Impact of food availability and light on A. lixula larval growth - data analysis

```
library('dplyr')
```

```
## Warning: package 'dplyr' was built under R version 4.4.2
```

```
##
## Adjuntando el paquete: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library('readr')
```

```
## Warning: package 'readr' was built under R version 4.4.2
```

```
library('ggplot2')
```

```
## Warning: package 'ggplot2' was built under R version 4.4.2
```

```
library('knitr')
library('tidyr')
```

```
## Warning: package 'tidyr' was built under R version 4.4.2
```

```
library('emmeans')
```

```
## Welcome to emmeans.
## Caution: You lose important information if you filter this package's results.
## See '? untidy'
```

```
library('rstan')
```

```
## Cargando paquete requerido: StanHeaders
```

```
##
## rstan version 2.32.6 (Stan version 2.32.2)
```

```
## For execution on a local, multicore CPU with excess RAM we recommend calling
## options(mc.cores = parallel::detectCores()).
## To avoid recompilation of unchanged Stan programs, we recommend calling
## rstan_options(auto_write = TRUE)
## For within-chain threading using `reduce_sum()` or `map_rect()` Stan functions,
## change `threads_per_chain` option:
## rstan_options(threads_per_chain = 1)
```

```
## Do not specify '-march=native' in 'LOCAL_CPPFLAGS' or a Makevars file
```

```
##
## Adjuntando el paquete: 'rstan'

## The following object is masked from 'package:tidyr':
##
##     extract
```

```
rstan::rstan_options(auto_write = TRUE)
library('brms')
```

```
## Warning: package 'brms' was built under R version 4.4.2

## Cargando paquete requerido: Rcpp

## Loading 'brms' package (version 2.22.0). Useful instructions
## can be found by typing help('brms'). A more detailed introduction
## to the package is available through vignette('brms_overview').

##
## Adjuntando el paquete: 'brms'

## The following object is masked from 'package:rstan':
##
##     loo

## The following object is masked from 'package:stats':
##
##     ar
```

```
options(mc.cores = parallel::detectCores())  # run all cores
library('bayesplot')
```

```
## Warning: package 'bayesplot' was built under R version 4.4.2

## This is bayesplot version 1.11.1

## - Online documentation and vignettes at mc-stan.org/bayesplot

## - bayesplot theme set to bayesplot::theme_default()

##    * Does _not_ affect other ggplot2 plots

##    * See ?bayesplot_theme_set for details on theme setting

##
## Adjuntando el paquete: 'bayesplot'

## The following object is masked from 'package:brms':
##
##     rhat
```

```
library('marginaleffects')
library('ggdist')
```

```
## Warning: package 'ggdist' was built under R version 4.4.2

##
## Adjuntando el paquete: 'ggdist'

## The following objects are masked from 'package:brms':
##
##     dstudent_t, pstudent_t, qstudent_t, rstudent_t
```

```
nchain = 4
niter  = 2500
moment_matching = TRUE
```

1. Data overview

Making a data set containing only the data pertaining to *A. lixula*.

```
Al_df <-  read_delim("larval_morphology.csv", delim = ",",
                  col_types = "fffnfiffffiniif")
Al_df = drop_na(Al_df, length)
# make Al_df$larva by concatenating Al_df$species with Al_df$larva
Al_df$larva <- as.factor(paste0(Al_df$species, Al_df$larva))
Al_df <- Al_df[Al_df$species == "Al",]
#ensure correct order for levels
Al_df<-Al_df %>% mutate(lit = factor(lit, levels = c("DD", "LD", "LL")))
Al_df<-Al_df %>% mutate(rod = factor(rod, levels = c("BR", "PO", "ALA")))
head(Al_df)
```

```
## # A tibble: 6 x 15
##   larva side  rod   length ate   Food_conc Food_species  fed   lit   condition
##   <fct> <fct> <fct>  <dbl> <fct>     <int> <fct>         <fct> <fct> <fct>
## 1 Al1   R     BR      96.7 NO           10 D_tertiolecta Fed   LD    FSW
## 2 Al1   R     PO     112.  NO           10 D_tertiolecta Fed   LD    FSW
## 3 Al1   L     BR      94.4 NO           10 D_tertiolecta Fed   LD    FSW
## 4 Al1   L     PO     110.  NO           10 D_tertiolecta Fed   LD    FSW
## 5 Al2   R     BR      89.8 YES          10 D_tertiolecta Fed   LD    FSW
## 6 Al2   R     PO     111.  YES          10 D_tertiolecta Fed   LD    FSW
## # i 5 more variables: larvae_per_well <int>, lar_ml <dbl>, hpf <int>,
## #   dpf <int>, species <fct>
```

```
Al_df <- Al_df[Al_df$length > 0,]
Al_df <- Al_df[! is.na(Al_df$length),]
print(paste0('There are ', dim(Al_df)[1], ' measures from ', length(unique(Al_df$larva)), ' individual l
```

```
## [1] "There are 729 measures from 161 individual larvae."
```

The chunk below produces a data summary for each condition. In column n we also calculate the number of observations.

```
Al_df %>% group_by(species,dpf, lit, rod, fed, lar_ml) %>%
  summarise(mean = mean(length, na.rm = TRUE), stdev = sd(length, na.rm = TRUE),
            n = n())
```

```
## `summarise()` has grouped output by 'species', 'dpf', 'lit', 'rod', 'fed'. You
## can override using the `.groups` argument.
```

```
## # A tibble: 23 x 9
## # Groups:   species, dpf, lit, rod, fed [23]
##    species   dpf lit   rod   fed     lar_ml  mean stdev     n
##    <fct>   <int> <fct> <fct> <fct>    <dbl> <dbl> <dbl> <int>
##  1 Al          3 LD    BR    Fed       12.5  95.9  4.59    35
##  2 Al          3 LD    BR    Starved   12.5  96.0  8.36    25
##  3 Al          3 LD    PO    Fed       12.5 115.  19.5     36
##  4 Al          3 LD    PO    Starved   12.5 127.  13.7     24
##  5 Al          3 LD    ALA   Starved   12.5  80.0  7.01     5
```

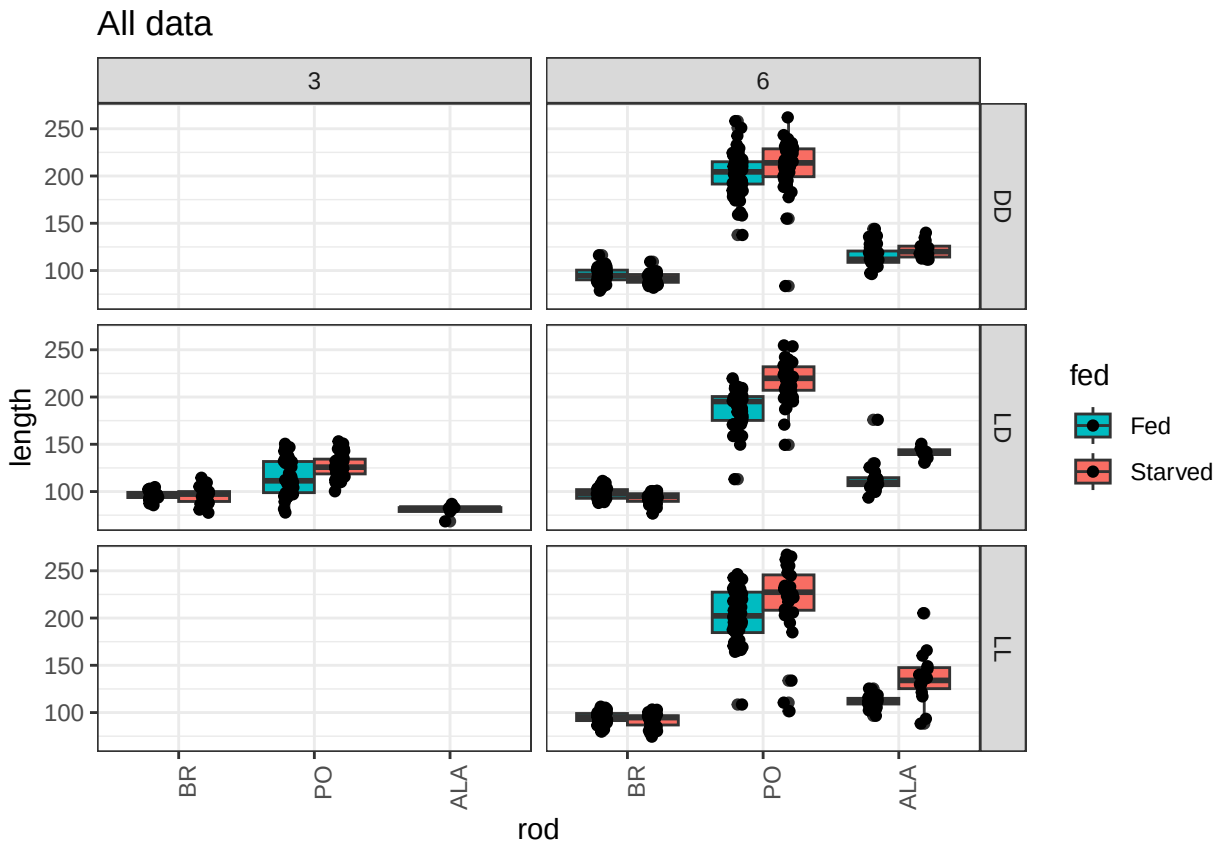
```
##  6 Al          6 DD    BR    Fed       12.5  95.2  7.31    54
##  7 Al          6 DD    BR    Starved   12.5  91.9  5.58    40
##  8 Al          6 DD    PO    Fed       12.5 202.  23.0     53
##  9 Al          6 DD    PO    Starved   12.5 210.  29.0     40
## 10 Al          6 DD    ALA   Fed       12.5 116.  10.7     36
## # i 13 more rows
```

Experimental setup and aim

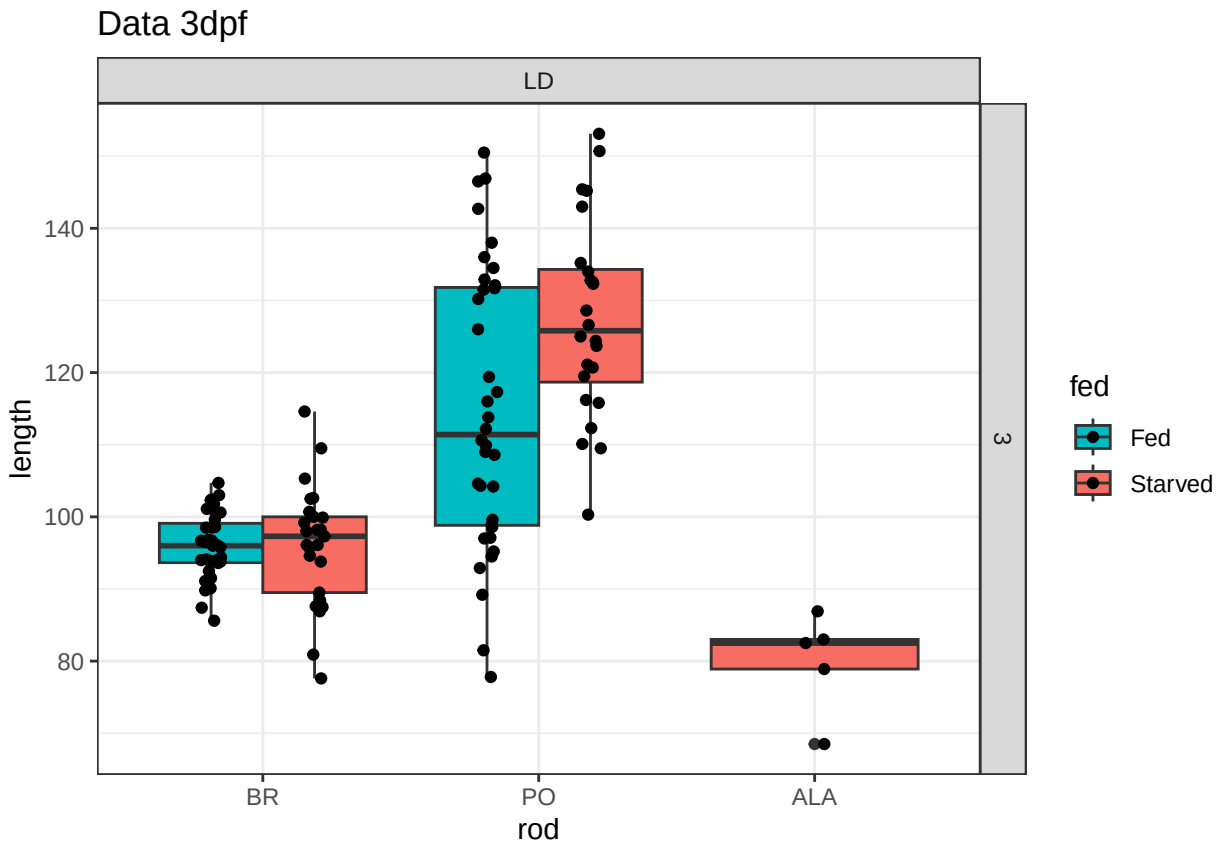
We are interested in investigating how the light dark cycle (lit) influences the phenotypic response to food availability (fed): larvae grow much shorter arms when food is abundant to save maternal storages; on the contrary, when food is scarce they develop much longer arms to maximize their capability to collect food. Three sets of spicules have been measured: Body Rod (BR), Post Oral (PO), and Anterolateral (ALA) arms .

Plot data overview

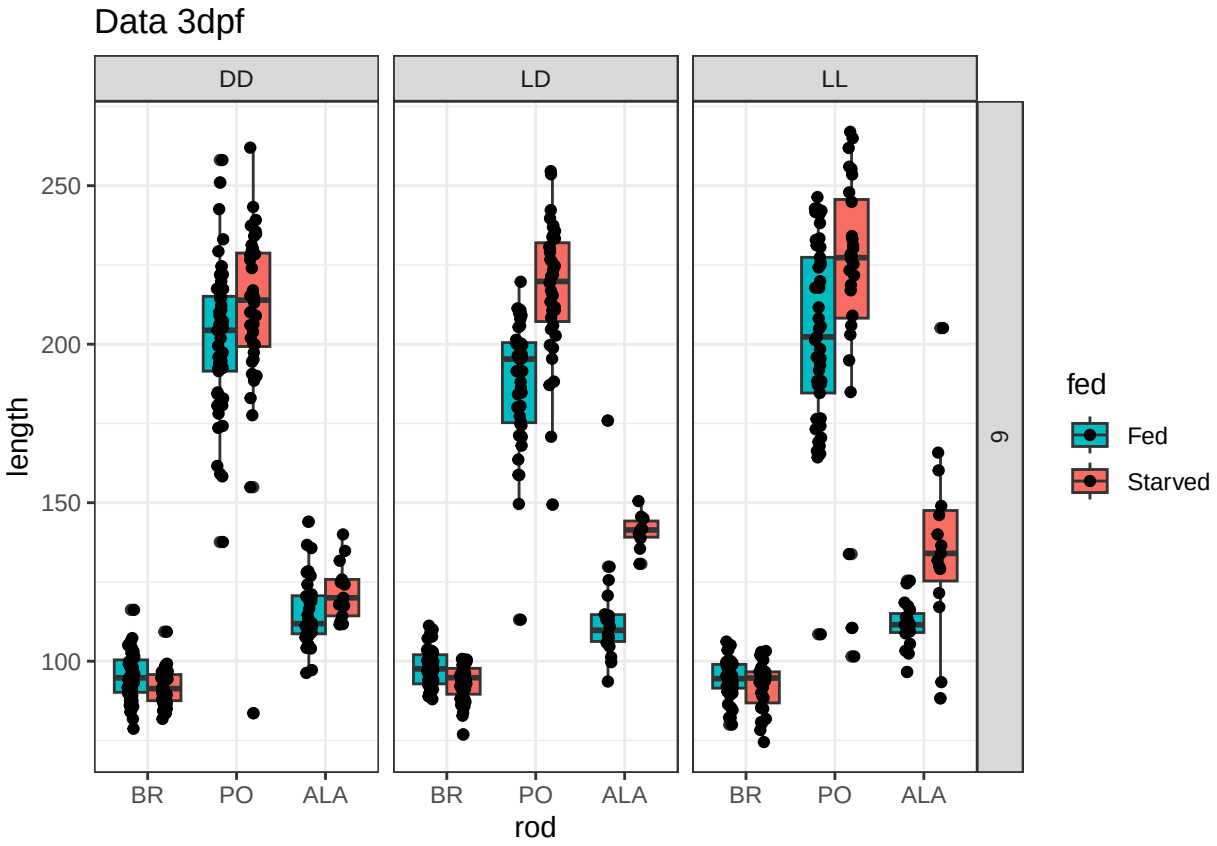
```
Al_df %>%
  ggplot(aes(y=length,x=rod, fill=fed)) +
 geom_boxplot(position = position_dodge(width = 0.75)) +
    geom_jitter(position = position_jitterdodge(jitter.width = 0.15, dodge.width = 0.75))+
    facet_grid(cols= vars(dpf),
               rows=vars(lit)
               ) +
    scale_fill_manual(values=c("#00BBC1", "#F86D63"))+
 #geom_violin()+
  theme_bw()+
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  ggtitle("All data")
```




```
Al_df %>%
  filter(dpf=="3")%>%
  ggplot(aes(y=length,x=rod, fill=fed)) +
  facet_grid(dpf~lit) +
  geom_boxplot(position = position_dodge(width = 0.75)) +
  geom_jitter(position = position_jitterdodge(jitter.width = 0.15, dodge.width = 0.75))+
  scale_fill_manual(values=c("#00BBC1", "#F86D63"))+
 #geom_violin()+
  theme_bw()+
  theme(axis.text.x = element_text(angle = 0, hjust = 0.5)) +
  ggtitle("Data 3dpf")
```




```
Al_df %>%
  filter(dpf=="6")%>%
  ggplot(aes(y=length,x=rod, fill=fed)) +
  facet_grid(dpf~lit) +
  geom_boxplot(position = position_dodge(width = 0.75)) +
  geom_jitter(position = position_jitterdodge(jitter.width = 0.15, dodge.width = 0.75))+
  scale_fill_manual(values=c("#00BBC1", "#F86D63"))+
 #geom_violin()+
  theme_bw()+
  theme(axis.text.x = element_text(angle = 0, hjust = 0.5)) +
  ggtitle("Data 3dpf")
```



For the statistical analysis we select only larvae at 6dpf.

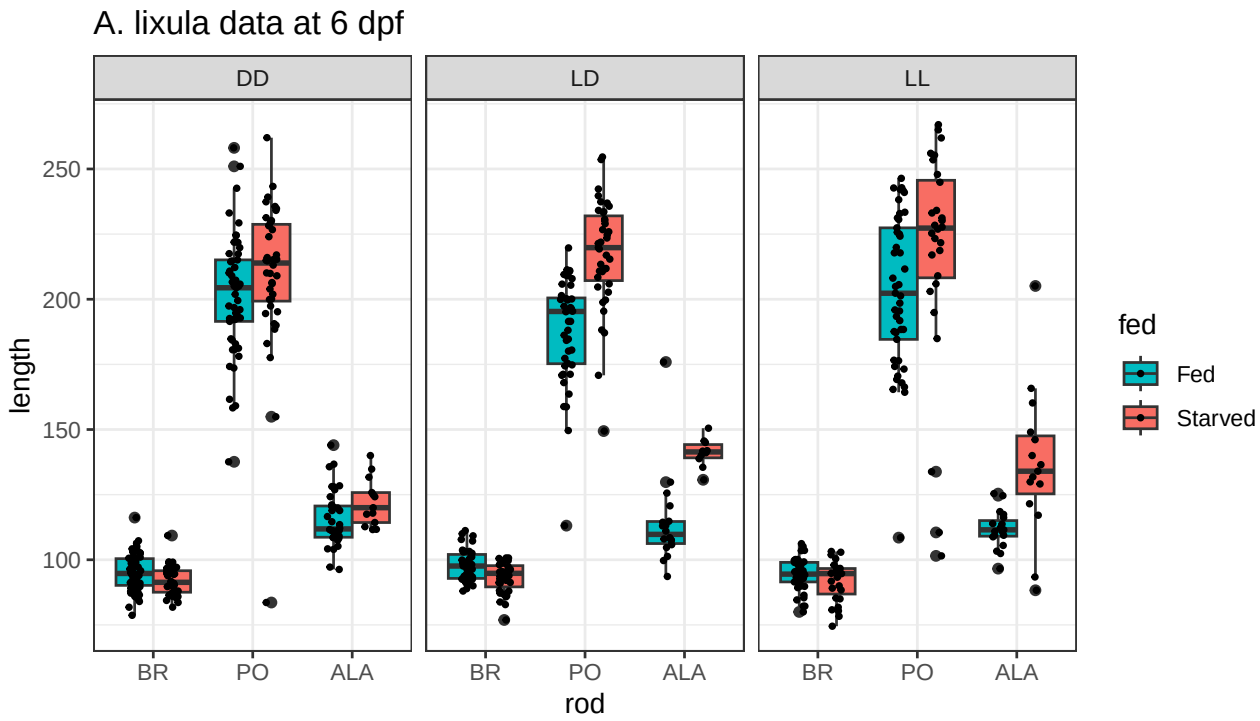
```
Al_df <- Al_df[Al_df$dpf == "6",]
Al_df
```

```
## # A tibble: 604 x 15
##    larva side  rod   length ate   Food_conc Food_species fed     lit   condition
##    <fct> <fct> <fct>  <dbl> <fct>     <int> <fct>        <fct>   <fct> <fct>
##  1 Al42  R     PO     237.  NO            0 NO           Starved LD    FSW
##  2 Al42  L     BR      85.8 NO            0 NO           Starved LD    FSW
##  3 Al42  L     PO     233.  NO            0 NO           Starved LD    FSW
##  4 Al43  R     BR     101.  NO            0 NO           Starved LD    FSW
##  5 Al43  R     PO     227.  NO            0 NO           Starved LD    FSW
##  6 Al43  R     ALA    141.  NO            0 NO           Starved LD    FSW
##  7 Al43  L     BR      86.2 NO            0 NO           Starved LD    FSW
##  8 Al43  L     PO     236.  NO            0 NO           Starved LD    FSW
##  9 Al43  L     ALA    142.  NO            0 NO           Starved LD    FSW
## 10 Al44  R     BR      95.3 NO            0 NO           Starved LD    FSW
## # i 594 more rows
## # i 5 more variables: larvae_per_well <int>, lar_ml <dbl>, hpf <int>,
## #   dpf <int>, species <fct>
```

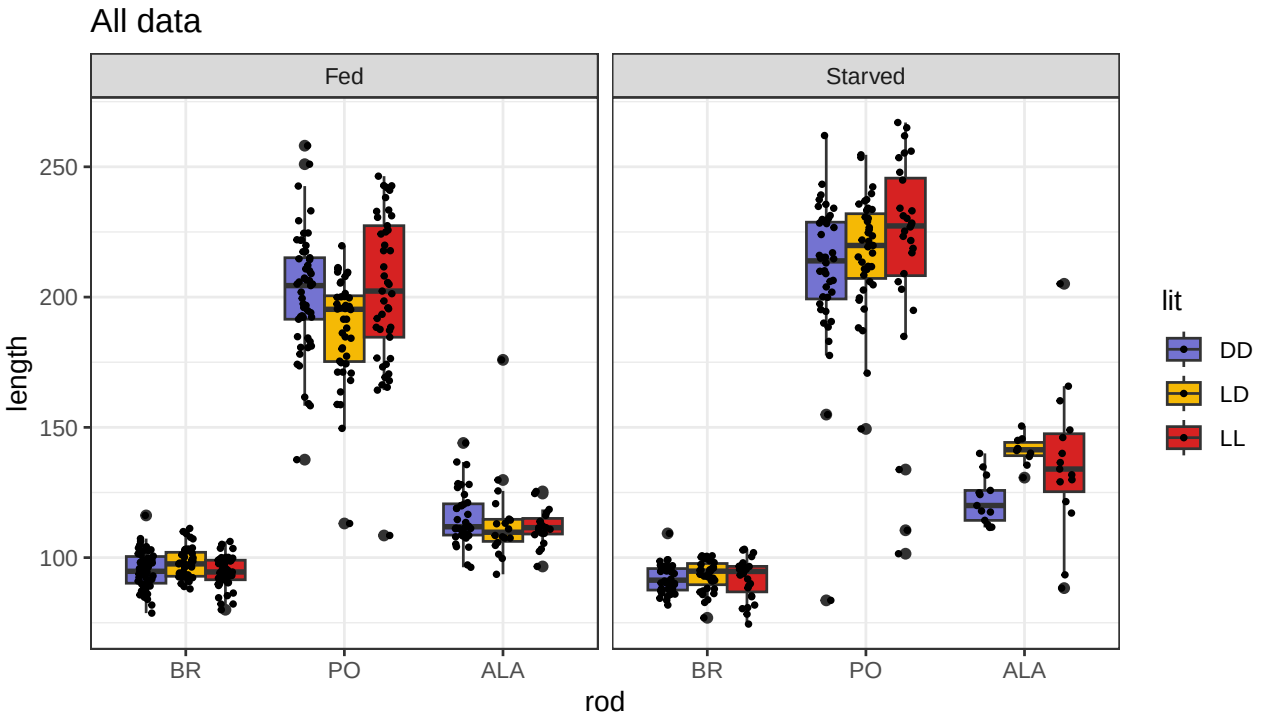
#Have a look at actual data at 6dpf to check best model

```
Al_df %>%
  ggplot(aes(y=length,x=rod, fill=fed)) +
  facet_grid(~ lit) +
    geom_boxplot(position = position_dodge(width = 0.75)) +
    geom_jitter(position = position_jitterdodge(jitter.width = 0.25, dodge.width = 0.75), size=0.7)+
```

```
  scale_fill_manual(values=c("#00BBC1", "#F86D63"))+
  theme_bw()+
  theme(axis.text.x = element_text(angle = 0, hjust = 0.5)) +
  ggtitle("A. lixula data at 6 dpf")
```




```
Al_df %>%
  ggplot(aes(y=length,x=rod, fill=lit, )) +
    facet_grid(~ fed) +
    geom_boxplot(position = position_dodge(width = 0.75)) +
    geom_jitter(position = position_jitterdodge(jitter.width = 0.25, dodge.width = 0.75), size=0.7)+
    scale_fill_manual(values=c("#7473d1", "#f5b905","#d62222" ))+
 #geom_violin()+
  theme_bw()+
  theme(axis.text.x = element_text(angle = 0, hjust = 0.5)) +
  ggtitle("All data")
```



2. Statistics

For the statistical analysis length is scaled by SD and centered at the data mean (L).

```
meanL <- mean(Al_df$length)
sdL <- sd(Al_df$length)
Al_df$L  <- as.numeric(scale(Al_df$length))
Al_df <- droplevels(Al_df)
```

Prior predictive test

Set priors on slope. Weakly informative priors are used to guide the model.

We are interested in investigating how feeding (fed), and light exposure (lit) influence arm length. Moreover, three sets of spicules have been measured Body Rod (BR), Post Oral (PO), and Anterolateral (ALA).

M0 Single intercept

Each treatment should be replicated sufficiently within each larva to capture the treatment effect accurately. Typically, having at least 3-5 measurements per treatment per larva can provide a reasonable balance between model complexity and data sufficiency.

Ideally, we would represent the data as a nested structure, with larvae nested within species. This would allow us to estimate the variance components for the species and larva levels. However, given the low number of measures per larva, it might be challenging to estimate these variance components reliably. Therefore, we will start with a simpler model that includes only the larva level as a random effect.

```
get_prior(bf(L ~  1 + (1|larva), sigma ~ 1), data=Al_df)
```

```
##                   prior     class      coef group resp  dpar nlpar lb ub
##  student_t(3, -0.5, 2.5) Intercept
##     student_t(3, 0, 2.5)        sd                                    0
```

```
##     student_t(3, 0, 2.5)        sd           larva                   0
##     student_t(3, 0, 2.5)        sd Intercept larva                   0
##     student_t(3, 0, 2.5) Intercept                       sigma
##        source
##       default
##       default
##  (vectorized)
##  (vectorized)
##       default
```

```
si_priors <- c(
  set_prior("normal(0, 0.5)", class = "Intercept"),  # prior for intercept
  set_prior("student_t(3, 0, 0.5)", class = "sd", group = "larva"),
  set_prior("student_t(3, 0, 0.5)", dpar = "sigma", class = "Intercept")
  )
```

```
si_priors <- c(
  set_prior("student_t(5, 0, 2)", class = "Intercept"),  #  prior for intercept

  set_prior("student_t(3, 0, 0.5)", class = "sd", group = "larva"),

  set_prior("student_t(5, 0, 1)", dpar = "sigma", class = "Intercept")  # prior for residual sd
)
```

The zeroth model is built to check the effect of the group level and see how the data is distributed overall. The nesting structure explicitly acknowledges the hierarchical nature of the data. This helps to avoid pseudoreplication and ensures that the estimates of variance components are not biased.

```
Al_intercept_mod <- brm(
  bf(L ~ 1 + (1|larva), sigma ~ 1),
  family = gaussian,
  data=Al_df, prior = si_priors,
  chains = nchain,
  iter = niter, warmup = niter/2,
  save_pars = save_pars(all = TRUE),
  )
Al_intercept_mod
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = log
## Formula: L ~ 1 + (1 | larva)
##          sigma ~ 1
##    Data: Al_df (Number of observations: 604)
##   Draws: 4 chains, each with iter = 2500; warmup = 1250; thin = 1;
##          total post-warmup draws = 5000
##
## Multilevel Hyperparameters:
## ~larva (Number of levels: 130)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.04      0.03     0.00     0.12 1.00     4289     3222
##
## Regression Coefficients:
##                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept           0.00      0.04    -0.08     0.08 1.00    11165     3514
## sigma_Intercept     0.00      0.03    -0.06     0.06 1.00    12035     3606
##
```

```
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
default_prior(bf(L ~  rod + (1|larva), sigma ~ rod), data=Al_df)
```

```
##                     prior     class      coef group resp  dpar nlpar lb ub
##                    (flat)         b
##                    (flat)         b    rodALA
##                    (flat)         b     rodPO
##  student_t(3, -0.5, 2.5) Intercept
##     student_t(3, 0, 2.5)        sd                                    0
##     student_t(3, 0, 2.5)        sd           larva                    0
##     student_t(3, 0, 2.5)        sd Intercept larva                    0
##                    (flat)         b                         sigma
##                    (flat)         b    rodALA               sigma
##                    (flat)         b     rodPO               sigma
##     student_t(3, 0, 2.5) Intercept                         sigma
##        source
##       default
##  (vectorized)
##  (vectorized)
##       default
##       default
##  (vectorized)
##  (vectorized)
##       default
##  (vectorized)
##  (vectorized)
##       default
```

```
priors <- c(
  set_prior("student_t(5, 0, 2)", class = "Intercept"),  #  prior for intercept
  set_prior("normal(0, 2)", class = "b"),

  set_prior("student_t(3, 0, 0.5)", class = "sd", group = "larva"),

  set_prior("student_t(5, 0, 2)", dpar = "sigma", class = "Intercept"),  # prior for residual sd
  set_prior("normal(0, 1)", class = "b", dpar="sigma")
)
```

M1 Rod model

```
Al_rod_mod <- brm(
  bf(L ~  rod + (1|larva), sigma ~ rod),
  family = gaussian,
  data=Al_df, prior = priors,
  chains = nchain,
  iter = niter, warmup = niter/2,
  save_pars = save_pars(all = TRUE),
  control = list(adapt_delta =0.99),
  )
Al_rod_mod
```

```
##  Family: gaussian
```

```
##   Links: mu = identity; sigma = log
## Formula: L ~ rod + (1 | larva)
##          sigma ~ rod
##    Data: Al_df (Number of observations: 604)
##   Draws: 4 chains, each with iter = 2500; warmup = 1250; thin = 1;
##          total post-warmup draws = 5000
##
## Multilevel Hyperparameters:
## ~larva (Number of levels: 130)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.07      0.01     0.04     0.09 1.00     1201     1918
##
## Regression Coefficients:
##                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept          -0.91      0.01    -0.93    -0.90 1.00     5659     4013
## sigma_Intercept    -2.29      0.07    -2.42    -2.15 1.00     1472     2402
## rodPO               2.00      0.03     1.94     2.07 1.00     7545     3282
## rodALA              0.47      0.03     0.41     0.53 1.00     8145     3572
## sigma_rodPO         1.63      0.08     1.46     1.79 1.00     1973     2652
## sigma_rodALA        1.14      0.10     0.95     1.35 1.00     2250     3011
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

M2 Rod Fed model

```
Al_rod_fed_mod <- brm(
  bf(L ~  rod*fed + (1|larva), sigma ~ rod*fed),
  family = gaussian,
  data=Al_df, prior = priors,
  chains = nchain,
  iter = niter, warmup = niter/2,
  save_pars = save_pars(all = TRUE),
  control = list(adapt_delta =0.99),
  )
Al_rod_fed_mod
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = log
## Formula: L ~ rod * fed + (1 | larva)
##          sigma ~ rod * fed
##    Data: Al_df (Number of observations: 604)
##   Draws: 4 chains, each with iter = 2500; warmup = 1250; thin = 1;
##          total post-warmup draws = 5000
##
## Multilevel Hyperparameters:
## ~larva (Number of levels: 130)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.07      0.01     0.05     0.08 1.00     1209     2190
##
## Regression Coefficients:
##                         Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## Intercept                  -0.89      0.01    -0.91    -0.86 1.00     5296
```

```
## sigma_Intercept            -2.27      0.08    -2.42    -2.11 1.00     1797
## rodPO                       1.85      0.04     1.77     1.92 1.00     6537
## rodALA                      0.33      0.03     0.27     0.38 1.00     7145
## fedStarved                 -0.06      0.02    -0.10    -0.03 1.00     4858
## rodPO:fedStarved            0.37      0.07     0.24     0.50 1.00     6889
## rodALA:fedStarved           0.40      0.06     0.28     0.52 1.00     6765
## sigma_rodPO                 1.47      0.10     1.27     1.66 1.00     2357
## sigma_rodALA                0.75      0.12     0.51     1.00 1.00     3015
## sigma_fedStarved           -0.13      0.12    -0.37     0.10 1.00     2789
## sigma_rodPO:fedStarved      0.32      0.15     0.03     0.61 1.00     3058
## sigma_rodALA:fedStarved     0.61      0.19     0.23     0.98 1.00     3587
##                         Tail_ESS
## Intercept                   4008
## sigma_Intercept             1938
## rodPO                       3441
## rodALA                      4007
## fedStarved                  4084
## rodPO:fedStarved            3678
## rodALA:fedStarved           4018
## sigma_rodPO                 2666
## sigma_rodALA                3396
## sigma_fedStarved            3483
## sigma_rodPO:fedStarved      3068
## sigma_rodALA:fedStarved     3954
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

M3 Rod Lit model

```
Al_rod_lit_mod <- brm(
  bf(L ~  rod*lit + (1|larva), sigma ~ rod*lit),
  family = gaussian,
  data=Al_df, prior = priors,
  chains = nchain,
  iter = niter, warmup = niter/2,
  control = list(adapt_delta =0.99),
  save_pars = save_pars(all = TRUE)
  )
Al_rod_lit_mod
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = log
## Formula: L ~ rod * lit + (1 | larva)
##          sigma ~ rod * lit
##    Data: Al_df (Number of observations: 604)
##   Draws: 4 chains, each with iter = 2500; warmup = 1250; thin = 1;
##          total post-warmup draws = 5000
##
## Multilevel Hyperparameters:
## ~larva (Number of levels: 130)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.06      0.01     0.04     0.08 1.00      737      640
```

```
##
## Regression Coefficients:
##                     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept              -0.92      0.01    -0.95    -0.89 1.00     3699     4060
## sigma_Intercept        -2.21      0.09    -2.40    -2.03 1.00     1553     2801
## rodPO                   2.01      0.05     1.91     2.11 1.00     3816     3214
## rodALA                  0.42      0.03     0.36     0.48 1.00     5253     3913
## litLD                   0.03      0.02    -0.01     0.08 1.00     3601     4007
## litLL                  -0.01      0.02    -0.05     0.04 1.00     3537     3696
## rodPO:litLD            -0.09      0.07    -0.24     0.05 1.00     4306     3713
## rodALA:litLD            0.08      0.08    -0.07     0.23 1.00     6431     3625
## rodPO:litLL             0.08      0.09    -0.10     0.26 1.00     5160     3741
## rodALA:litLL            0.11      0.08    -0.05     0.27 1.00     5985     3984
## sigma_rodPO             1.45      0.12     1.21     1.68 1.00     2061     2947
## sigma_rodALA            0.59      0.15     0.30     0.90 1.00     2141     3180
## sigma_litLD            -0.09      0.13    -0.35     0.17 1.00     2014     2782
## sigma_litLL            -0.10      0.14    -0.38     0.19 1.00     1816     3313
## sigma_rodPO:litLD       0.08      0.18    -0.25     0.43 1.00     2216     3243
## sigma_rodALA:litLD      0.68      0.22     0.23     1.12 1.00     2516     3656
## sigma_rodPO:litLL       0.41      0.18     0.05     0.76 1.00     2310     3748
## sigma_rodALA:litLL      0.85      0.22     0.41     1.29 1.00     2533     3802
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

M4 Rod Fed Lit model

```
Al_rod_fed_lit_mod <- brm(
  bf(L ~  rod*fed*lit + (1|larva), sigma ~ rod*fed*lit),
  family = gaussian,
  data=Al_df, prior = priors,
  chains = nchain,
  iter = niter, warmup = niter/2,
  control=list(adapt_delta=0.999),
  save_pars = save_pars(all = TRUE)
  )
Al_rod_fed_lit_mod
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = log
## Formula: L ~ rod * fed * lit + (1 | larva)
##          sigma ~ rod * fed * lit
##    Data: Al_df (Number of observations: 604)
##   Draws: 4 chains, each with iter = 2500; warmup = 1250; thin = 1;
##          total post-warmup draws = 5000
##
## Multilevel Hyperparameters:
## ~larva (Number of levels: 130)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.06      0.01     0.04     0.08 1.00     1006     2073
##
## Regression Coefficients:
##                              Estimate Est.Error l-95% CI u-95% CI Rhat
```

```
## Intercept                         -0.90      0.02    -0.93    -0.86 1.00
## sigma_Intercept                   -2.14      0.11    -2.34    -1.93 1.00
## rodPO                              1.92      0.06     1.80     2.03 1.00
## rodALA                             0.36      0.04     0.29     0.44 1.00
## fedStarved                        -0.06      0.03    -0.12    -0.00 1.00
## litLD                              0.05      0.03    -0.01     0.10 1.00
## litLL                             -0.02      0.03    -0.07     0.04 1.00
## rodPO:fedStarved                   0.22      0.10     0.01     0.42 1.00
## rodALA:fedStarved                  0.17      0.06     0.04     0.30 1.00
## rodPO:litLD                       -0.28      0.08    -0.45    -0.13 1.00
## rodALA:litLD                      -0.07      0.09    -0.24     0.11 1.00
## rodPO:litLL                        0.05      0.10    -0.15     0.25 1.00
## rodALA:litLL                      -0.07      0.05    -0.18     0.03 1.00
## fedStarved:litLD                  -0.02      0.04    -0.10     0.05 1.00
## fedStarved:litLL                   0.01      0.04    -0.07     0.10 1.00
## rodPO:fedStarved:litLD             0.39      0.14     0.13     0.66 1.00
## rodALA:fedStarved:litLD            0.38      0.11     0.16     0.59 1.00
## rodPO:fedStarved:litLL             0.10      0.19    -0.28     0.48 1.00
## rodALA:fedStarved:litLL            0.36      0.15     0.05     0.66 1.00
## sigma_rodPO                        1.26      0.14     0.98     1.53 1.00
## sigma_rodALA                       0.51      0.17     0.17     0.86 1.00
## sigma_fedStarved                  -0.35      0.18    -0.69     0.00 1.00
## sigma_litLD                       -0.31      0.18    -0.65     0.03 1.00
## sigma_litLL                       -0.22      0.17    -0.54     0.11 1.00
## sigma_rodPO:fedStarved             0.57      0.22     0.14     1.01 1.00
## sigma_rodALA:fedStarved            0.22      0.29    -0.34     0.79 1.00
## sigma_rodPO:litLD                  0.18      0.22    -0.25     0.62 1.00
## sigma_rodALA:litLD                 0.78      0.27     0.26     1.32 1.00
## sigma_rodPO:litLL                  0.46      0.22     0.02     0.89 1.00
## sigma_rodALA:litLL                -0.13      0.29    -0.69     0.42 1.00
## sigma_fedStarved:litLD             0.47      0.25    -0.03     0.96 1.00
## sigma_fedStarved:litLL             0.43      0.27    -0.10     0.96 1.00
## sigma_rodPO:fedStarved:litLD      -0.63      0.31    -1.25    -0.01 1.00
## sigma_rodALA:fedStarved:litLD     -1.49      0.46    -2.37    -0.59 1.00
## sigma_rodPO:fedStarved:litLL      -0.29      0.34    -0.94     0.37 1.00
## sigma_rodALA:fedStarved:litLL      0.97      0.43     0.17     1.82 1.00
##                                Bulk_ESS Tail_ESS
## Intercept                          2306     3432
## sigma_Intercept                    1998     2688
## rodPO                              2742     3386
## rodALA                             3399     3187
## fedStarved                         2196     3081
## litLD                              2193     3139
## litLL                              2190     2761
## rodPO:fedStarved                   2759     2717
## rodALA:fedStarved                  3501     3862
## rodPO:litLD                        3011     3683
## rodALA:litLD                       3689     3157
## rodPO:litLL                        3500     3447
## rodALA:litLL                       3897     3968
## fedStarved:litLD                   2236     3244
## fedStarved:litLL                   2480     3085
## rodPO:fedStarved:litLD             2946     3307
## rodALA:fedStarved:litLD            3291     3562
```

```
## rodPO:fedStarved:litLL            3914     3597
## rodALA:fedStarved:litLL           5718     3950
## sigma_rodPO                       2410     2778
## sigma_rodALA                      2133     2934
## sigma_fedStarved                  1704     2645
## sigma_litLD                       2090     3150
## sigma_litLL                       1979     2549
## sigma_rodPO:fedStarved            1933     2437
## sigma_rodALA:fedStarved           2056     2996
## sigma_rodPO:litLD                 2346     3147
## sigma_rodALA:litLD                2738     3161
## sigma_rodPO:litLL                 2374     3117
## sigma_rodALA:litLL                2248     2766
## sigma_fedStarved:litLD            1717     2647
## sigma_fedStarved:litLL            1993     2808
## sigma_rodPO:fedStarved:litLD      2031     3032
## sigma_rodALA:fedStarved:litLD     2836     3745
## sigma_rodPO:fedStarved:litLL      2304     3533
## sigma_rodALA:fedStarved:litLL     2336     3146
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

3. Evaluate models using LOO

```
Al_intercept_mod = add_criterion(Al_intercept_mod,criterion = "loo",
                                 moment_match = TRUE, reloo = TRUE)
```

```
## No problematic observations found. Returning the original 'loo' object.
```

```
Al_rod_mod = add_criterion(Al_rod_mod, criterion = "loo",
                                 moment_match = TRUE, reloo = TRUE)
```

```
## No problematic observations found. Returning the original 'loo' object.
```

```
Al_rod_lit_mod = add_criterion(Al_rod_lit_mod, criterion = "loo",
                                 moment_match = TRUE, reloo = TRUE)
```

```
## Warning: Some Pareto k diagnostic values are too high. See help('pareto-k-diagnostic') for details.
```

```
## 2 problematic observation(s) found.
## The model will be refit 2 times.
```

```
##
## Fitting model 1 out of 2 (leaving out observation 192)
```

```
## Start sampling
```

```
##
## Fitting model 2 out of 2 (leaving out observation 305)
```

```
## Start sampling
```

```
Al_rod_fed_mod = add_criterion(Al_rod_fed_mod, criterion = "loo",
                                 moment_match = TRUE, reloo = TRUE)
```

```
## Warning: Some Pareto k diagnostic values are too high. See help('pareto-k-diagnostic') for details.
```

```
## 1 problematic observation(s) found.
## The model will be refit 1 times.

##
## Fitting model 1 out of 1 (leaving out observation 158)

## Start sampling
```

```
Al_rod_fed_lit_mod = add_criterion(Al_rod_fed_lit_mod, criterion = "loo",
                                   moment_match = TRUE, reloo = TRUE)
```

```
## Warning: Some Pareto k diagnostic values are too high. See help('pareto-k-diagnostic') for details.

## 3 problematic observation(s) found.
## The model will be refit 3 times.

##
## Fitting model 1 out of 3 (leaving out observation 158)

## Start sampling

##
## Fitting model 2 out of 3 (leaving out observation 408)

## Start sampling

##
## Fitting model 3 out of 3 (leaving out observation 442)

## Start sampling
```

```
# Perform LOO comparison
loo_results <- loo_compare(Al_intercept_mod,
                           Al_rod_mod,
                           Al_rod_fed_mod,
                           Al_rod_lit_mod,
                           Al_rod_fed_lit_mod
                           )
loo_results
```

```
##                     elpd_diff se_diff
## Al_rod_fed_lit_mod    0.0       0.0
## Al_rod_fed_mod      -20.9      10.8
## Al_rod_lit_mod      -51.7      14.1
## Al_rod_mod          -57.5      17.2
## Al_intercept_mod   -871.4      31.9
```

```
best_model_name <- rownames(loo_results)[1]
best_model <- get(best_model_name)

# Print the name of the best model
print(paste("The best model is:", best_model_name))
```

```
## [1] "The best model is: Al_rod_fed_lit_mod"
```

Model Equation

The model assumes a normal distribution for the response variable:

$$Y_i \sim \mathcal{N}(\mu_i, \sigma_i)$$

where:

Linear Predictor for the Mean (μ_i):

$$\mu_i = \beta_0 + X_i\boldsymbol{\beta} + u_{J_1[i]}Z_{1,i}$$

- β_0 (Intercept): The population-level intercept.
- $X_i\boldsymbol{\beta}$: Fixed effects (population-level predictors) with centered design matrix.
- $u_{J_1[i]}$: Random effect for group-level predictor, where $J_1[i]$ is the grouping index.
- $Z_{1,i}$: Group-level predictor values.
- $u_{J_1[i]}$ follows a normal distribution:

$$u_{J_1[i]} \sim \mathcal{N}(0, \sigma_u)$$

  where σ_u is the standard deviation of the group-level effect.

Linear Predictor for the Standard Deviation (σ_i):

$$\log(\sigma_i) = \alpha_0 + X_{\sigma,i}\boldsymbol{\alpha}$$

- α_0 (Intercept_sigma): Population-level intercept for the variance structure.
- $X_{\sigma,i}\boldsymbol{\alpha}$: Fixed effects for the variance model.

Prior Distributions:

$$\boldsymbol{\beta} \sim \mathcal{N}(0, 2), \quad \beta_0 \sim t_5(0, 2)$$

$$\boldsymbol{\alpha} \sim \mathcal{N}(0, 1), \quad \alpha_0 \sim t_5(0, 2)$$

$$\sigma_u \sim t_3(0, 0.5)$$

This structure allows the model to estimate both the mean and the variance of growth (Y) while accounting for hierarchical effects from group-level predictors.

```
#saveRDS(best_model, file = paste0("./model_objects/", best_model_name, ".rds"))
```