

Centaurea Project

DG, IM, BS

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This is the Rmarkdown file for the Centaurea project containing the code required to replicate the analysis and the plots.

We begin by loading the required packages for the rest of the script.

```
library(ggeffects)
library(gridExtra)
library(cowplot)
library(lme4)
library(MuMIn)
library(sjPlot)
library(tidyverse)
```

Next, we load in our dataset.

```
data <- read_tsv("donnees_centauree.csv")

data <- data %>%
  mutate(light = PAR/reference) %>%
  rename("species" = "espece",
         "population" = "pop")

data$species <- factor(data$species, levels = c("mac", "cor"))

head(data)
```

```
## # A tibble: 6 x 14
##   Plante Date_de_germinat~ Cotyledons Taille_Dec_05 Taille_Fev_06 Taille_Mars_06
##   <dbl> <chr>                <dbl>         <dbl>         <dbl>         <dbl>
## 1     1 <NA>                    NA             0             0             0
## 2     2 <NA>                    NA             0             0             0
## 3     3 <NA>                    NA             0             0             0
## 4     4 05/04/2006          11.1           0             0             0
## 5     5 <NA>                    NA             0             0             0
## 6     6 17/10/2005          8.03           0             0             0
## # ... with 8 more variables: Taille_Juin_06 <dbl>, Taille_Sept_06 <dbl>,
## #   traitement <chr>, PAR <dbl>, reference <dbl>, species <fct>,
## #   population <chr>, light <dbl>
```

We will now split the dataset into two part. The first part will be used to model the probability of germination, and the second part will be used to model the rosette size growth.

```
didnotgerm <- data %>%
  filter(is.na(Date_de_germination)) %>%
  mutate(germination = 0)
```

```

didgerm <- data %>%
  filter(!is.na(Date_de_germination)) %>%
  mutate(germination = 1)

germ_data <- full_join(didnotgerm, didgerm) %>%
  select(-c(Date_de_germination:reference))

rm(didnotgerm, didgerm)

head(germ_data)

## # A tibble: 6 x 5
##   Plante species population light germination
##   <dbl> <fct>   <chr>      <dbl>      <dbl>
## 1     1 mac     rog        1.02        0
## 2     2 mac     rog        0.954       0
## 3     3 mac     rog        0.816       0
## 4     5 mac     rog        0.987       0
## 5     7 mac     rog        0.876       0
## 6     8 mac     rog        0.910       0

rosette_data <- data %>%
  rename("2005-12-01" = "Taille_Dec_05",
        "2006-02-01" = "Taille_Fev_06",
        "2006-03-01" = "Taille_Mars_06",
        "2006-06-01" = "Taille_Juin_06",
        "2006-09-01" = "Taille_Sept_06") %>%
  gather(key = "Date",
        value = "Rosette_size",
        "2005-12-01":"2006-09-01") %>%
  select(-c(traitement:reference)) %>%
  group_by(Plante) %>%
  filter(Rosette_size == max(Rosette_size),
        Rosette_size > 0) %>%
  distinct(Plante, .keep_all = TRUE)

rosette_data$Date_de_germination <- as.Date(rosette_data$Date_de_germination, format = "%d/%m/%Y")
rosette_data$Date <- as.Date(rosette_data$Date, format = "%Y-%m-%d")

rosette_data <- rosette_data %>%
  mutate(time_after_germ = difftime(Date, Date_de_germination, units = "days")) %>%
  filter(time_after_germ > 0)

rosette_data$time_after_germ <- as.numeric(rosette_data$time_after_germ)

rm(data)

head(rosette_data)

## # A tibble: 6 x 9
## # Groups:   Plante [6]
##   Plante Date_de_germination Cotyledons species population light Date
##   <dbl> <date>                <dbl> <fct>   <chr>      <dbl> <date>
## 1    230 2005-10-17              9.18 mac     rog        0.297 2005-12-01

```

```
## 2      527 2005-10-17          9.39 cor      E1          0.103 2005-12-01
## 3      589 2005-11-07          8.53 cor      E2          0.194 2005-12-01
## 4      609 2005-10-17          9.4  mac      rog          1      2005-12-01
## 5      683 2005-10-17          8.4  mac      nav          1      2005-12-01
## 6      686 2005-10-17         11.8  mac      nav          1      2005-12-01
## # ... with 2 more variables: Rosette_size <dbl>, time_after_germ <dbl>
```

Now, we will build and plot the germination model.

```
germ_mod1 <- glmer(germination~light*species+(1+species|population), data = germ_data, family = "binomial")
```

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

```
germ_mod2 <- glmer(germination~light*species+(1|population), data = germ_data, family = "binomial")
```

```
germ_mod3 <- glm(germination~light*species, data = germ_data, family = "binomial")
```

```
anova(germ_mod1, germ_mod2) # (1+species|population) not sig better
```

```
## Data: germ_data
```

```
## Models:
```

```
## germ_mod2: germination ~ light * species + (1 | population)
```

```
## germ_mod1: germination ~ light * species + (1 + species | population)
```

```
##          npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
```

```
## germ_mod2      5 956.49 979.92 -473.25   946.49
```

```
## germ_mod1      7 957.10 989.90 -471.55   943.10 3.3901  2      0.1836
```

```
anova(germ_mod2, germ_mod3) # however including (1|population) is supported
```

```
## Data: germ_data
```

```
## Models:
```

```
## germ_mod3: germination ~ light * species
```

```
## germ_mod2: germination ~ light * species + (1 | population)
```

```
##          npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
```

```
## germ_mod3      4 967.67 986.41 -479.83   959.67
```

```
## germ_mod2      5 956.49 979.92 -473.25   946.49 13.175  1 0.0002836 ***
```

```
## ---
```

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

```
summary(germ_mod2) # all terms are sig
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
```

```
## Approximation) [glmerMod]
```

```
## Family: binomial ( logit )
```

```
## Formula: germination ~ light * species + (1 | population)
```

```
## Data: germ_data
```

```
##
```

```
##          AIC      BIC  logLik deviance df.resid
```

```
##      956.5      979.9  -473.2   946.5       795
```

```
##
```

```
## Scaled residuals:
```

```
##      Min      1Q  Median      3Q      Max
```

```
## -2.6174 -0.8036  0.4320  0.7310  2.0336
```

```
##
```

```
## Random effects:
```

```
## Groups      Name      Variance Std.Dev.
```

```
## population (Intercept) 0.1461   0.3823
```

```
## Number of obs: 800, groups: population, 4
```

```
##
## Fixed effects:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -1.4520    0.3677  -3.949 7.84e-05 ***
## light          1.9987    0.3359   5.951 2.67e-09 ***
## speciescor     2.2425    0.5133   4.369 1.25e-05 ***
## light:speciescor -1.3574    0.4807  -2.824 0.00474 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr) light  spcscr
## light      -0.614
## speciescor -0.716  0.440
## lght:spcscr  0.429 -0.699 -0.586

germ_mod4 <- update(germ_mod2, .~. -light:species)
anova(germ_mod2, germ_mod4)

## Data: germ_data
## Models:
## germ_mod4: germination ~ light + species + (1 | population)
## germ_mod2: germination ~ light * species + (1 | population)
##           npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## germ_mod4    4 962.51 981.25 -477.26   954.51
## germ_mod2    5 956.49 979.92 -473.25   946.49 8.018  1 0.004631 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

AICc(germ_mod1, germ_mod2, germ_mod3, germ_mod4)

##           df      AICc
## germ_mod1  7 957.2447
## germ_mod2  5 956.5690
## germ_mod3  4 967.7192
## germ_mod4  4 962.5617

logLik(germ_mod4)

## 'log Lik.' -477.2557 (df=4)

germ_mod <- germ_mod2

rm(germ_mod1, germ_mod2, germ_mod3, germ_mod4)

germ_pred <- ggpredict(germ_mod, terms = c("light [all]", "species"), type = "fixed") %>%
  rename("species" = "group")

germ_pred$species <- recode_factor(germ_pred$species, mac = "C. maculosa", cor = "C. corymbosa")

germplot <- ggplot(data = germ_data,
  aes(x = light, y = germination)) +
  geom_point(data = germ_data %>%
    filter(species == "mac"),
    aes(x = light, y = germination),
    size = 3, alpha = 0.1, colour = "#F8766D") +
  geom_point(data = germ_data %>%
```

```

        filter(species == "cor"),
        aes(x = light, y = germination),
        size = 3, alpha = 0.1, colour = "#00BFC4") +
geom_line(data = germ_pred,
        aes(y = predicted, x = x, colour = species),
        size = 1.5) +
geom_ribbon(data = germ_pred,
        aes(y = predicted, x = x, ymin = conf.low, ymax = conf.high, colour = species, fill = species),
        alpha = 0.1) +
labs(y = "P(Germination)",
     x = "Light (received PAR / reference PAR)") +
scale_x_continuous(breaks = c(0,0.25,0.5,0.75,1)) +
theme_cowplot() +
theme(legend.position = c(0.65,0.25),
      legend.title = element_blank())

ggsave(filename = "Figure2.png",
      plot = germplot,
      dpi = 600,
      width = 5,
      height = 5,
      type="cairo-png"
      )

rm(germ_pred, germ_mod, germplot)

```

And finally, we build and plot the model for rosette size.

```

rosette_mod1 <- lmer(Rosette_size ~ light*species*Cotyledons*time_after_germ+(1+species|population),
                    data = rosette_data)

```

```

## Warning: Some predictor variables are on very different scales: consider
## rescaling

```

```

## boundary (singular) fit: see ?isSingular

```

```

rosette_mod2 <- lmer(Rosette_size ~ light*species*Cotyledons*time_after_germ+(1|population),
                    data = rosette_data)

```

```

## Warning: Some predictor variables are on very different scales: consider
## rescaling

```

```

rosette_mod3 <- lm(Rosette_size~light*species*Cotyledons*time_after_germ,
                  data = rosette_data)

```

```

anova(rosette_mod1, rosette_mod2) # no difference in L.ratio, AIC support simpler model

```

```

## refitting model(s) with ML (instead of REML)

```

```

## Data: rosette_data

```

```

## Models:

```

```

## rosette_mod2: Rosette_size ~ light * species * Cotyledons * time_after_germ +

```

```

## rosette_mod2:      (1 | population)

```

```

## rosette_mod1: Rosette_size ~ light * species * Cotyledons * time_after_germ +

```

```

## rosette_mod1:      (1 + species | population)

```

```

##               npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)

```

```

## rosette_mod2    18 3262.4 3331.9 -1613.2   3226.4

```

```

## rosette_mod1    20 3266.4 3343.6 -1613.2    3226.4 0.0033  2    0.9984
anova(rosette_mod2, rosette_mod3) # no difference in L.ratio again, and AIC would marginally support si

## refitting model(s) with ML (instead of REML)

## Data: rosette_data
## Models:
## rosette_mod3: Rosette_size ~ light * species * Cotyledons * time_after_germ
## rosette_mod2: Rosette_size ~ light * species * Cotyledons * time_after_germ +
## rosette_mod2:      (1 | population)
##           npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## rosette_mod3    17 3260.4 3326.0 -1613.2    3226.4
## rosette_mod2    18 3262.4 3331.9 -1613.2    3226.4      0 1      1
# going with simpler = better if both explain the data just as well, we will move on with a lm

rosette_mod4 <- lm(Rosette_size~light*species*Cotyledons*time_after_germ, data = rosette_data)
summary(rosette_mod4)

##
## Call:
## lm(formula = Rosette_size ~ light * species * Cotyledons * time_after_germ,
##     data = rosette_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -56.900 -17.122   1.634  15.195  94.885
##
## Coefficients:
##              Estimate Std. Error t value
## (Intercept)    -1.000e+02  6.673e+01  -1.499
## light           1.953e+02  7.816e+01   2.499
## speciescor      6.228e+01  7.039e+01   0.885
## Cotyledons      6.916e+00  7.779e+00   0.889
## time_after_germ  5.208e-01  2.829e-01   1.841
## light:speciescor -1.362e+02  8.564e+01  -1.591
## light:Cotyledons -1.009e+01  8.721e+00  -1.157
## speciescor:Cotyledons -2.944e+00  8.055e+00  -0.365
## light:time_after_germ -5.884e-01  3.273e-01  -1.797
## speciescor:time_after_germ -2.191e-01  3.022e-01  -0.725
## Cotyledons:time_after_germ -1.637e-02  3.638e-02  -0.450
## light:speciescor:Cotyledons  7.049e+00  9.273e+00   0.760
## light:speciescor:time_after_germ  4.765e-01  3.596e-01   1.325
## light:Cotyledons:time_after_germ  2.963e-02  3.982e-02   0.744
## speciescor:Cotyledons:time_after_germ  7.531e-03  3.796e-02   0.198
## light:speciescor:Cotyledons:time_after_germ -2.075e-02  4.230e-02  -0.491
##              Pr(>|t|)
## (Intercept)      0.1348
## light            0.0129 *
## speciescor       0.3770
## Cotyledons       0.3746
## time_after_germ  0.0665 .
## light:speciescor 0.1126
## light:Cotyledons 0.2480
## speciescor:Cotyledons 0.7150

```

```

## light:time_after_germ          0.0732 .
## speciescor:time_after_germ     0.4690
## Cotyledons:time_after_germ     0.6531
## light:speciescor:Cotyledons    0.4477
## light:speciescor:time_after_germ 0.1860
## light:Cotyledons:time_after_germ 0.4574
## speciescor:Cotyledons:time_after_germ 0.8428
## light:speciescor:Cotyledons:time_after_germ 0.6240
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 24.87 on 334 degrees of freedom
## Multiple R-squared:  0.4144, Adjusted R-squared:  0.3881
## F-statistic: 15.76 on 15 and 334 DF,  p-value: < 2.2e-16

rosette_mod5 <- update(rosette_mod4, .~. -light:species:Cotyledons:time_after_germ) # try remove 4 way
anova(rosette_mod4, rosette_mod5) # removal is supported by lrt

## Analysis of Variance Table
##
## Model 1: Rosette_size ~ light * species * Cotyledons * time_after_germ
## Model 2: Rosette_size ~ light + species + Cotyledons + time_after_germ +
##   light:species + light:Cotyledons + species:Cotyledons + light:time_after_germ +
##   species:time_after_germ + Cotyledons:time_after_germ + light:species:Cotyledons +
##   light:species:time_after_germ + light:Cotyledons:time_after_germ +
##   species:Cotyledons:time_after_germ
##   Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1      334 206578
## 2      335 206727 -1    -148.85 0.2407  0.624

summary(rosette_mod5)

##
## Call:
## lm(formula = Rosette_size ~ light + species + Cotyledons + time_after_germ +
##   light:species + light:Cotyledons + species:Cotyledons + light:time_after_germ +
##   species:time_after_germ + Cotyledons:time_after_germ + light:species:Cotyledons +
##   light:species:time_after_germ + light:Cotyledons:time_after_germ +
##   species:Cotyledons:time_after_germ, data = rosette_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -57.221 -16.961   1.406  15.143  94.973
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -7.389e+01  4.009e+01  -1.843  0.066177
## light          1.644e+02  4.608e+01   3.567  0.000414
## speciescor     3.326e+01  3.813e+01   0.872  0.383666
## Cotyledons     3.661e+00  4.057e+00   0.902  0.367534
## time_after_germ 3.981e-01  1.319e-01   3.018  0.002742
## light:speciescor -1.006e+02  4.519e+01  -2.226  0.026700
## light:Cotyledons -6.359e+00  4.254e+00  -1.495  0.135842
## speciescor:Cotyledons 6.113e-01  3.513e+00   0.174  0.861965
## light:time_after_germ -4.445e-01  1.452e-01  -3.061  0.002382

```

```
## speciescor:time_after_germ          -8.163e-02  1.131e-01  -0.722  0.471084
## Cotyledons:time_after_germ          -1.295e-04  1.508e-02  -0.009  0.993155
## light:speciescor:Cotyledons         2.834e+00  3.485e+00   0.813  0.416721
## light:speciescor:time_after_germ    3.103e-01  1.201e-01   2.584  0.010181
## light:Cotyledons:time_after_germ     1.124e-02  1.341e-02   0.838  0.402567
## speciescor:Cotyledons:time_after_germ -1.032e-02  1.078e-02  -0.958  0.338988
##
## (Intercept)                          .
## light                                ***
## speciescor
## Cotyledons
## time_after_germ                      **
## light:speciescor                     *
## light:Cotyledons
## speciescor:Cotyledons
## light:time_after_germ                **
## speciescor:time_after_germ
## Cotyledons:time_after_germ
## light:speciescor:Cotyledons
## light:speciescor:time_after_germ     *
## light:Cotyledons:time_after_germ
## speciescor:Cotyledons:time_after_germ
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 24.84 on 335 degrees of freedom
## Multiple R-squared:  0.414, Adjusted R-squared:  0.3895
## F-statistic: 16.9 on 14 and 335 DF, p-value: < 2.2e-16
```

```
rosette_mod6 <- update(rosette_mod5, .~. -species:Cotyledons:time_after_germ) # try remove non sig 3 wa
anova(rosette_mod5, rosette_mod6) # removal supported by lrt
```

```
## Analysis of Variance Table
```

```
##
```

```
## Model 1: Rosette_size ~ light + species + Cotyledons + time_after_germ +
##   light:species + light:Cotyledons + species:Cotyledons + light:time_after_germ +
##   species:time_after_germ + Cotyledons:time_after_germ + light:species:Cotyledons +
##   light:species:time_after_germ + light:Cotyledons:time_after_germ +
##   species:Cotyledons:time_after_germ
## Model 2: Rosette_size ~ light + species + Cotyledons + time_after_germ +
##   light:species + light:Cotyledons + species:Cotyledons + light:time_after_germ +
##   species:time_after_germ + Cotyledons:time_after_germ + light:species:Cotyledons +
##   light:species:time_after_germ + light:Cotyledons:time_after_germ
##   Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1      335 206727
## 2      336 207293 -1    -565.8 0.9169  0.339
```

```
summary(rosette_mod6)
```

```
##
```

```
## Call:
```

```
## lm(formula = Rosette_size ~ light + species + Cotyledons + time_after_germ +
##   light:species + light:Cotyledons + species:Cotyledons + light:time_after_germ +
##   species:time_after_germ + Cotyledons:time_after_germ + light:species:Cotyledons +
##   light:species:time_after_germ + light:Cotyledons:time_after_germ,
```



```

##      data = rosette_data)
##
## Residuals:
##      Min        1Q    Median        3Q        Max
## -56.681 -17.587   1.456  15.643  94.999
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -86.77135     37.75418  -2.298  0.022157 *
## light          160.41230     45.88834   3.496  0.000536 ***
## speciescor      44.67347     36.21522   1.234  0.218231
## Cotyledons       5.61158      3.50830   1.600  0.110645
## time_after_germ  0.46345      0.11290   4.105  5.08e-05 ***
## light:speciescor -87.60715     43.10551  -2.032  0.042900 *
## light:Cotyledons -6.65707      4.24161  -1.569  0.117480
## speciescor:Cotyledons -1.21813     2.94765  -0.413  0.679684
## light:time_after_germ -0.43541     0.14487  -3.005  0.002851 **
## speciescor:time_after_germ -0.14307     0.09316  -1.536  0.125556
## Cotyledons:time_after_germ -0.01069     0.01028  -1.040  0.298968
## light:speciescor:Cotyledons 2.28542     3.43707   0.665  0.506551
## light:speciescor:time_after_germ 0.26661     0.11105   2.401  0.016903 *
## light:Cotyledons:time_after_germ 0.01441     0.01299   1.110  0.267887
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 24.84 on 336 degrees of freedom
## Multiple R-squared:  0.4124, Adjusted R-squared:  0.3896
## F-statistic: 18.14 on 13 and 336 DF,  p-value: < 2.2e-16

rosette_mod7 <- update(rosette_mod6, .~. -light:Cotyledons:time_after_germ) # remove non sig 3 way int
anova(rosette_mod6,rosette_mod7) # removal supported by lrt

## Analysis of Variance Table
##
## Model 1: Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:Cotyledons + species:Cotyledons + light:time_after_germ +
##      species:time_after_germ + Cotyledons:time_after_germ + light:species:Cotyledons +
##      light:species:time_after_germ + light:Cotyledons:time_after_germ
## Model 2: Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:Cotyledons + species:Cotyledons + light:time_after_germ +
##      species:time_after_germ + Cotyledons:time_after_germ + light:species:Cotyledons +
##      light:species:time_after_germ
##      Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1      336 207293
## 2      337 208052 -1    -759.83 1.2316 0.2679

summary(rosette_mod7)

##
## Call:
## lm(formula = Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:Cotyledons + species:Cotyledons + light:time_after_germ +
##      species:time_after_germ + Cotyledons:time_after_germ + light:species:Cotyledons +
##      light:species:time_after_germ, data = rosette_data)
##

```

```
## Residuals:
##      Min       1Q   Median       3Q      Max
## -56.790 -16.437   1.633  15.960  94.432
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -6.875e+01  3.410e+01  -2.016  0.044549 *
## light           1.334e+02  3.892e+01   3.428  0.000683 ***
## speciescor      4.484e+01  3.623e+01   1.238  0.216638
## Cotyledons      3.472e+00  2.932e+00   1.184  0.237205
## time_after_germ  3.804e-01  8.452e-02   4.500  9.37e-06 ***
## light:speciescor -8.866e+01  4.311e+01  -2.057  0.040498 *
## light:Cotyledons -3.628e+00  3.248e+00  -1.117  0.264769
## speciescor:Cotyledons -9.979e-01  2.942e+00  -0.339  0.734681
## light:time_after_germ -3.126e-01  9.353e-02  -3.342  0.000925 ***
## speciescor:time_after_germ -1.548e-01  9.259e-02  -1.672  0.095453 .
## Cotyledons:time_after_germ -2.656e-04  4.171e-03  -0.064  0.949267
## light:speciescor:Cotyledons 2.142e+00  3.436e+00   0.623  0.533485
## light:speciescor:time_after_germ 2.794e-01  1.105e-01   2.529  0.011897 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 24.85 on 337 degrees of freedom
## Multiple R-squared:  0.4102, Adjusted R-squared:  0.3892
## F-statistic: 19.53 on 12 and 337 DF,  p-value: < 2.2e-16

rosette_mod8 <- update(rosette_mod7, .~. -light:species:Cotyledons) # remove non sig 3 way int
anova(rosette_mod7,rosette_mod8) # removal supported by lrt

## Analysis of Variance Table
##
## Model 1: Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:Cotyledons + species:Cotyledons + light:time_after_germ +
##      species:time_after_germ + Cotyledons:time_after_germ + light:species:Cotyledons +
##      light:species:time_after_germ
## Model 2: Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:Cotyledons + species:Cotyledons + light:time_after_germ +
##      species:time_after_germ + Cotyledons:time_after_germ + light:species:time_after_germ
##   Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1     337 208052
## 2     338 208292 -1    -239.88 0.3885 0.5335

summary(rosette_mod8)

##
## Call:
## lm(formula = Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:Cotyledons + species:Cotyledons + light:time_after_germ +
##      species:time_after_germ + Cotyledons:time_after_germ + light:species:time_after_germ,
##      data = rosette_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -56.340 -16.174   1.323  15.670  94.521
##
```

```
## Coefficients:
##
##          Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -5.247e+01  2.189e+01  -2.397 0.017079 *
## light          1.144e+02  2.411e+01   4.744 3.10e-06 ***
## speciescor      2.724e+01  2.267e+01   1.202 0.230339
## Cotyledons      1.846e+00  1.338e+00   1.380 0.168516
## time_after_germ  3.612e-01  7.864e-02   4.593 6.19e-06 ***
## light:speciescor -6.694e+01  2.537e+01  -2.639 0.008711 **
## light:Cotyledons -1.729e+00  1.123e+00  -1.539 0.124643
## speciescor:Cotyledons  7.364e-01  9.552e-01   0.771 0.441284
## light:time_after_germ -2.939e-01  8.849e-02  -3.321 0.000995 ***
## speciescor:time_after_germ -1.363e-01  8.760e-02  -1.556 0.120756
## Cotyledons:time_after_germ -8.413e-05  4.157e-03  -0.020 0.983866
## light:speciescor:time_after_germ  2.595e-01  1.057e-01   2.456 0.014561 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 24.82 on 338 degrees of freedom
## Multiple R-squared:  0.4095, Adjusted R-squared:  0.3903
## F-statistic: 21.31 on 11 and 338 DF,  p-value: < 2.2e-16

rosette_mod9 <- update(rosette_mod8, .~. -Cotyledons:time_after_germ) # remove non sig int
anova(rosette_mod8,rosette_mod9) # removal supported by lrt

## Analysis of Variance Table
##
## Model 1: Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:Cotyledons + species:Cotyledons + light:time_after_germ +
##      species:time_after_germ + Cotyledons:time_after_germ + light:species:time_after_germ
## Model 2: Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:Cotyledons + species:Cotyledons + light:time_after_germ +
##      species:time_after_germ + light:species:time_after_germ
##   Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1      338 208292
## 2      339 208293 -1    -0.2524 4e-04 0.9839

summary(rosette_mod9)

##
## Call:
## lm(formula = Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:Cotyledons + species:Cotyledons + light:time_after_germ +
##      species:time_after_germ + light:species:time_after_germ,
##      data = rosette_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -56.347 -16.144   1.343  15.665  94.516
##
## Coefficients:
##
##          Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -52.41257    21.69338  -2.416 0.016217 *
## light          114.51523    22.99363   4.980 1.01e-06 ***
## speciescor      27.29194    22.48151   1.214 0.225603
## Cotyledons       1.83434     1.21059   1.515 0.130643
```

```

## time_after_germ          0.36072      0.07550      4.778 2.65e-06 ***
## light:speciescor        -66.97719     25.27764     -2.650 0.008435 **
## light:Cotyledons        -1.73678      1.04779     -1.658 0.098331 .
## speciescor:Cotyledons     0.73519      0.95187      0.772 0.440440
## light:time_after_germ    -0.29427      0.08598     -3.422 0.000696 ***
## speciescor:time_after_germ -0.13653      0.08652     -1.578 0.115484
## light:speciescor:time_after_germ 0.25971      0.10493      2.475 0.013810 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 24.79 on 339 degrees of freedom
## Multiple R-squared:  0.4095, Adjusted R-squared:  0.3921
## F-statistic: 23.51 on 10 and 339 DF,  p-value: < 2.2e-16

rosette_mod10 <- update(rosette_mod9, .~. -species:time_after_germ)
anova(rosette_mod9,rosette_mod10) # removal supported by lrt

## Analysis of Variance Table
##
## Model 1: Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:Cotyledons + species:Cotyledons + light:time_after_germ +
##      species:time_after_germ + light:species:time_after_germ
## Model 2: Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:Cotyledons + species:Cotyledons + light:time_after_germ +
##      light:species:time_after_germ
##   Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1      339 208293
## 2      340 209823 -1   -1530.1 2.4903 0.1155

summary(rosette_mod10)

##
## Call:
## lm(formula = Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:Cotyledons + species:Cotyledons + light:time_after_germ +
##      light:species:time_after_germ, data = rosette_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -56.362 -16.486   2.065  15.260  95.197
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -26.86014     14.46809   -1.857 0.064246 .
## light           89.05898     16.42142    5.423 1.11e-07 ***
## speciescor     -4.52924      9.96166   -0.455 0.649639
## Cotyledons      1.51633      1.19632    1.268 0.205843
## time_after_germ  0.25747      0.03776    6.819 4.21e-11 ***
## light:speciescor -34.17620     14.41609   -2.371 0.018312 *
## light:Cotyledons -1.62212      1.04756   -1.548 0.122437
## speciescor:Cotyledons 1.02723      0.93575    1.098 0.273084
## light:time_after_germ -0.18260      0.04895   -3.731 0.000224 ***
## light:speciescor:time_after_germ 0.10679      0.04034    2.647 0.008494 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
##
## Residual standard error: 24.84 on 340 degrees of freedom
## Multiple R-squared:  0.4052, Adjusted R-squared:  0.3894
## F-statistic: 25.73 on 9 and 340 DF,  p-value: < 2.2e-16

rosette_mod11 <- update(rosette_mod10, .~. -species:Cotyledons) # remove non sig int
anova(rosette_mod10,rosette_mod11) # removal supported by lrt

## Analysis of Variance Table
##
## Model 1: Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:Cotyledons + species:Cotyledons + light:time_after_germ +
##      light:species:time_after_germ
## Model 2: Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:Cotyledons + light:time_after_germ +
##      light:species:time_after_germ
##   Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1     340 209823
## 2     341 210566 -1    -743.69 1.2051 0.2731

summary(rosette_mod11)

##
## Call:
## lm(formula = Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:Cotyledons + light:time_after_germ +
##      light:species:time_after_germ, data = rosette_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -56.87 -17.30   2.55  15.52  95.35
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -34.25695     12.80714   -2.675 0.007837 **
## light           88.53082     16.41931    5.392 1.31e-07 ***
## speciescor      2.14164      7.89588    0.271 0.786375
## Cotyledons      2.54649      0.74222    3.431 0.000675 ***
## time_after_germ  0.26041      0.03768    6.912 2.36e-11 ***
## light:speciescor -30.09781     13.93333   -2.160 0.031459 *
## light:Cotyledons -1.90537      1.01559   -1.876 0.061492 .
## light:time_after_germ -0.18142      0.04895   -3.706 0.000245 ***
## light:speciescor:time_after_germ  0.10262      0.04017    2.554 0.011070 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 24.85 on 341 degrees of freedom
## Multiple R-squared:  0.4031, Adjusted R-squared:  0.3891
## F-statistic: 28.78 on 8 and 341 DF,  p-value: < 2.2e-16

rosette_mod12 <- update(rosette_mod11, .~. -light:Cotyledons) # remove marg. sig. int
anova(rosette_mod11,rosette_mod12) # removal supported marginally

## Analysis of Variance Table
##
## Model 1: Rosette_size ~ light + species + Cotyledons + time_after_germ +
```

```

##      light:species + light:Cotyledons + light:time_after_germ +
##      light:species:time_after_germ
## Model 2: Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:time_after_germ + light:species:time_after_germ
##   Res.Df    RSS Df Sum of Sq      F Pr(>F)
## 1      341 210566
## 2      342 212740 -1    -2173.5 3.5199 0.06149 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

summary(rosette_mod12) # all terms sig or are included in sig ints

##
## Call:
## lm(formula = Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:time_after_germ + light:species:time_after_germ,
##      data = rosette_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -56.590 -17.204   2.006  15.818  94.473
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -22.46487    11.19977   -2.006 0.045661 *
## light           69.91133    13.12861    5.325 1.83e-07 ***
## speciescor      4.65179     7.81031    0.596 0.551839
## Cotyledons      1.31872     0.35148    3.752 0.000206 ***
## time_after_germ  0.25110     0.03749    6.699 8.67e-11 ***
## light:speciescor -32.75407    13.91218   -2.354 0.019120 *
## light:time_after_germ -0.16957     0.04872   -3.481 0.000565 ***
## light:speciescor:time_after_germ  0.10012     0.04030    2.485 0.013451 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 24.94 on 342 degrees of freedom
## Multiple R-squared:  0.3969, Adjusted R-squared:  0.3846
## F-statistic: 32.16 on 7 and 342 DF,  p-value: < 2.2e-16

rosette_mod13 <- update(rosette_mod12, ~. -light:species:time_after_germ)
anova(rosette_mod12, rosette_mod13) # supported to be kept in

## Analysis of Variance Table
##
## Model 1: Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:time_after_germ + light:species:time_after_germ
## Model 2: Rosette_size ~ light + species + Cotyledons + time_after_germ +
##      light:species + light:time_after_germ
##   Res.Df    RSS Df Sum of Sq      F Pr(>F)
## 1      342 212740
## 2      343 216580 -1    -3839.7 6.1728 0.01345 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

rosette_mod14 <- update(rosette_mod12, ~. -light:species)
anova(rosette_mod12, rosette_mod14) # supported to be kept in

```

```
## Analysis of Variance Table
##
## Model 1: Rosette_size ~ light + species + Cotyledons + time_after_germ +
##       light:species + light:time_after_germ + light:species:time_after_germ
## Model 2: Rosette_size ~ light + species + Cotyledons + time_after_germ +
##       light:time_after_germ + light:species:time_after_germ
##   Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1      342 212740
## 2      343 216188 -1      -3448 5.5429 0.01912 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
rosette_mod <- rosette_mod12
```

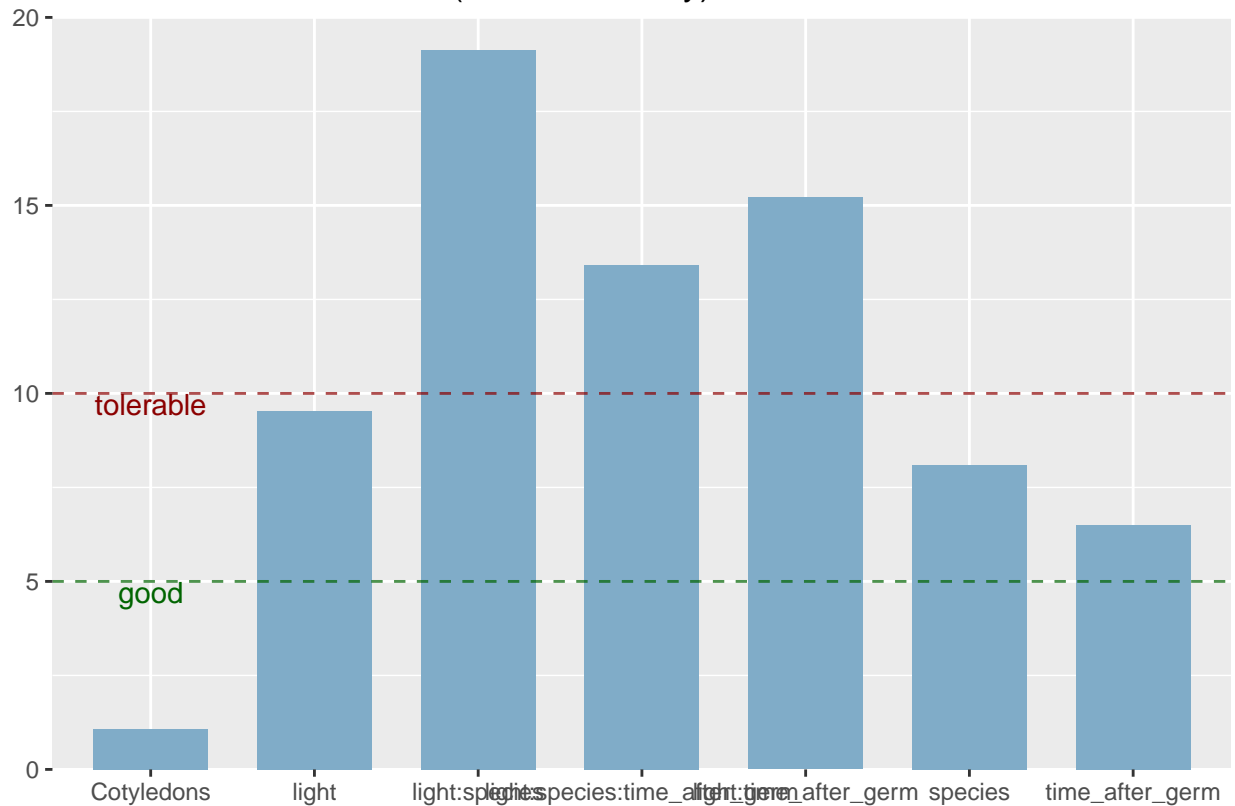
```
plot_model(rosette_mod, type = "diag")
```

```
## Registered S3 methods overwritten by 'car':
```

```
##   method                      from
## influence.merMod              lme4
## cooks.distance.influence.merMod lme4
## dfbeta.influence.merMod        lme4
## dfbetas.influence.merMod        lme4
```

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

Variance Inflation Factors (multicollinearity)



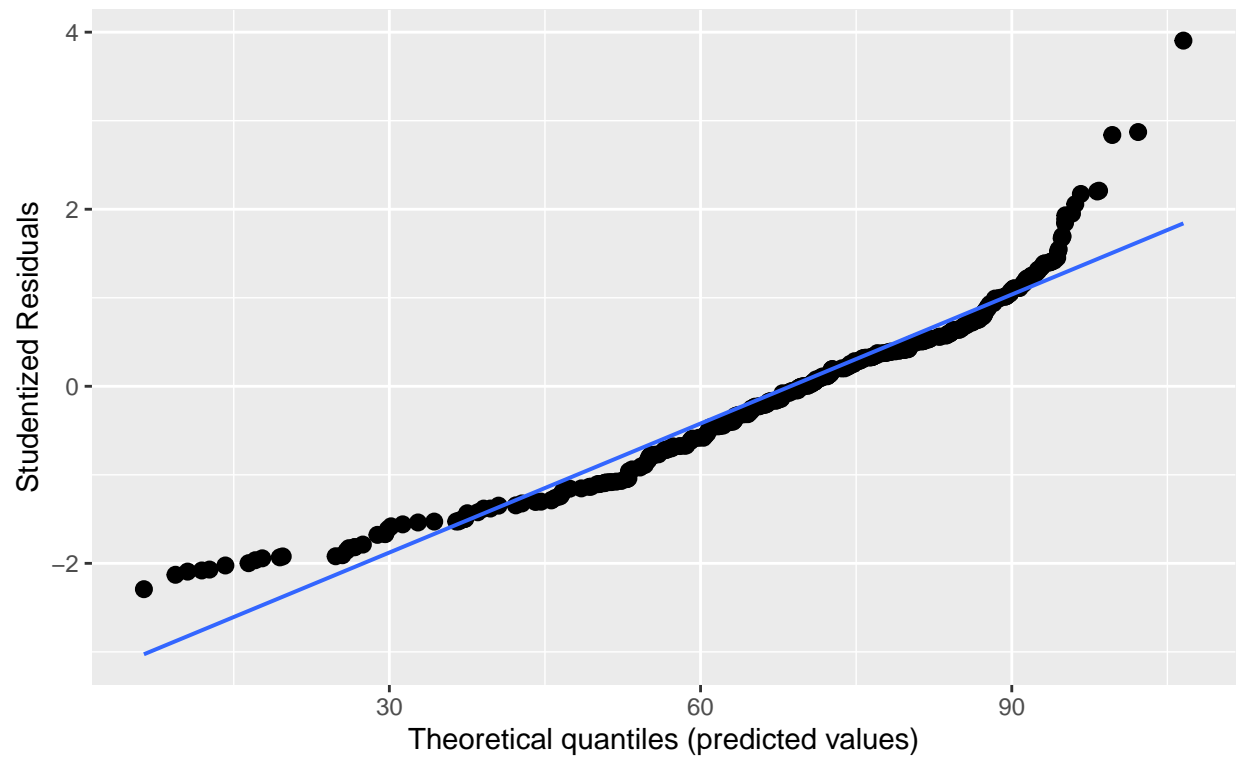
```
##
```

```
## [[2]]
```

```
## `geom_smooth()` using formula 'y ~ x'
```

Non-normality of residuals and outliers

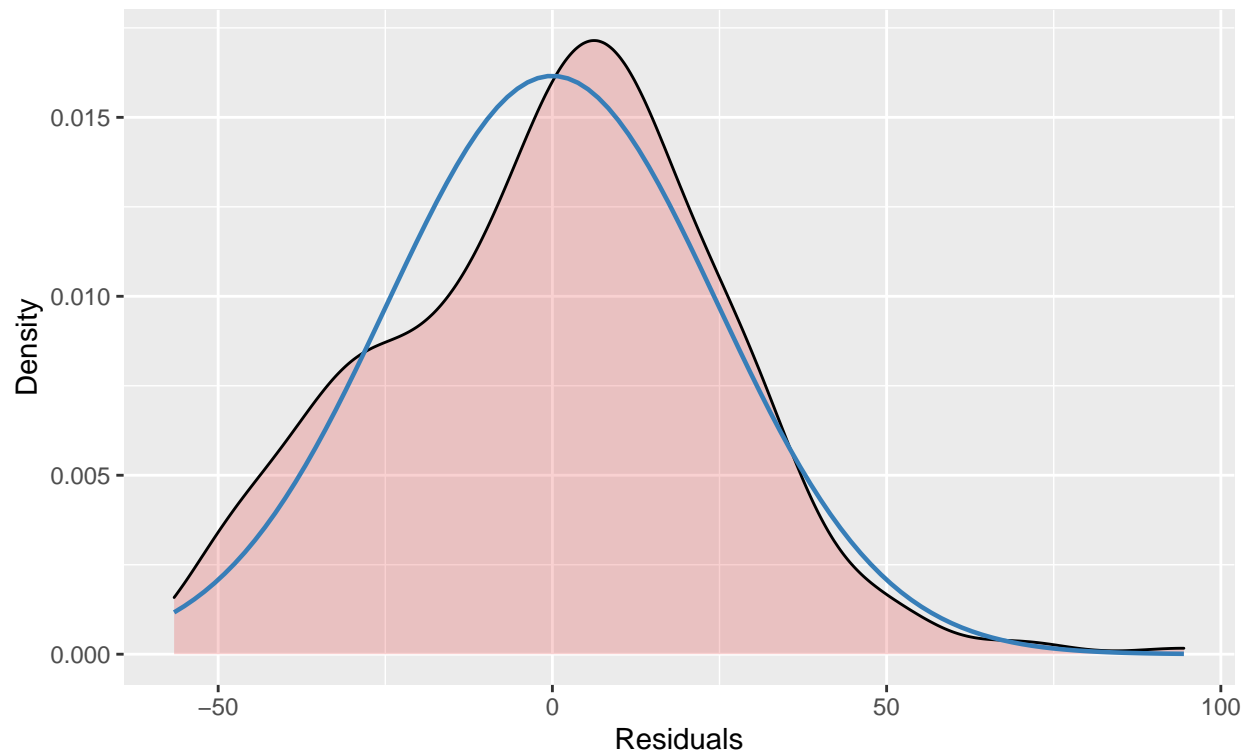
Dots should be plotted along the line



```
##  
## [[3]]
```


Non-normality of residuals

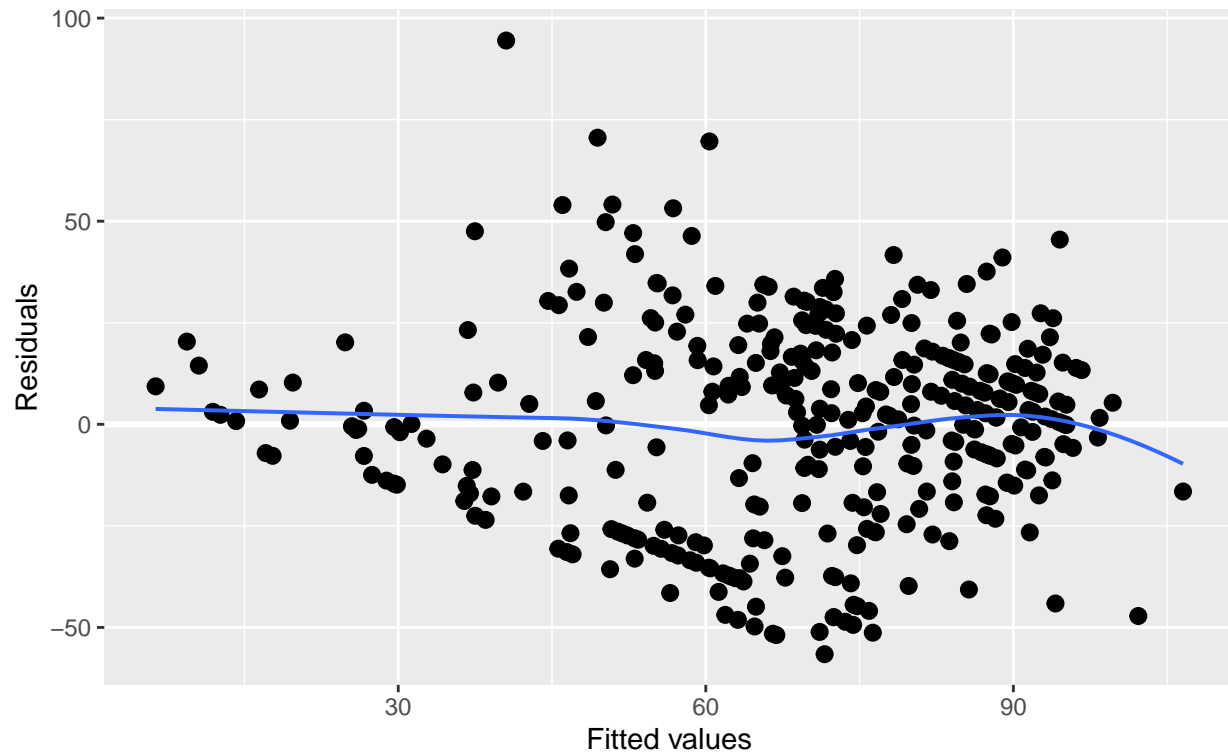
Distribution should look like normal curve



```
##  
## [[4]]  
## `geom_smooth()` using formula 'y ~ x'
```

Homoscedasticity (constant variance of residuals)

Amount and distance of points scattered above/below line is equal or randomly spread



```
mod_list <- paste0("rosette_mod",1:14)
Akaike <- NULL
LL <- NULL

for ( i in 1:length(mod_list)){
  Akaike[i] = AICc(get(mod_list[i]),k = 2)
  LL[i] = logLik(get(mod_list[i]))
}

mod_sum <- data.frame(mod_list, Akaike, LL)
mod_sum
```

```
##      mod_list  Akaike      LL
## 1  rosette_mod1 3290.159 -1623.803
## 2  rosette_mod2 3285.762 -1623.848
## 3  rosette_mod3 3262.275 -1613.216
## 4  rosette_mod4 3262.275 -1613.216
## 5  rosette_mod5 3260.318 -1613.342
## 6  rosette_mod6 3259.078 -1613.820
## 7  rosette_mod7 3258.175 -1614.461
## 8  rosette_mod8 3256.408 -1614.662
## 9  rosette_mod9 3254.251 -1614.662
## 10 rosette_mod10 3254.668 -1615.943
## 11 rosette_mod11 3253.774 -1616.562
## 12 rosette_mod12 3255.249 -1618.360
## 13 rosette_mod13 3259.402 -1621.490
```

```

## 14 rosette_mod14 3258.769 -1621.173
# recheck random effect structure with min. ad. mod

re1 <- lmer(Rosette_size ~ light + species + Cotyledons + time_after_germ +
  light:species + light:time_after_germ + light:species:time_after_germ+(1+species|population),
  data = rosette_data)

## boundary (singular) fit: see ?isSingular

re2 <- lmer(Rosette_size ~ light + species + Cotyledons + time_after_germ +
  light:species + light:time_after_germ + light:species:time_after_germ+(1|population),
  data = rosette_data)

anova(re1, re2)

## refitting model(s) with ML (instead of REML)

## Data: rosette_data
## Models:
## re2: Rosette_size ~ light + species + Cotyledons + time_after_germ +
## re2:      light:species + light:time_after_germ + light:species:time_after_germ +
## re2:      (1 | population)
## re1: Rosette_size ~ light + species + Cotyledons + time_after_germ +
## re1:      light:species + light:time_after_germ + light:species:time_after_germ +
## re1:      (1 + species | population)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## re2    10 3256.7 3295.3 -1618.4   3236.7
## re1    12 3260.6 3306.9 -1618.3   3236.6 0.0769  2      0.9623

anova(re2, rosette_mod) # still not worth including

## refitting model(s) with ML (instead of REML)

## Data: rosette_data
## Models:
## rosette_mod: Rosette_size ~ light + species + Cotyledons + time_after_germ +
## rosette_mod:      light:species + light:time_after_germ + light:species:time_after_germ
## re2: Rosette_size ~ light + species + Cotyledons + time_after_germ +
## re2:      light:species + light:time_after_germ + light:species:time_after_germ +
## re2:      (1 | population)
##      npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## rosette_mod    9 3254.7 3289.4 -1618.4   3236.7
## re2            10 3256.7 3295.3 -1618.4   3236.7    0  1      1

samp_test <- data.frame(matrix(nrow = 8))

byspe <- rosette_data %>%
  group_by(species)

for (i in 1:1000) {
  samp <- sample_n(byspe, 100)
  lm_samp <- lm(Rosette_size ~ light + species + Cotyledons + time_after_germ +
    light:species + light:time_after_germ + light:species:time_after_germ, data = samp)

  samp_test <- cbind(samp_test, lm_samp$coefficients)
}

```

```

samp <- sample_n(byspe, 113)
lm_samp <- lm(Rosette_size ~ light + species + Cotyledons + time_after_germ +
  light:species + light:time_after_germ + light:species:time_after_germ, data = samp)

samp_test <- cbind(samp_test, lm_samp$coefficients)

colnames(samp_test) <- paste0("Model", 1:ncol(samp_test))

samp_test <- samp_test %>%
  select(-Model1)

samples <- as.data.frame(t(samp_test))

summary(samples)

```

```

##      (Intercept)          light          speciescor          Cotyledons
## Min.      :-56.496   Min.      : 42.93   Min.      :-26.8613   Min.      :0.006876
## 1st Qu.: -30.060   1st Qu.: 67.47   1st Qu.: 0.8398   1st Qu.:0.981054
## Median : -24.529   Median : 72.69   Median : 5.2225   Median :1.222776
## Mean    : -24.554   Mean    : 73.13   Mean     : 5.2769   Mean     :1.221563
## 3rd Qu.: -18.988   3rd Qu.: 78.87   3rd Qu.: 10.1279   3rd Qu.:1.465756
## Max.     :  2.526   Max.     :105.87   Max.     : 25.3030   Max.     :2.375630
## time_after_germ light:speciescor light:time_after_germ
## Min.      :0.1623   Min.      :-73.842   Min.      :-0.31091
## 1st Qu.: 0.2436   1st Qu.: -41.301   1st Qu.: -0.20215
## Median : 0.2627   Median : -31.998   Median : -0.18126
## Mean     : 0.2624   Mean     : -32.925   Mean     : -0.18190
## 3rd Qu.: 0.2802   3rd Qu.: -24.460   3rd Qu.: -0.15995
## Max.     : 0.3852   Max.      : 9.777   Max.     : -0.07206
## light:speciescor:time_after_germ
## Min.      :0.01875
## 1st Qu.: 0.07617
## Median : 0.09777
## Mean     : 0.09907
## 3rd Qu.: 0.11813
## Max.     : 0.22346

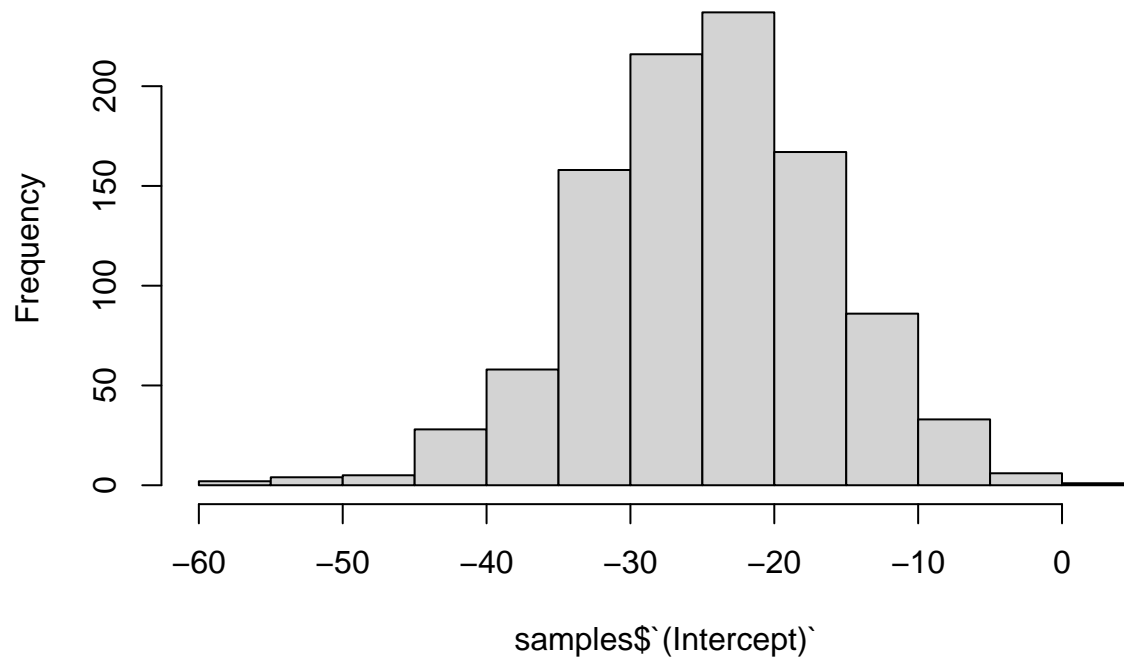
```

```

hist(samples$` (Intercept) `)

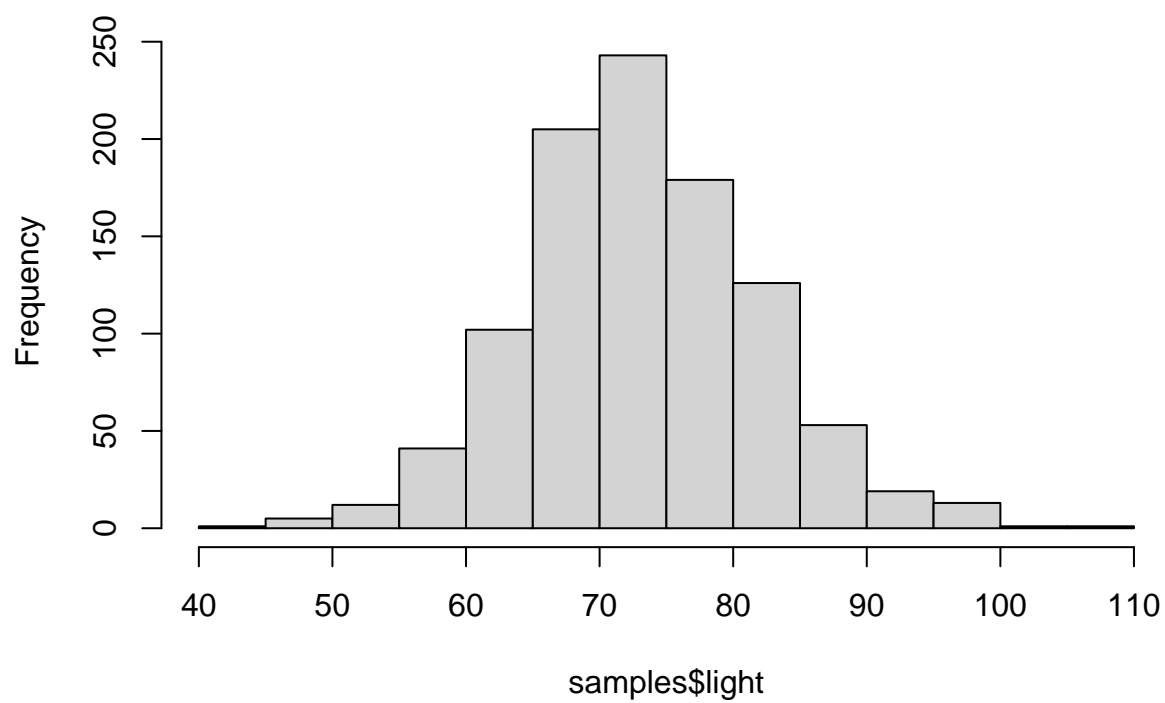
```

Histogram of samples\$(Intercept)\$



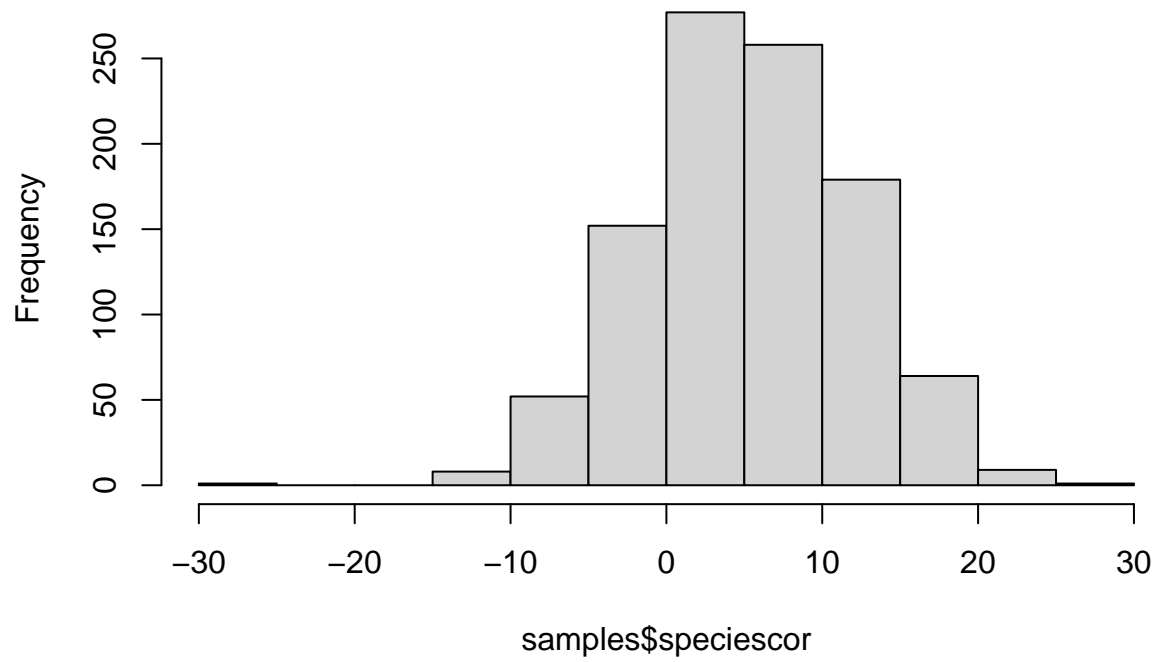
```
hist(samples$light)
```

Histogram of samples\$light



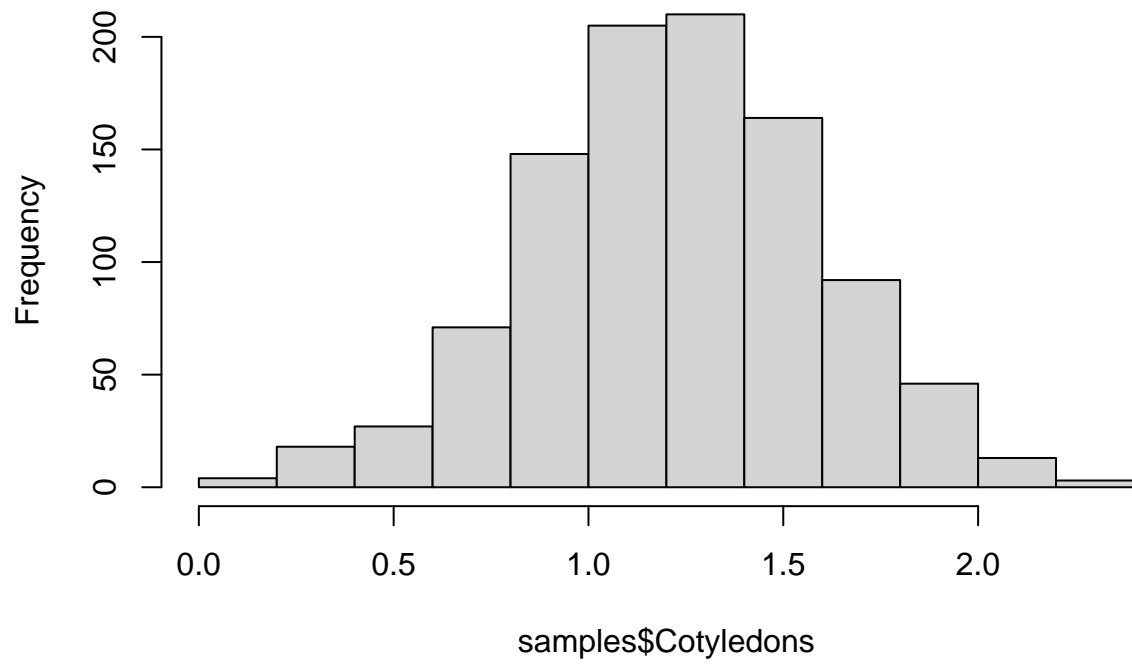
```
hist(samples$speciescor)
```

Histogram of samples\$speciescor

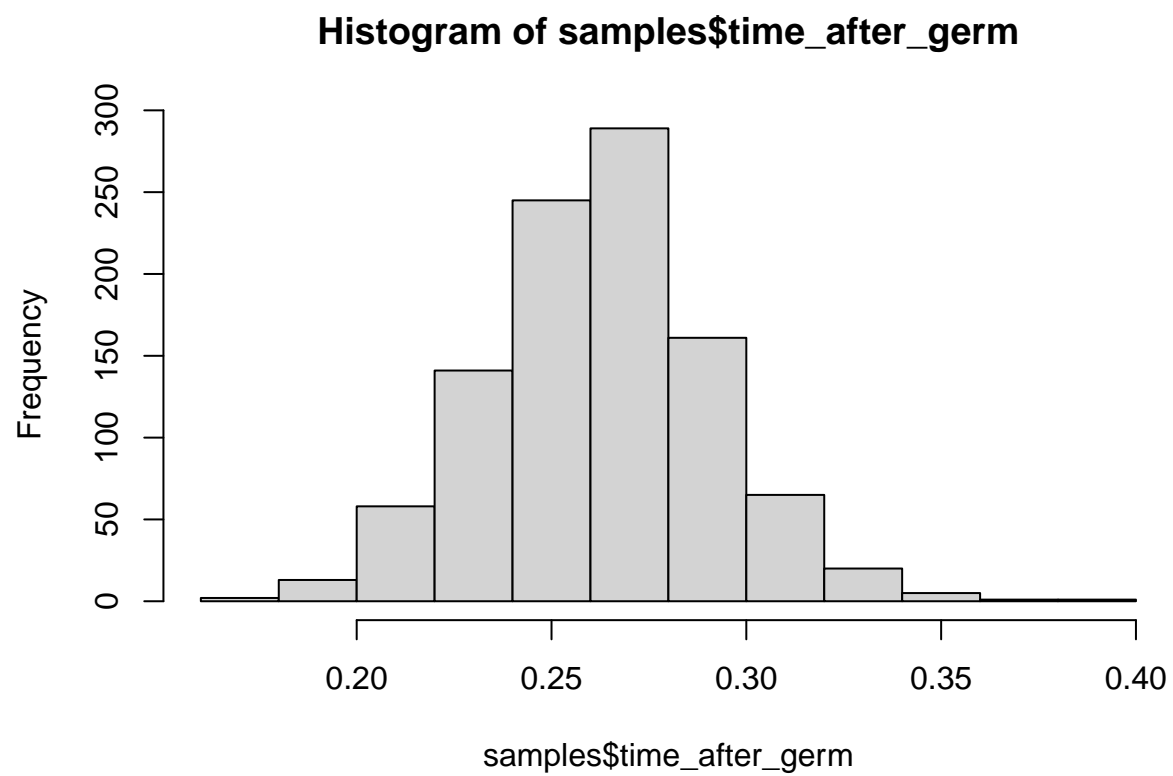


```
hist(samples$Cotyledons)
```

Histogram of samples\$Cotyledons

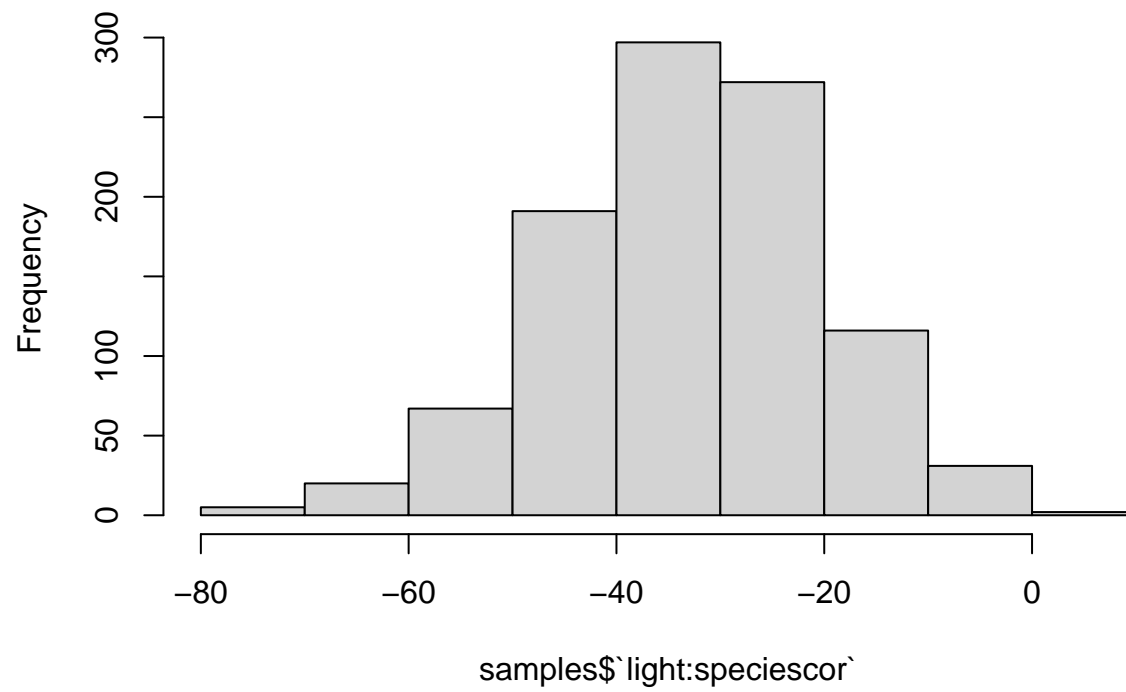


```
hist(samples$time_after_germ)
```

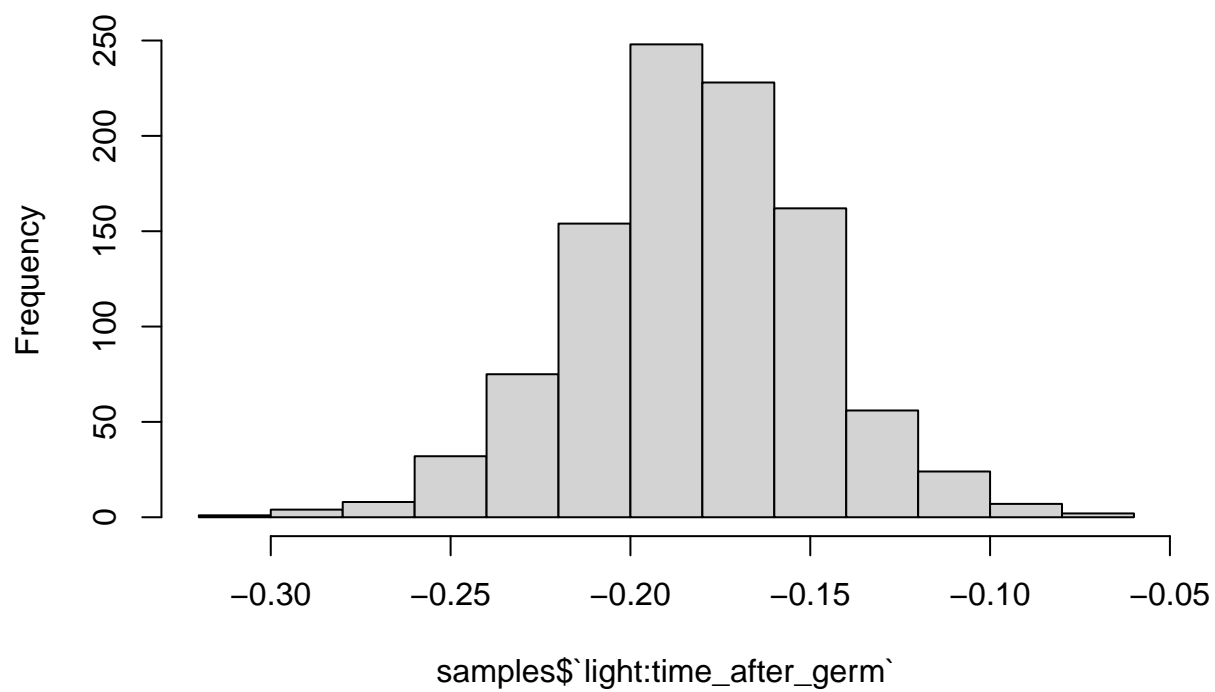
```
hist(samples$`light:speciescor`)
```

Histogram of samples\$`light:speciescor`



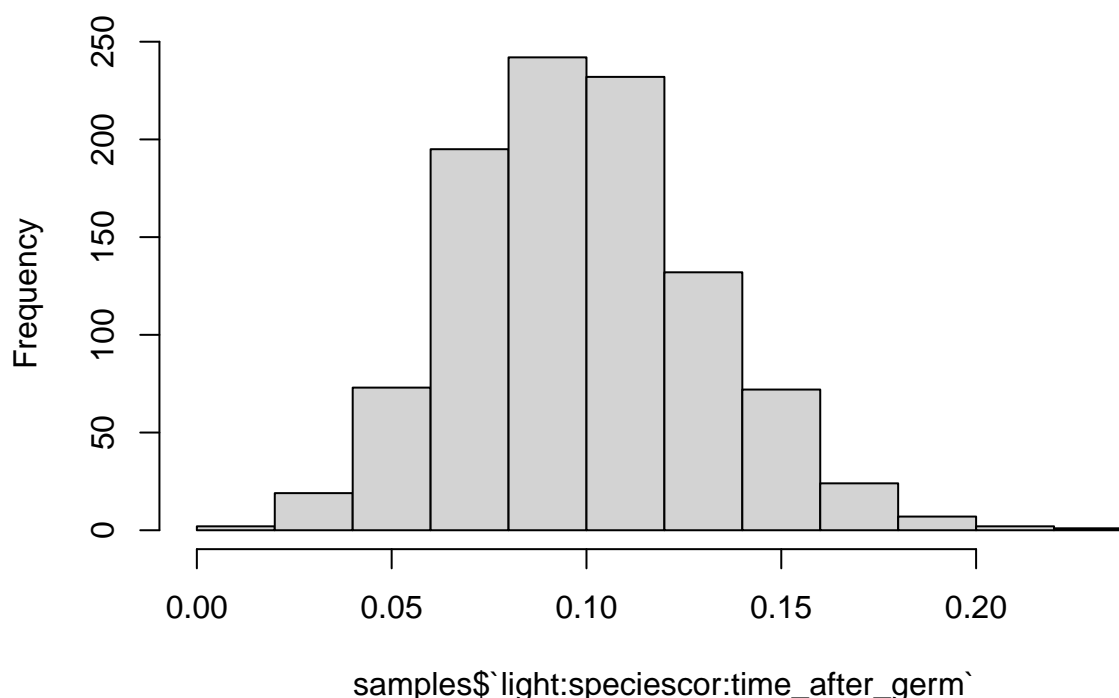
```
hist(samples$`light:time_after_germ`)
```

Histogram of samples`light:time_after_germ`



```
hist(samples`light:speciescor:time_after_germ`)
```

Histogram of samples`light:speciescor:time_after_germ`



```
rm(list = mod_list)
rm(re1, re2, mod_list, Akaike, i, LL, samp, samp_test, samples)

rosette_pred1 <- ggpredict(rosette_mod, terms = c("light", "species"), type = "fixed") %>%
  rename("species" = "group")

rosette_pred2 <- ggpredict(rosette_mod, terms = c("Cotyledons", "species"), type = "fixed") %>%
  rename("species" = "group")

rosette_pred3 <- ggpredict(rosette_mod, terms = c("time_after_germ", "species"), type = "fixed") %>%
  rename("species" = "group")

rosette_pred1$species <- recode_factor(rosette_pred1$species, mac = "C. maculosa", cor = "C. corymbosa")
rosette_pred2$species <- recode_factor(rosette_pred2$species, mac = "C. maculosa", cor = "C. corymbosa")
rosette_pred3$species <- recode_factor(rosette_pred3$species, mac = "C. maculosa", cor = "C. corymbosa")

A <- ggplot(data = rosette_data,
  aes(x = light, y = Rosette_size)) +
  geom_point(data = rosette_data %>%
    filter(species == "mac"),
    aes(x = light, y = Rosette_size),
    size = 4, alpha = 0.3, colour = "#F8766D") +
  geom_point(data = rosette_data %>%
    filter(species == "cor"),
    aes(x = light, y = Rosette_size),
    size = 4, alpha = 0.3, colour = "#00BFC4") +
```

```

geom_line(data = rosette_pred1,
          aes(y = predicted, x = x, colour = species),
          size = 1.5) +
geom_ribbon(data = rosette_pred1,
           aes(y = predicted, x = x, ymin = conf.low, ymax = conf.high, colour = species, fill = species),
           alpha = 0.1) +
labs(y = "Maximum rosette size (mm)",
     x = "Light (received PAR / reference PAR)",
     title = "A") +
scale_x_continuous(expand = c(0, 0), limits = c(0,1.09)) +
scale_y_continuous(expand = c(0, 0), limits = c(0,150)) +
theme_cowplot() +
theme(legend.position = "none")

B <- ggplot(data = rosette_data,
           aes(x = Cotyledons, y = Rosette_size)) +
geom_point(data = rosette_data %>%
           filter(species == "mac"),
           aes(x = Cotyledons, y = Rosette_size),
           size = 3, alpha = 0.3, colour = "#F8766D") +
geom_point(data = rosette_data %>%
           filter(species == "cor"),
           aes(x = Cotyledons, y = Rosette_size),
           size = 3, alpha = 0.3, colour = "#00BFC4") +
geom_line(data = rosette_pred2,
          aes(y = predicted, x = x, colour = species),
          size = 1.5) +
geom_ribbon(data = rosette_pred2,
           aes(y = predicted, x = x, ymin = conf.low, ymax = conf.high, colour = species, fill = species),
           alpha = 0.1) +
labs(y = "Maximum rosette size (mm)",
     x = "Cotyledon size (mm)",
     title = "B") +
scale_x_continuous(expand = c(0, 0), limits = c(0,26)) +
scale_y_continuous(expand = c(0, 0), limits = c(0,150)) +
theme_cowplot() +
theme(axis.title.y=element_blank(),
      # axis.text.y=element_blank(),
      legend.position = "none",
      legend.title = element_blank())

C <- ggplot(data = rosette_data,
           aes(x = time_after_germ, y = Rosette_size)) +
geom_point(data = rosette_data %>%
           filter(species == "mac"),
           aes(x = time_after_germ, y = Rosette_size),
           size = 3, alpha = 0.3, colour = "#F8766D") +
geom_point(data = rosette_data %>%
           filter(species == "cor"),
           aes(x = time_after_germ, y = Rosette_size),
           size = 3, alpha = 0.3, colour = "#00BFC4") +
geom_line(data = rosette_pred3,
          aes(y = predicted, x = x, colour = species),

```

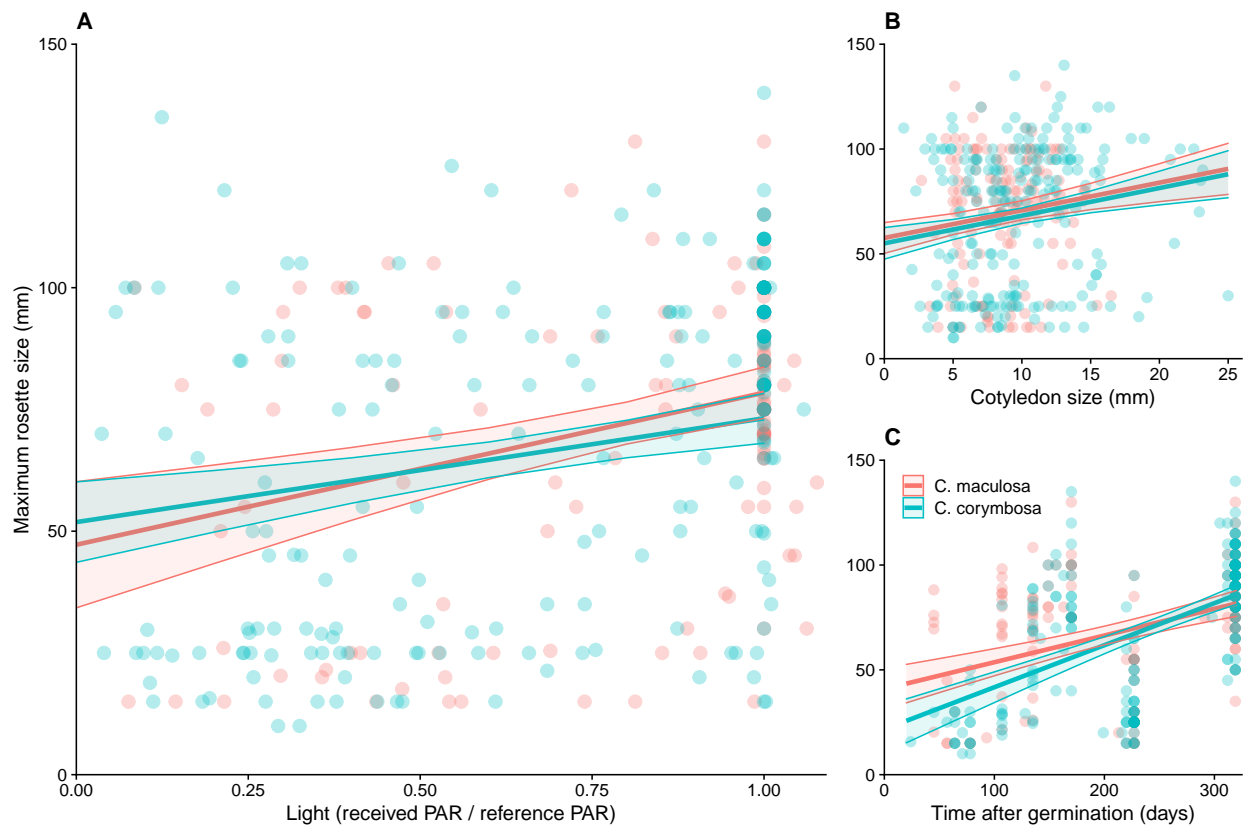
```

      size = 1.5) +
geom_ribbon(data = rosette_pred3,
          aes(y = predicted, x = x, ymin = conf.low, ymax = conf.high, colour = species, fill = spe
          alpha = 0.1) +
labs(y = "Maximum rosette size (mm)",
     x = "Time after germination (days)",
     title = "C") +
scale_x_continuous(expand = c(0, 0), limits = c(0,325)) +
scale_y_continuous(expand = c(0, 0), limits = c(0,150)) +
theme_cowplot() +
theme(axis.title.y=element_blank(),
      legend.position = c(0.05,0.9),
      legend.title = element_blank())

layout <- rbind(c(1,1,2),
               c(1,1,3))

ABC <- grid.arrange(A,B,C, layout_matrix=layout)

```



```

ggsave(filename="Figure1.png",
        plot = ABC,
        dpi = 600,
        width = 12,
        height = 8,
        type="cairo-png")

```

```
rm(A, B, C, ABC, rosette_mod, rosette_pred1, rosette_pred2, rosette_pred3)
```