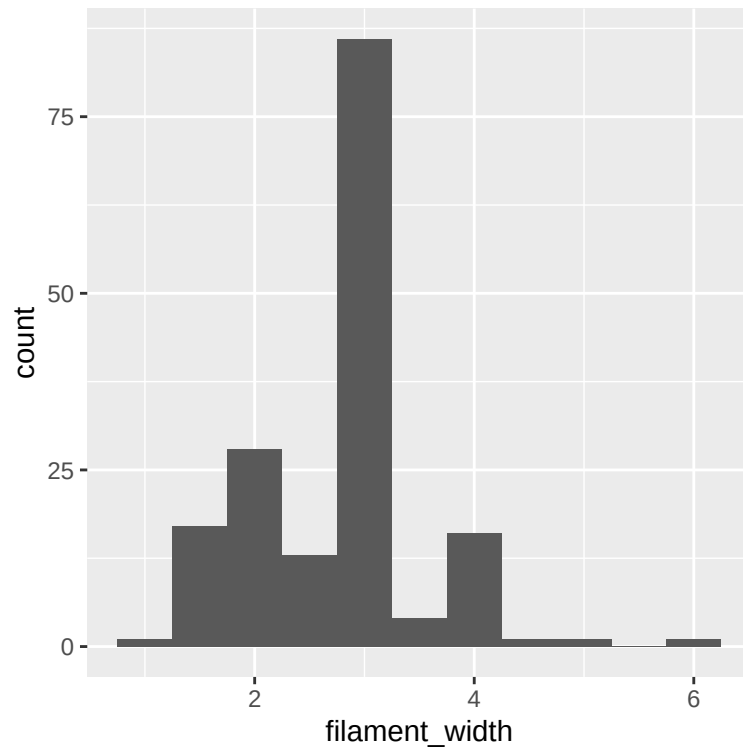
```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
qqp(c(na.exclude(effusa$filament_width)), "gamma", shape = gamma$estimate[[1]],  
  rate = gamma$estimate[[2]])
```

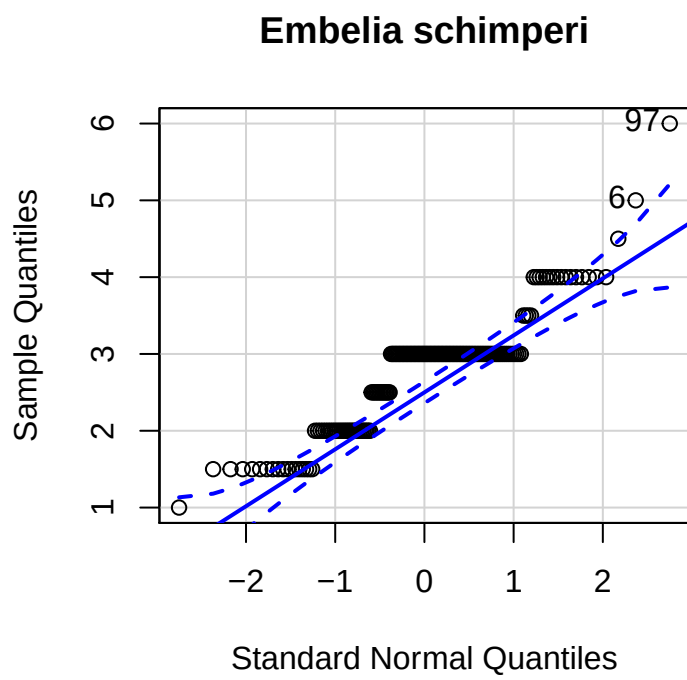


```
## [1] 56 57
histnormFwS <- ggplot(schimp, aes(filament_width))
histnormFwS + geom_histogram(binwidth = 0.5) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))

## Warning: Removed 26 rows containing non-finite values (stat_bin).
```

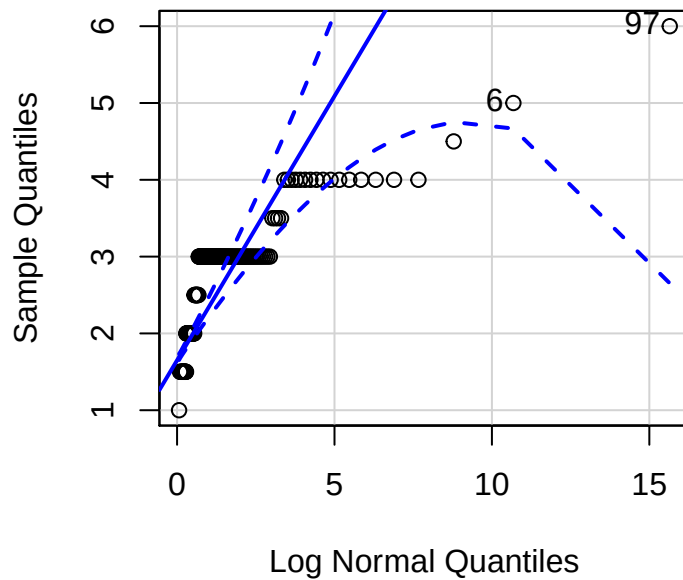


```
qqp(schimp$filament_width, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia schimperii")
```



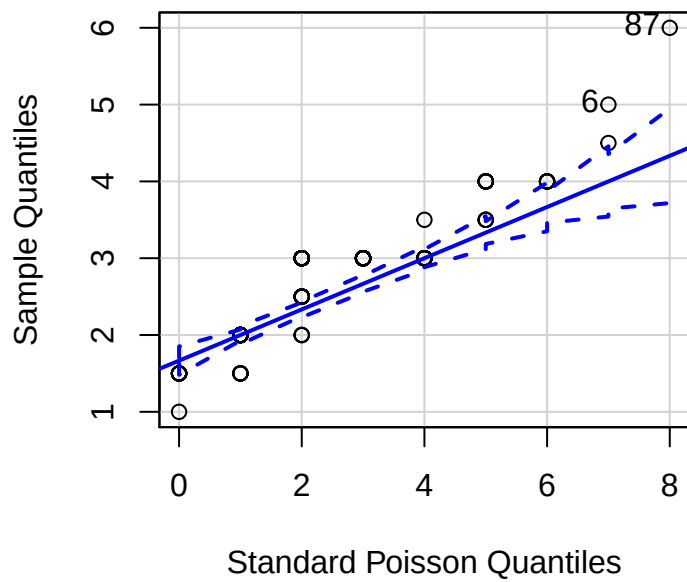
```
## [1] 97 6
```

```
qqp(schimp$filament_width, "lnorm", xlab = "Log Normal Quantiles",
    ylab = "Sample Quantiles")
```

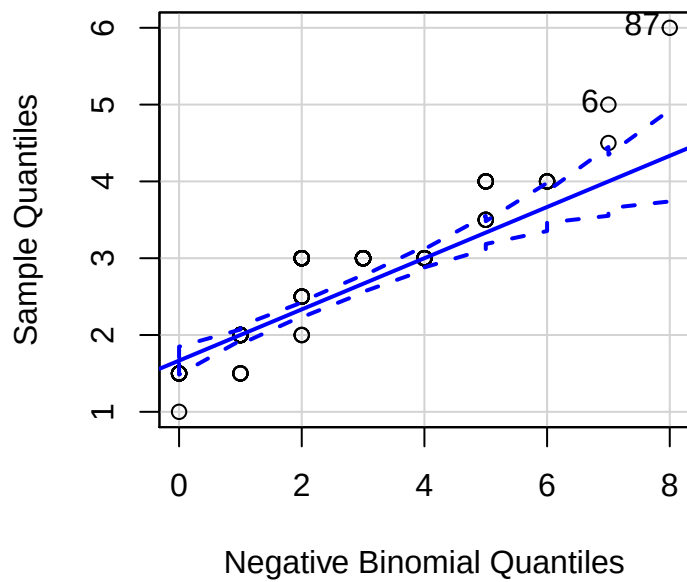


```
## [1] 97 6
```

```
poisson <- fitdistr(c(na.exclude(as.integer(schimp$filament_width))),
    "Poisson")
qqp(c(na.exclude(schimp$filament_width)), "pois", lambda = poisson$estimate,
    xlab = "Standard Poisson Quantiles", ylab = "Sample Quantiles")
```



```
## [1] 87 6
nbinom <- fitdistr(c(na.exclude(as.integer(schimp$filament_width))),
  "Negative Binomial")
qqp(c(na.exclude(schimp$filament_width)), "nbinom", size = nbinom$estimate[[1]],
  mu = nbinom$estimate[[2]], xlab = "Negative Binomial Quantiles",
  ylab = "Sample Quantiles")
```

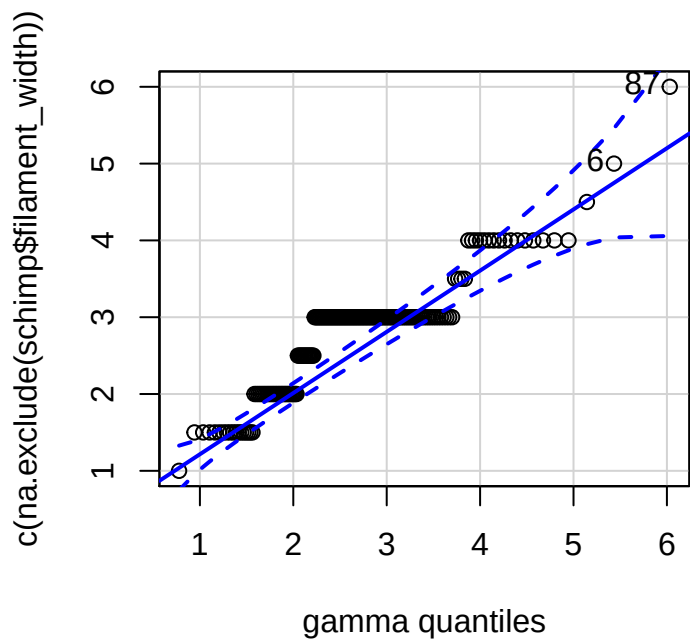
```
## [1] 87 6
```

```
gamma <- fitdistr(c(na.exclude(as.integer(schimp$filament_width))),  
  "gamma")
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

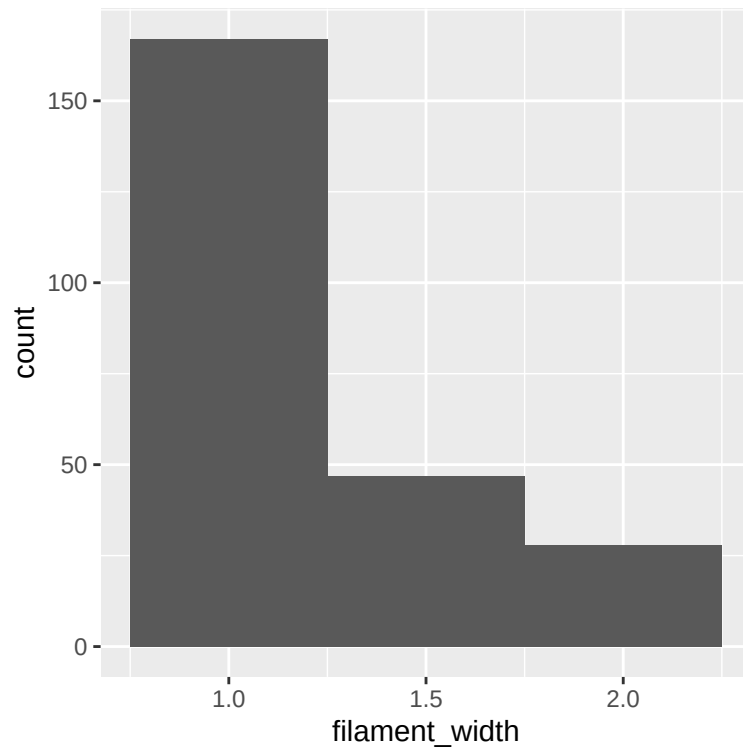
```
qqp(c(na.exclude(schimp$filament_width)), "gamma", shape = gamma$estimate[[1]],  
  rate = gamma$estimate[[2]])
```



```
## [1] 87 6
```

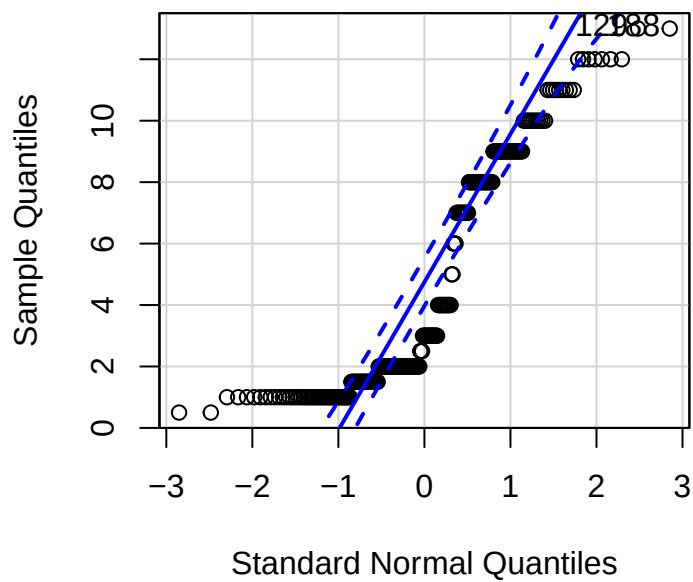
```
histnormFWT <- ggplot(tsjer, aes(filament_width))
histnormFWT + geom_histogram(binwidth = 0.5) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 13 rows containing non-finite values (stat_bin).
```



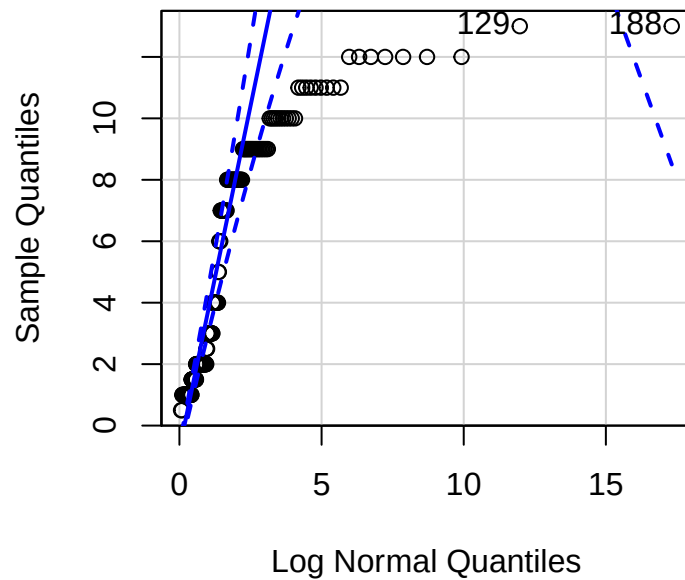
```
qqp(tsjer$filament_length, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia tsjeriamcottam")
```

Embelia tsjeriamcottam



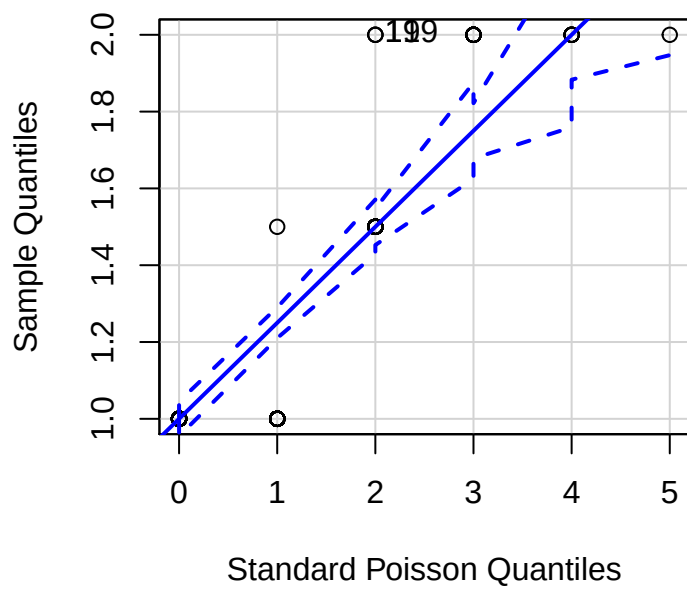
```
## [1] 129 188
```

```
qqp(tsjer$filament_length, "lnorm", xlab = "Log Normal Quantiles",
    ylab = "Sample Quantiles")
```

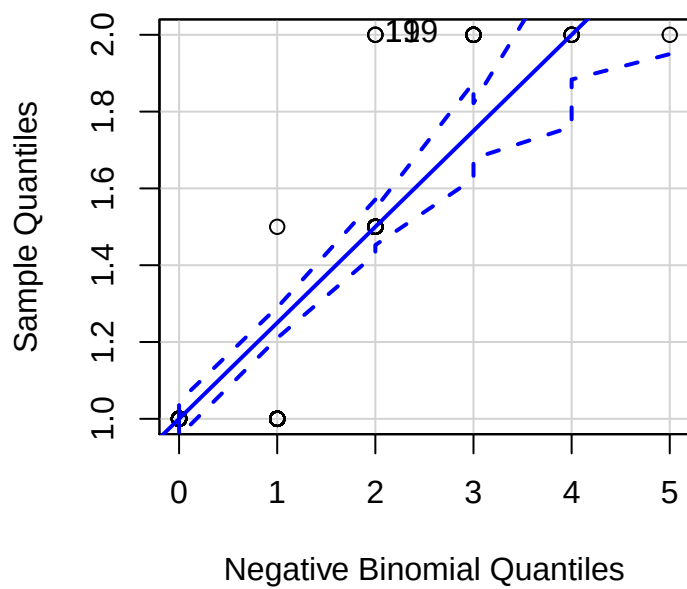


```
## [1] 129 188
```

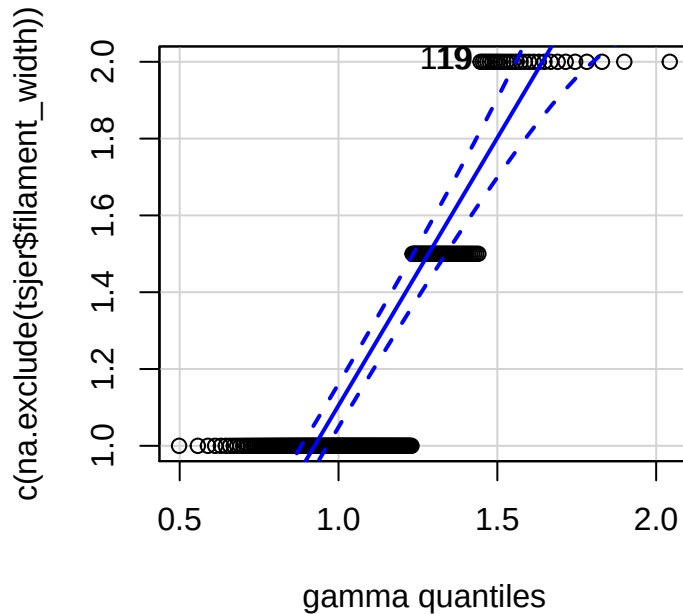
```
poisson <- fitdistr(c(na.exclude(as.integer(tsjer$filament_width))),
    "Poisson")
qqp(c(na.exclude(tsjer$filament_width)), "pois", lambda = poisson$estimate,
    xlab = "Standard Poisson Quantiles", ylab = "Sample Quantiles")
```



```
## [1] 19 119
nbinom <- fitdistr(c(na.exclude(as.integer(tsjer$filament_width))),
  "Negative Binomial")
qqp(c(na.exclude(tsjer$filament_width)), "nbinom", size = nbinom$estimate[[1]],
  mu = nbinom$estimate[[2]], xlab = "Negative Binomial Quantiles",
  ylab = "Sample Quantiles")
```



```
## [1] 19 119
gamma <- fitdistr(c(na.exclude(as.integer(tsjer$filament_width))),
  "gamma")
qqp(c(na.exclude(tsjer$filament_width)), "gamma", shape = gamma$estimate[[1]],
  rate = gamma$estimate[[2]])
```



```
## [1] 19 119
```

Once again, the distribution of the **filament width** is too far from a normal distribution or any other tested distributions (log normal, poisson, negative binomial, gamma) to conduct a linear regression model. Considering the quality of the data (the width of the filaments is too small for a microruler measuring at a resolution of 0.1 mm to record a potential variation), it does not seem appropriate to go into more complex statistical methods because the results would not be reliable.

3.4.4 Statistical tests - Length of fusion of the filaments to the petals (emergence point of the filament)

Embelia effusa

Number of observations

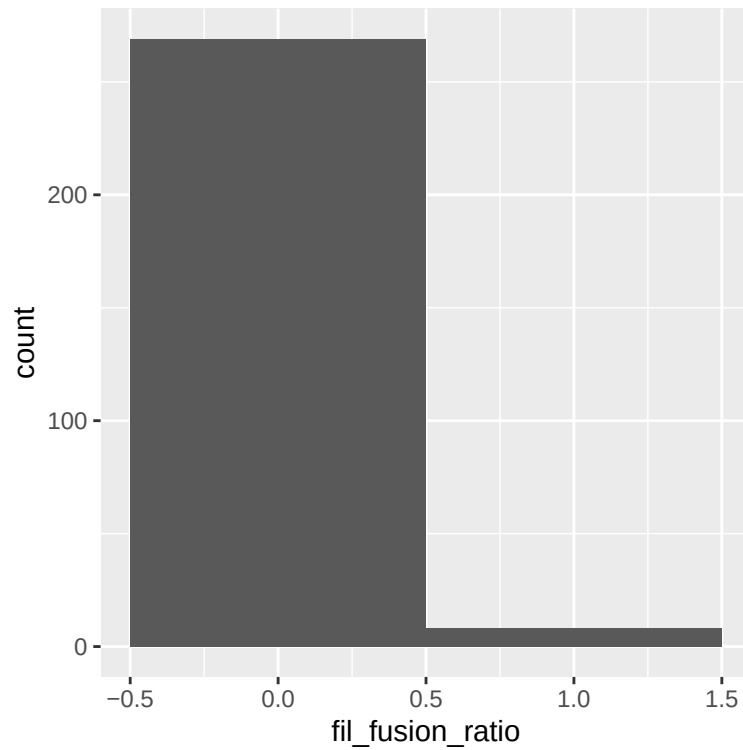
```
aggregate(fil_fusion_ratio ~ sex + species, data = effusa, function(x) length(x))
```

```
##      sex species fil_fusion_ratio
## 1 female  effusa             148
## 2  male   effusa             129
```

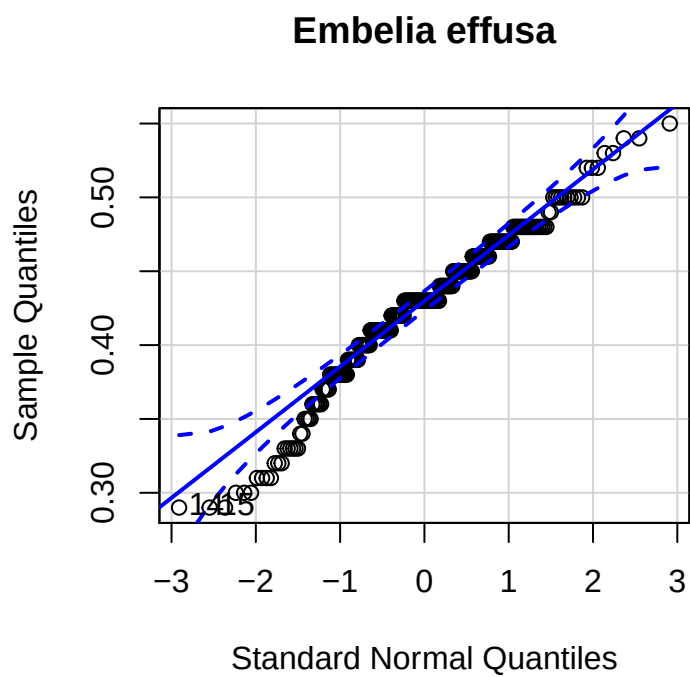
Distribution

```
histnormFfE <- ggplot(effusa, aes(fil_fusion_ratio))
histnormFfE + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
"lightsalmon"))
```

```
## Warning: Removed 15 rows containing non-finite values (stat_bin).
```



```
qqp(effusa$fil_fusion_ratio, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia effusa")
```



```
## [1] 14 15
```


Build model

```
lmFfE <- lmer(fil_fusion_ratio ~ sex + (1 | spec_ID), effusa,  
  REML = FALSE)
```

Display results

```
summary(lmFfE)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']  
## Formula: fil_fusion_ratio ~ sex + (1 | spec_ID)  
## Data: effusa  
##  
##           AIC          BIC    logLik deviance df.resid  
##    -899.3    -884.8    453.6   -907.3      273  
##  
## Scaled residuals:  
##      Min       1Q   Median       3Q      Max  
## -3.2900 -0.4921  0.0300  0.6008  2.9468  
##  
## Random effects:  
## Groups Name Variance Std.Dev.  
## spec_ID (Intercept) 0.0002596 0.01611  
## Residual 0.0021117 0.04595  
## Number of obs: 277, groups: spec_ID, 8  
##  
## Fixed effects:  
##              Estimate Std. Error t value  
## (Intercept) 0.424681 0.008951 47.443  
## sexmale 0.008586 0.012746 0.674  
##  
## Correlation of Fixed Effects:  
##      (Intr)  
## sexmale -0.702
```

```
confint(lmFfE)
```

```
## Computing profile confidence intervals ...  
##              2.5 %      97.5 %  
## .sig01 0.00890776 0.03103069  
## .sigma 0.04232978 0.05012372  
## (Intercept) 0.40513496 0.44481765  
## sexmale -0.01991020 0.03644428
```

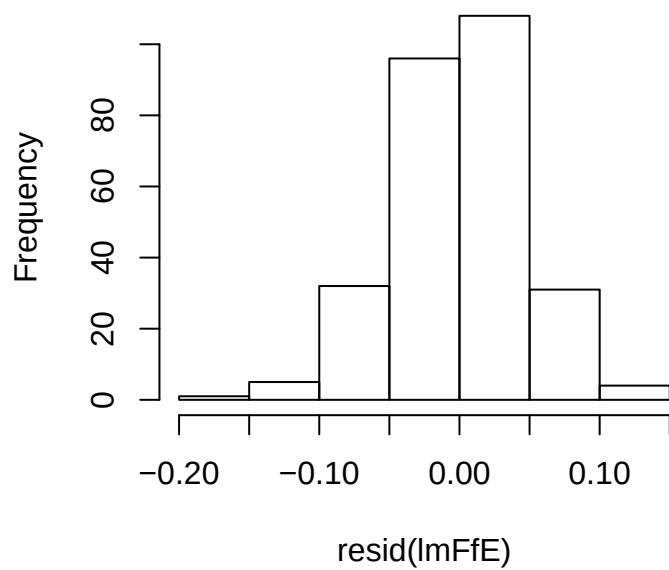
```
Anova(lmFfE)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)  
##  
## Response: fil_fusion_ratio  
##      Chisq Df Pr(>Chisq)  
## sex 0.4537 1 0.5006
```

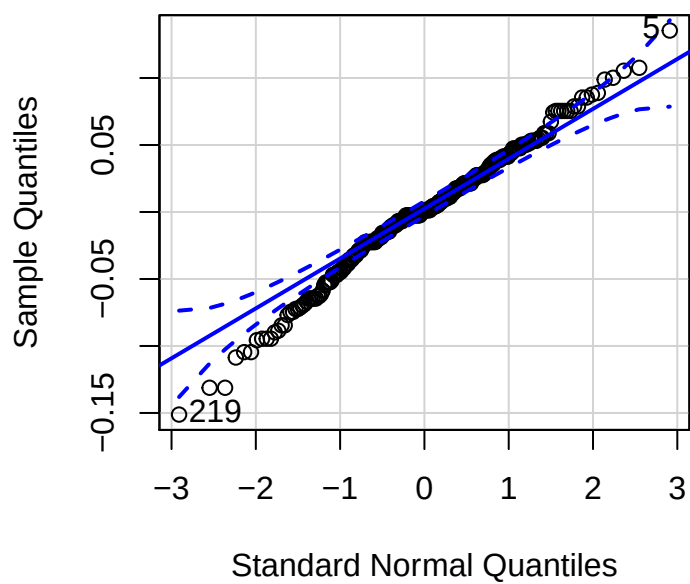
Check normality of residuals

```
hist(resid(lmFfE))
```

Histogram of resid(lmFfE)



```
qqp(resid(lmFfE), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

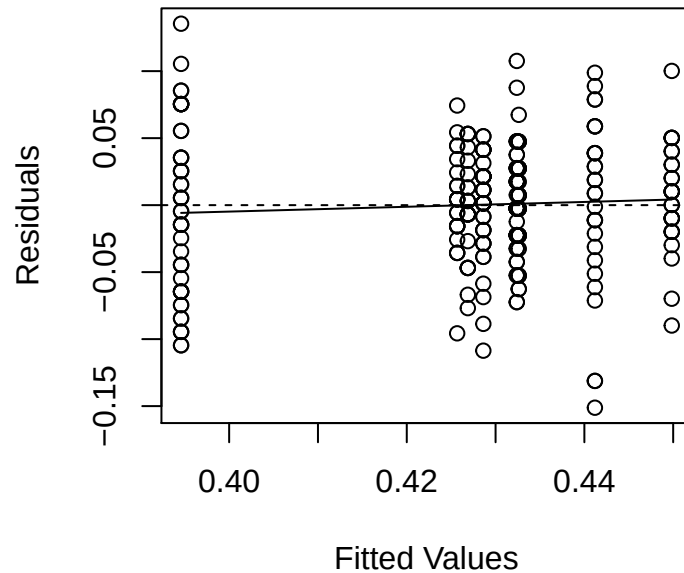


```
## 219 5
## 204 5
```

Check model fit

```
plot(fitted(lmFfE), residuals(lmFfE), xlab = "Fitted Values",  
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")  
abline(h = 0, lty = 2)  
lines(smooth.spline(fitted(lmFfE), residuals(lmFfE)))
```

Linear mixed model using maximum likelih



Embelia schimperi

Number of observations

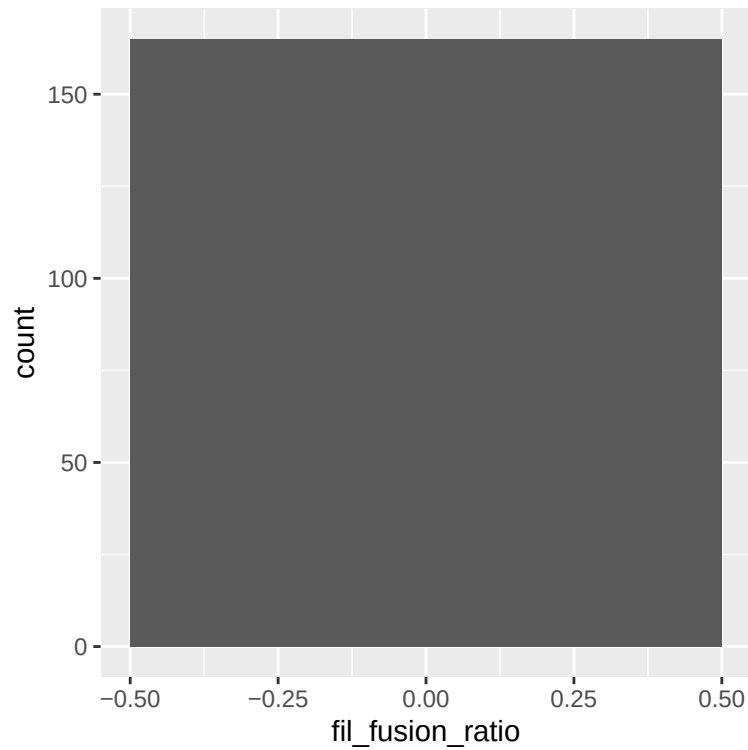
```
aggregate(fil_fusion_ratio ~ sex + species, data = schimp, function(x) length(x))
```

```
##      sex  species fil_fusion_ratio  
## 1 female schimperi             83  
## 2  male schimperi             82
```

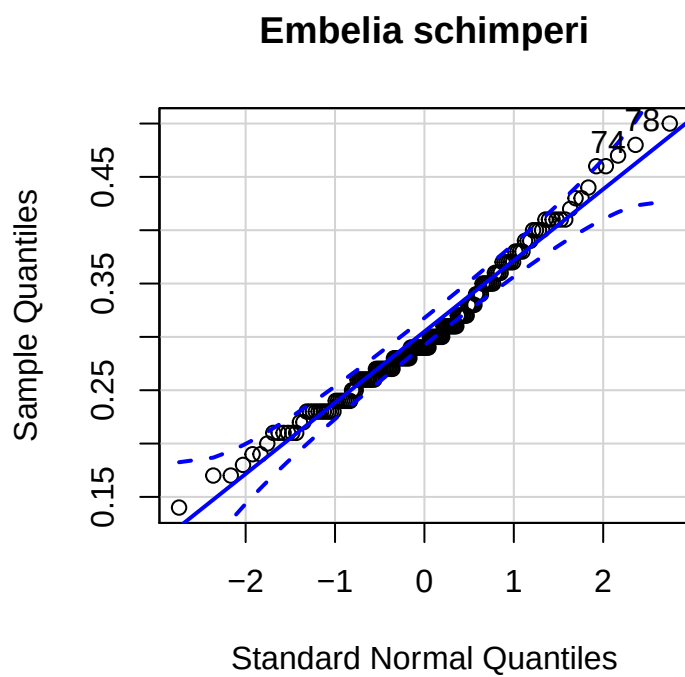
Distribution

```
histnormFfS <- ggplot(schimp, aes(fil_fusion_ratio))  
histnormFfS + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",  
  "lightsalmon"))
```

```
## Warning: Removed 29 rows containing non-finite values (stat_bin).
```



```
qqp(schimp$fil_fusion_ratio, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia schimperi")
```



```
## [1] 78 74
```

Build model

```
lmFfS <- lmer(fil_fusion_ratio ~ sex + (1 | spec_ID), schimp,  
  REML = FALSE)
```

Display results

```
summary(lmFfS)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']  
## Formula: fil_fusion_ratio ~ sex + (1 | spec_ID)  
## Data: schimp  
##  
##           AIC          BIC    logLik deviance df.resid  
##    -520.1    -507.7     264.0   -528.1      161  
##  
## Scaled residuals:  
##      Min       1Q   Median       3Q      Max  
## -2.9542 -0.6342  0.0073  0.6686  4.2113  
##  
## Random effects:  
## Groups Name          Variance Std.Dev.  
## spec_ID (Intercept) 0.002092 0.04574  
## Residual              0.002121 0.04605  
## Number of obs: 165, groups: spec_ID, 6  
##  
## Fixed effects:  
##              Estimate Std. Error t value  
## (Intercept)  0.33026    0.02710  12.186  
## sexmale      -0.02849    0.03821  -0.746  
##  
## Correlation of Fixed Effects:  
##              (Intr)  
## sexmale -0.709
```

```
confint(lmFfS)
```

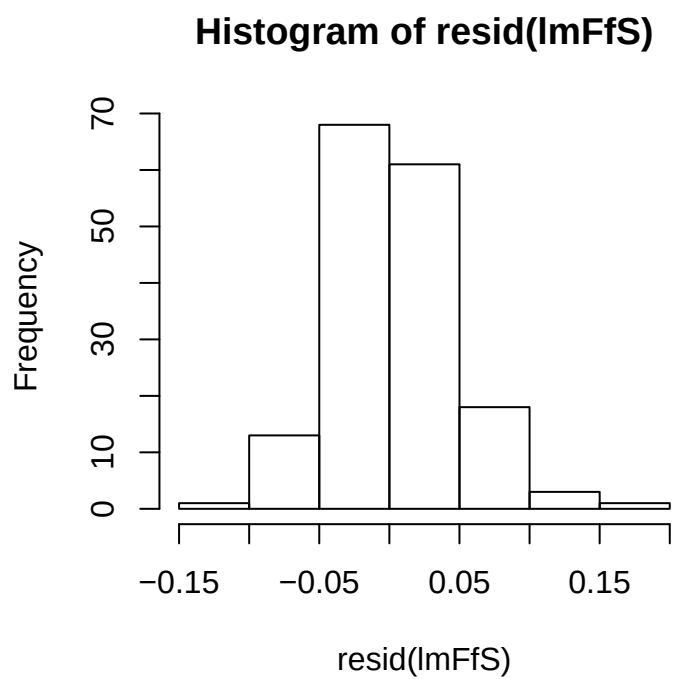
```
## Computing profile confidence intervals ...  
##              2.5 %      97.5 %  
## .sig01      0.02764135 0.09285605  
## .sigma      0.04142284 0.05161637  
## (Intercept) 0.26790458 0.39309744  
## sexmale     -0.11699446 0.05974884
```

```
Anova(lmFfS)
```

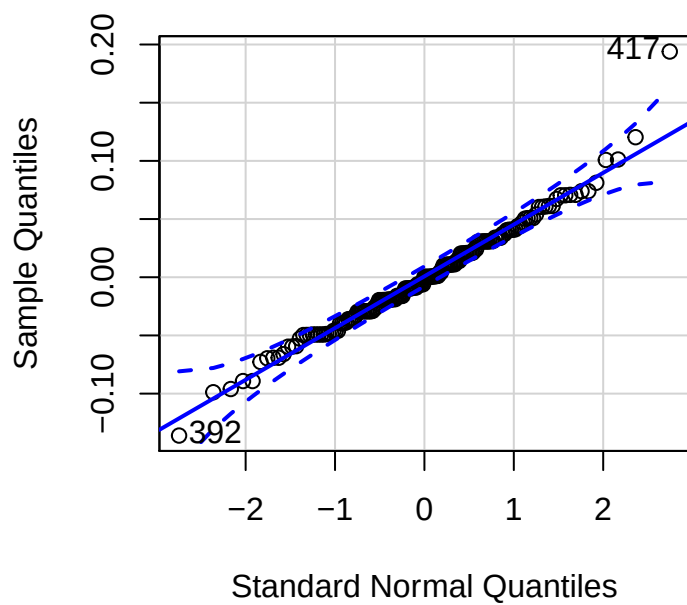
```
## Analysis of Deviance Table (Type II Wald chisquare tests)  
##  
## Response: fil_fusion_ratio  
##      Chisq Df Pr(>Chisq)  
## sex 0.5561  1    0.4558
```

Check normality of residuals

```
hist(resid(lmFfS))
```



```
qqp(resid(lmFfS), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

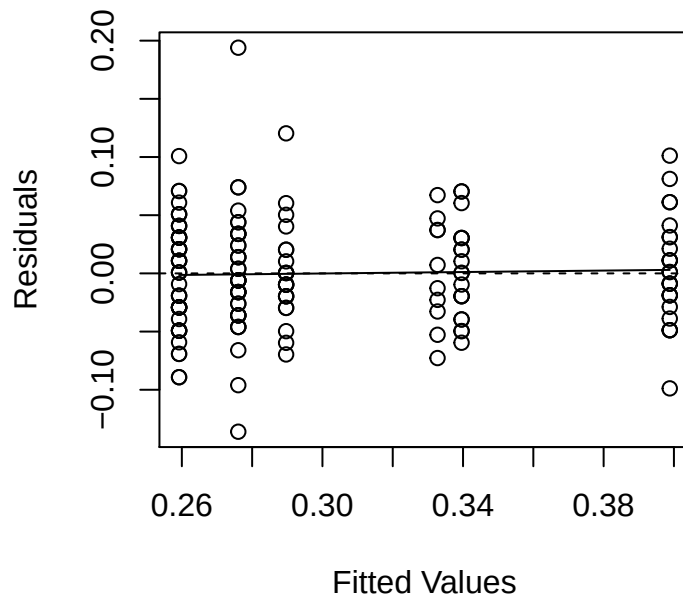


```
## 417 392
## 107 88
```

Check model fit

```
plot(fitted(lmFfS), residuals(lmFfS), xlab = "Fitted Values",  
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")  
abline(h = 0, lty = 2)  
lines(smooth.spline(fitted(lmFfS), residuals(lmFfS)))
```

Linear mixed model using maximum likelih



Embelia tsjeriamcottam

Number of observations

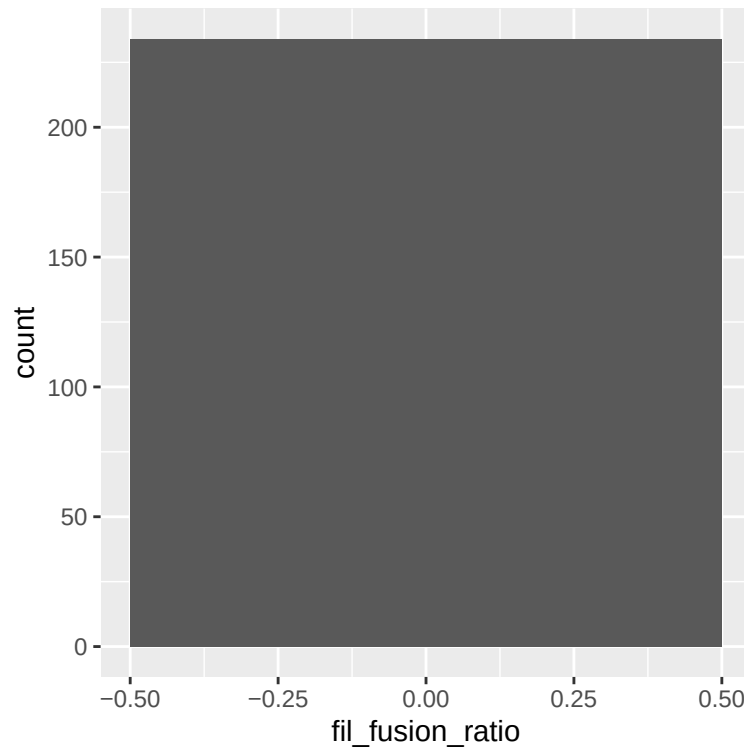
```
aggregate(fil_fusion_ratio ~ sex + species, data = tsjer, function(x) length(x))
```

```
##      sex      species fil_fusion_ratio  
## 1 female tsjeriamcottam             117  
## 2 male   tsjeriamcottam             117
```

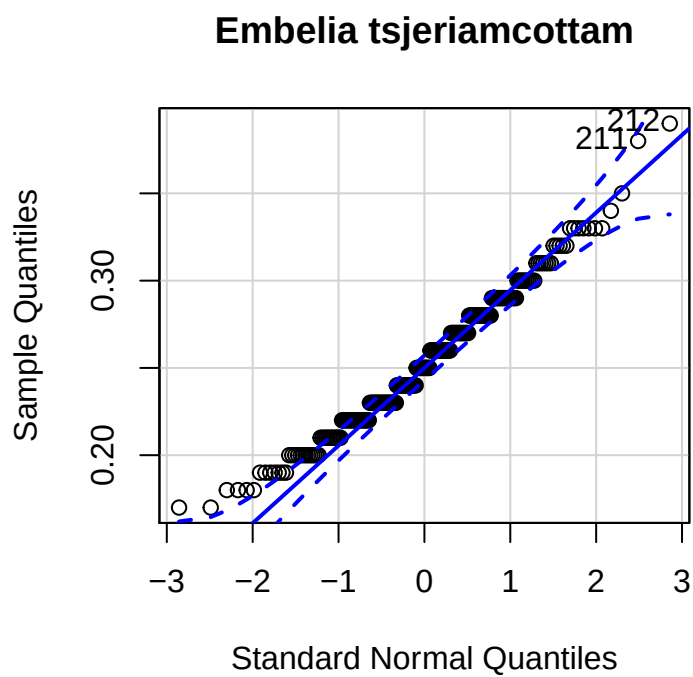
Distribution

```
histnormFfT <- ggplot(tsjer, aes(fil_fusion_ratio))  
histnormFfT + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",  
  "lightsalmon"))
```

```
## Warning: Removed 21 rows containing non-finite values (stat_bin).
```



```
qqp(tsjer$fil_fusion_ratio, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia tsjeriamcottam")
```



```
## [1] 212 211
```


Build model

```
lmFfT <- lmer(fil_fusion_ratio ~ sex + (1 | spec_ID), tsjer,  
             REML = FALSE)
```

Display results

```
summary(lmFfT)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']  
## Formula: fil_fusion_ratio ~ sex + (1 | spec_ID)  
## Data: tsjer  
##  
##           AIC          BIC    logLik deviance df.resid  
##    -923.5    -909.7     465.7   -931.5        230  
##  
## Scaled residuals:  
##      Min       1Q   Median       3Q      Max  
## -2.72077 -0.59497 -0.07056  0.69376  2.57965  
##  
## Random effects:  
## Groups Name Variance Std.Dev.  
## spec_ID (Intercept) 0.0004112 0.02028  
## Residual          0.0010122 0.03182  
## Number of obs: 234, groups: spec_ID, 7  
##  
## Fixed effects:  
##              Estimate Std. Error t value  
## (Intercept)  0.23473    0.01210   19.401  
## sexmale      0.04121    0.01617    2.549  
##  
## Correlation of Fixed Effects:  
##          (Intr)  
## sexmale -0.748
```

```
confint(lmFfT)
```

```
## Computing profile confidence intervals ...  
##              2.5 %    97.5 %  
## .sig01      0.011087602 0.04077130  
## .sigma      0.029092244 0.03499237  
## (Intercept) 0.206702233 0.26279653  
## sexmale     0.004505711 0.07915098
```

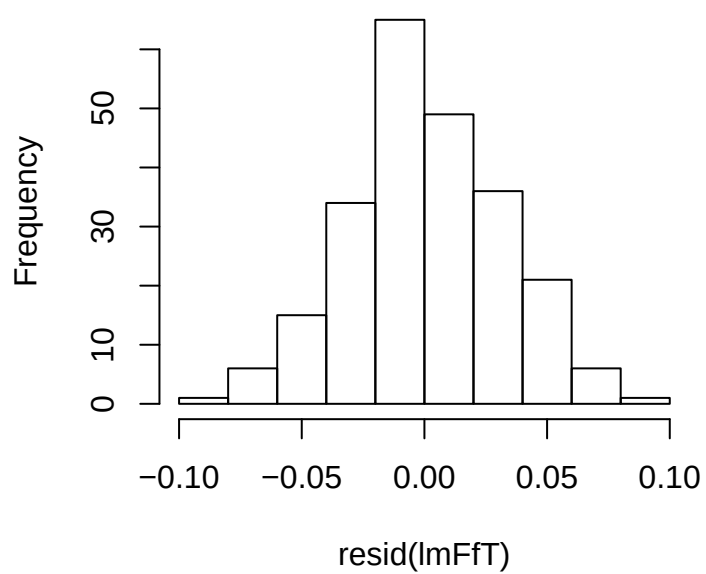
```
Anova(lmFfT)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)  
##  
## Response: fil_fusion_ratio  
##      Chisq Df Pr(>Chisq)  
## sex 6.4971  1  0.01081 *  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

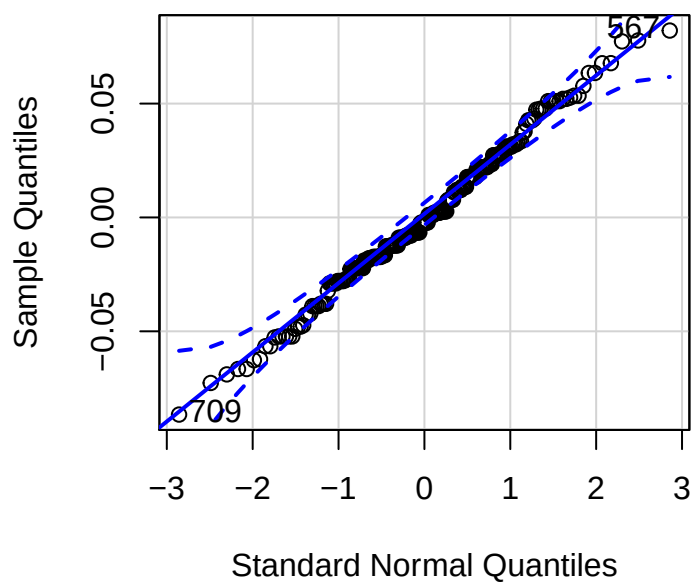
Check normality of residuals

```
hist(resid(lmFfT))
```

Histogram of resid(lmFfT)



```
qqp(resid(lmFfT), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

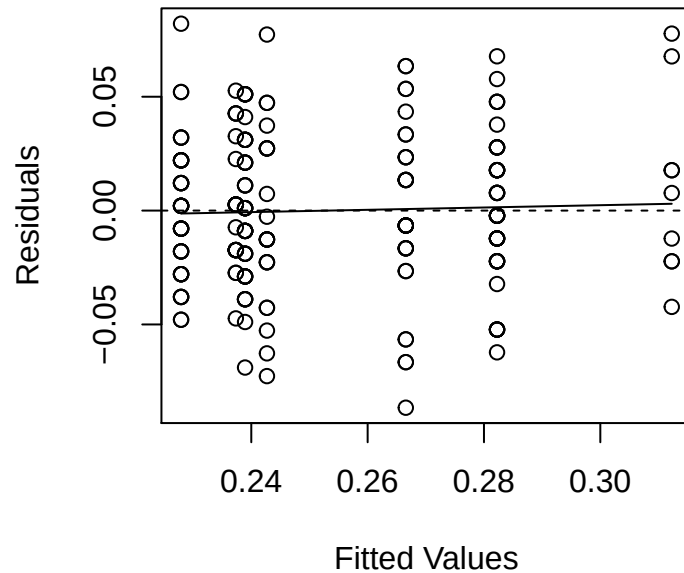


```
## 709 567
## 203 79
```

Check model fit

```
plot(fitted(lmFfT), residuals(lmFfT), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmFfT), residuals(lmFfT)))
```

Linear mixed model using maximum likelih



3.5 Anthers

3.5.1 Descriptive statistics

Anther length

Mean

```
aggregate(anther_length ~ sex + species, data = flwr, mean)
```

##	sex	species	anther_length
## 1	female	effusa	6.324818
## 2	male	effusa	4.931452
## 3	female	schimperi	6.956790
## 4	male	schimperi	12.006173
## 5	female	tsjeriamcottam	4.995327
## 6	male	tsjeriamcottam	7.885321

Variance

```
aggregate(anther_length ~ sex + species, data = flwr, var)
```

##	sex	species	anther_length
## 1	female	effusa	0.4764384
## 2	male	effusa	0.5420109
## 3	female	schimperi	1.5387346

```
## 4   male      schimperi      0.8155864
## 5 female tsjeriamcottam      0.2947893
## 6   male tsjeriamcottam      4.1881159
```

Standard deviation

```
aggregate(anther_length ~ sex + species, data = flwr, sd)
```

```
##      sex      species anther_length
## 1 female      effusa      0.6902452
## 2   male      effusa      0.7362139
## 3 female      schimperi      1.2404574
## 4   male      schimperi      0.9030982
## 5 female tsjeriamcottam      0.5429450
## 6   male tsjeriamcottam      2.0464887
```

Anther width

Mean

```
aggregate(anther_width ~ sex + species, data = flwr, mean)
```

```
##      sex      species anther_width
## 1 female      effusa      4.648905
## 2   male      effusa      5.945161
## 3 female      schimperi      4.864198
## 4   male      schimperi      7.265432
## 5 female tsjeriamcottam      3.158879
## 6   male tsjeriamcottam      5.697248
```

Variance

```
aggregate(anther_width ~ sex + species, data = flwr, var)
```

```
##      sex      species anther_width
## 1 female      effusa      0.7479584
## 2   male      effusa      0.7785943
## 3 female      schimperi      1.0063272
## 4   male      schimperi      1.1755401
## 5 female tsjeriamcottam      0.1773497
## 6   male tsjeriamcottam      0.4908257
```

Standard deviation

```
aggregate(anther_width ~ sex + species, data = flwr, sd)
```

```
##      sex      species anther_width
## 1 female      effusa      0.8648459
## 2   male      effusa      0.8823799
## 3 female      schimperi      1.0031586
## 4   male      schimperi      1.0842233
## 5 female tsjeriamcottam      0.4211290
## 6   male tsjeriamcottam      0.7005895
```

3.5.2 Statistical tests - Anther length

Embelia effusa

Number of observations

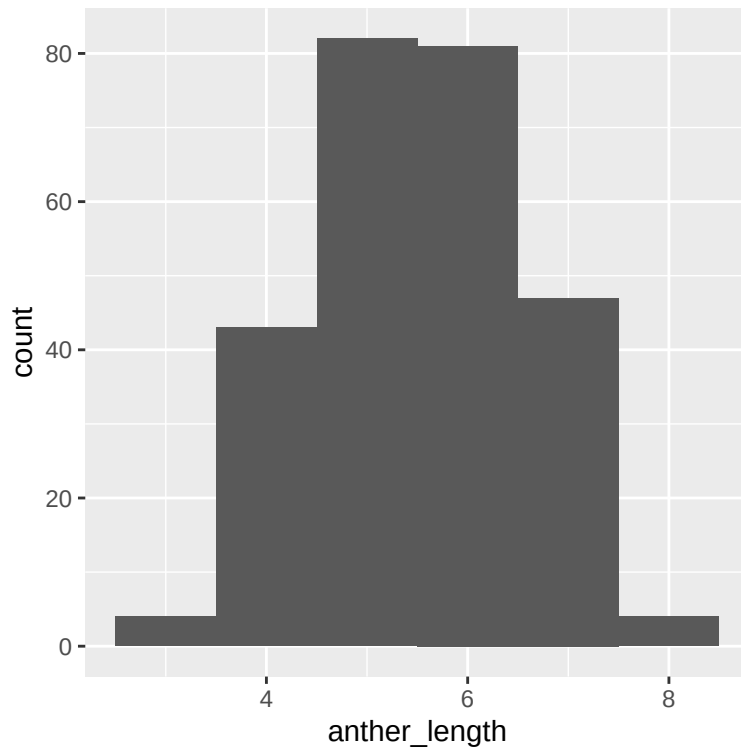
```
aggregate(anther_length ~ sex + species, data = effusa, function(x) length(x))
```

```
##      sex species anther_length
## 1 female  effusa           137
## 2 male   effusa           124
```

Distribution

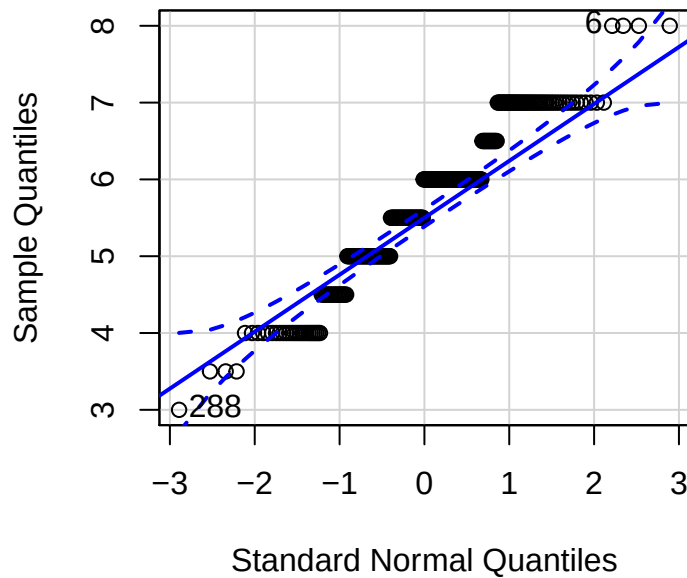
```
histnormAlE <- ggplot(effusa, aes(anther_length))
histnormAlE + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 31 rows containing non-finite values (stat_bin).
```



```
qqp(effusa$anther_length, "norm", xlab = "Standard Normal Quantiles",
  ylab = "Sample Quantiles", main = "Embelia effusa")
```

Embelia effusa



```
## [1] 288 6
```

Build model

```
lmAlE <- lmer(anther_length ~ sex + (1 | spec_ID), effusa, REML = FALSE)
```

Display results

```
summary(lmAlE)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: anther_length ~ sex + (1 | spec_ID)
## Data: effusa
##
##      AIC      BIC    logLik deviance df.resid
##    427.6    441.9   -209.8    419.6     257
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.7565 -0.6928  0.1551  0.5050  2.4325
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## spec_ID  (Intercept)  0.2307     0.4804
## Residual                    0.2638     0.5137
## Number of obs: 261, groups:  spec_ID, 8
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   6.2696     0.2446  25.635
## sexmale      -1.4328     0.3462  -4.139
```

```
##
## Correlation of Fixed Effects:
##      (Intr)
## sexmale -0.707

confint(lmAIE)

## Computing profile confidence intervals ...

##           2.5 %    97.5 %
## .sig01      0.3074823  0.8728728
## .sigma      0.4719528  0.5618730
## (Intercept)  5.7257515  6.8118417
## sexmale     -2.2014839 -0.6647288

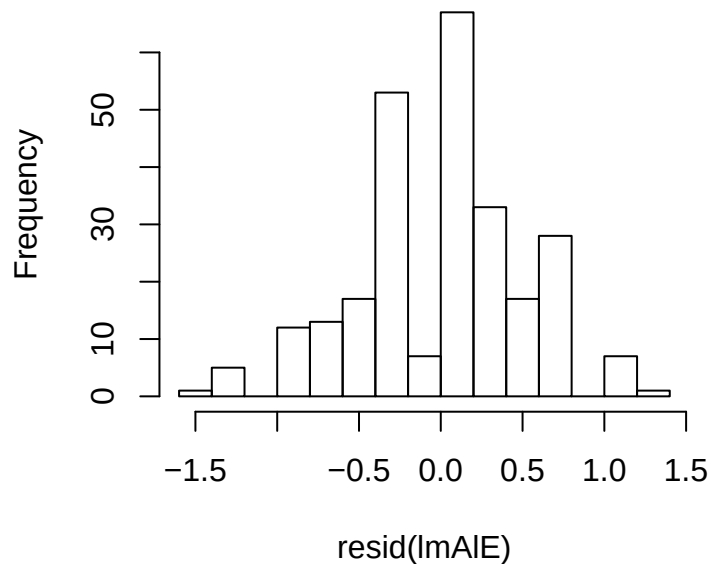
Anova(lmAIE)

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: anther_length
##      Chisq Df Pr(>Chisq)
## sex 17.131  1  3.488e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

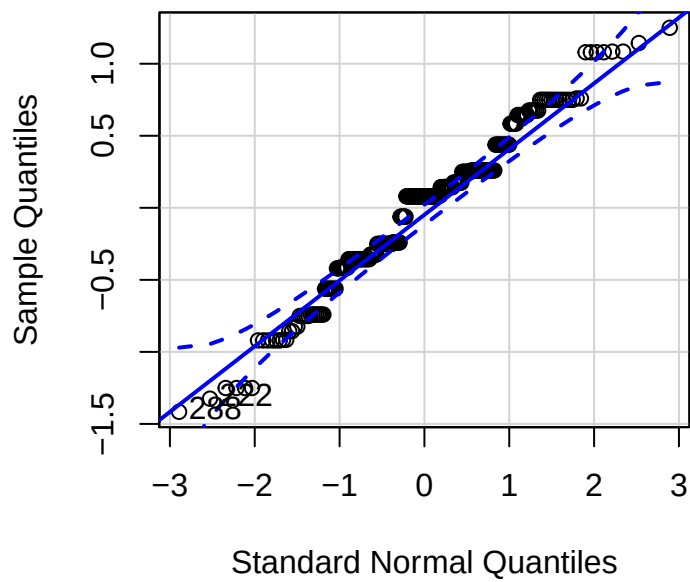
Check normality of residuals

hist(resid(lmAIE))
```

Histogram of resid(lmAIE)



```
qqp(resid(lmAIE), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

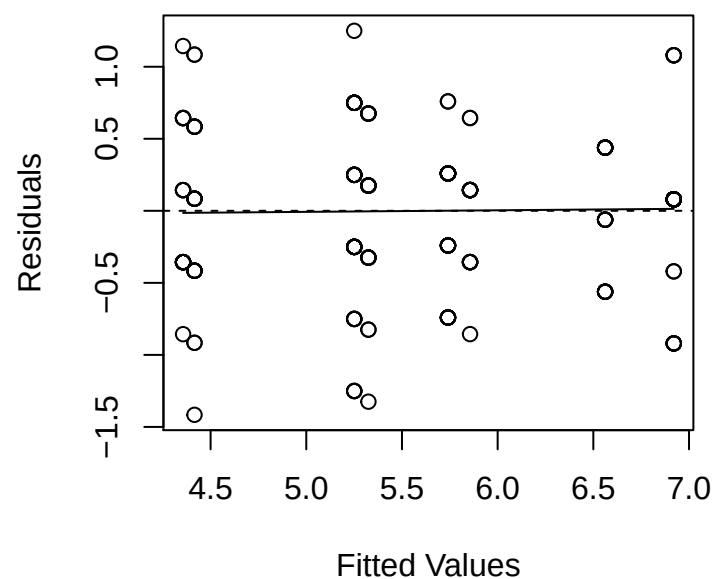


```
## 288 222
## 258 196
```

Check model fit

```
plot(fitted(lmA1E), residuals(lmA1E), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmA1E), residuals(lmA1E)))
```


Linear mixed model using maximum likelih



Embelia schimperi

Number of observations

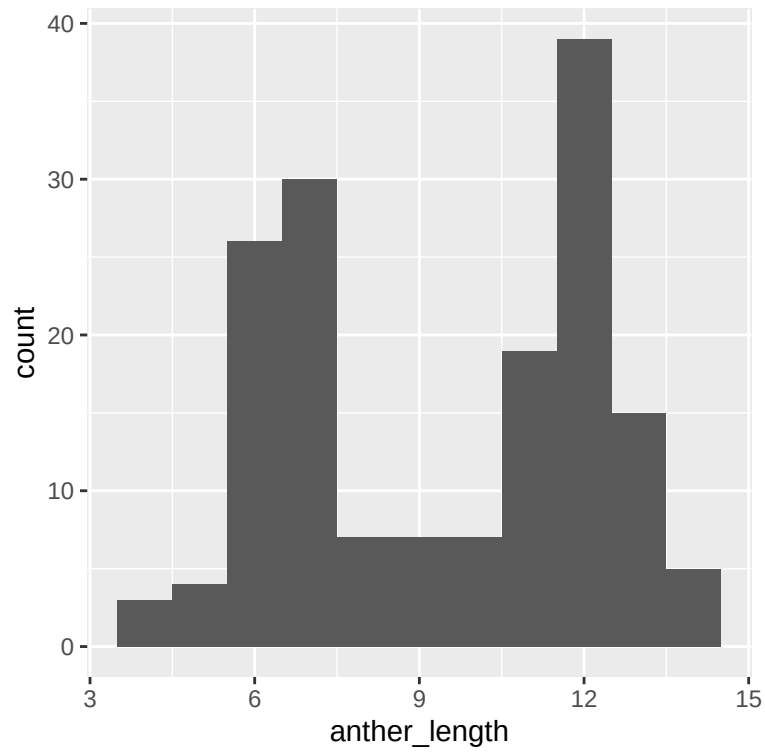
```
aggregate(anther_length ~ sex + species, data = schimp, function(x) length(x))
```

```
##      sex  species anther_length
## 1 female schimperi           81
## 2  male schimperi           81
```

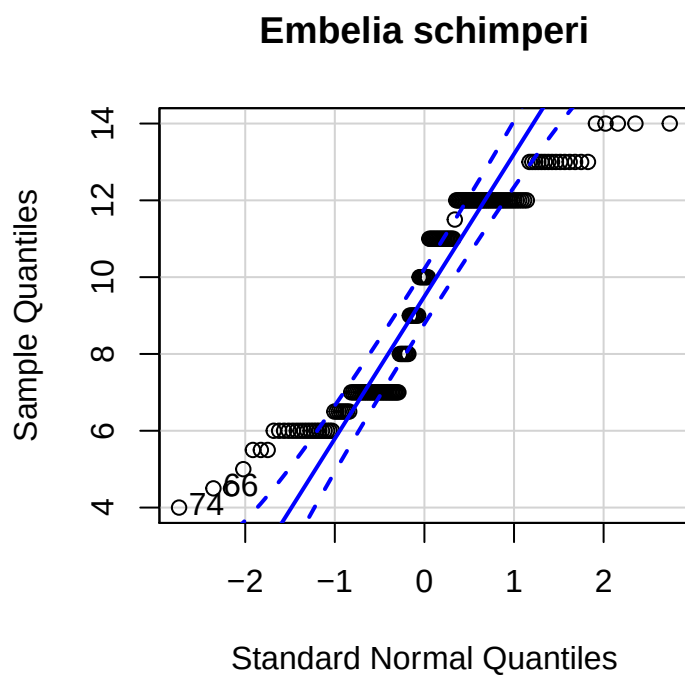
Distribution

```
histnormA1S <- ggplot(schimp, aes(anther_length))
histnormA1S + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 32 rows containing non-finite values (stat_bin).
```



```
qqp(schimp$anther_length, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia schimperi")
```



```
## [1] 74 66
```

Build model

```
lmA1S <- lmer(anther_length ~ sex + (1 | spec_ID), schimp, REML = FALSE)
```

Display results

```
summary(lmA1S)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: anther_length ~ sex + (1 | spec_ID)
## Data: schimp
##
##      AIC      BIC    logLik deviance df.resid
##    435.2    447.6   -213.6    427.2     158
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4102 -0.5354  0.0004   0.4071   3.5844
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 0.8616  0.9282
## Residual              0.7217  0.8496
## Number of obs: 162, groups: spec_ID, 6
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   7.3532    0.5479   13.42
## sexmale       4.6290    0.7728    5.99
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.709
```

```
confint(lmA1S)
```

```
## Computing profile confidence intervals ...
##
##              2.5 %   97.5 %
## .sig01      0.5458941 1.905695
## .sigma      0.7632753 0.953416
## (Intercept) 6.0905302 8.643830
## sexmale     2.8115548 6.417446
```

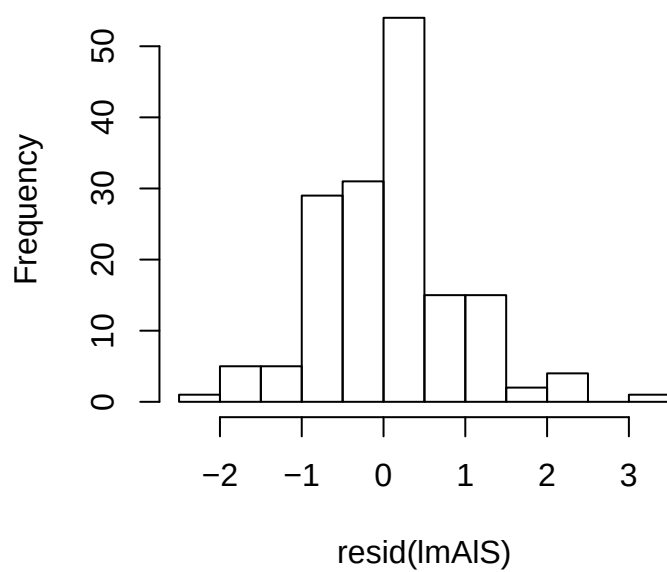
```
Anova(lmA1S)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: anther_length
##      Chisq Df Pr(>Chisq)
## sex 35.876  1 2.103e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

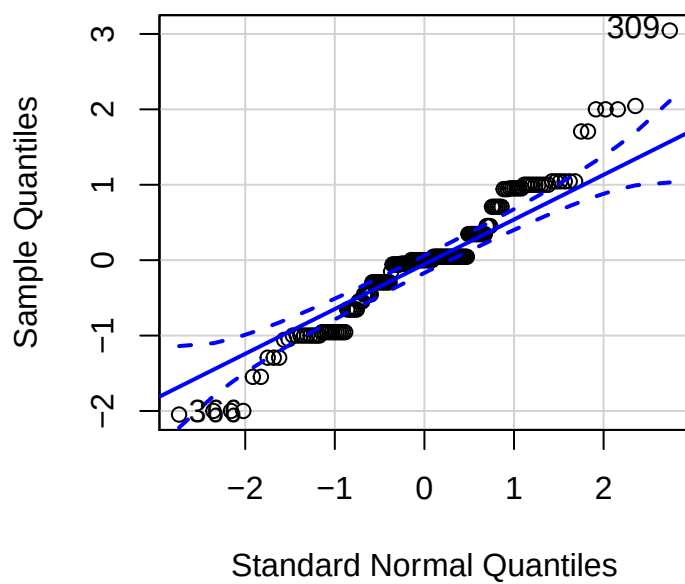
Check normality of residuals

```
hist(resid(lmA1S))
```

Histogram of resid(lmAIS)



```
qqp(resid(lmAIS), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

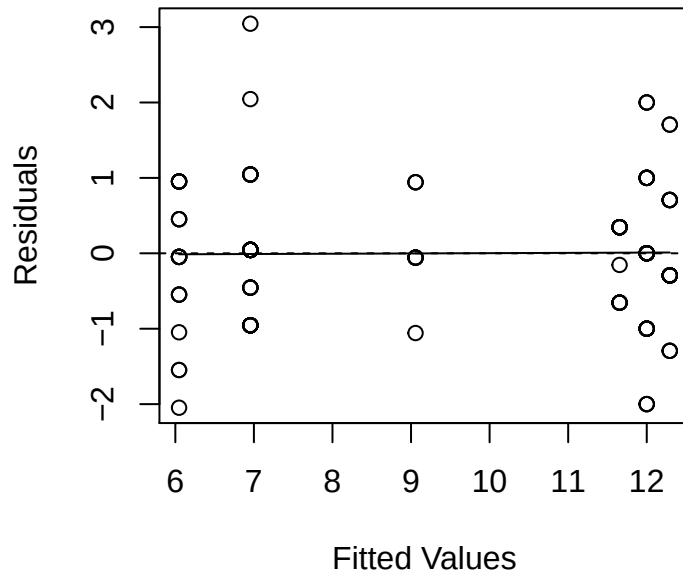


```
## 309 366
## 16 66
```

Check model fit

```
plot(fitted(lmAlS), residuals(lmAlS), xlab = "Fitted Values",  
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")  
abline(h = 0, lty = 2)  
lines(smooth.spline(fitted(lmAlS), residuals(lmAlS)))
```

Linear mixed model using maximum likelih



Embelia tsjeriamcottam

Number of observations

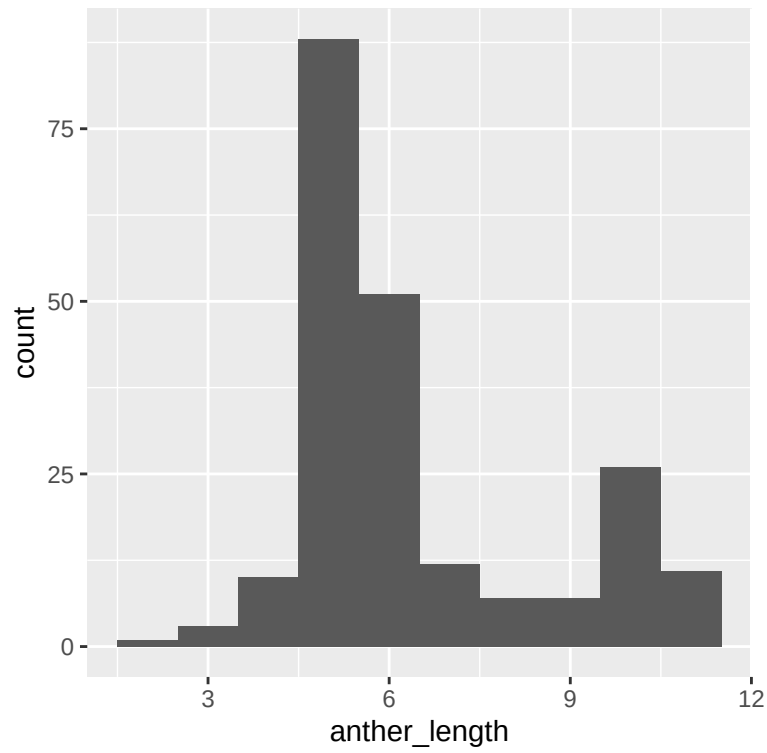
```
aggregate(anther_length ~ sex + species, data = tsjer, function(x) length(x))
```

```
##      sex      species anther_length  
## 1 female tsjeriamcottam          107  
## 2  male tsjeriamcottam          109
```

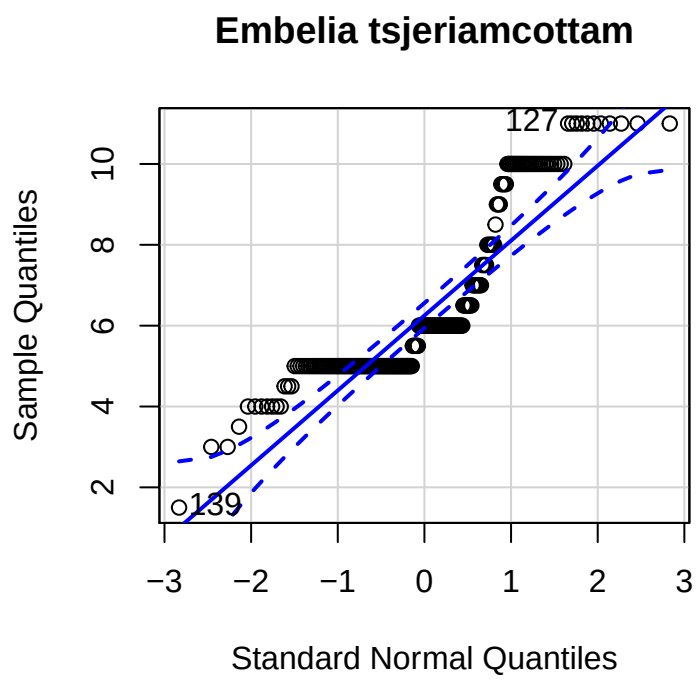
Distribution

```
histnormALT <- ggplot(tsjer, aes(anther_length))  
histnormALT + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",  
  "lightsalmon"))
```

```
## Warning: Removed 39 rows containing non-finite values (stat_bin).
```



```
qqp(tsjer$anther_length, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia tsjeriamcottam")
```



```
## [1] 139 127
```

Build model

```
lmAlt <- lmer(anther_length ~ sex + (1 | spec_ID), tsjer, REML = FALSE)
```

Display results

```
summary(lmAlt)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: anther_length ~ sex + (1 | spec_ID)
## Data: tsjer
##
##      AIC      BIC    logLik deviance df.resid
##    543.8    557.3   -267.9    535.8      212
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -10.7848  -0.0733  -0.0629   0.2630   1.5436
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 1.4685  1.2118
## Residual          0.6098  0.7809
## Number of obs: 216, groups: spec_ID, 7
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  4.9670    0.7040    7.056
## sexmale      2.4806    0.9326    2.660
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.755
```

```
confint(lmAlt)
```

```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01      0.7682113 2.2942213
## .sigma      0.7116129 0.8621599
## (Intercept) 3.3740051 6.5596842
## sexmale     0.3700407 4.5876562
```

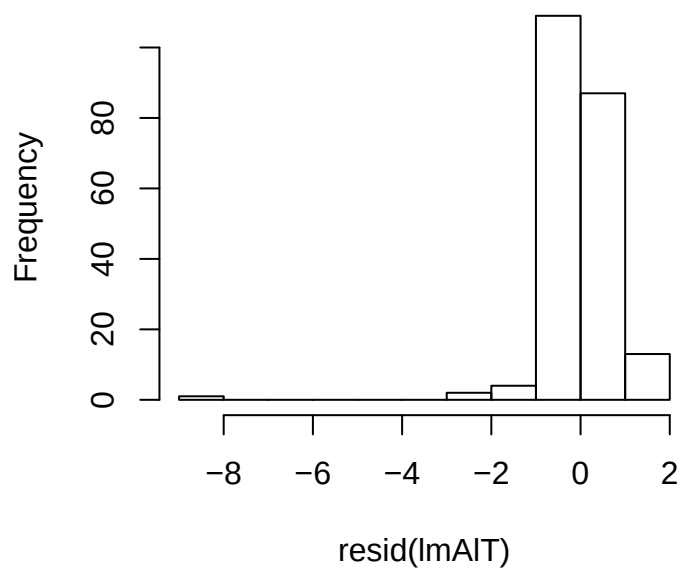
```
Anova(lmAlt)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: anther_length
##      Chisq Df Pr(>Chisq)
## sex 7.0755  1  0.007815 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

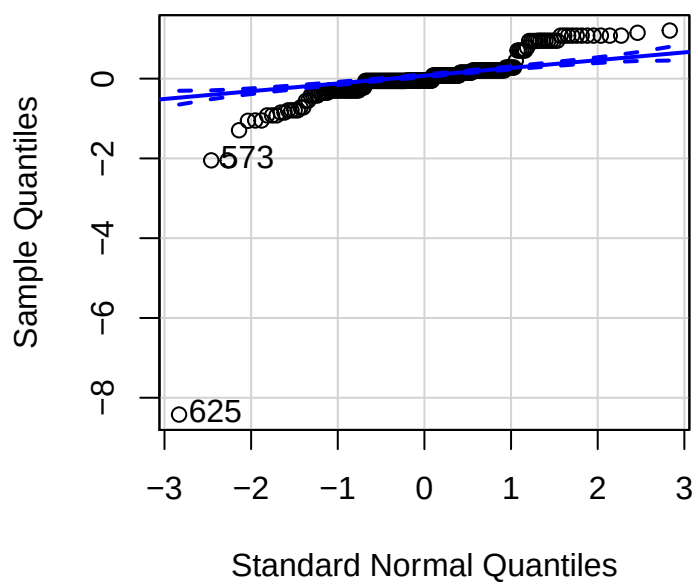
Check normality of residuals

```
hist(resid(lmAlt))
```

Histogram of resid(lmAIT)



```
qqp(resid(lmAIT), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

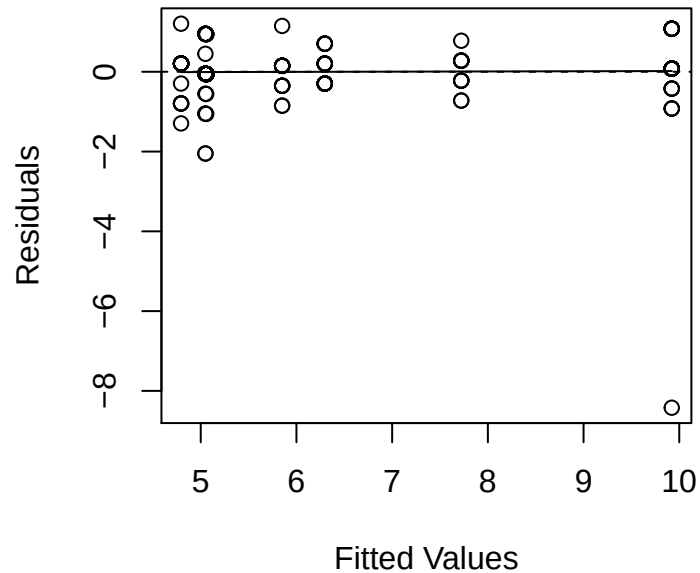


```
## 625 573
## 120 80
```


Check model fit

```
plot(fitted(lmALT), residuals(lmALT), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
lines(smooth.spline(fitted(lmALT), residuals(lmALT)))
```

Linear mixed model using maximum likelih



3.5.3 Statistical tests - Anther width

Embelia effusa

Number of observations

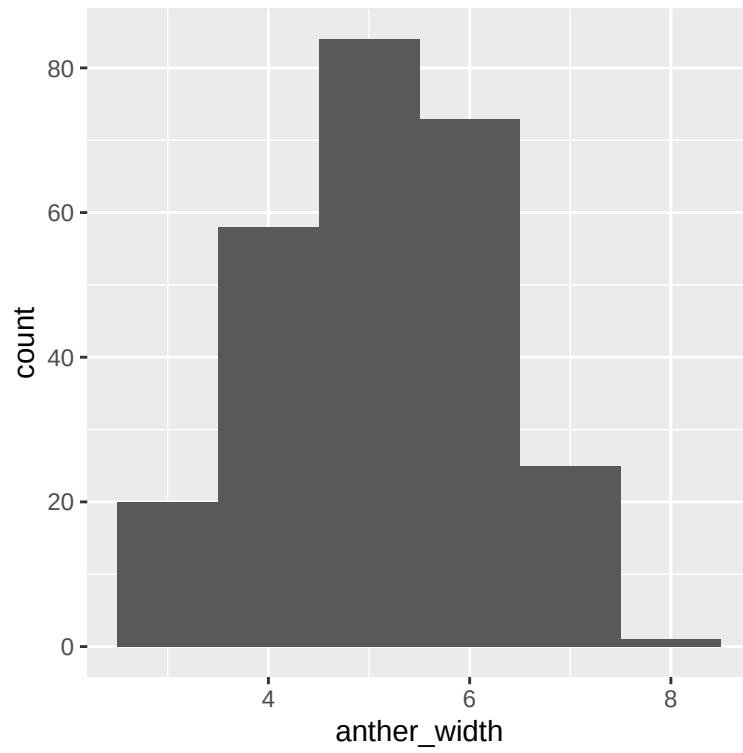
```
aggregate(anther_width ~ sex + species, data = effusa, function(x) length(x))
```

```
##      sex species anther_width
## 1 female  effusa           137
## 2  male   effusa           124
```

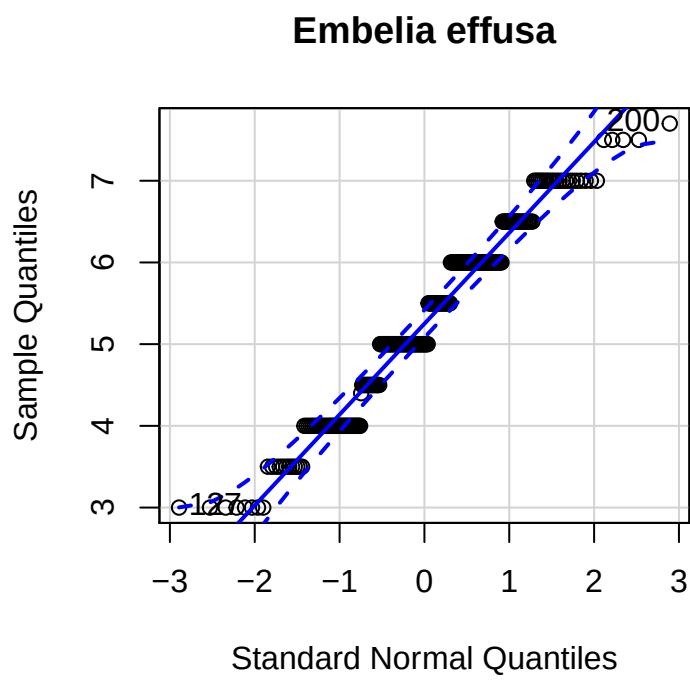
Distribution

```
histnormAwE <- ggplot(effusa, aes(anther_width))
histnormAwE + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 31 rows containing non-finite values (stat_bin).
```



```
qqp(effusa$anther_width, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia effusa")
```



```
## [1] 200 127
```

Build model

```
lmAwE <- lmer(anther_width ~ sex + (1 | spec_ID), effusa, REML = FALSE)
```

Display results

```
summary(lmAwE)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: anther_width ~ sex + (1 | spec_ID)
## Data: effusa
##
##      AIC      BIC    logLik deviance df.resid
##    473.2    487.5   -232.6    465.2     257
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.06405 -0.49867 -0.07874  0.68386  3.09905
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 0.4709  0.6862
## Residual              0.3090  0.5559
## Number of obs: 261, groups: spec_ID, 8
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  4.5594     0.3467  13.149
## sexmale      1.2228     0.4906   2.492
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.707
```

```
confint(lmAwE)
```

```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01      0.4433669 1.2413020
## .sigma      0.5107748 0.6081013
## (Intercept) 3.7883213 5.3287331
## sexmale     0.1330215 2.3121441
```

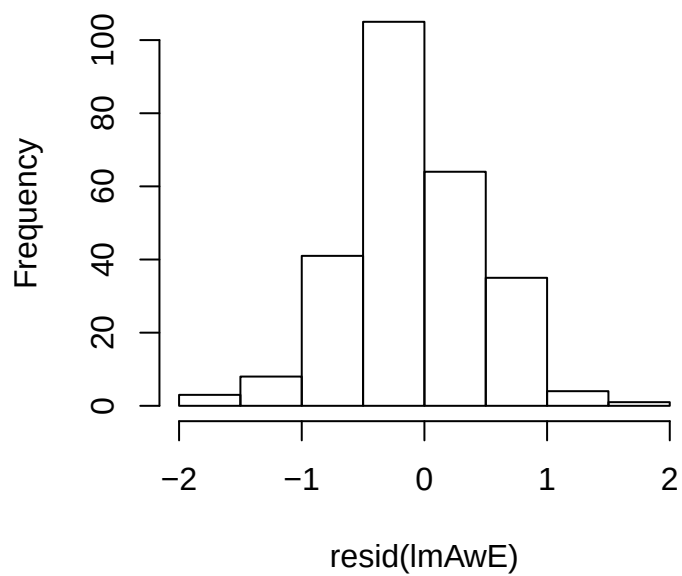
```
Anova(lmAwE)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: anther_width
##      Chisq Df Pr(>Chisq)
## sex  6.212  1  0.01269 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

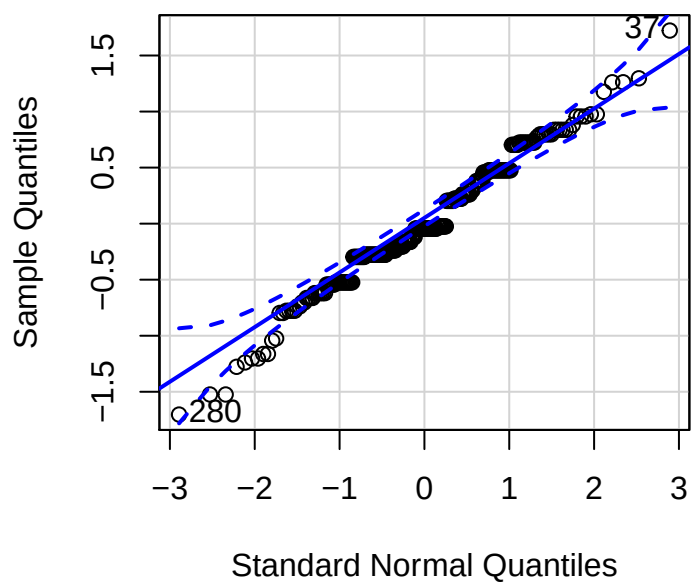
Check normality of residuals

```
hist(resid(lmAwE))
```

Histogram of resid(lmAwE)



```
qqp(resid(lmAwE), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

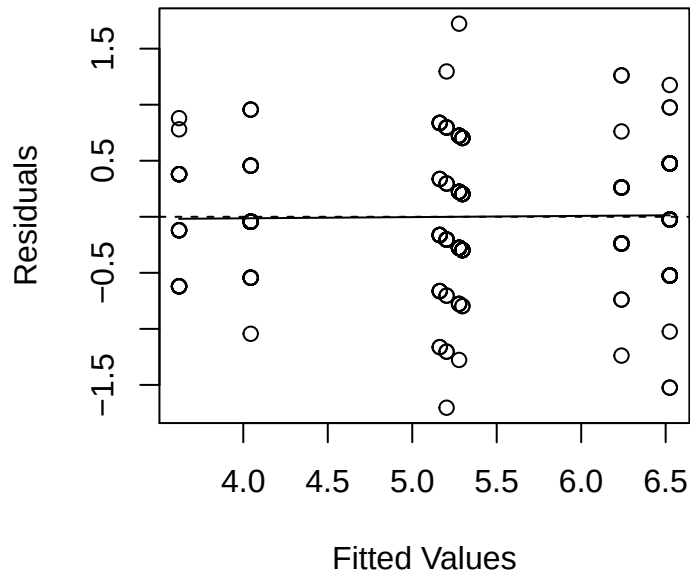


```
## 37 280
## 35 250
```

Check model fit

```
plot(fitted(lmAwE), residuals(lmAwE), xlab = "Fitted Values",  
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")  
abline(h = 0, lty = 2)  
lines(smooth.spline(fitted(lmAwE), residuals(lmAwE)))
```

Linear mixed model using maximum likelih



Embelia schimperi

Number of observations

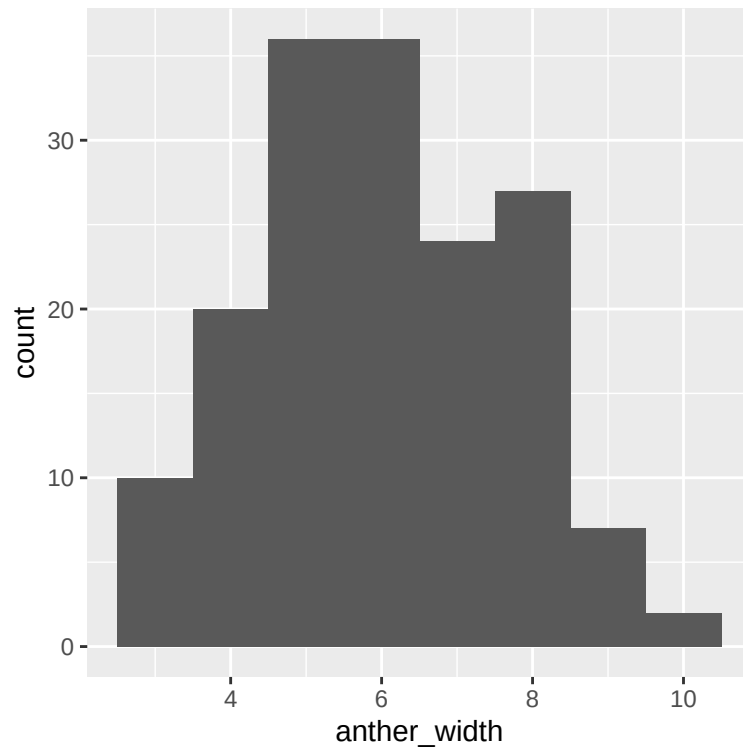
```
aggregate(anther_width ~ sex + species, data = schimp, function(x) length(x))
```

```
##      sex  species anther_width  
## 1 female schimperi           81  
## 2  male schimperi           81
```

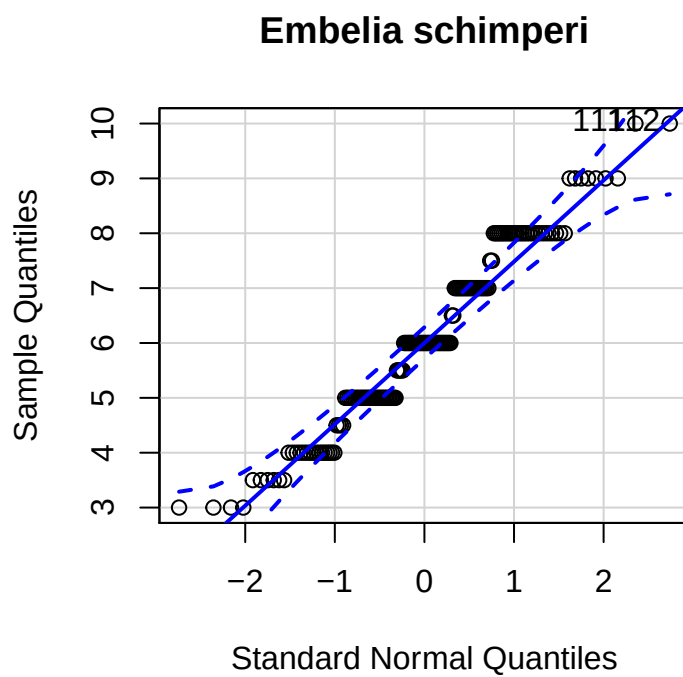
Distribution

```
histnormAwS <- ggplot(schimp, aes(anther_width))  
histnormAwS + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",  
  "lightsalmon"))
```

```
## Warning: Removed 32 rows containing non-finite values (stat_bin).
```



```
qqp(schimp$anther_width, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia schimperi")
```



```
## [1] 111 112
```

Build model

```
lmAwS <- lmer(anther_width ~ sex + (1 | spec_ID), schimp, REML = FALSE)
```

Display results

```
summary(lmAwS)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: anther_width ~ sex + (1 | spec_ID)
## Data: schimp
##
##      AIC      BIC    logLik deviance df.resid
##    415.9    428.2   -203.9    407.9      158
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.31792 -0.64803 -0.05115  0.56476  2.65215
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 0.5616  0.7494
## Residual            0.6477  0.8048
## Number of obs: 162, groups: spec_ID, 6
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  5.0203    0.4459   11.260
## sexmale      2.0823    0.6284    3.314
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.710
```

```
confint(lmAwS)
```

```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01      0.4400187 1.5404547
## .sigma      0.7231132 0.9031558
## (Intercept) 3.9946764 6.0662856
## sexmale     0.6072294 3.5315083
```

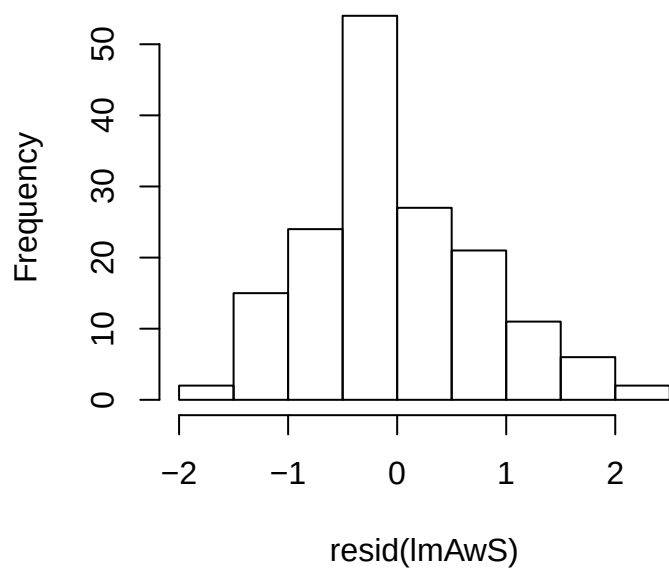
```
Anova(lmAwS)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: anther_width
##      Chisq Df Pr(>Chisq)
## sex 10.98  1 0.0009211 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

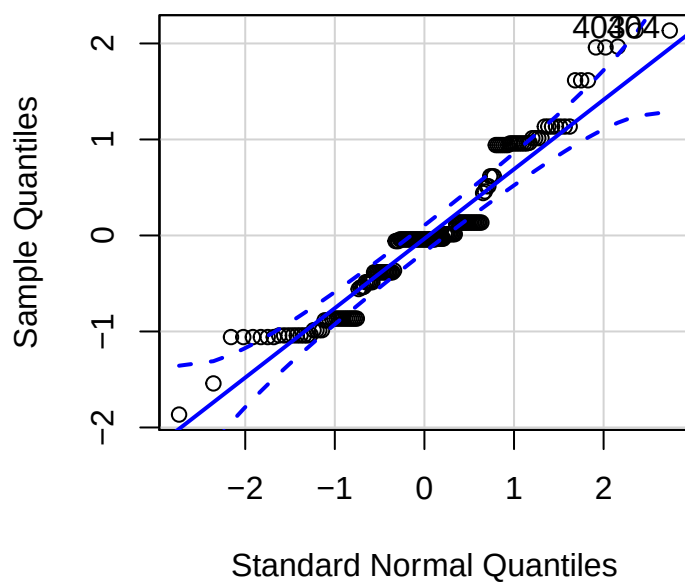
Check normality of residuals

```
hist(resid(lmAwS))
```

Histogram of resid(lmAwS)



```
qqp(resid(lmAwS), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

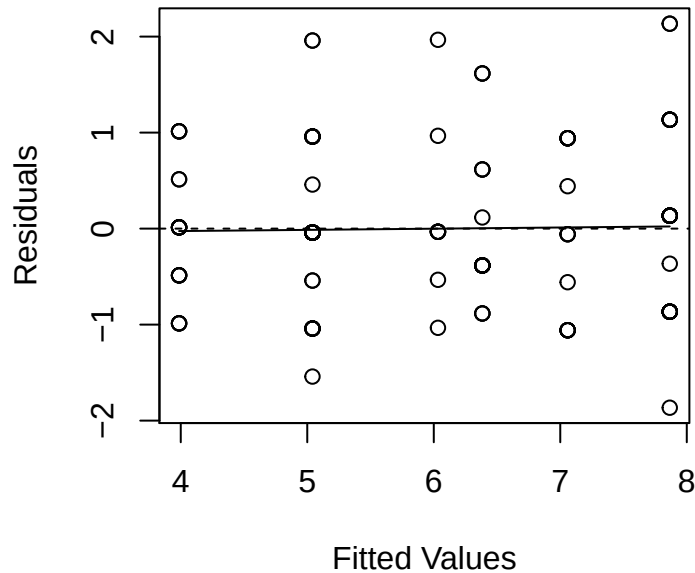


```
## 403 404
## 95 96
```


Check model fit

```
plot(fitted(lmAwS), residuals(lmAwS), xlab = "Fitted Values",  
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")  
abline(h = 0, lty = 2)  
lines(smooth.spline(fitted(lmAwS), residuals(lmAwS)))
```

Linear mixed model using maximum likelih



Embelia tsjeriamcottam

Number of observations

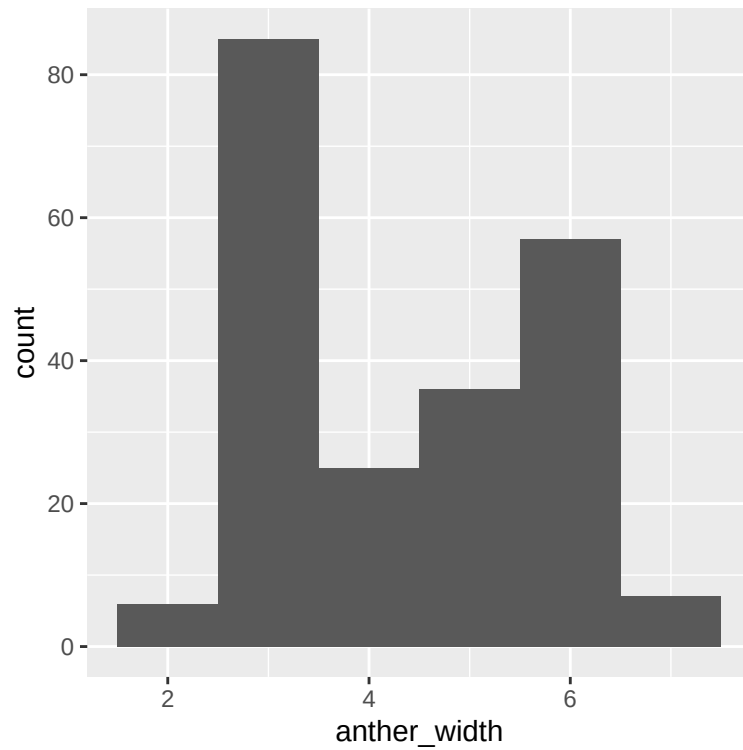
```
aggregate(anther_width ~ sex + species, data = tsjer, function(x) length(x))
```

```
##      sex      species anther_width  
## 1 female tsjeriamcottam         107  
## 2  male tsjeriamcottam         109
```

Distribution

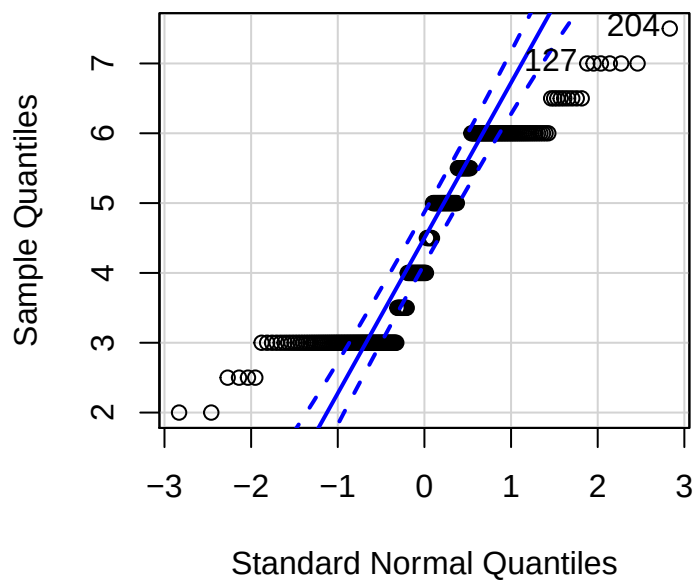
```
histnormAwT <- ggplot(tsjer, aes(anther_width))  
histnormAwT + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",  
  "lightsalmon"))
```

```
## Warning: Removed 39 rows containing non-finite values (stat_bin).
```



```
qqp(tsjer$anther_width, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia tsjeriamcottam")
```

Embelia tsjeriamcottam



```
## [1] 204 127
```

Build model

```
lmAwT <- lmer(anther_width ~ sex + (1 | spec_ID), tsjer, REML = FALSE)
```

Display results

```
summary(lmAwT)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: anther_width ~ sex + (1 | spec_ID)
## Data: tsjer
##
##      AIC      BIC    logLik deviance df.resid
##    296.5    310.0   -144.2    288.5      212
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.5562 -0.3217 -0.1379  0.1871  2.4215
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 0.1768  0.4204
## Residual            0.2003  0.4475
## Number of obs: 216, groups: spec_ID, 7
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   3.1970     0.2468  12.954
## sexmale       2.4832     0.3277   7.578
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.753
```

```
confint(lmAwT)
```

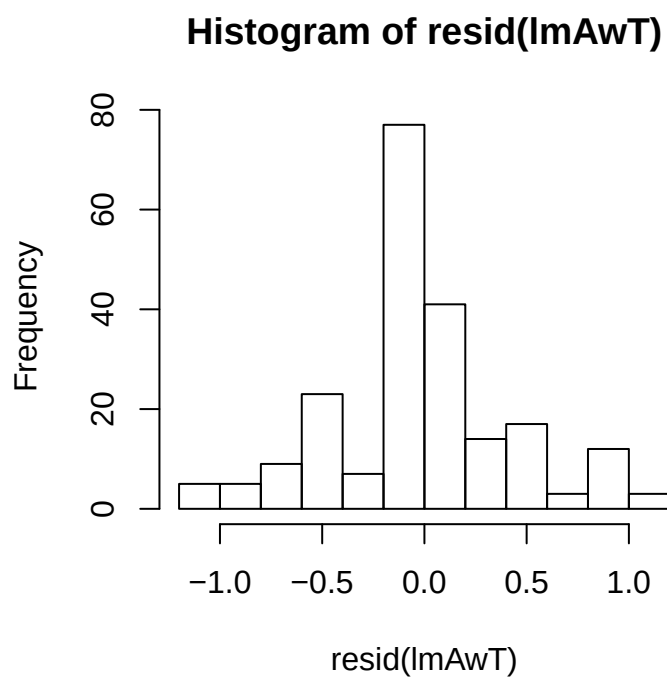
```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01      0.2581059 0.8078894
## .sigma      0.4078219 0.4941455
## (Intercept) 2.6368477 3.7584926
## sexmale     1.7382977 3.2251828
```

```
Anova(lmAwT)
```

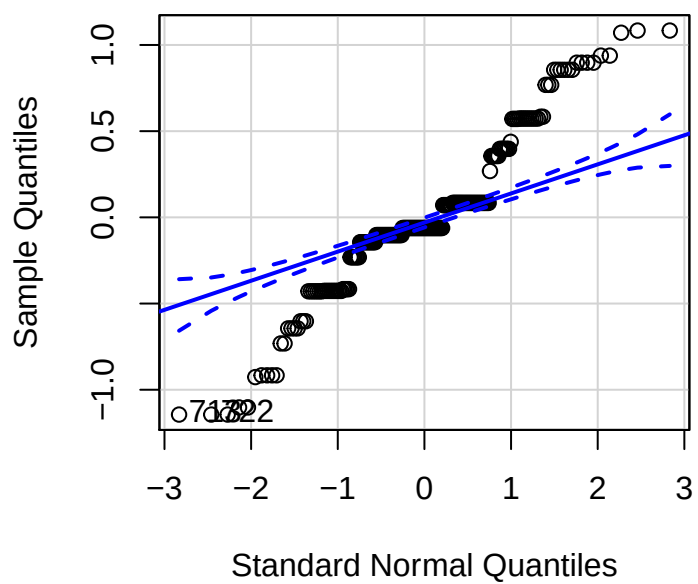
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: anther_width
##      Chisq Df Pr(>Chisq)
## sex  57.429  1 3.503e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Check normality of residuals

```
hist(resid(lmAwT))
```



```
qqp(resid(lmAwT), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

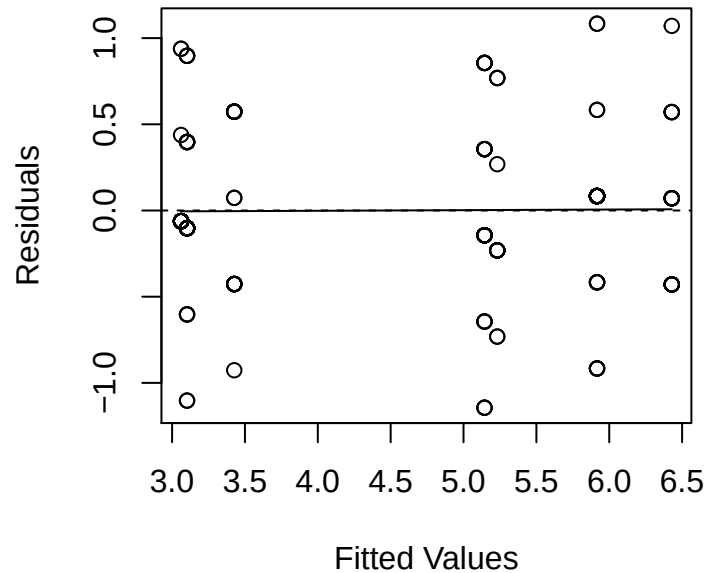


```
## 713 722
## 191 199
```

Check model fit

```
plot(fitted(lmAwT), residuals(lmAwT), xlab = "Fitted Values",  
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")  
abline(h = 0, lty = 2)  
lines(smooth.spline(fitted(lmAwT), residuals(lmAwT)))
```

Linear mixed model using maximum likelih



3.6 Ovary diameter

3.6.1 Descriptive statistics

Mean

```
aggregate(ovary_diameter ~ sex + species, data = flwr, mean)
```

##	sex	species	ovary_diameter
## 1	female	effusa	9.953125
## 2	male	effusa	3.596154
## 3	female	schimperi	11.875000
## 4	male	schimperi	4.857143
## 5	female	tsjeriamcottam	8.100000
## 6	male	tsjeriamcottam	3.250000

Variance

```
aggregate(ovary_diameter ~ sex + species, data = flwr, var)
```

##	sex	species	ovary_diameter
## 1	female	effusa	4.5219254
## 2	male	effusa	0.8203846
## 3	female	schimperi	1.7861842
## 4	male	schimperi	3.5035714

```
## 5 female tsjeriamcottam      1.1041667
## 6  male tsjeriamcottam      0.3913043
```

Standard deviation

```
aggregate(ovary_diameter ~ sex + species, data = flwr, sd)
```

```
##      sex      species ovary_diameter
## 1 female      effusa      2.1264819
## 2  male      effusa      0.9057509
## 3 female  schimperi      1.3364820
## 4  male  schimperi      1.8717830
## 5 female tsjeriamcottam      1.0507934
## 6  male tsjeriamcottam      0.6255432
```

3.6.2 Statistical tests

Embelia effusa

Number of observations

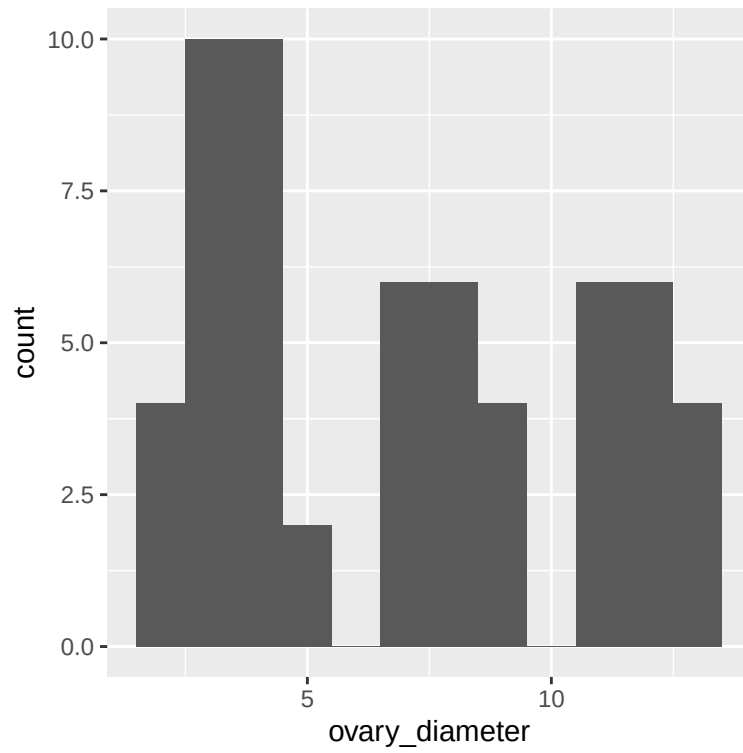
```
aggregate(ovary_diameter ~ sex + species, data = effusa, function(x) length(x))
```

```
##      sex species ovary_diameter
## 1 female  effusa             32
## 2  male  effusa             26
```

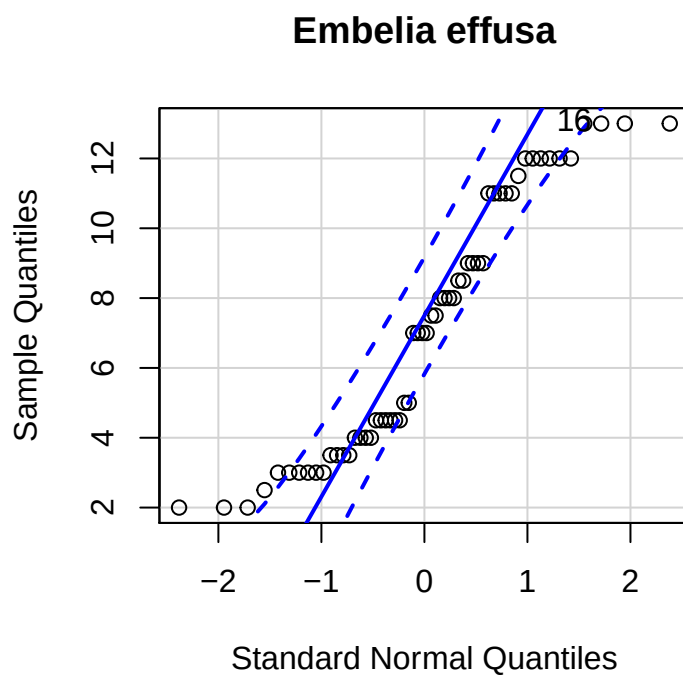
Distribution

```
histnormOE <- ggplot(effusa, aes(ovary_diameter))
histnormOE + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 234 rows containing non-finite values (stat_bin).
```



```
qqp(effusa$ovary_diameter, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia effusa")
```



```
## [1] 1 6
```

Build model

```
lmOE <- lmer(ovary_diameter ~ sex + (1 | spec_ID), effusa, REML = FALSE)
```

Display results

```
summary(lmOE)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: ovary_diameter ~ sex + (1 | spec_ID)
## Data: effusa
##
##      AIC      BIC    logLik deviance df.resid
##    151.3    159.6     -71.7    143.3      54
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.2071 -0.6596  0.0864  0.6371  2.0196
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 2.3022  1.5173
## Residual            0.4176  0.6462
## Number of obs: 58, groups: spec_ID, 8
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   9.8728    0.7678  12.859
## sexmale      -6.4312    1.0874  -5.914
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.706
```

```
confint(lmOE)
```

```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01      0.9780864  2.7474384
## .sigma      0.5376290  0.7969236
## (Intercept) 8.1666053 11.5774634
## sexmale     -8.8460209 -4.0179481
```

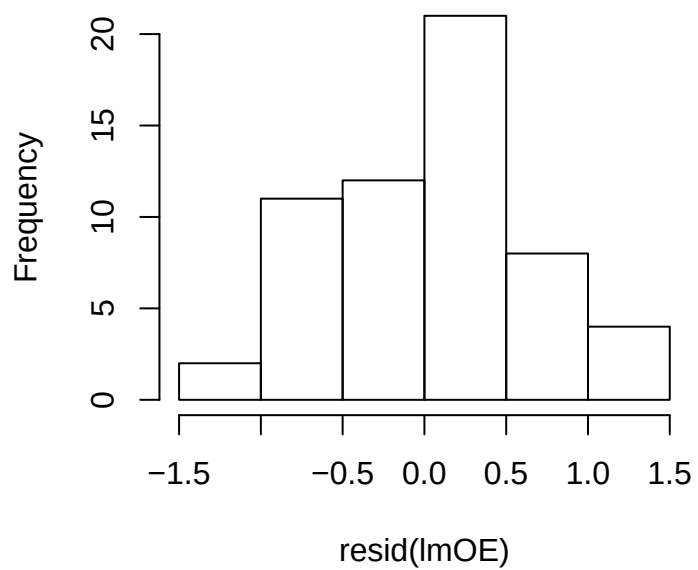
```
Anova(lmOE)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: ovary_diameter
##      Chisq Df Pr(>Chisq)
## sex 34.981  1  3.33e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

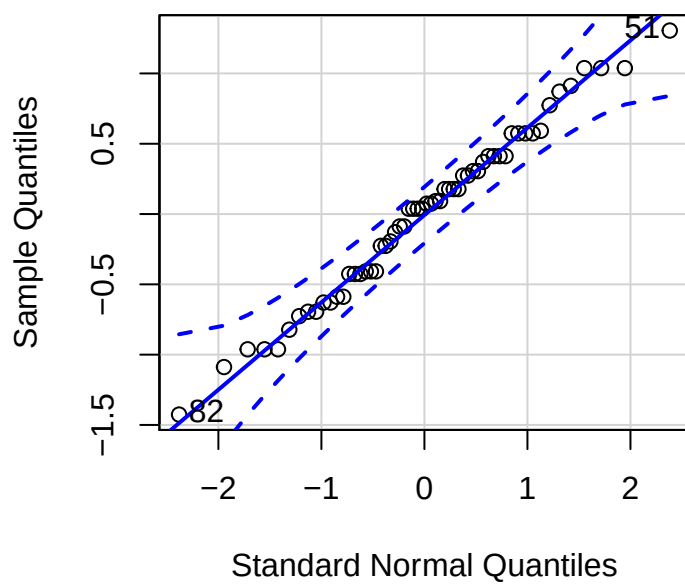
Check normality of residuals

```
hist(resid(lmOE))
```


Histogram of resid(lmOE)



```
qqp(resid(lmOE), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

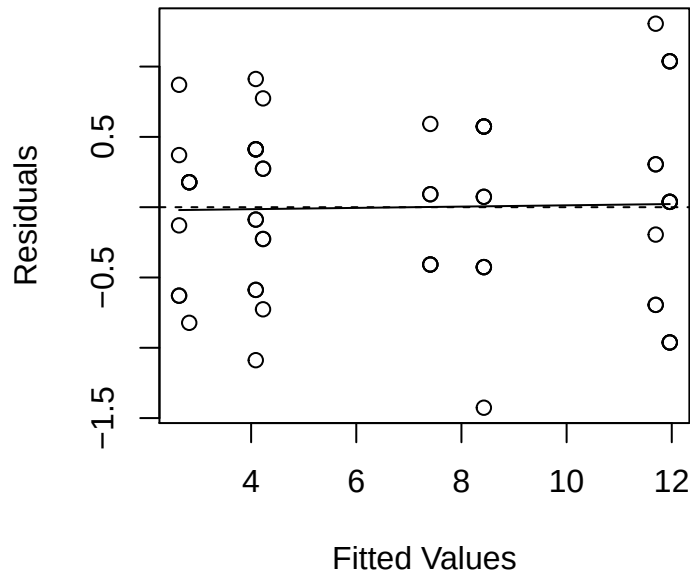


```
## 82 51
## 17 11
```

Check model fit

```
plot(fitted(lmOE), residuals(lmOE), xlab = "Fitted Values", ylab = "Residuals",  
     main = "Linear mixed model using maximum likelihood")  
abline(h = 0, lty = 2)  
lines(smooth.spline(fitted(lmOE), residuals(lmOE)))
```

Linear mixed model using maximum likelih



Embelia schimperi

Number of observations

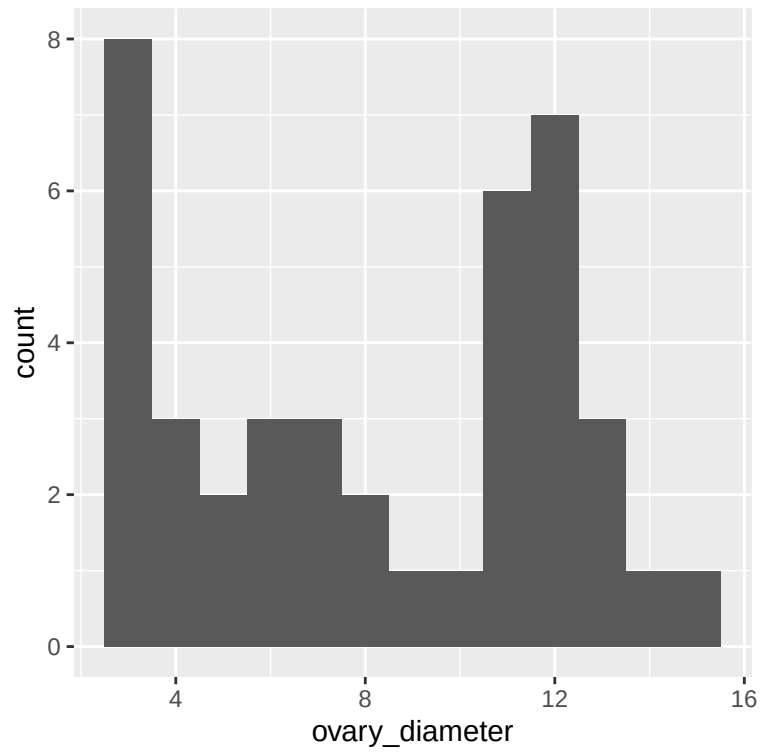
```
aggregate(ovary_diameter ~ sex + species, data = schimp, function(x) length(x))
```

```
##      sex  species ovary_diameter  
## 1 female schimperi             20  
## 2  male schimperi             21
```

Distribution

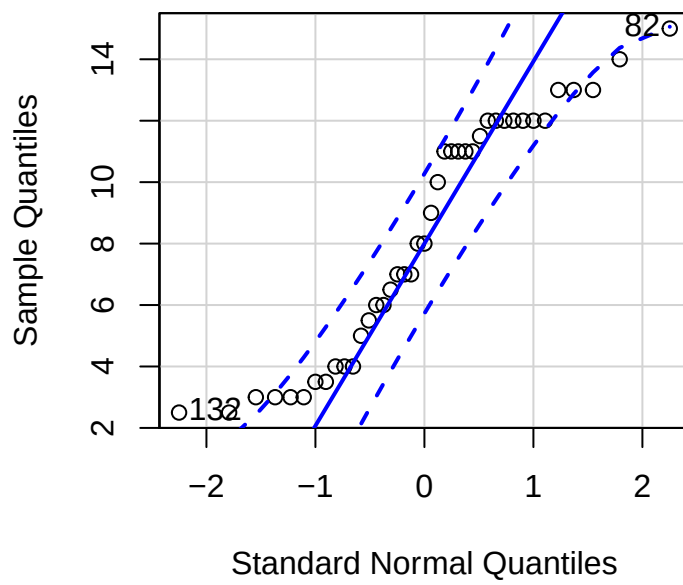
```
histnormOS <- ggplot(schimp, aes(ovary_diameter))  
histnormOS + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",  
  "lightsalmon"))
```

```
## Warning: Removed 153 rows containing non-finite values (stat_bin).
```



```
qqp(schimp$ovary_diameter, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia schimperi")
```

Embelia schimperi



```
## [1] 82 132
```

Build model

```
lmOS <- lmer(ovary_diameter ~ sex + (1 | spec_ID), schimp, REML = FALSE)
```

Display results

```
summary(lmOS)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: ovary_diameter ~ sex + (1 | spec_ID)
## Data: schimp
##
##      AIC      BIC    logLik deviance df.resid
##    132.6    139.5     -62.3    124.6      37
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.58176 -0.49446  0.01249  0.72670  1.67226
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 1.8359  1.3550
## Residual          0.8222  0.9068
## Number of obs: 41, groups: spec_ID, 6
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  12.2577    0.8145  15.048
## sexmale      -6.9208    1.1480  -6.029
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.710
```

```
confint(lmOS)
```

```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01      0.7871101  2.794015
## .sigma      0.7296729  1.169031
## (Intercept) 10.3896924 14.163440
## sexmale     -9.5887517 -4.262362
```

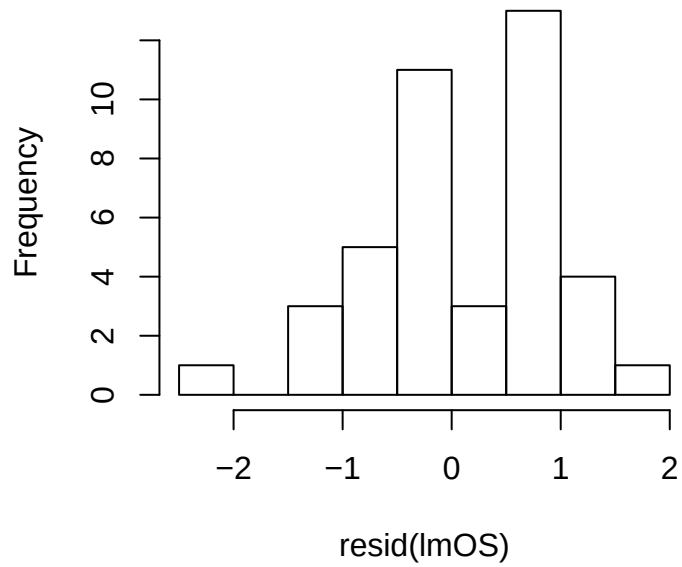
```
Anova(lmOS)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: ovary_diameter
##      Chisq Df Pr(>Chisq)
## sex 36.344  1 1.654e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

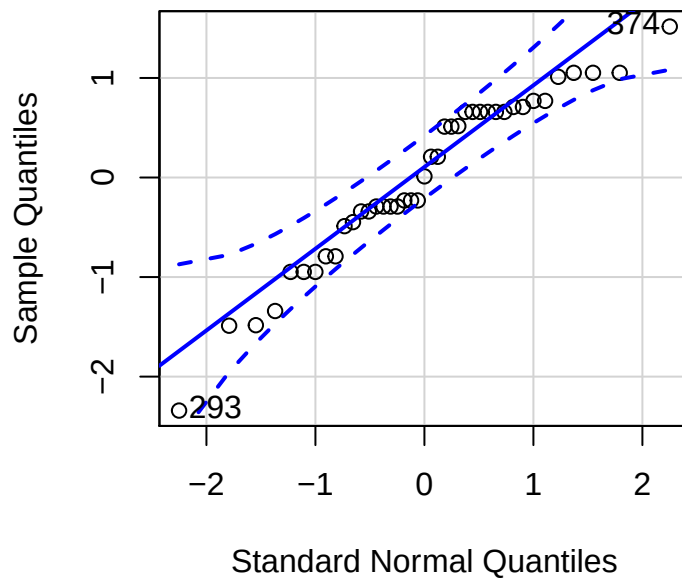
Check normality of residuals

```
hist(resid(lmOS))
```

Histogram of resid(lmOS)



```
qqp(resid(lmOS), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

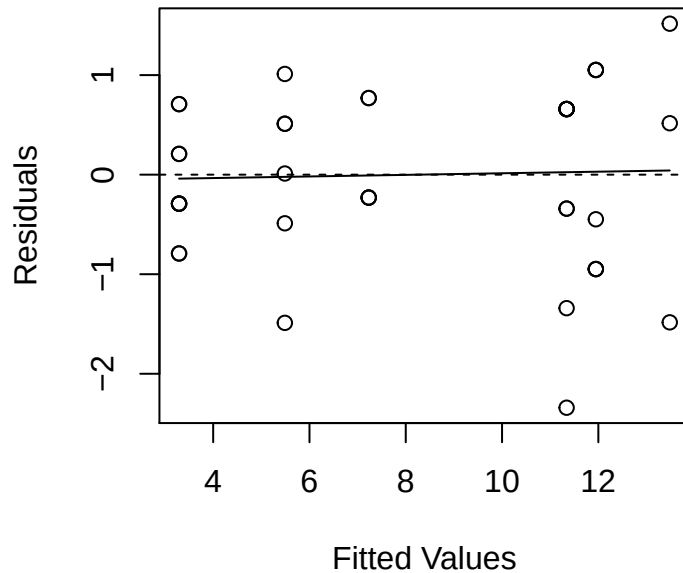


```
## 293 374
##    1  18
```

Check model fit

```
plot(fitted(lmOS), residuals(lmOS), xlab = "Fitted Values", ylab = "Residuals",  
     main = "Linear mixed model using maximum likelihood")  
abline(h = 0, lty = 2)  
lines(smooth.spline(fitted(lmOS), residuals(lmOS)))
```

Linear mixed model using maximum likelih



Embelia tsjeriamcottam

Number of observations

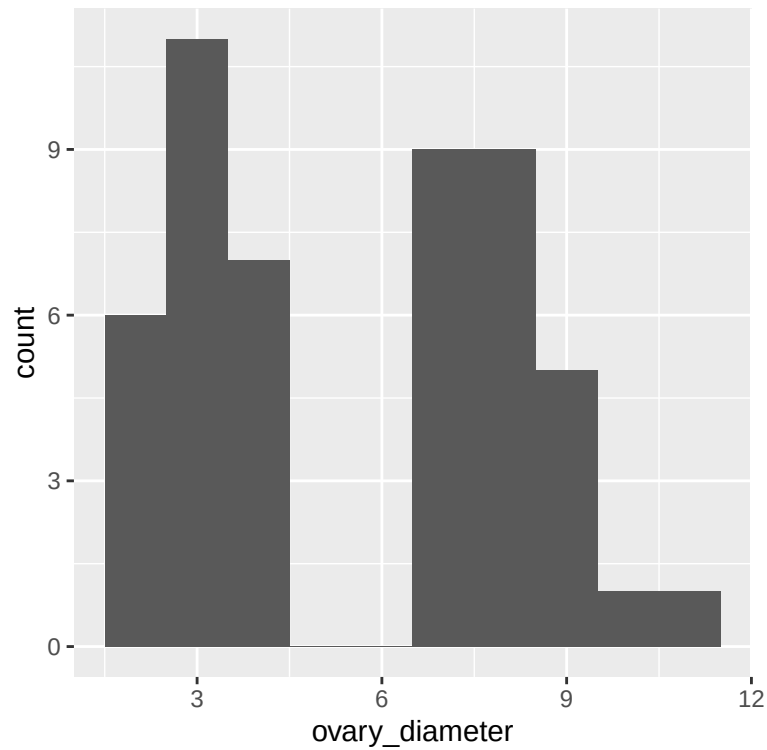
```
aggregate(ovary_diameter ~ sex + species, data = tsjer, function(x) length(x))
```

```
##      sex      species ovary_diameter  
## 1 female tsjeriamcottam           25  
## 2  male tsjeriamcottam           24
```

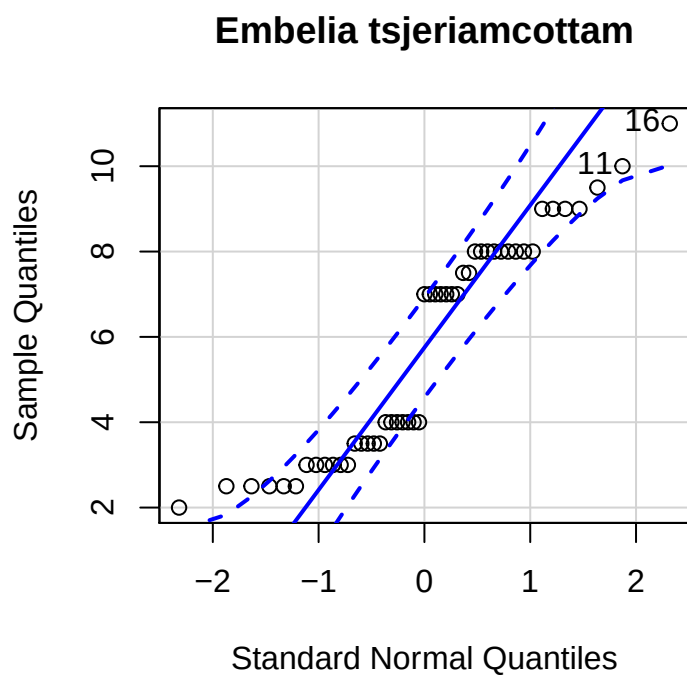
Distribution

```
histnormOT <- ggplot(tsjer, aes(ovary_diameter))  
histnormOT + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",  
  "lightsalmon"))
```

```
## Warning: Removed 206 rows containing non-finite values (stat_bin).
```



```
qqp(tsjer$ovary_diameter, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia tsjeriamcottam")
```



```
## [1] 16 11
```

Build model

```
lmOT <- lmer(ovary_diameter ~ sex + (1 | spec_ID), tsjer, REML = FALSE)
```

Display results

```
summary(lmOT)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: ovary_diameter ~ sex + (1 | spec_ID)
## Data: tsjer
##
##      AIC      BIC    logLik deviance df.resid
##    108.9    116.5    -50.5    100.9      45
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.6143 -0.7087  0.0839  0.5216  3.4804
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 0.3364  0.5800
## Residual          0.3467  0.5888
## Number of obs: 49, groups: spec_ID, 7
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   7.9862    0.3568   22.38
## sexmale      -4.8478    0.4799  -10.10
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.744
```

```
confint(lmOT)
```

```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01      0.3305177  1.1480372
## .sigma      0.4827636  0.7400706
## (Intercept) 7.1695157  8.7866479
## sexmale     -5.9308073 -3.7696550
```

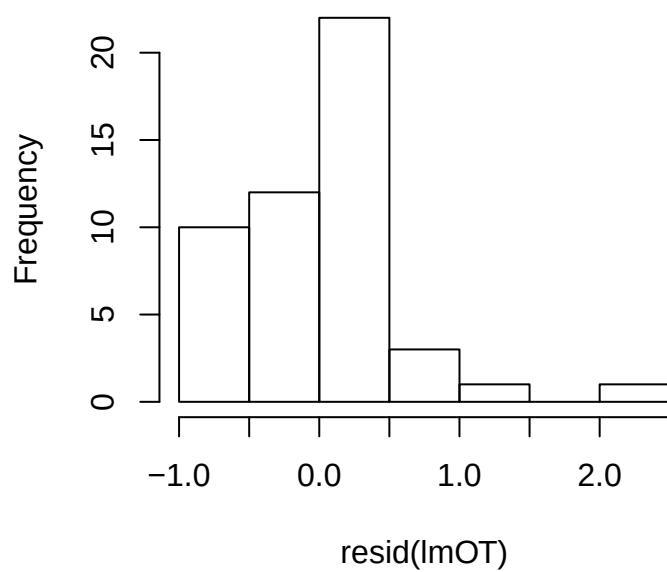
```
Anova(lmOT)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: ovary_diameter
##      Chisq Df Pr(>Chisq)
## sex 102.06  1 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

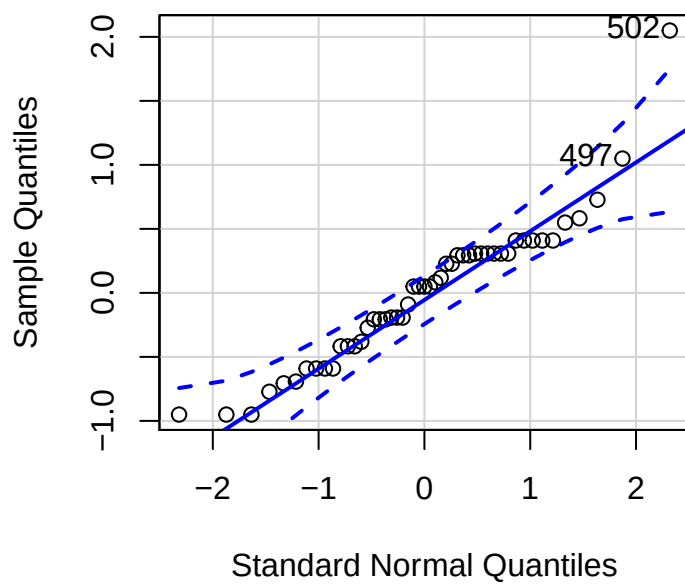
Check normality of residuals

```
hist(resid(lmOT))
```


Histogram of resid(lmOT)



```
qqp(resid(lmOT), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

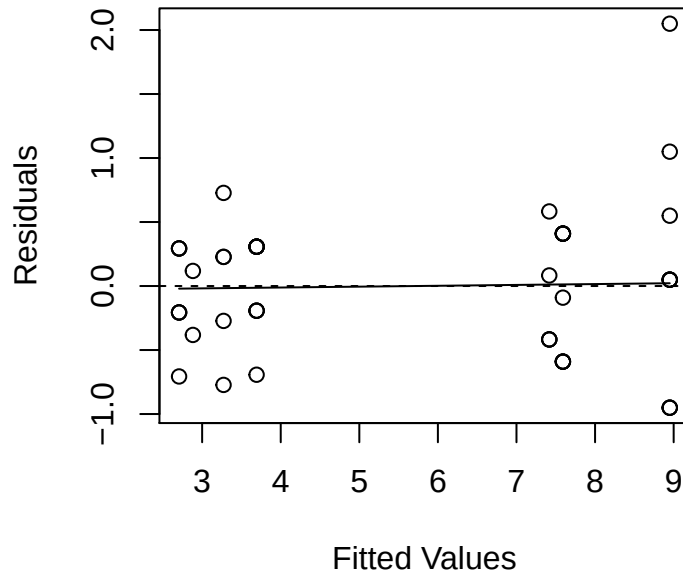


```
## 502 497
## 4 3
```

Check model fit

```
plot(fitted(lmOT), residuals(lmOT), xlab = "Fitted Values", ylab = "Residuals",  
     main = "Linear mixed model using maximum likelihood")  
abline(h = 0, lty = 2)  
lines(smooth.spline(fitted(lmOT), residuals(lmOT)))
```

Linear mixed model using maximum likelih



3.7 Style length

3.7.1 Descriptive statistics

Mean

```
aggregate(style_length ~ sex + species, data = flwr, mean)
```

##	sex	species	style_length
## 1	female	effusa	14.750000
## 2	male	effusa	1.346154
## 3	female	schimperi	18.473684
## 4	male	schimperi	1.547619
## 5	female	tsjeriamcottam	8.120000
## 6	male	tsjeriamcottam	1.687500

Variance

```
aggregate(style_length ~ sex + species, data = flwr, var)
```

##	sex	species	style_length
## 1	female	effusa	8.5322581
## 2	male	effusa	0.2353846
## 3	female	schimperi	12.1520468
## 4	male	schimperi	0.1476190

```
## 5 female tsjeriamcottam 1.0475000
## 6 male tsjeriamcottam 0.2350543
```

Standard deviation

```
aggregate(style_length ~ sex + species, data = flwr, sd)
```

```
##      sex      species style_length
## 1 female      effusa  2.9210029
## 2 male      effusa  0.4851645
## 3 female    schimperi  3.4859786
## 4 male      schimperi  0.3842122
## 5 female tsjeriamcottam  1.0234745
## 6 male tsjeriamcottam  0.4848240
```

3.7.2 Statistical tests - Style length

Embelia effusa

Number of observations

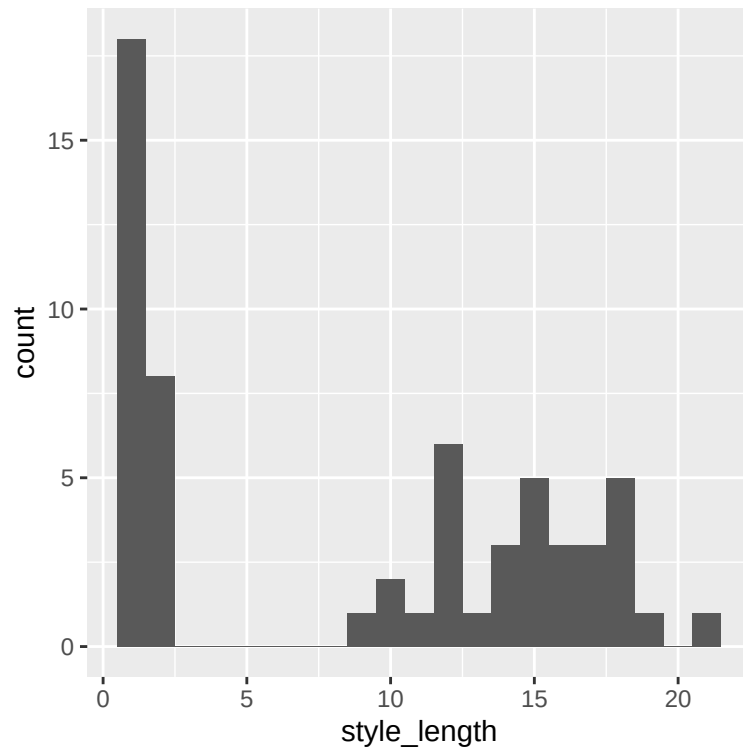
```
aggregate(style_length ~ sex + species, data = effusa, function(x) length(x))
```

```
##      sex species style_length
## 1 female  effusa          32
## 2 male   effusa          26
```

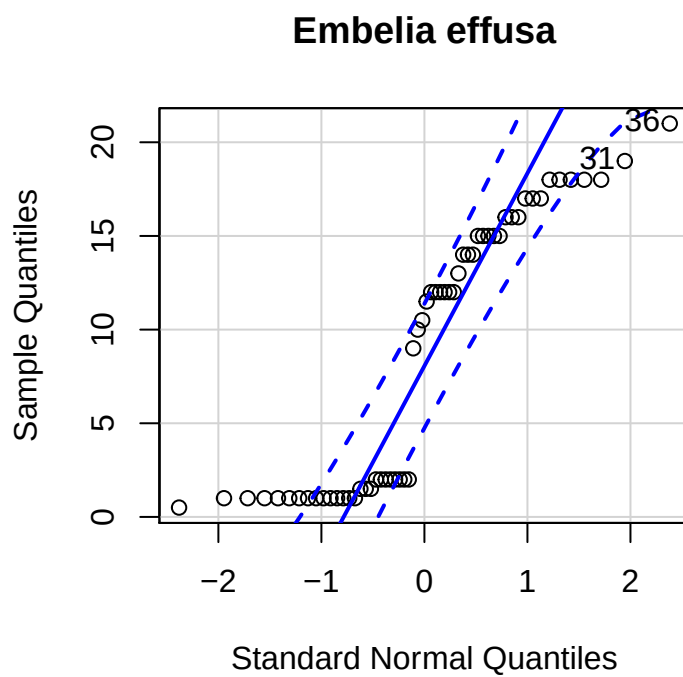
Distribution

```
histnormStyE <- ggplot(effusa, aes(style_length))
histnormStyE + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 234 rows containing non-finite values (stat_bin).
```



```
qqp(effusa$style_length, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia effusa")
```



```
## [1] 36 31
```

Build model

```
lmStyE <- lmer(style_length ~ sex + (1 | spec_ID), effusa, REML = FALSE)
```

Display results

```
summary(lmStyE)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: style_length ~ sex + (1 | spec_ID)
## Data: effusa
##
##      AIC      BIC    logLik deviance df.resid
##    260.8    269.1   -126.4    252.8      54
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.43979 -0.18985 -0.07873  0.26825  2.82739
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 0.4209  0.6488
## Residual          4.2528  2.0622
## Number of obs: 58, groups: spec_ID, 8
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  14.7429    0.4918   29.98
## sexmale     -13.4507    0.7188  -18.71
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.684
```

```
confint(lmStyE)
```

```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01         0.000000  1.667278
## .sigma         1.714913  2.545090
## (Intercept)  13.625198 15.852701
## sexmale     -15.081914 -11.867214
```

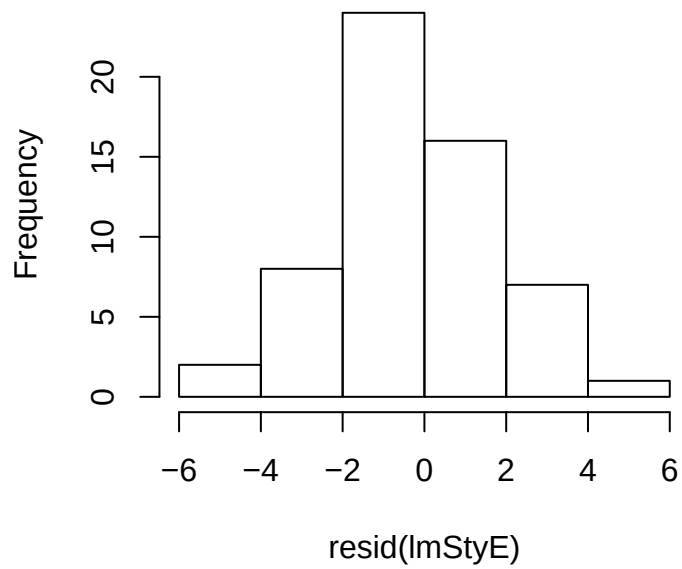
```
Anova(lmStyE)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: style_length
##      Chisq Df Pr(>Chisq)
## sex 350.19  1 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

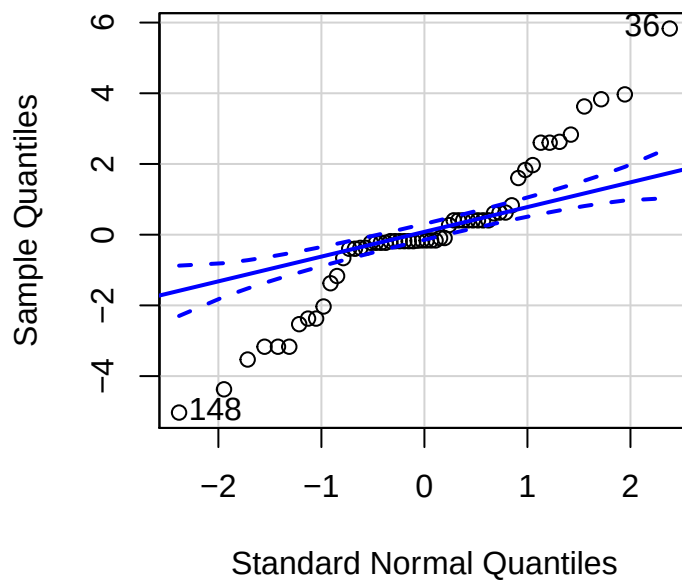
Check normality of residuals

```
hist(resid(lmStyE))
```

Histogram of resid(lmStyE)



```
qqp(resid(lmStyE), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```

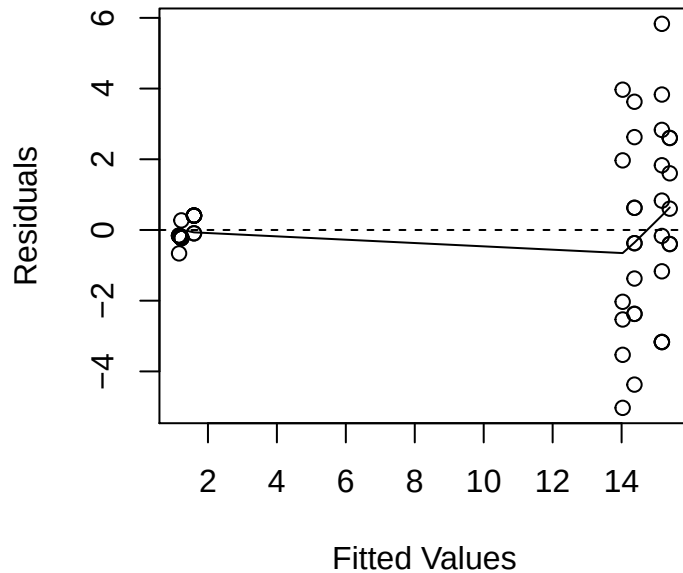


```
## 36 148
## 8 30
```

Check model fit

```
plot(fitted(lmStyE), residuals(lmStyE), xlab = "Fitted Values",  
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")  
abline(h = 0, lty = 2)  
lines(smooth.spline(fitted(lmStyE), residuals(lmStyE)))
```

Linear mixed model using maximum likelih



Embelia schimperi

Number of observations

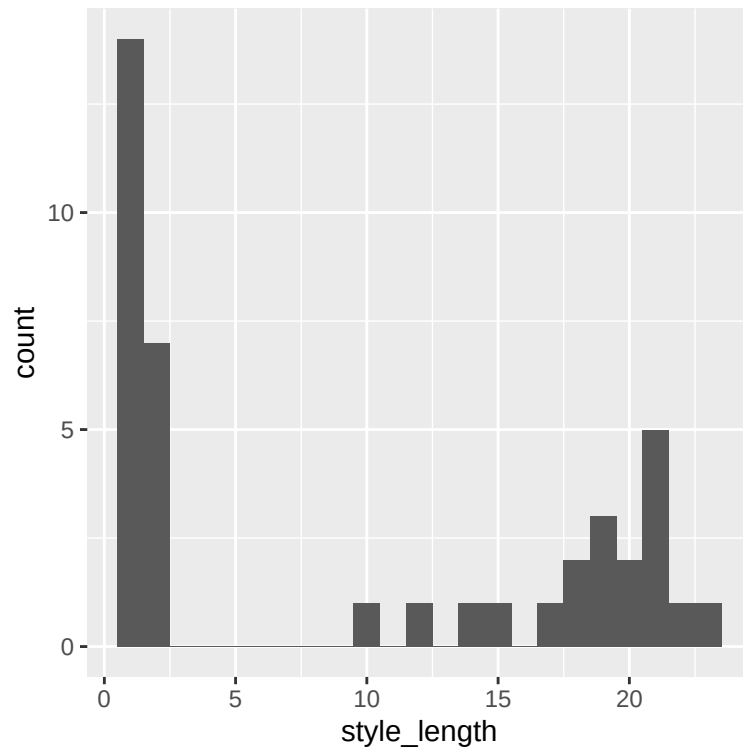
```
aggregate(style_length ~ sex + species, data = schimp, function(x) length(x))
```

```
##      sex  species style_length  
## 1 female schimperi          19  
## 2  male schimperi          21
```

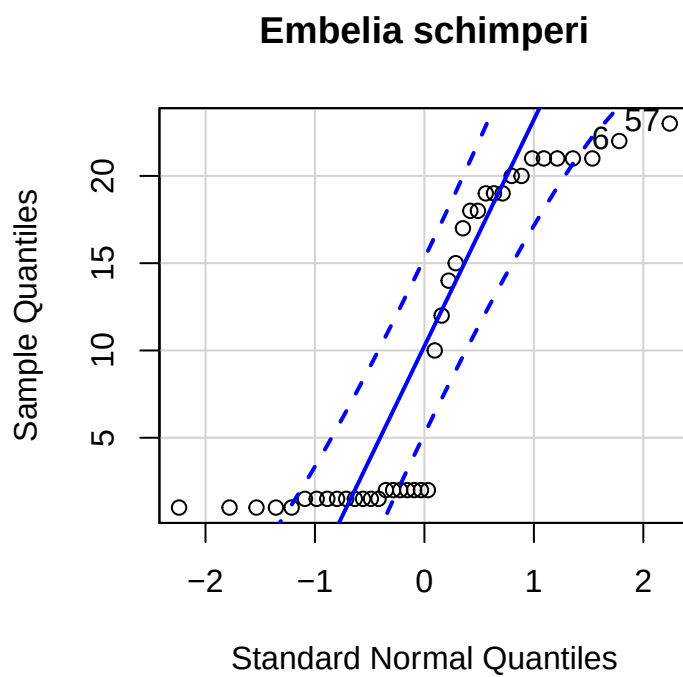
Distribution

```
histnormStyS <- ggplot(schimp, aes(style_length))  
histnormStyS + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",  
  "lightsalmon"))
```

```
## Warning: Removed 154 rows containing non-finite values (stat_bin).
```



```
qqp(schimp$style_length, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia schimperi")
```



```
## [1] 57 6
```


Build model

```
lmStyS <- lmer(style_length ~ sex + (1 | spec_ID), schimp, REML = FALSE)
```

```
## boundary (singular) fit: see ?isSingular
```

Display results

```
summary(lmStyS)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: style_length ~ sex + (1 | spec_ID)
## Data: schimp
##
##      AIC      BIC    logLik deviance df.resid
##    190.0    196.8    -91.0    182.0      36
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.5994 -0.2091 -0.0202  0.2236  1.9227
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 0.000 0.000
## Residual 5.542 2.354
## Number of obs: 40, groups: spec_ID, 6
##
## Fixed effects:
## Estimate Std. Error t value
## (Intercept) 18.4737 0.5401 34.20
## sexmale -16.9261 0.7454 -22.71
##
## Correlation of Fixed Effects:
## (Intr)
## sexmale -0.725
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```
confint(lmStyS)
```

```
## Computing profile confidence intervals ...
```

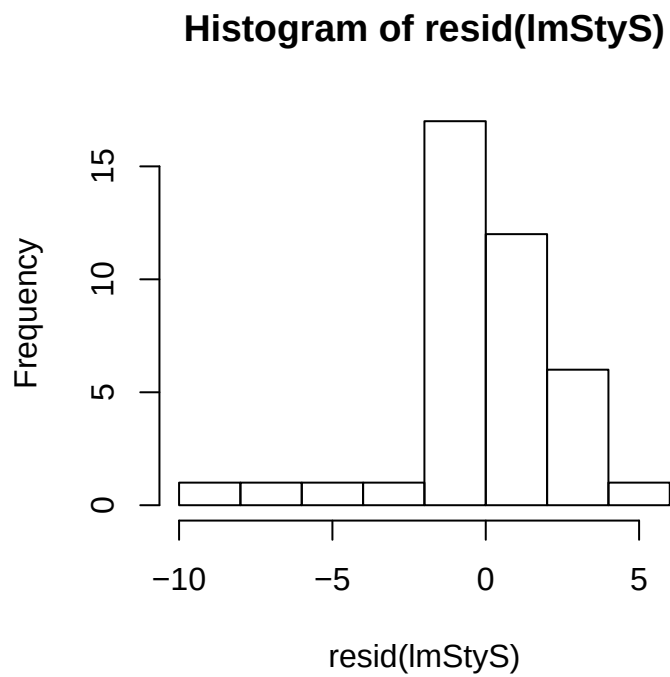
```
##           2.5 %    97.5 %
## .sig01      0.000000  1.311091
## .sigma      1.919322  2.981942
## (Intercept) 17.367100 19.616435
## sexmale    -18.472046 -15.364796
```

```
Anova(lmStyS)
```

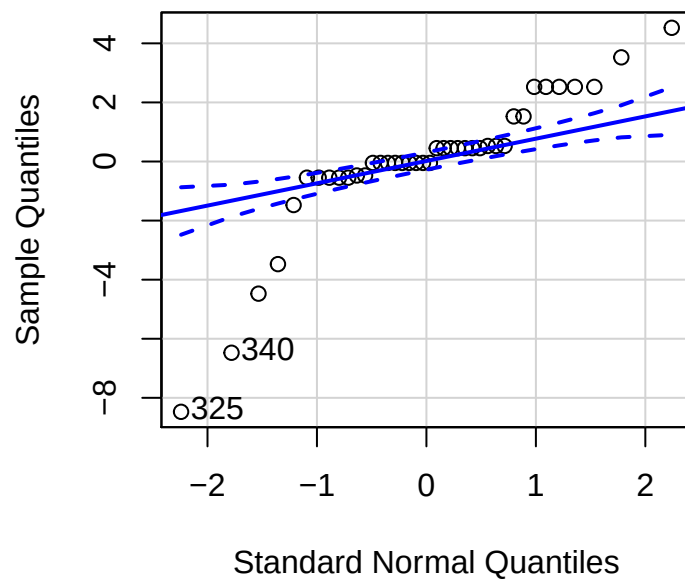
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: style_length
##      Chisq Df Pr(>Chisq)
## sex 515.63 1 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Check normality of residuals

```
hist(resid(lmStyS))
```



```
qqp(resid(lmStyS), "norm", xlab = "Standard Normal Quantiles",  
     ylab = "Sample Quantiles")
```

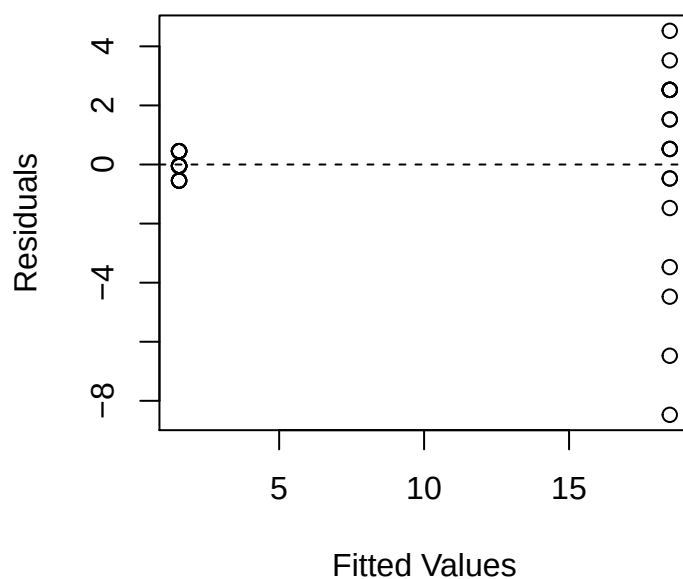


```
## 325 340
##    7 10
```

Check model fit

```
plot(fitted(lmStyS), residuals(lmStyS), xlab = "Fitted Values",
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")
abline(h = 0, lty = 2)
```

Linear mixed model using maximum likelih



```
# lines(smooth.spline(fitted(lmStyS), residuals(lmStyS)))
```

Embelia tsjeriamcottam

Number of observations

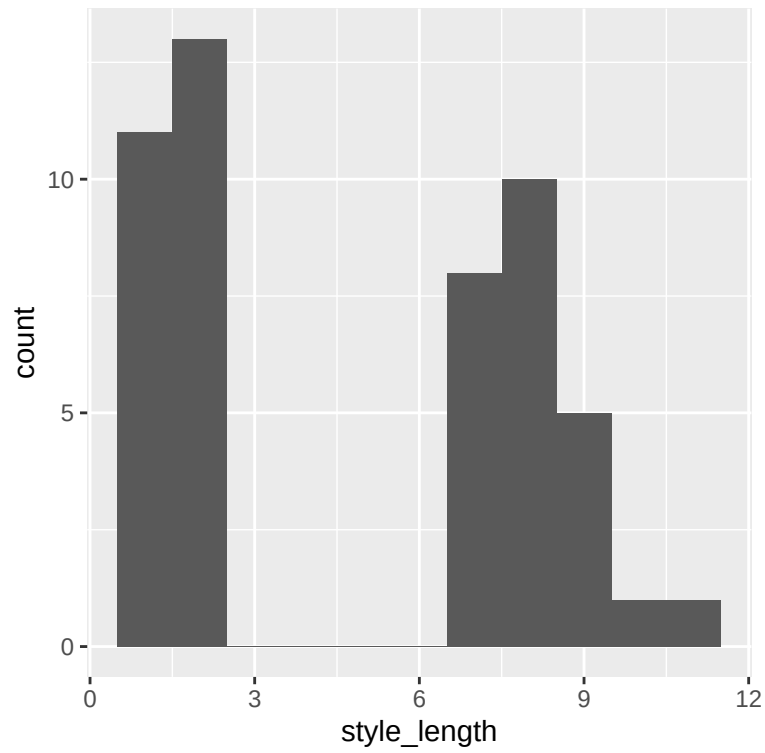
```
aggregate(style_length ~ sex + species, data = tsjer, function(x) length(x))
```

```
##      sex      species style_length
## 1 female tsjeriamcottam         25
## 2  male tsjeriamcottam         24
```

Distribution

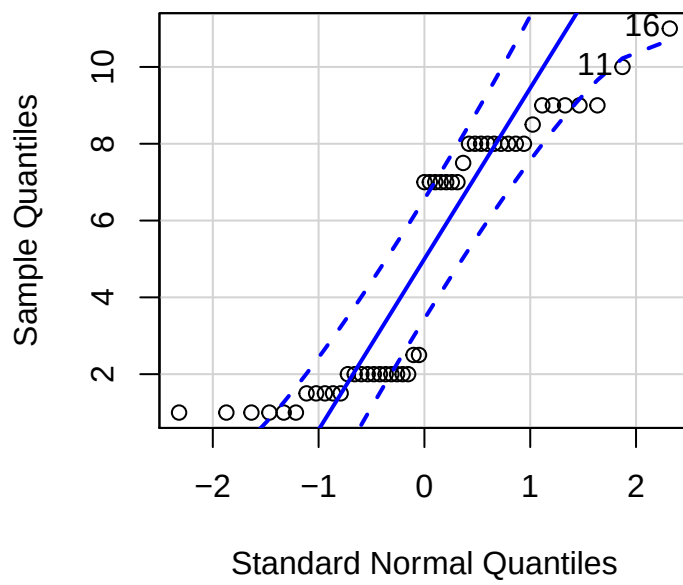
```
histnormStyT <- ggplot(tsjer, aes(style_length))
histnormStyT + geom_histogram(binwidth = 1) + scale_fill_manual(values = c("cornflowerblue",
  "lightsalmon"))
```

```
## Warning: Removed 206 rows containing non-finite values (stat_bin).
```



```
qqp(tsjer$style_length, "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles", main = "Embelia tsjeriamcottam")
```

Embelia tsjeriamcottam



```
## [1] 16 11
```

Build model

```
lmStyT <- lmer(style_length ~ sex + (1 | spec_ID), tsjer, REML = FALSE)
```

Display results

```
summary(lmStyT)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: style_length ~ sex + (1 | spec_ID)
## Data: tsjer
##
##      AIC      BIC    logLik deviance df.resid
##    103.5    111.1    -47.7    95.5      45
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.6251 -0.4763  0.0644  0.4115  3.7629
##
## Random effects:
## Groups Name Variance Std.Dev.
## spec_ID (Intercept) 0.303  0.5505
## Residual          0.310  0.5568
## Number of obs: 49, groups: spec_ID, 7
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   7.9748    0.3385   23.56
## sexmale      -6.3614    0.4552  -13.97
##
## Correlation of Fixed Effects:
##              (Intr)
## sexmale -0.744
```

```
confint(lmStyT)
```

```
## Computing profile confidence intervals ...
##
##              2.5 %    97.5 %
## .sig01      0.3095388 1.0941689
## .sigma      0.4563446 0.7001636
## (Intercept) 7.1952192 8.7334408
## sexmale     -7.3870599 -5.3318228
```

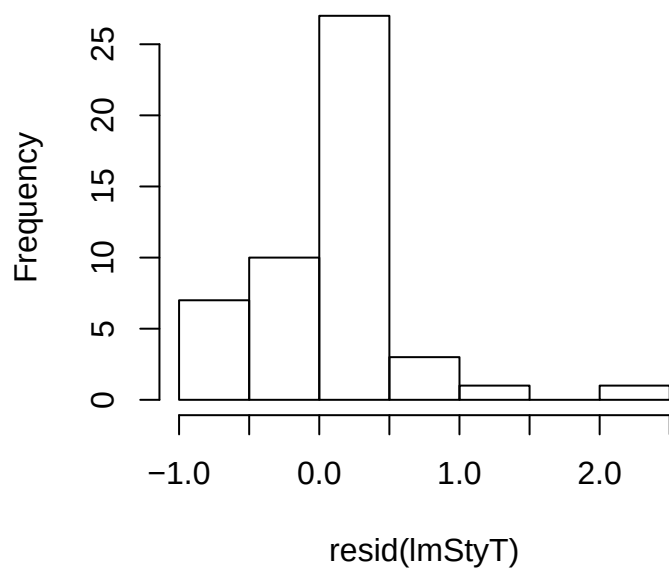
```
Anova(lmStyT)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: style_length
##      Chisq Df Pr(>Chisq)
## sex 195.29  1 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

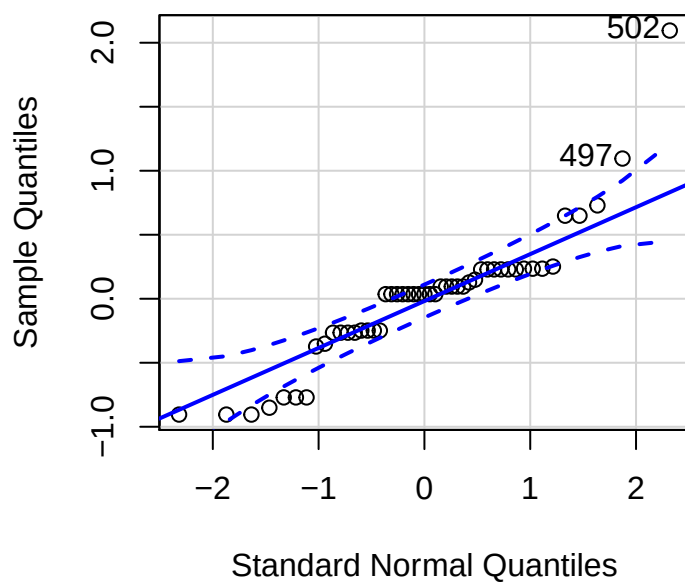
Check normality of residuals

```
hist(resid(lmStyT))
```

Histogram of resid(lmStyT)



```
qqp(resid(lmStyT), "norm", xlab = "Standard Normal Quantiles",
     ylab = "Sample Quantiles")
```



```
## 502 497
## 4 3
```

Check model fit

```
plot(fitted(lmStyT), residuals(lmStyT), xlab = "Fitted Values",  
     ylab = "Residuals", main = "Linear mixed model using maximum likelihood")  
abline(h = 0, lty = 2)  
lines(smooth.spline(fitted(lmStyT), residuals(lmStyT)))
```

Linear mixed model using maximum likelih

