Impact of food availability, larval concentration and light on P. lividus larval growth - data analysis

```
library('dplyr')
library('readr')
library('ggplot2')
library('ggdist')
library('knitr')
library('tidyr')
library('emmeans')
library('rstan')
rstan::rstan_options(auto_write = TRUE)
library('brms')
options(mc.cores = parallel::detectCores())  # run all cores
library('bayesplot')
library('marginaleffects')
library('ggdist')
```

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

1. Data overview

Making a data set containing only the data on *P. lividus*.

```
Pl_df <-  read_delim("larval_morphology.csv", delim = ",",
                  col_types = "fffnfiffffiniif")
Pl_df = drop_na(Pl_df, length)
# make Pl_df$larva by concatenating Pl_df$species with Pl_df$larva
Pl_df$larva <- as.factor(paste0(Pl_df$species, Pl_df$larva))
Pl_df <- Pl_df[Pl_df$species == "Pl",]
Pl_df <- Pl_df[Pl_df$length > 0,]
Pl_df <- Pl_df[! is.na(Pl_df$length),]
#ensure correct order for levels
Pl_df<-Pl_df %>% mutate(lit = factor(lit, levels = c("DD", "LD", "LL")))
Pl_df<-Pl_df %>% mutate(rod = factor(rod, levels = c("BR", "PO", "ALA")))

print(paste0('There are ', dim(Pl_df)[1], ' measures from ', length(unique(Pl_df$larva)), ' individual l
```

```
## [1] "There are 1152 measures from 211 individual larvae."
```

```
head(Pl_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 Pl1   R     BR      199. YES          10 D_tertiolecta Fed   DD    FSW
## 2 Pl1   R     PO      160. YES          10 D_tertiolecta Fed   DD    FSW
```

```
## 3 Pl1   R     ALA     189. YES          10 D_tertiolecta Fed   DD    FSW
## 4 Pl1   L     BR      195. YES          10 D_tertiolecta Fed   DD    FSW
## 5 Pl1   L     PO      143. YES          10 D_tertiolecta Fed   DD    FSW
## 6 Pl1   L     ALA     195. YES          10 D_tertiolecta Fed   DD    FSW
## # i 5 more variables: larvae_per_well <int>, lar_ml <dbl>, hpf <int>,
## #   dpf <int>, species <fct>
```

For the statistical analysis a few transformation are required. First both length and larvae concentration (lar_ml) are scaled (L and C respectively).

```
meanL <- mean(Pl_df$length)
sdL <- sd(Pl_df$length)
meanC <- mean(Pl_df$lar_ml)
sdC <- sd(Pl_df$lar_ml)
Pl_df$L  <- as.numeric(scale(Pl_df$length))
Pl_df$C  <- as.numeric(scale(Pl_df$lar_ml))
Pl_df <- droplevels(Pl_df) # drop factor levels which are absent
head(Pl_df)
```

```
## # A tibble: 6 x 17
##   larva side  rod   length ate   Food_conc Food_species  fed   lit   condition
##   <fct> <fct> <fct>  <dbl> <fct>     <int> <fct>         <fct> <fct> <fct>
## 1 Pl1   R     BR      199. YES          10 D_tertiolecta Fed   DD    FSW
## 2 Pl1   R     PO      160. YES          10 D_tertiolecta Fed   DD    FSW
## 3 Pl1   R     ALA     189. YES          10 D_tertiolecta Fed   DD    FSW
## 4 Pl1   L     BR      195. YES          10 D_tertiolecta Fed   DD    FSW
## 5 Pl1   L     PO      143. YES          10 D_tertiolecta Fed   DD    FSW
## 6 Pl1   L     ALA     195. YES          10 D_tertiolecta Fed   DD    FSW
## # i 7 more variables: larvae_per_well <int>, lar_ml <dbl>, hpf <int>,
## #   dpf <int>, species <fct>, L <dbl>, C <dbl>
```

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

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

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

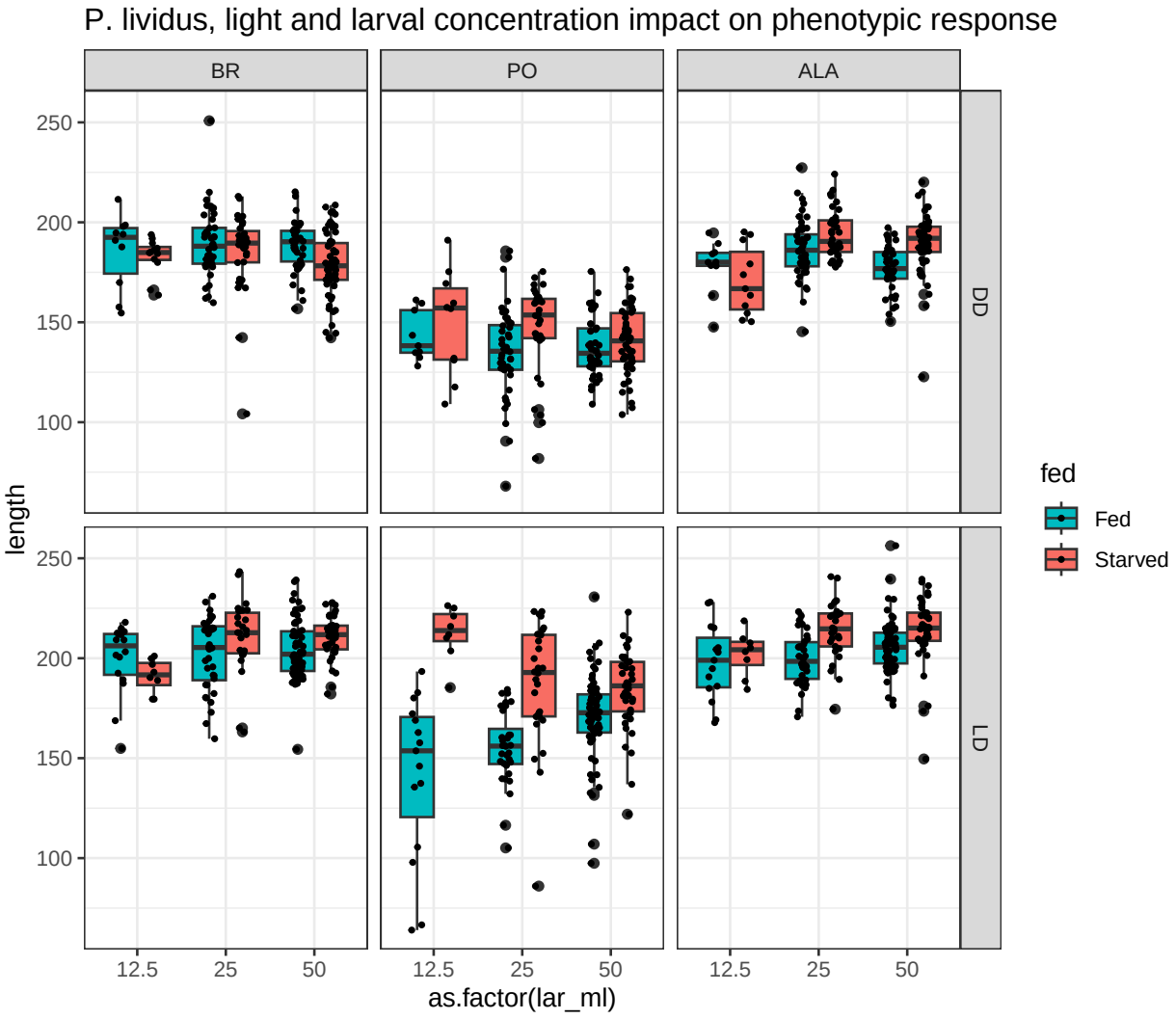
```
## # A tibble: 36 x 10
## # Groups:   species, dpf, condition, lit, lar_ml, rod [18]
##    species   dpf condition lit   lar_ml rod   fed      mean stdev     n
##    <fct>   <int> <fct>     <fct>  <dbl> <fct> <fct>   <dbl> <dbl> <int>
##  1 Pl          3 FSW       DD      12.5 BR    Fed      186. 18.8     10
##  2 Pl          3 FSW       DD      12.5 BR    Starved  183.  9.27    12
##  3 Pl          3 FSW       DD      12.5 PO    Fed      143. 12.5      9
##  4 Pl          3 FSW       DD      12.5 PO    Starved  150. 26.5     10
##  5 Pl          3 FSW       DD      12.5 ALA   Fed      178. 13.5     10
##  6 Pl          3 FSW       DD      12.5 ALA   Starved  171. 17.1     11
##  7 Pl          3 FSW       DD      25   BR    Fed      189. 16.8     42
##  8 Pl          3 FSW       DD      25   BR    Starved  185. 20.0     35
##  9 Pl          3 FSW       DD      25   PO    Fed      135. 22.6     44
## 10 Pl          3 FSW       DD      25   PO    Starved  147. 23.0     32
## # i 26 more rows
```

2. Experimental set-up and aim

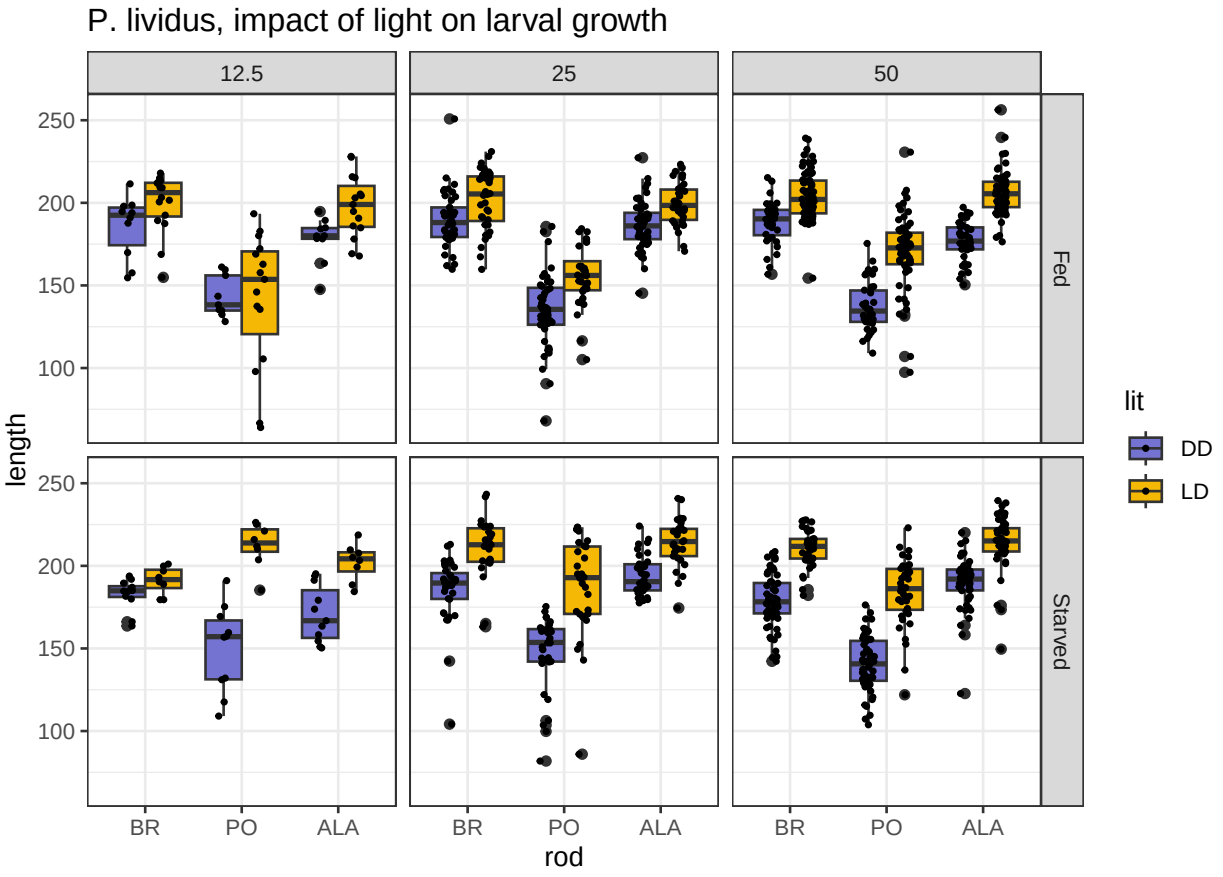
We are interested in investigating how the light dark cycle (lit) and the larval concentration (lar_ml) influence the phenotypic response to food availability (fed): larvae grow much shorter arms when food is abundant to save maternal storages; on the contrary, when food is scarce they develop much longer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

PLOT DATA OVERVIEW

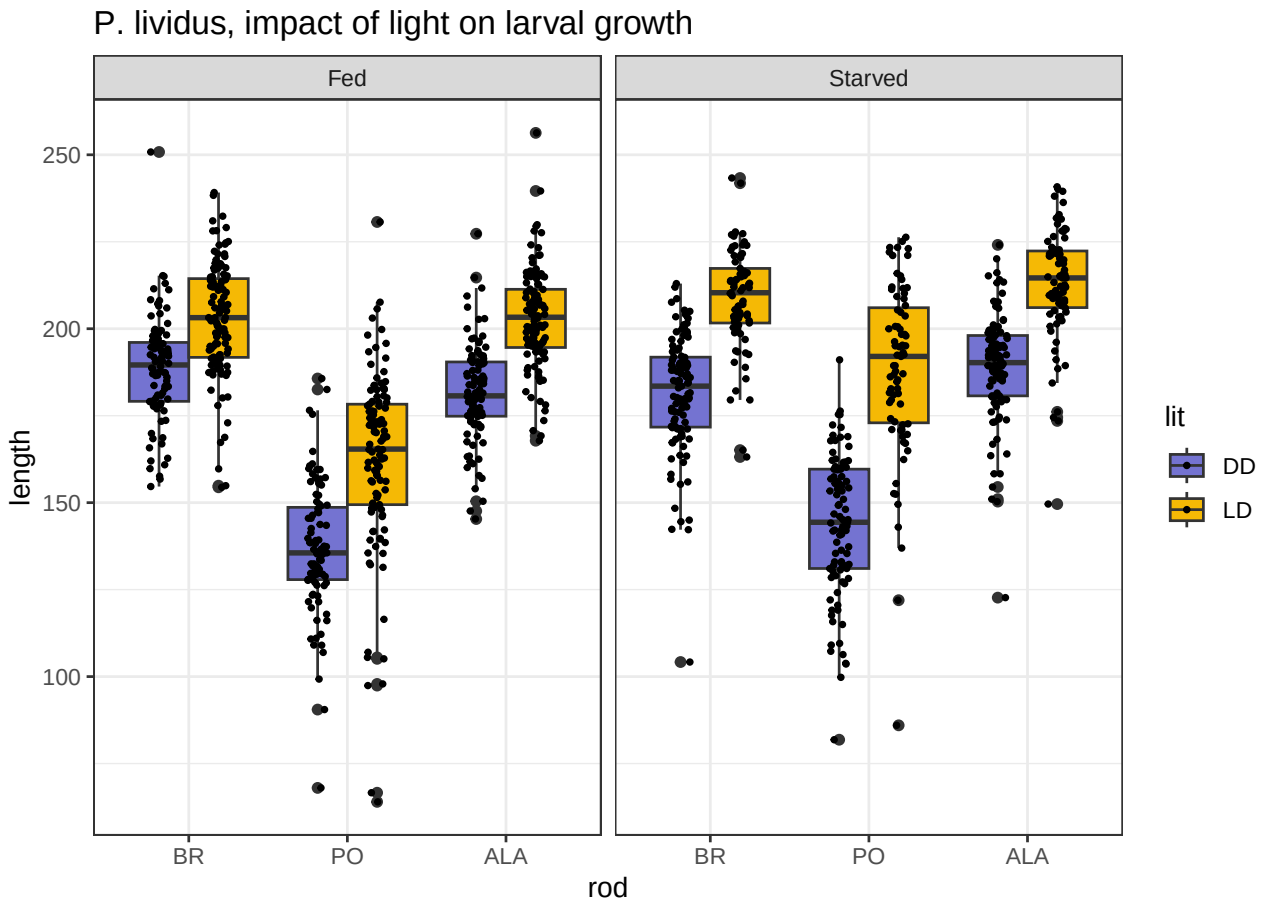
```
plot1<- Pl_df %>%
  ggplot(aes(y=length,x=as.factor(lar_ml), fill=fed)) +
  facet_grid(lit~rod ) +
     geom_boxplot(position = position_dodge(width = 0.75)) +
    geom_jitter(position = position_jitterdodge(jitter.width = 0.25, dodge.width = 0.75), size=0.7)+
  scale_fill_manual(values=c("#00BBC1", "#F86D63"))+
 #geom_violin()+
  theme_bw()+
  theme(axis.text.x = element_text(angle = 0, hjust = 0.5)) +
  ggtitle("P. lividus, light and larval concentration impact on phenotypic response")

plot1
```



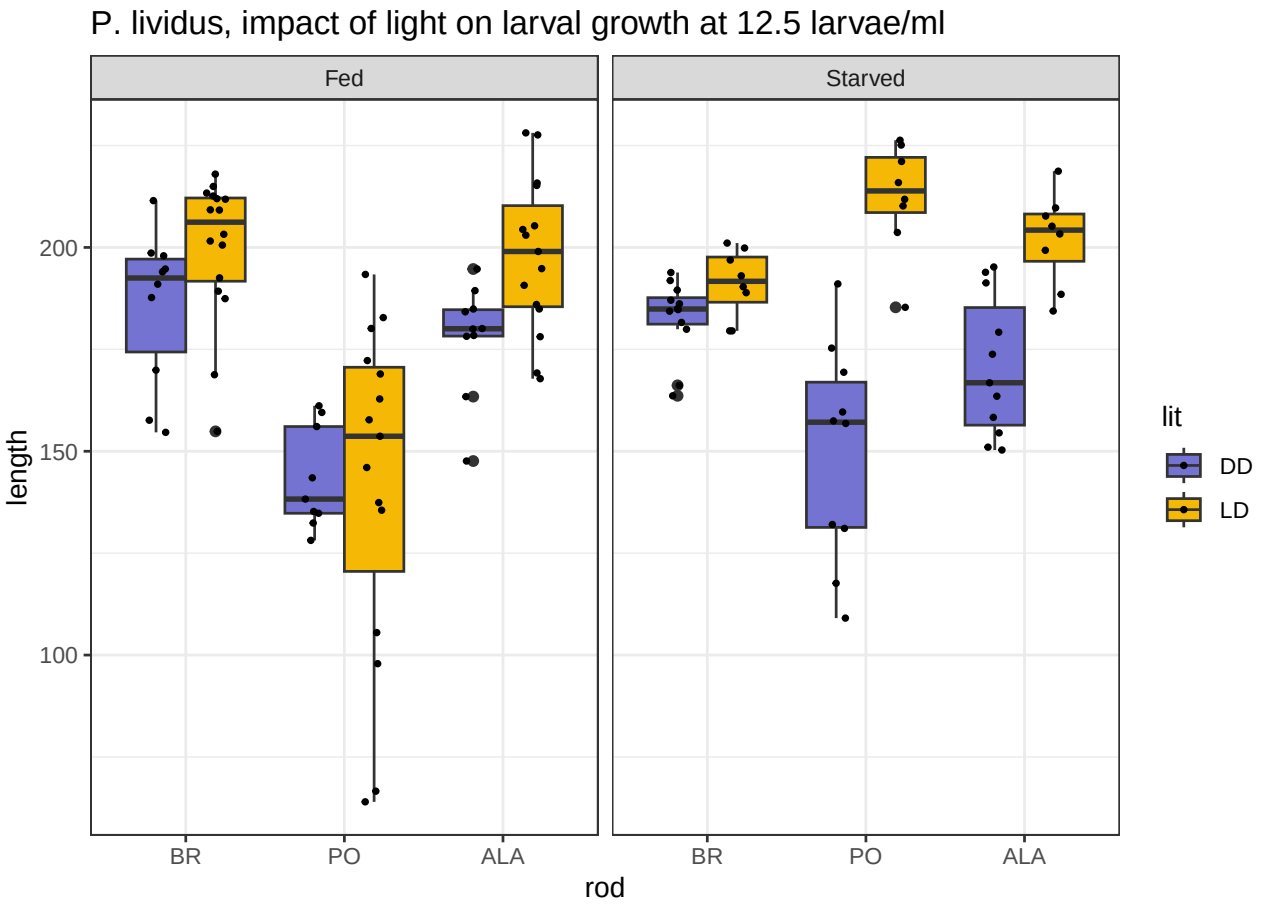

```
Pl_df %>%
  ggplot(aes(y=length,x=rod, fill=lit, )) +
    facet_grid(fed~lar_ml) +
    geom_boxplot(position = position_dodge(width = 0.75)) +
    geom_jitter(position = position_jitterdodge(jitter.width = 0.25, dodge.width = 0.75), size=0.7)+
    scale_fill_manual(values=c("#7473d1", "#f5b905","#d62222"))+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




```
Pl_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" )) +
  theme_bw()+
  theme(axis.text.x = element_text(angle = 0, hjust = 0.5)) +
  ggtitle("P. lividus, impact of light on larval growth")
```




```
Pl_df %>%
  filter(lar_ml==12.5) %>%
  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("P. lividus, impact of light on larval growth at 12.5 larvae/ml")
```



3. Statistics

Prior preditive test

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

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=Pl_df)
```

```
##                   prior     class      coef group resp  dpar nlpar lb ub
##  student_t(3, 0.2, 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"),
  set_prior("student_t(3, 0, 0.5)", class = "sd", group = "larva"), # Student's t prior for group-level
  set_prior("student_t(3, 0, 0.5)", dpar = "sigma", class = "Intercept")  # Student's t prior for resid
)
```

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.

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

```
##  Family: gaussian
##   Links: mu = identity; sigma = log
## Formula: L ~ 1 + (1 | larva)
##          sigma ~ 1
##    Data: Pl_df (Number of observations: 1152)
##   Draws: 4 chains, each with iter = 2500; warmup = 1250; thin = 1;
##          total post-warmup draws = 5000
##
## Multilevel Hyperparameters:
## ~larva (Number of levels: 211)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.47      0.04     0.40     0.55 1.00     2292     3149
##
## Regression Coefficients:
##                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept          -0.00      0.04    -0.09     0.08 1.00     4211     3828
## sigma_Intercept    -0.12      0.02    -0.16    -0.08 1.00     5969     3649
##
## 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).
```

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

```
##                   prior     class      coef group resp  dpar nlpar lb ub
##                  (flat)         b
##                  (flat)         b    rodALA
##                  (flat)         b     rodPO
##  student_t(3, 0.2, 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

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

```
##  Family: gaussian
##   Links: mu = identity; sigma = log
## Formula: L ~ rod + (1 | larva)
##          sigma ~ rod
##    Data: Pl_df (Number of observations: 1152)
##   Draws: 4 chains, each with iter = 2500; warmup = 1250; thin = 1;
##          total post-warmup draws = 5000
##
## Multilevel Hyperparameters:
## ~larva (Number of levels: 211)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.56      0.03     0.50     0.63 1.00      917     1660
```

```
##
## Regression Coefficients:
##                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept           0.41      0.04     0.33     0.49 1.01      879     1649
## sigma_Intercept    -1.12      0.09    -1.31    -0.95 1.01      677     1347
## rodPO              -1.33      0.04    -1.42    -1.24 1.00     7099     3863
## rodALA              0.00      0.03    -0.06     0.06 1.00     7849     3814
## sigma_rodPO         0.90      0.11     0.69     1.13 1.01      720     1605
## sigma_rodALA        0.43      0.14     0.17     0.70 1.01      693     1425
##
## 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 C Rod model

```
Pl_rod_C_mod <- brm(
  bf(L ~  rod*C + (1|larva), sigma ~ rod),
  family = gaussian,
  data=Pl_df, prior = priors,
  chains = nchain,
  iter = niter, warmup = niter/2,
  save_pars = save_pars(all = TRUE)
  )
Pl_rod_C_mod
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = log
## Formula: L ~ rod * C + (1 | larva)
##          sigma ~ rod
##    Data: Pl_df (Number of observations: 1152)
##   Draws: 4 chains, each with iter = 2500; warmup = 1250; thin = 1;
##          total post-warmup draws = 5000
##
## Multilevel Hyperparameters:
## ~larva (Number of levels: 211)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.56      0.03     0.50     0.63 1.01      775     1873
##
## Regression Coefficients:
##                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept           0.41      0.04     0.33     0.50 1.00      592     1295
## sigma_Intercept    -1.11      0.09    -1.30    -0.93 1.01      545     1085
## rodPO              -1.33      0.05    -1.42    -1.24 1.00     6722     3445
## rodALA              0.00      0.03    -0.06     0.06 1.00     6494     3719
## C                   0.02      0.04    -0.07     0.10 1.00      670     1233
## rodPO:C             0.04      0.05    -0.05     0.13 1.00     7031     4041
## rodALA:C            0.05      0.03    -0.01     0.11 1.00     6711     3491
## sigma_rodPO         0.89      0.11     0.68     1.13 1.01      600     1172
## sigma_rodALA        0.41      0.14     0.15     0.68 1.01      550     1132
##
## 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 C Rod Fed model

```
Pl_rod_C_fed_mod <- brm(
  bf(L ~  rod*C*fed + (1|larva), sigma ~ rod*fed),
  family = gaussian,
  data=Pl_df, prior = priors,
  chains = nchain,
  iter = niter, warmup = niter/2,
   save_pars = save_pars(all = TRUE)
  )
```

```
## Warning: Bulk Effective Samples Size (ESS) is too low, indicating posterior means and medians may be
## Running the chains for more iterations may help. See
## https://mc-stan.org/misc/warnings.html#bulk-ess
```

```
Pl_rod_C_fed_mod
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = log
## Formula: L ~ rod * C * fed + (1 | larva)
##          sigma ~ rod * fed
##    Data: Pl_df (Number of observations: 1152)
##   Draws: 4 chains, each with iter = 2500; warmup = 1250; thin = 1;
##          total post-warmup draws = 5000
##
## Multilevel Hyperparameters:
## ~larva (Number of levels: 211)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.59      0.03     0.53     0.65 1.00      767     1517
##
## Regression Coefficients:
##                          Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## Intercept                    0.47      0.06     0.35     0.58 1.00      743
## sigma_Intercept             -1.05      0.09    -1.23    -0.86 1.00     1051
## rodPO                       -1.57      0.06    -1.68    -1.46 1.00     4204
## rodALA                      -0.14      0.04    -0.22    -0.07 1.00     4225
## C                            0.05      0.06    -0.07     0.16 1.01      507
## fedStarved                  -0.11      0.09    -0.27     0.06 1.00      526
## rodPO:C                      0.19      0.05     0.09     0.30 1.00     3982
## rodALA:C                     0.02      0.04    -0.06     0.09 1.00     3941
## rodPO:fedStarved             0.54      0.09     0.36     0.71 1.00     3965
## rodALA:fedStarved            0.31      0.06     0.18     0.43 1.00     4384
## C:fedStarved                -0.06      0.09    -0.24     0.11 1.01      341
## rodPO:C:fedStarved          -0.36      0.09    -0.52    -0.19 1.00     4116
## rodALA:C:fedStarved          0.05      0.06    -0.07     0.17 1.00     3990
## sigma_rodPO                  0.72      0.12     0.49     0.96 1.00     1162
## sigma_rodALA                 0.16      0.14    -0.12     0.45 1.00     1031
## sigma_fedStarved            -0.46      0.15    -0.74    -0.14 1.00      787
## sigma_rodPO:fedStarved       0.60      0.19     0.23     0.96 1.00      862
## sigma_rodALA:fedStarved      0.87      0.21     0.44     1.27 1.00      816
##                          Tail_ESS
## Intercept                    1417
## sigma_Intercept              1931
## rodPO                        3879
## rodALA                       3737
```

```
## C                           1026
## fedStarved                   942
## rodPO:C                     3592
## rodALA:C                    3640
## rodPO:fedStarved            3342
## rodALA:fedStarved           3360
## C:fedStarved                 865
## rodPO:C:fedStarved          3697
## rodALA:C:fedStarved         3887
## sigma_rodPO                 2203
## sigma_rodALA                1792
## sigma_fedStarved            1246
## sigma_rodPO:fedStarved      1471
## sigma_rodALA:fedStarved     1286
##
## 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 C Rod Lit model

```
Pl_rod_C_lit_mod <- brm(
  bf(L ~  rod*C*lit + (1|larva), sigma ~ rod*lit),
  family = gaussian,
  data=Pl_df, prior = priors,
  chains = nchain,
  iter = niter, warmup = niter/2,
   save_pars = save_pars(all = TRUE)
  )
Pl_rod_C_lit_mod
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = log
## Formula: L ~ rod * C * lit + (1 | larva)
##          sigma ~ rod * lit
##    Data: Pl_df (Number of observations: 1152)
##   Draws: 4 chains, each with iter = 2500; warmup = 1250; thin = 1;
##          total post-warmup draws = 5000
##
## Multilevel Hyperparameters:
## ~larva (Number of levels: 211)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.38      0.03     0.32     0.44 1.00      610     1370
##
## Regression Coefficients:
##                     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept               0.07      0.05    -0.03     0.16 1.00     2368     3301
## sigma_Intercept        -0.82      0.08    -0.97    -0.67 1.00     2482     3121
## rodPO                  -1.51      0.05    -1.62    -1.41 1.00     5500     4217
## rodALA                 -0.00      0.04    -0.09     0.09 1.00     4655     3799
## C                      -0.06      0.05    -0.15     0.04 1.00     1856     2828
## litLD                   0.70      0.06     0.58     0.83 1.00     2166     2966
## rodPO:C                 0.03      0.05    -0.08     0.13 1.00     4562     4029
## rodALA:C                0.06      0.04    -0.03     0.15 1.00     4148     3802
```

```
## rodPO:litLD            0.38      0.09     0.21     0.56 1.00     7314     4378
## rodALA:litLD           0.03      0.06    -0.09     0.16 1.00     4616     3697
## C:litLD                0.14      0.07     0.01     0.27 1.00     1764     2448
## rodPO:C:litLD          0.01      0.09    -0.16     0.18 1.00     5958     4284
## rodALA:C:litLD        -0.04      0.06    -0.16     0.09 1.00     4525     3989
## sigma_rodPO            0.30      0.10     0.10     0.51 1.00     2831     3738
## sigma_rodALA           0.00      0.12    -0.22     0.23 1.00     2663     3610
## sigma_litLD           -0.38      0.18    -0.75    -0.07 1.00      608     1172
## sigma_rodPO:litLD      0.82      0.21     0.43     1.26 1.00      674     1334
## sigma_rodALA:litLD     0.50      0.25     0.05     1.01 1.00      671     1404
##
## 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).
```

M5 C Rod Fed Lit model

```
Pl_rod_C_fed_lit_mod <- brm(
  bf(L ~  rod*C*fed*lit + (1|larva), sigma ~ rod*fed*lit),
  family = gaussian,
  data=Pl_df, prior = priors,
  chains = nchain,
  iter = niter, warmup = niter/2,
  save_pars = save_pars(all = TRUE)
  )
Pl_rod_C_fed_lit_mod
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = log
## Formula: L ~ rod * C * fed * lit + (1 | larva)
##          sigma ~ rod * fed * lit
##    Data: Pl_df (Number of observations: 1152)
##   Draws: 4 chains, each with iter = 2500; warmup = 1250; thin = 1;
##          total post-warmup draws = 5000
##
## Multilevel Hyperparameters:
## ~larva (Number of levels: 211)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.40      0.03     0.34     0.45 1.00      850     1198
##
## Regression Coefficients:
##                              Estimate Est.Error l-95% CI u-95% CI Rhat
## Intercept                        0.21      0.07     0.06     0.35 1.00
## sigma_Intercept                 -0.87      0.09    -1.05    -0.69 1.00
## rodPO                           -1.76      0.07    -1.91    -1.62 1.00
## rodALA                          -0.27      0.06    -0.39    -0.16 1.00
## C                               -0.01      0.07    -0.16     0.13 1.00
## fedStarved                      -0.26      0.10    -0.45    -0.07 1.00
## litLD                            0.47      0.09     0.29     0.66 1.00
## rodPO:C                          0.02      0.08    -0.14     0.17 1.00
## rodALA:C                        -0.10      0.06    -0.22     0.01 1.00
## rodPO:fedStarved                 0.47      0.10     0.27     0.68 1.00
## rodALA:fedStarved                0.48      0.08     0.31     0.65 1.00
## C:fedStarved                    -0.07      0.10    -0.25     0.13 1.00
```

```
## rodPO:litLD                        0.34      0.11     0.12     0.55 1.00
## rodALA:litLD                       0.24      0.08     0.08     0.39 1.00
## C:litLD                            0.07      0.09    -0.11     0.25 1.00
## fedStarved:litLD                   0.47      0.13     0.20     0.72 1.00
## rodPO:C:fedStarved                -0.03      0.11    -0.23     0.18 1.00
## rodALA:C:fedStarved                0.26      0.09     0.09     0.43 1.00
## rodPO:C:litLD                      0.28      0.11     0.06     0.50 1.00
## rodALA:C:litLD                     0.18      0.08     0.03     0.33 1.00
## rodPO:fedStarved:litLD             0.24      0.17    -0.09     0.58 1.00
## rodALA:fedStarved:litLD           -0.31      0.13    -0.55    -0.06 1.00
## C:fedStarved:litLD                 0.15      0.13    -0.11     0.40 1.00
## rodPO:C:fedStarved:litLD          -0.61      0.17    -0.94    -0.28 1.00
## rodALA:C:fedStarved:litLD         -0.40      0.13    -0.66    -0.15 1.00
## sigma_rodPO                        0.32      0.13     0.06     0.57 1.00
## sigma_rodALA                      -0.19      0.14    -0.47     0.09 1.00
## sigma_fedStarved                  -0.13      0.16    -0.45     0.18 1.00
## sigma_litLD                       -0.24      0.16    -0.58     0.06 1.00
## sigma_rodPO:fedStarved             0.19      0.20    -0.19     0.61 1.00
## sigma_rodALA:fedStarved            0.51      0.23     0.07     0.98 1.00
## sigma_rodPO:litLD                  0.56      0.20     0.17     0.98 1.00
## sigma_rodALA:litLD                 0.45      0.24    -0.01     0.94 1.00
## sigma_fedStarved:litLD            -0.63      0.26    -1.11    -0.08 1.00
## sigma_rodPO:fedStarved:litLD       0.71      0.32     0.05     1.30 1.00
## sigma_rodALA:fedStarved:litLD      0.68      0.35    -0.04     1.33 1.00
##                                Bulk_ESS Tail_ESS
## Intercept                          1369     1902
## sigma_Intercept                    2481     3319
## rodPO                              2513     3828
## rodALA                             2283     3228
## C                                  1290     1777
## fedStarved                         1420     1922
## litLD                              1381     2050
## rodPO:C                            2743     3610
## rodALA:C                           2494     3365
## rodPO:fedStarved                   3230     3823
## rodALA:fedStarved                  2566     2993
## C:fedStarved                       1324     2315
## rodPO:litLD                        3070     3676
## rodALA:litLD                       2467     3422
## C:litLD                            1343     2112
## fedStarved:litLD                   1222     1845
## rodPO:C:fedStarved                 2950     3803
## rodALA:C:fedStarved                2850     3497
## rodPO:C:litLD                      2918     3683
## rodALA:C:litLD                     2715     3455
## rodPO:fedStarved:litLD             4099     4102
## rodALA:fedStarved:litLD            2969     3725
## C:fedStarved:litLD                 1261     1985
## rodPO:C:fedStarved:litLD           3701     4022
## rodALA:C:fedStarved:litLD          3396     3697
## sigma_rodPO                        2425     2951
## sigma_rodALA                       2731     3629
## sigma_fedStarved                   1234     1931
## sigma_litLD                        1114     2066
```

```
## sigma_rodPO:fedStarved            1436     2269
## sigma_rodALA:fedStarved           1381     2304
## sigma_rodPO:litLD                 1291     2148
## sigma_rodALA:litLD                1184     1982
## sigma_fedStarved:litLD            1015     1294
## sigma_rodPO:fedStarved:litLD      1182     1397
## sigma_rodALA:fedStarved:litLD     1211     1496
##
## 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).
```

4. Models evaluation using LOO

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

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

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

```
## Warning: Some Pareto k diagnostic values are too high. See help('pareto-k-diagnostic') for details.
## 7 problematic observation(s) found.
## The model will be refit 7 times.
##
## Fitting model 1 out of 7 (leaving out observation 114)
## Start sampling
##
## Fitting model 2 out of 7 (leaving out observation 279)
## Start sampling
##
## Fitting model 3 out of 7 (leaving out observation 340)
## Start sampling
##
## Fitting model 4 out of 7 (leaving out observation 440)
## Start sampling
##
## Fitting model 5 out of 7 (leaving out observation 490)
## Start sampling
##
## Fitting model 6 out of 7 (leaving out observation 683)
## Start sampling
##
## Fitting model 7 out of 7 (leaving out observation 1021)
## Start sampling
```

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

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

```
## 5 problematic observation(s) found.
## The model will be refit 5 times.
```

```
##
## Fitting model 1 out of 5 (leaving out observation 114)
```

```
## Start sampling
```

```
##
## Fitting model 2 out of 5 (leaving out observation 215)
```

```
## Start sampling
```

```
##
## Fitting model 3 out of 5 (leaving out observation 279)
```

```
## Start sampling
```

```
##
## Fitting model 4 out of 5 (leaving out observation 508)
```

```
## Start sampling
```

```
##
## Fitting model 5 out of 5 (leaving out observation 1021)
```

```
## Start sampling
```

```
Pl_rod_C_lit_mod = add_criterion(Pl_rod_C_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.
```

```
## 6 problematic observation(s) found.
## The model will be refit 6 times.
```

```
##
## Fitting model 1 out of 6 (leaving out observation 114)
```

```
## Start sampling
```

```
##
## Fitting model 2 out of 6 (leaving out observation 279)
```

```
## Start sampling
```

```
##
## Fitting model 3 out of 6 (leaving out observation 683)
```

```
## Start sampling
```

```
##
## Fitting model 4 out of 6 (leaving out observation 733)
```

```
## Start sampling
```

```
##
## Fitting model 5 out of 6 (leaving out observation 736)
```

```
## Start sampling
```

```
##
## Fitting model 6 out of 6 (leaving out observation 1021)

## Start sampling
```

```
Pl_rod_C_fed_mod = add_criterion(Pl_rod_C_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.

## 12 problematic observation(s) found.
## The model will be refit 12 times.

##
## Fitting model 1 out of 12 (leaving out observation 114)

## Start sampling

##
## Fitting model 2 out of 12 (leaving out observation 215)

## Start sampling

##
## Fitting model 3 out of 12 (leaving out observation 218)

## Start sampling

##
## Fitting model 4 out of 12 (leaving out observation 279)

## Start sampling

##
## Fitting model 5 out of 12 (leaving out observation 432)

## Start sampling

##
## Fitting model 6 out of 12 (leaving out observation 440)

## Start sampling

##
## Fitting model 7 out of 12 (leaving out observation 490)

## Start sampling

##
## Fitting model 8 out of 12 (leaving out observation 505)

## Start sampling

##
## Fitting model 9 out of 12 (leaving out observation 508)

## Start sampling

##
## Fitting model 10 out of 12 (leaving out observation 645)

## Start sampling

##
## Fitting model 11 out of 12 (leaving out observation 683)

## Start sampling
```

```
##
## Fitting model 12 out of 12 (leaving out observation 1021)

## Start sampling
```

```
Pl_rod_C_fed_lit_mod = add_criterion(Pl_rod_C_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.

## 20 problematic observation(s) found.
## The model will be refit 20 times.

##
## Fitting model 1 out of 20 (leaving out observation 114)

## Start sampling

##
## Fitting model 2 out of 20 (leaving out observation 279)

## Start sampling

##
## Fitting model 3 out of 20 (leaving out observation 495)

## Start sampling

##
## Fitting model 4 out of 20 (leaving out observation 508)

## Start sampling

##
## Fitting model 5 out of 20 (leaving out observation 642)

## Start sampling

##
## Fitting model 6 out of 20 (leaving out observation 645)

## Start sampling

##
## Fitting model 7 out of 20 (leaving out observation 683)

## Start sampling

##
## Fitting model 8 out of 20 (leaving out observation 716)

## Start sampling

##
## Fitting model 9 out of 20 (leaving out observation 728)

## Start sampling

##
## Fitting model 10 out of 20 (leaving out observation 733)

## Start sampling

##
## Fitting model 11 out of 20 (leaving out observation 736)

## Start sampling
```

```
##
## Fitting model 12 out of 20 (leaving out observation 782)
## Start sampling
##
## Fitting model 13 out of 20 (leaving out observation 785)
## Start sampling
##
## Fitting model 14 out of 20 (leaving out observation 800)
## Start sampling
##
## Fitting model 15 out of 20 (leaving out observation 803)
## Start sampling
##
## Fitting model 16 out of 20 (leaving out observation 807)
## Start sampling
##
## Fitting model 17 out of 20 (leaving out observation 810)
## Start sampling
##
## Fitting model 18 out of 20 (leaving out observation 813)
## Start sampling
##
## Fitting model 19 out of 20 (leaving out observation 991)
## Start sampling
##
## Fitting model 20 out of 20 (leaving out observation 1021)
## Start sampling
```

```r
# Perform LOO comparison
loo_results <- loo_compare(Pl_intercept_mod,
                           Pl_rod_mod,
                           Pl_rod_C_mod,
                           Pl_rod_C_fed_mod,
                           Pl_rod_C_lit_mod,
                           Pl_rod_C_fed_lit_mod
                           )

loo_results
```

```
##                       elpd_diff se_diff
## Pl_rod_C_fed_lit_mod    0.0       0.0
## Pl_rod_C_fed_mod      -24.7      15.6
## Pl_rod_C_lit_mod      -64.8      16.2
## Pl_rod_mod            -81.2      19.5
## Pl_rod_C_mod          -87.8      19.2
## Pl_intercept_mod     -672.2      33.5
```

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

# Save the best model to an RDS file
saveRDS(best_model, file = paste0(
  "./model_objects/", best_model_name, ".rds"))

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

```
## [1] "The best model is: Pl_rod_C_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.

```r
# Save the brms model to an RDS file
#saveRDS(best_model, file = paste0("./model_objects/", best_model_name, ".rds"))
```