Impact of food availability and light on S. purpuratus 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_match = TRUE
```

1. Data overview

Making a data set containing only the data on *S. purpuratus* larvae.

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

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

```
## [1] "There are 573 measures from 111 individual larvae."
```

```
head(Sp_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 Sp1   R     PO     105.  NO            5 D_tertiolecta Fed   LD    DMSO
## 2 Sp1   R     ALA    169.  NO            5 D_tertiolecta Fed   LD    DMSO
```

```
## 3 Sp1   L     BR     170   NO            5 D_tertiolecta Fed   LD    DMSO
## 4 Sp1   L     PO      92.7 NO            5 D_tertiolecta Fed   LD    DMSO
## 5 Sp2   R     BR     184   NO            5 D_tertiolecta Fed   LD    DMSO
## 6 Sp2   R     PO      80.9 NO            5 D_tertiolecta Fed   LD    DMSO
## # i 5 more variables: larvae_per_well <int>, lar_ml <dbl>, hpf <int>,
## #   dpf <int>, species <fct>
```

For the statistical analysis length needs to be scaled to L.

```
meanL <- mean(Sp_df$length)
sdL <- sd(Sp_df$length)

Sp_df$L  <- as.numeric(scale(Sp_df$length))
Sp_df <- droplevels(Sp_df) # drop factor levels which are absent
head(Sp_df)
```

```
## # A tibble: 6 x 16
##   larva side  rod   length ate   Food_conc Food_species  fed   lit   condition
##   <fct> <fct> <fct>  <dbl> <fct>     <int> <fct>         <fct> <fct> <fct>
## 1 Sp1   R     PO     105.  NO            5 D_tertiolecta Fed   LD    DMSO
## 2 Sp1   R     ALA    169.  NO            5 D_tertiolecta Fed   LD    DMSO
## 3 Sp1   L     BR     170   NO            5 D_tertiolecta Fed   LD    DMSO
## 4 Sp1   L     PO      92.7 NO            5 D_tertiolecta Fed   LD    DMSO
## 5 Sp2   R     BR     184   NO            5 D_tertiolecta Fed   LD    DMSO
## 6 Sp2   R     PO      80.9 NO            5 D_tertiolecta Fed   LD    DMSO
## # i 6 more variables: larvae_per_well <int>, lar_ml <dbl>, hpf <int>,
## #   dpf <int>, species <fct>, L <dbl>
```

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

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

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

```
## # A tibble: 8 x 9
## # Groups:   species, dpf, lar_ml, lit, condition [4]
##   species   dpf lar_ml lit   condition   fed      mean stdev     n
##   <fct>   <int>  <dbl> <fct> <fct>       <fct>   <dbl> <dbl> <int>
## 1 Sp          6     25 DD    DMSO        Fed      129.  36.2    71
## 2 Sp          6     25 DD    DMSO        Starved  131.  37.9    81
## 3 Sp          6     25 DD    TH_inh_10nM Fed      130.  38.1    40
## 4 Sp          6     25 DD    TH_inh_10nM Starved  130.  34.8    54
## 5 Sp          6     25 LD    DMSO        Fed      139.  34.3    96
## 6 Sp          6     25 LD    DMSO        Starved  147.  28.8    88
## 7 Sp          6     25 LD    TH_inh_10nM Fed      143.  31.1    86
## 8 Sp          6     25 LD    TH_inh_10nM Starved  142.  34.3    57
```

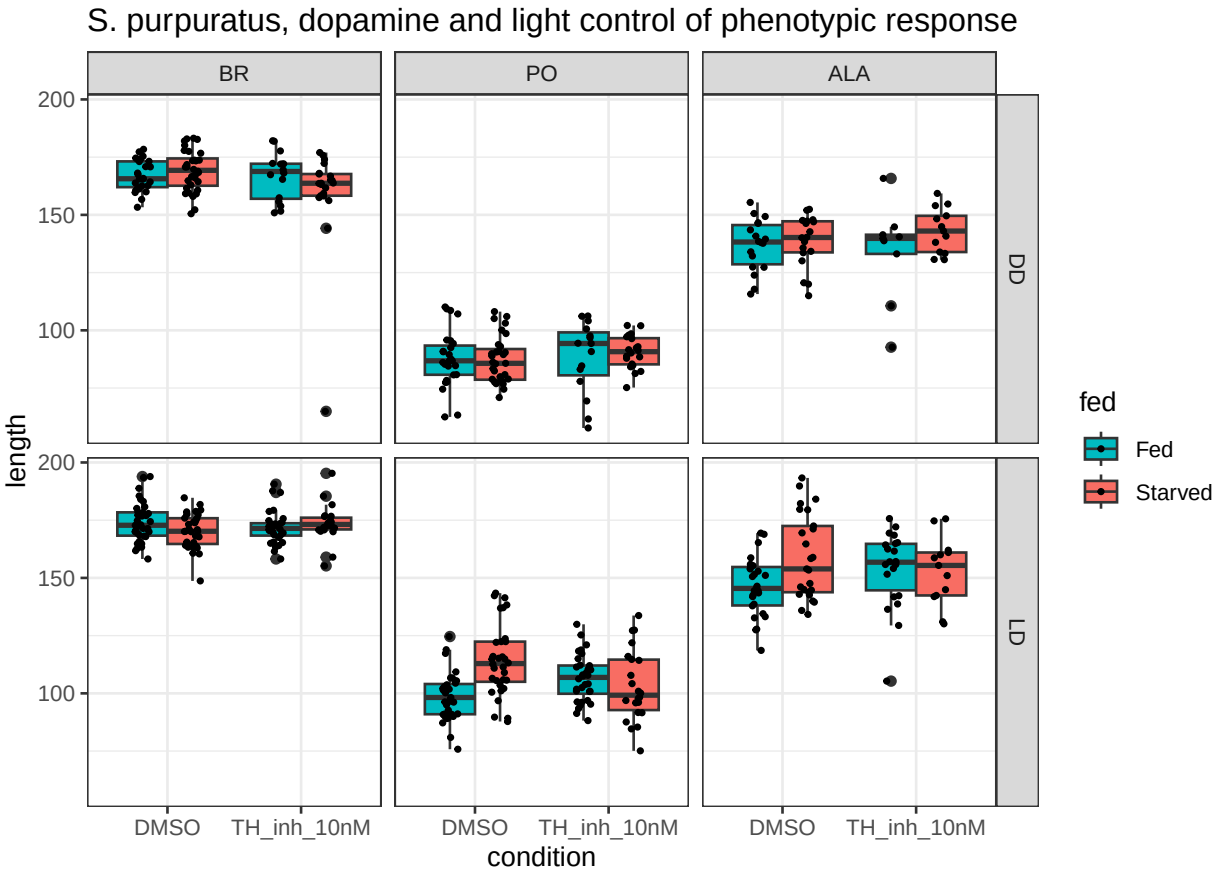
EXPERIMENTAL SETUP AND AIM

We are interested in investigating how the light-dark cycle (lit) influence the phenotypic response to food availability (fed): larvae grow much shorter arms when food is abundant enough to allow maternal storage; on the contrary, when food is scarce they develop much longer arms to maximize their capability to collect food. This response is controlled by a dopaminergic signalling. To interfere with this signalling we used an in

inhibitor of the TH (one of the enzymes involved in the dopamine synthesis) and DMSO as negative control. Three sets of spicules have been measured: Body Rod (BR), Post Oral (PO), and Anterolateral (ALA) arms.

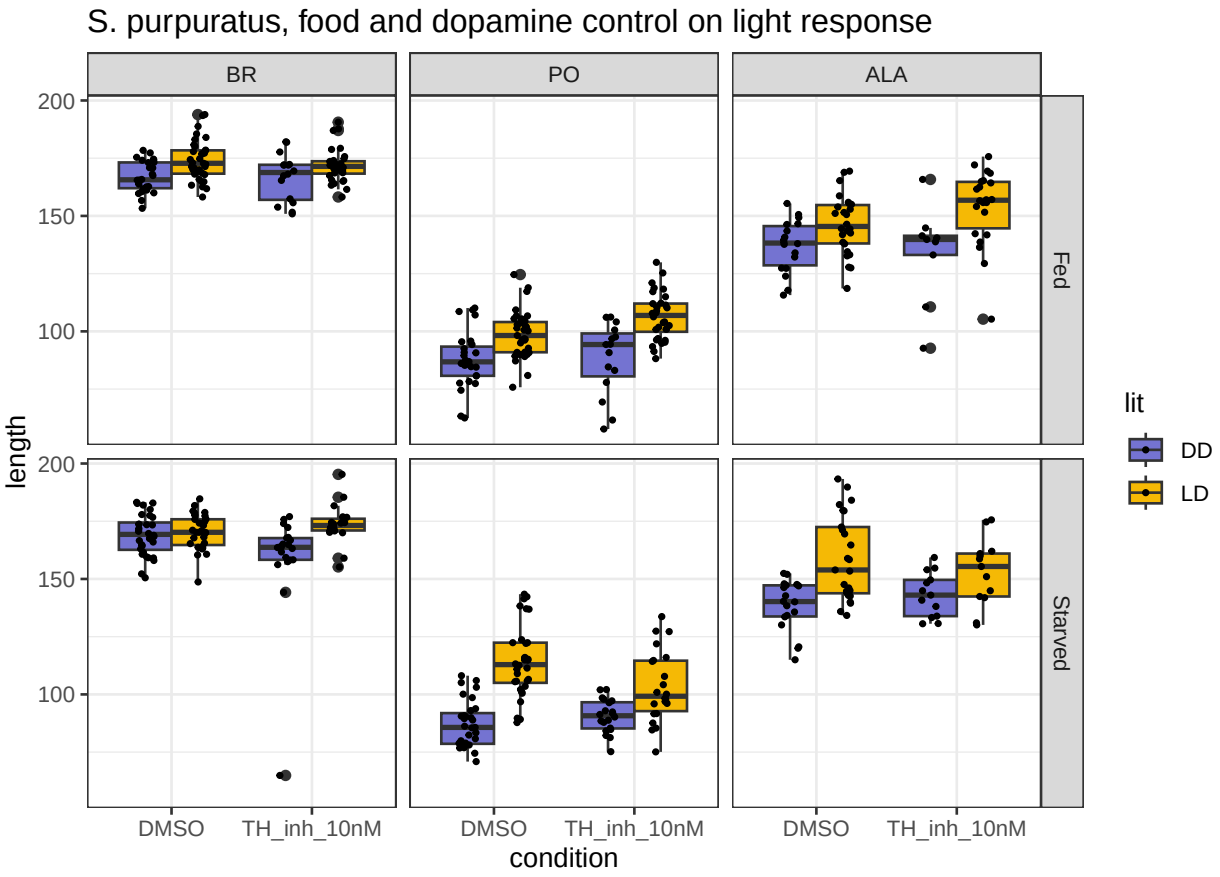
PLOT DATA OVERVIEW

```
Sp_df %>%
  ggplot(aes(y=length,x=condition, 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("S. purpuratus, dopamine and light control of phenotypic response")
```




```
Sp_df %>%
  ggplot(aes(y=length,x=condition, fill=lit, )) +
    facet_grid(fed~ 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("#7473d1", "#f5b905","#d62222"))+
 #geom_violin()+
  theme_bw()+
  theme(axis.text.x = element_text(angle = 0, hjust = 0.5)) +
```

```
  ggtitle("S. purpuratus, food and dopamine control on light response")
```



2. Statistics

PRIOR PREDICTIVE TEST

M0 Single intercept

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

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, sigma ~1), data=Sp_df)
```

```
##                  prior     class coef group resp  dpar nlpar lb ub  source
##  student_t(3, 0.2, 2.5) Intercept                                    default
##    student_t(3, 0, 2.5) Intercept                 sigma               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"), # 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.

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

```
##  Family: gaussian
##   Links: mu = identity; sigma = log
## Formula: L ~ 1 + (1 | larva)
##          sigma ~ 1
##    Data: Sp_df (Number of observations: 573)
##   Draws: 4 chains, each with iter = 2500; warmup = 1250; thin = 1;
##          total post-warmup draws = 5000
##
## Multilevel Hyperparameters:
## ~larva (Number of levels: 111)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.05      0.04     0.00     0.13 1.00     3742     2780
##
## 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    10618     3351
## sigma_Intercept     0.00      0.03    -0.06     0.06 1.00    12612     3364
##
## 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, sigma ~ rod), data=Sp_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
##                  (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
```

```
priors <- c(
  set_prior("normal(0, 1)", class = "Intercept"),  # prior for intercept
  set_prior("normal(0, 2)", class = "b"),
  set_prior("student_t(3, 0, 1)", class = "sd", group = "larva"),  # Student's t prior for group-level
  set_prior("student_t(3, 0, 1)", dpar = "sigma", class = "Intercept"),  # Student's t prior for residu

  set_prior("normal(0, 2)", class = "b", dpar = "sigma")
)
```

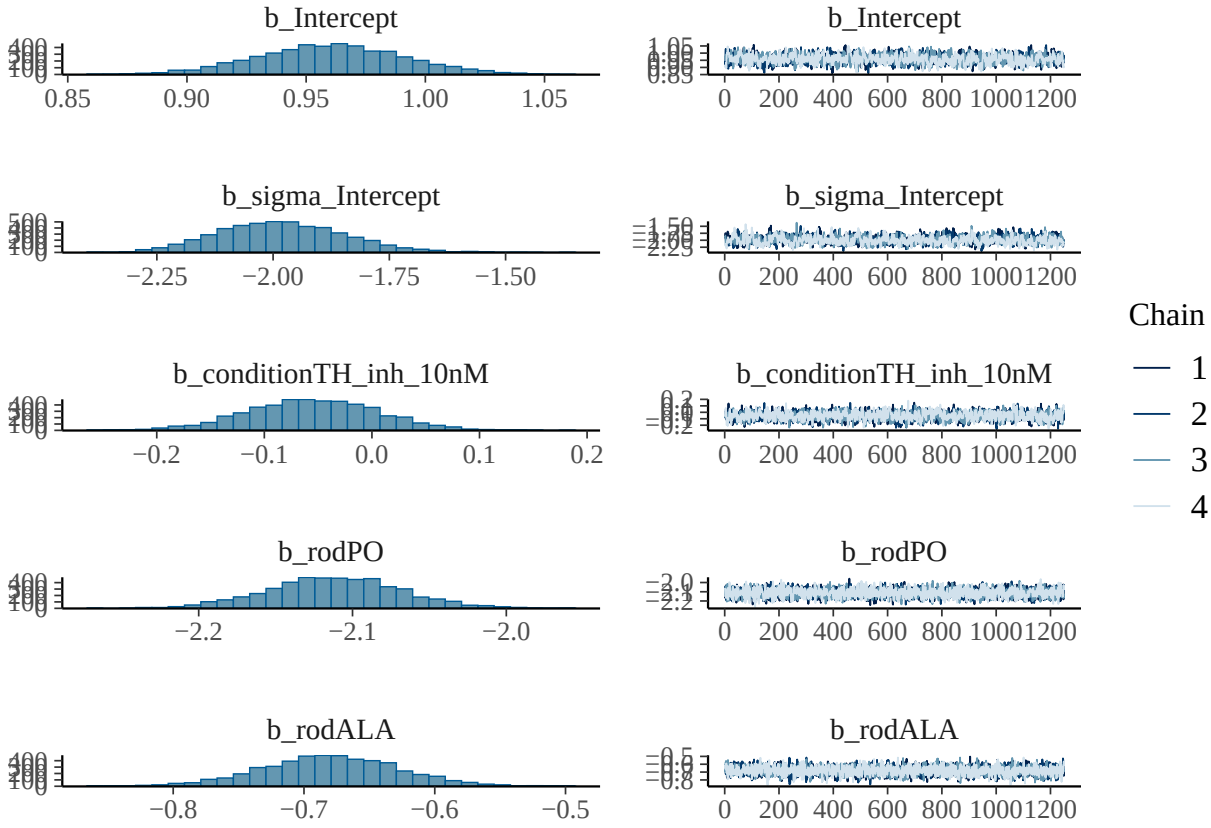
M1 Rod model

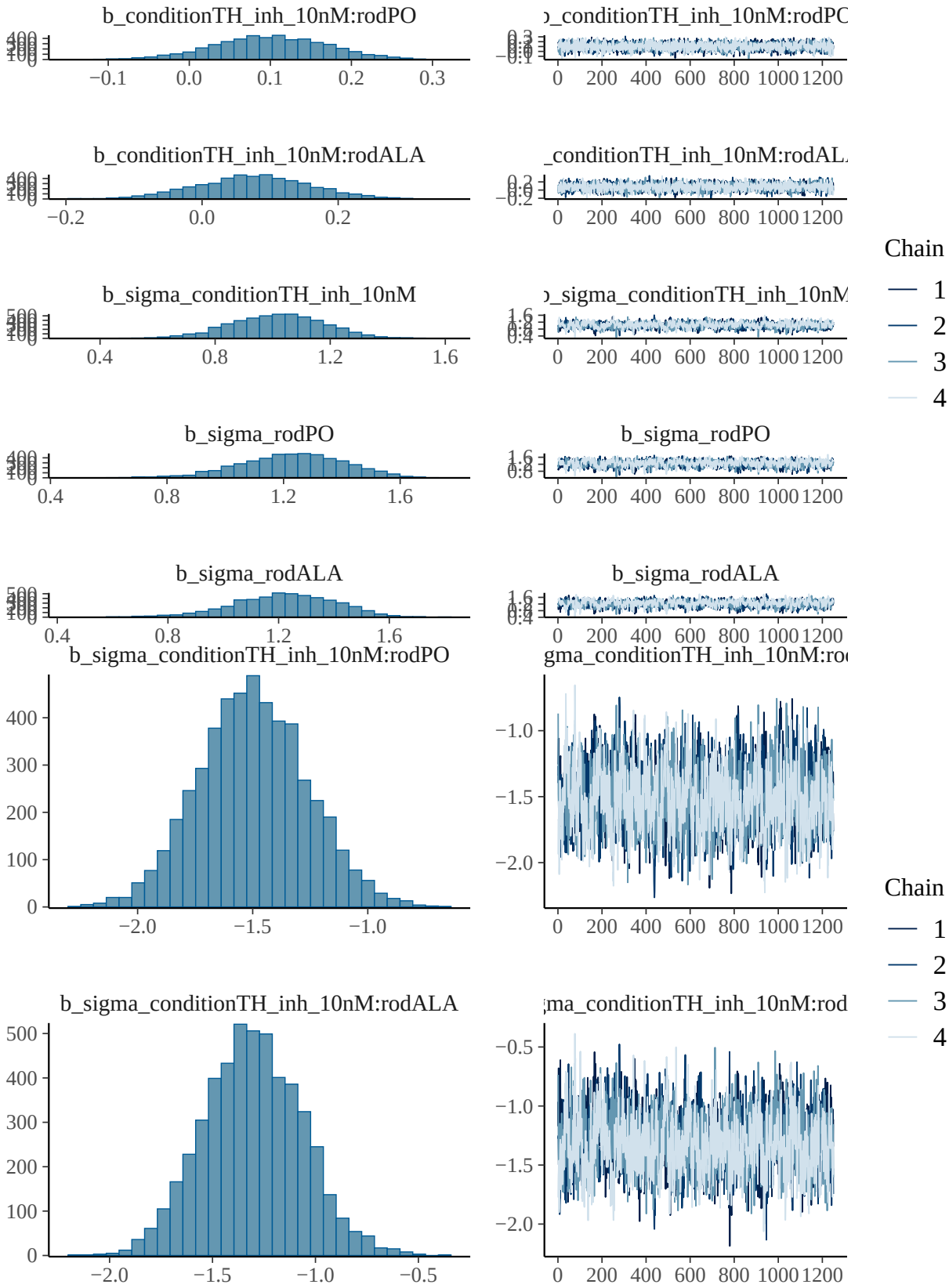
```
Sp_rod_mod <- brm(
  bf(L ~  condition*rod + (1|larva), sigma ~ condition*rod),
  family = gaussian,
  data=Sp_df, prior = priors,
  chains = nchain,
  iter = niter, warmup = niter/2,
  save_pars = save_pars(all = TRUE)
  )
Sp_rod_mod
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = log
## Formula: L ~ condition * rod + (1 | larva)
##          sigma ~ condition * rod
##    Data: Sp_df (Number of observations: 573)
##   Draws: 4 chains, each with iter = 2500; warmup = 1250; thin = 1;
##          total post-warmup draws = 5000
##
## Multilevel Hyperparameters:
## ~larva (Number of levels: 111)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.22      0.02     0.18     0.27 1.01     1118     1792
##
## Regression Coefficients:
##                                   Estimate Est.Error l-95% CI u-95% CI Rhat
## Intercept                             0.96      0.03     0.90     1.02 1.00
## sigma_Intercept                      -1.98      0.14    -2.23    -1.70 1.01
## conditionTH_inh_10nM                 -0.06      0.06    -0.18     0.06 1.00
## rodPO                                -2.11      0.04    -2.20    -2.03 1.00
## rodALA                               -0.68      0.05    -0.78    -0.58 1.00
## conditionTH_inh_10nM:rodPO            0.10      0.07    -0.04     0.23 1.00
## conditionTH_inh_10nM:rodALA           0.08      0.08    -0.09     0.24 1.00
## sigma_conditionTH_inh_10nM            1.02      0.16     0.69     1.32 1.01
## sigma_rodPO                           1.23      0.18     0.86     1.55 1.01
## sigma_rodALA                          1.22      0.18     0.83     1.55 1.01
## sigma_conditionTH_inh_10nM:rodPO     -1.50      0.24    -1.95    -1.03 1.01
## sigma_conditionTH_inh_10nM:rodALA    -1.30      0.24    -1.76    -0.82 1.01
```

```
##                                    Bulk_ESS Tail_ESS
## Intercept                              1301     2050
## sigma_Intercept                         739     1619
## conditionTH_inh_10nM                   2020     2890
## rodPO                                  4768     3790
## rodALA                                 4490     3514
## conditionTH_inh_10nM:rodPO             4103     3349
## conditionTH_inh_10nM:rodALA            4027     3530
## sigma_conditionTH_inh_10nM              774     1934
## sigma_rodPO                             810     1722
## sigma_rodALA                            809     1703
## sigma_conditionTH_inh_10nM:rodPO        891     1943
## sigma_conditionTH_inh_10nM:rodALA       927     2102
##
## 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).
```

```
plot(Sp_rod_mod, ask=FALSE, variable = "^b_", regex = TRUE)
```




b_conditionTH_inh_10nM:rodPO
b_conditionTH_inh_10nM:rodALA
b_sigma_conditionTH_inh_10nM
b_sigma_rodPO
b_sigma_rodALA
b_sigma_conditionTH_inh_10nM:rodPO
b_sigma_conditionTH_inh_10nM:rodALA
Chain
1
2
3
4

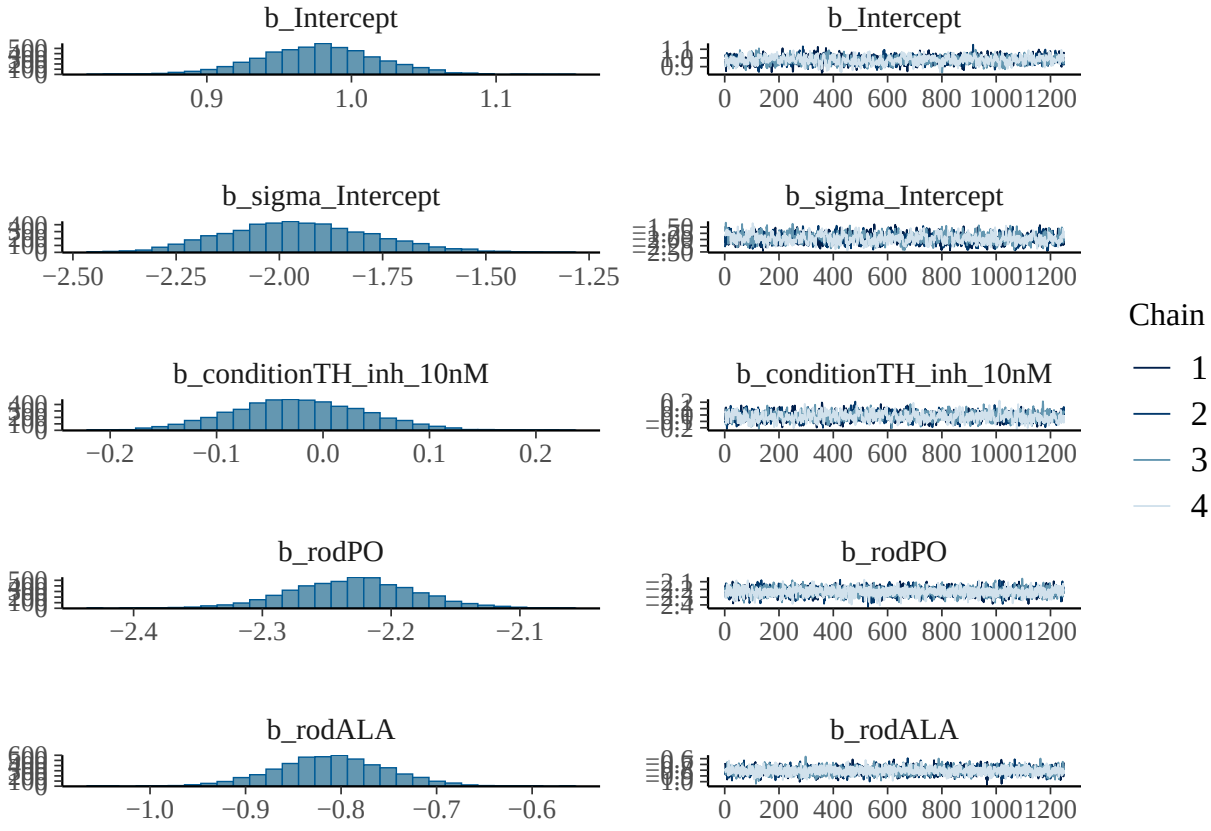
M2 Rod Fed model

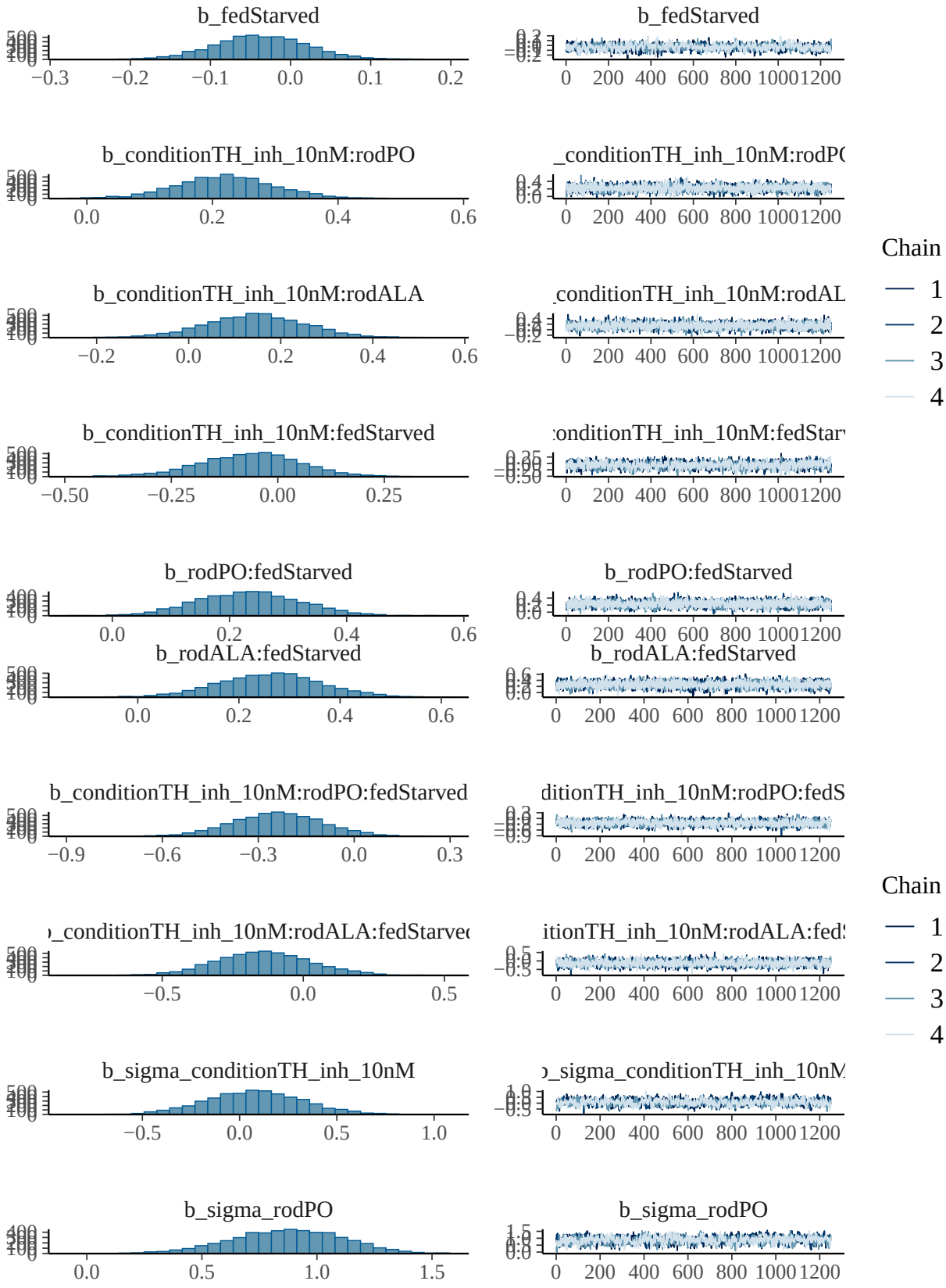
```
Sp_rod_fed_mod <- brm(
  bf(L ~  condition*rod*fed + (1|larva), sigma ~ condition*rod*fed),
  family = gaussian,
  data=Sp_df, prior = priors,
  chains = nchain,
  iter = niter, warmup = niter/2,
   save_pars = save_pars(all = TRUE)
  )
Sp_rod_fed_mod
```

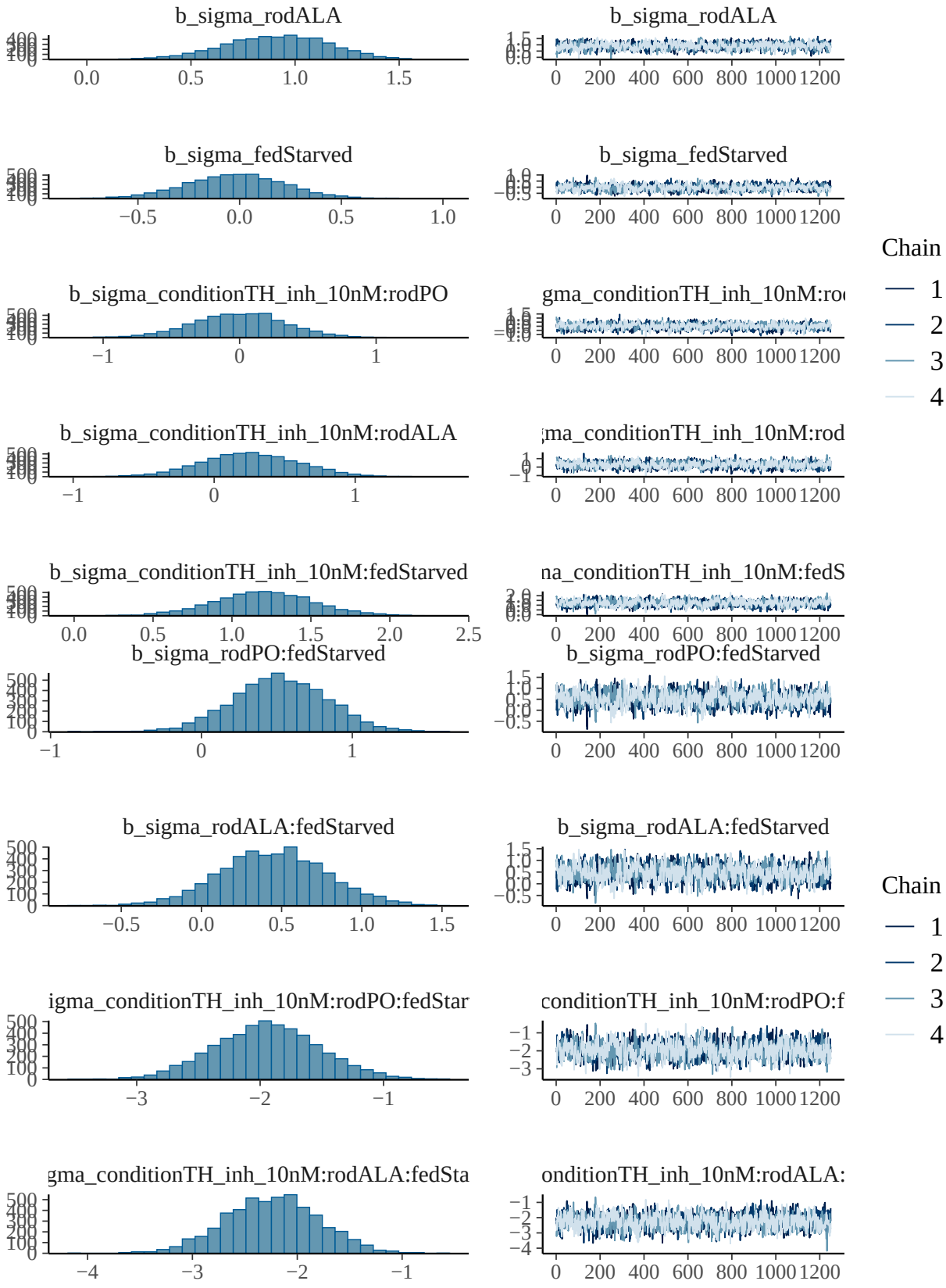
```
##  Family: gaussian
##   Links: mu = identity; sigma = log
## Formula: L ~ condition * rod * fed + (1 | larva)
##          sigma ~ condition * rod * fed
##    Data: Sp_df (Number of observations: 573)
##   Draws: 4 chains, each with iter = 2500; warmup = 1250; thin = 1;
##          total post-warmup draws = 5000
##
## Multilevel Hyperparameters:
## ~larva (Number of levels: 111)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.21      0.02     0.17     0.25 1.00     1399     2562
##
## Regression Coefficients:
##                                              Estimate Est.Error l-95% CI
## Intercept                                        0.98      0.04     0.89
## sigma_Intercept                                 -1.95      0.18    -2.28
## conditionTH_inh_10nM                            -0.02      0.06    -0.14
## rodPO                                           -2.23      0.05    -2.33
## rodALA                                          -0.81      0.06    -0.92
## fedStarved                                      -0.04      0.06    -0.15
## conditionTH_inh_10nM:rodPO                       0.22      0.08     0.07
## conditionTH_inh_10nM:rodALA                      0.14      0.11    -0.07
## conditionTH_inh_10nM:fedStarved                 -0.07      0.12    -0.31
## rodPO:fedStarved                                 0.23      0.09     0.07
## rodALA:fedStarved                                0.26      0.10     0.06
## conditionTH_inh_10nM:rodPO:fedStarved           -0.24      0.14    -0.51
## conditionTH_inh_10nM:rodALA:fedStarved          -0.14      0.17    -0.46
## sigma_conditionTH_inh_10nM                       0.08      0.25    -0.40
## sigma_rodPO                                      0.87      0.24     0.40
## sigma_rodALA                                     0.91      0.25     0.41
## sigma_fedStarved                                -0.02      0.24    -0.50
## sigma_conditionTH_inh_10nM:rodPO                -0.00      0.33    -0.67
## sigma_conditionTH_inh_10nM:rodALA                0.26      0.34    -0.40
## sigma_conditionTH_inh_10nM:fedStarved            1.20      0.31     0.58
## sigma_rodPO:fedStarved                           0.52      0.31    -0.10
## sigma_rodALA:fedStarved                          0.45      0.33    -0.20
## sigma_conditionTH_inh_10nM:rodPO:fedStarved     -1.94      0.43    -2.77
## sigma_conditionTH_inh_10nM:rodALA:fedStarved    -2.24      0.45    -3.11
##                                              u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept                                        1.06 1.00     1321     2262
## sigma_Intercept                                 -1.58 1.01      891     2055
```

```
## conditionTH_inh_10nM                              0.10 1.00     1166     2236
## rodPO                                            -2.13 1.00     3674     3297
## rodALA                                           -0.69 1.00     3630     3646
## fedStarved                                        0.08 1.00     1238     1851
## conditionTH_inh_10nM:rodPO                        0.38 1.00     3816     3503
## conditionTH_inh_10nM:rodALA                       0.35 1.00     3407     3633
## conditionTH_inh_10nM:fedStarved                   0.16 1.00     1578     2437
## rodPO:fedStarved                                  0.40 1.00     3789     3618
## rodALA:fedStarved                                 0.46 1.00     3787     3703
## conditionTH_inh_10nM:rodPO:fedStarved             0.03 1.00     3083     3657
## conditionTH_inh_10nM:rodALA:fedStarved            0.20 1.00     2868     3680
## sigma_conditionTH_inh_10nM                        0.57 1.01      893     1653
## sigma_rodPO                                       1.31 1.00      984     2179
## sigma_rodALA                                      1.37 1.00      932     2207
## sigma_fedStarved                                  0.45 1.01      870     1525
## sigma_conditionTH_inh_10nM:rodPO                  0.64 1.01      965     1884
## sigma_conditionTH_inh_10nM:rodALA                 0.93 1.01      943     1655
## sigma_conditionTH_inh_10nM:fedStarved             1.83 1.01      818     1839
## sigma_rodPO:fedStarved                            1.12 1.00      943     1669
## sigma_rodALA:fedStarved                           1.11 1.00      942     1699
## sigma_conditionTH_inh_10nM:rodPO:fedStarved      -1.09 1.00      926     2018
## sigma_conditionTH_inh_10nM:rodALA:fedStarved     -1.38 1.01      995     1742
##
## 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).
```

```
plot(Sp_rod_fed_mod, ask=FALSE, variable = "^b_", regex = TRUE)
```




b_fedStarved
b_fedStarved
b_conditionTH_inh_10nM:rodPO
_conditionTH_inh_10nM:rodPO
b_conditionTH_inh_10nM:rodALA
_conditionTH_inh_10nM:rodALA
b_conditionTH_inh_10nM:fedStarved
conditionTH_inh_10nM:fedStarved
b_rodPO:fedStarved
b_rodPO:fedStarved
b_rodALA:fedStarved
b_rodALA:fedStarved
b_conditionTH_inh_10nM:rodPO:fedStarved
ditionTH_inh_10nM:rodPO:fedStarved
_conditionTH_inh_10nM:rodALA:fedStarved
itionTH_inh_10nM:rodALA:fedStarved
b_sigma_conditionTH_inh_10nM
_sigma_conditionTH_inh_10nM
b_sigma_rodPO
b_sigma_rodPO
Chain
1
2
3
4
Chain
1
2
3
4


b_sigma_rodALA
b_sigma_fedStarved
b_sigma_conditionTH_inh_10nM:rodPO
b_sigma_conditionTH_inh_10nM:rodALA
b_sigma_conditionTH_inh_10nM:fedStarved
b_sigma_rodPO:fedStarved
b_sigma_rodALA:fedStarved
Chain
1
2
3
4

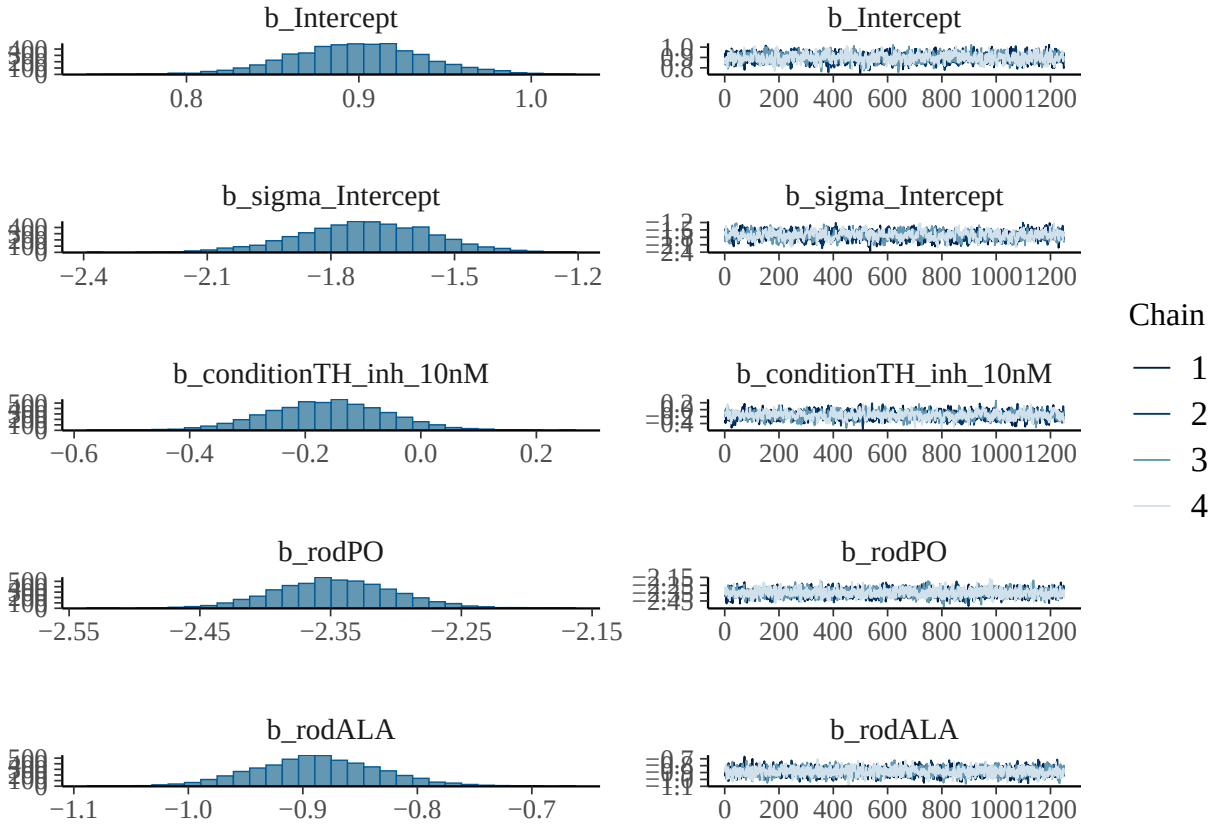
M3 Rod Lit model

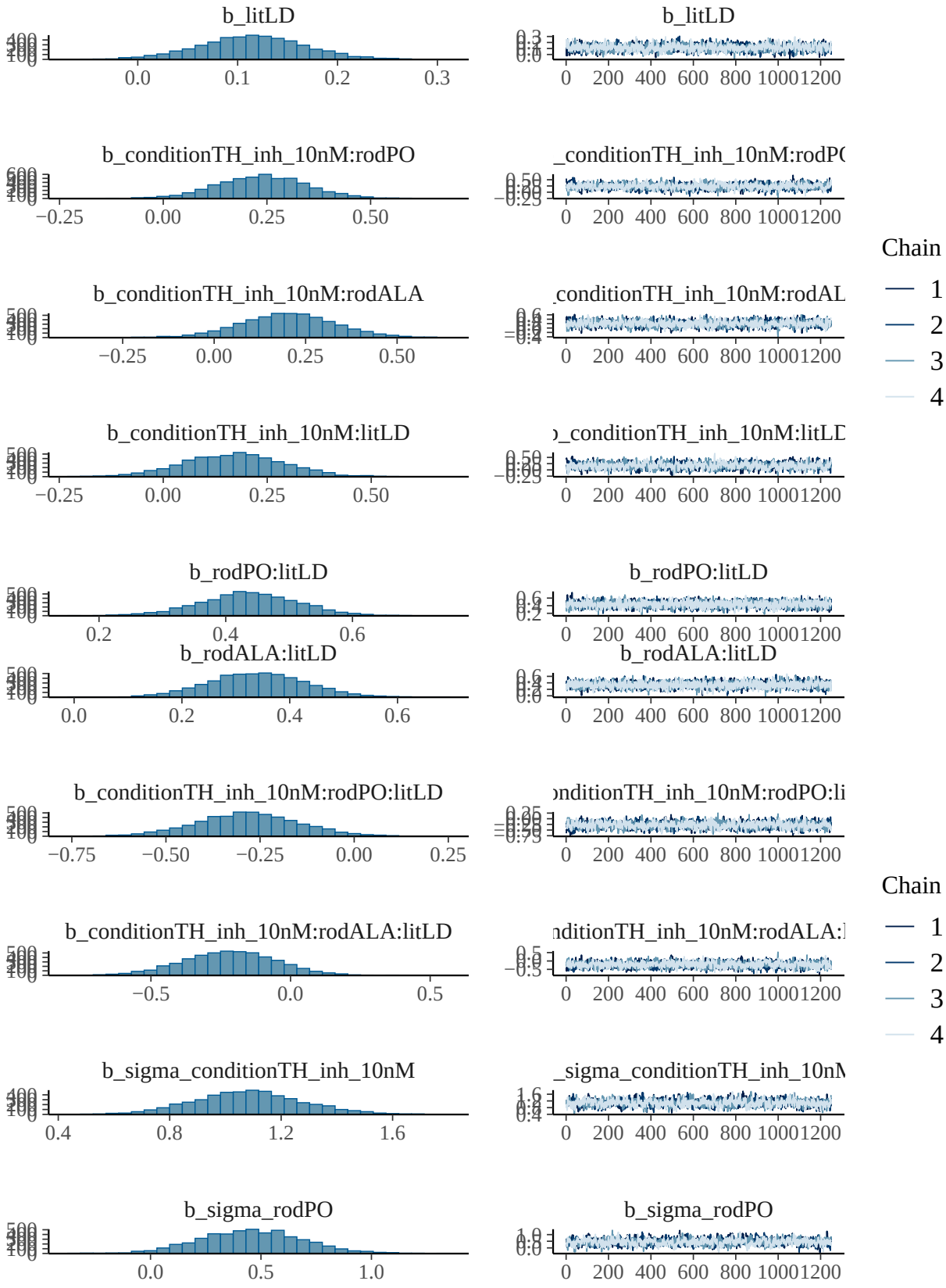
```
Sp_rod_lit_mod <- brm(
  bf(L ~  condition*rod*lit + (1|larva), sigma ~ condition*rod*lit),
  family = gaussian,
  data=Sp_df, prior = priors,
  chains = nchain,
  iter = niter, warmup = niter/2,
   save_pars = save_pars(all = TRUE)
  )
Sp_rod_lit_mod
```

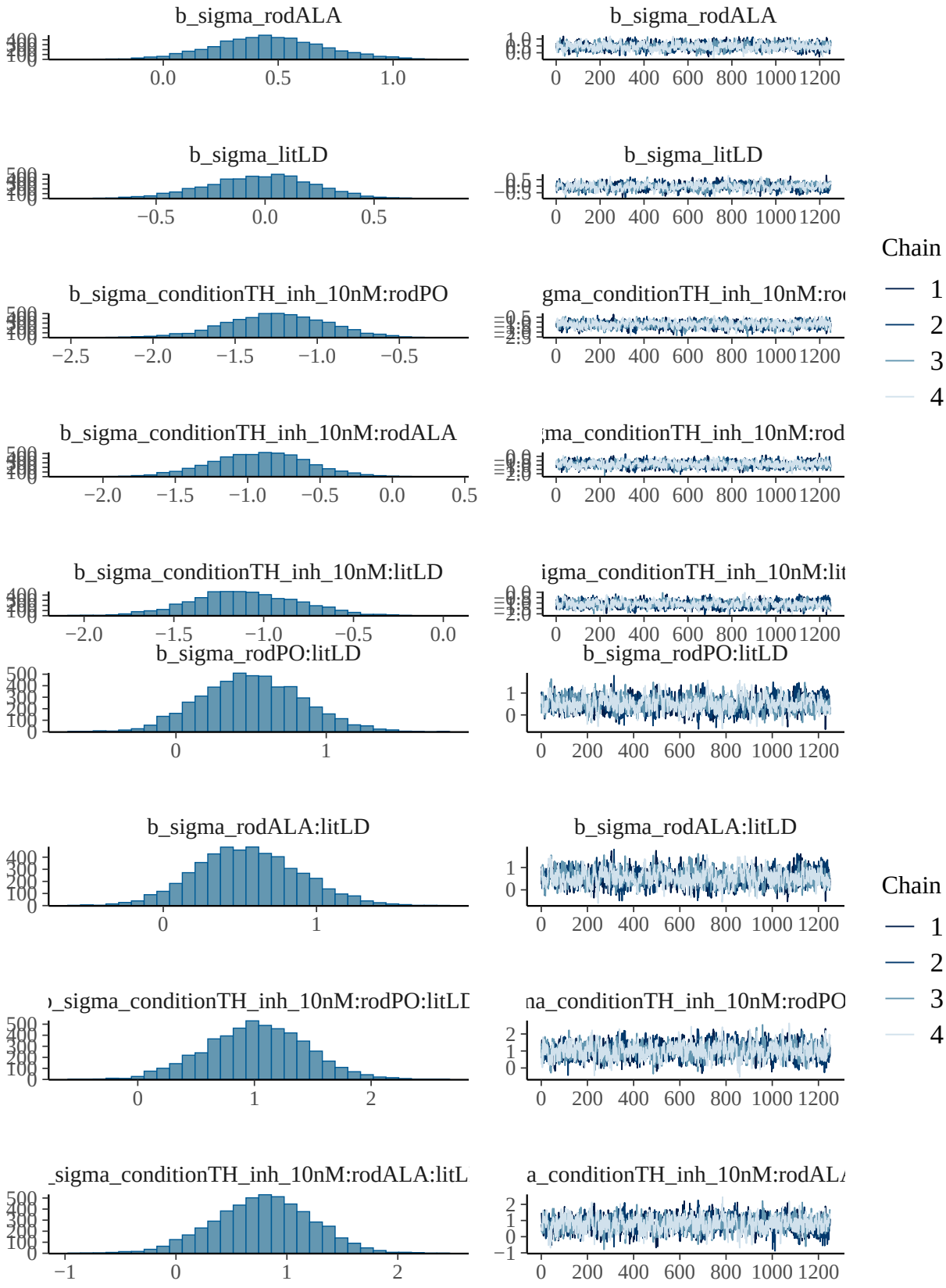
```
##  Family: gaussian
##   Links: mu = identity; sigma = log
## Formula: L ~ condition * rod * lit + (1 | larva)
##          sigma ~ condition * rod * lit
##    Data: Sp_df (Number of observations: 573)
##   Draws: 4 chains, each with iter = 2500; warmup = 1250; thin = 1;
##          total post-warmup draws = 5000
##
## Multilevel Hyperparameters:
## ~larva (Number of levels: 111)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.16      0.02     0.13     0.20 1.00      918     2145
##
## Regression Coefficients:
##                                        Estimate Est.Error l-95% CI u-95% CI
## Intercept                                  0.90      0.04     0.82     0.98
## sigma_Intercept                           -1.72      0.16    -2.04    -1.40
## conditionTH_inh_10nM                      -0.16      0.11    -0.37     0.04
## rodPO                                     -2.35      0.05    -2.43    -2.25
## rodALA                                    -0.89      0.05    -0.99    -0.78
## litLD                                      0.11      0.05     0.01     0.22
## conditionTH_inh_10nM:rodPO                 0.24      0.11     0.02     0.45
## conditionTH_inh_10nM:rodALA                0.20      0.13    -0.05     0.46
## conditionTH_inh_10nM:litLD                 0.17      0.12    -0.06     0.40
## rodPO:litLD                                0.44      0.08     0.28     0.59
## rodALA:litLD                               0.34      0.09     0.16     0.52
## conditionTH_inh_10nM:rodPO:litLD          -0.28      0.14    -0.55    -0.01
## conditionTH_inh_10nM:rodALA:litLD         -0.22      0.17    -0.55     0.10
## sigma_conditionTH_inh_10nM                 1.08      0.20     0.71     1.48
## sigma_rodPO                                0.46      0.23     0.02     0.91
## sigma_rodALA                               0.46      0.24     0.00     0.94
## sigma_litLD                               -0.02      0.24    -0.51     0.42
## sigma_conditionTH_inh_10nM:rodPO          -1.25      0.31    -1.89    -0.65
## sigma_conditionTH_inh_10nM:rodALA         -0.92      0.33    -1.57    -0.27
## sigma_conditionTH_inh_10nM:litLD          -1.10      0.30    -1.68    -0.52
## sigma_rodPO:litLD                          0.50      0.34    -0.12     1.19
## sigma_rodALA:litLD                         0.55      0.34    -0.09     1.25
## sigma_conditionTH_inh_10nM:rodPO:litLD     1.02      0.43     0.16     1.85
## sigma_conditionTH_inh_10nM:rodALA:litLD    0.79      0.44    -0.09     1.63
##                                        Rhat Bulk_ESS Tail_ESS
## Intercept                              1.00     1553     2534
## sigma_Intercept                        1.00      712     1602
```

```
## conditionTH_inh_10nM                    1.00     1080     1816
## rodPO                                   1.00     2522     2699
## rodALA                                  1.00     2812     3356
## litLD                                   1.00     1374     2270
## conditionTH_inh_10nM:rodPO              1.00     1215     2121
## conditionTH_inh_10nM:rodALA             1.00     1668     2397
## conditionTH_inh_10nM:litLD              1.00     1106     1826
## rodPO:litLD                             1.00     2329     2994
## rodALA:litLD                            1.00     2779     3541
## conditionTH_inh_10nM:rodPO:litLD        1.00     1294     2196
## conditionTH_inh_10nM:rodALA:litLD       1.00     1536     2762
## sigma_conditionTH_inh_10nM              1.00      802     1510
## sigma_rodPO                             1.00      746     1611
## sigma_rodALA                            1.00      802     1814
## sigma_litLD                             1.00      596     1289
## sigma_conditionTH_inh_10nM:rodPO        1.00      898     1501
## sigma_conditionTH_inh_10nM:rodALA       1.00      946     1762
## sigma_conditionTH_inh_10nM:litLD        1.00      760     1453
## sigma_rodPO:litLD                       1.00      616     1157
## sigma_rodALA:litLD                      1.00      688     1394
## sigma_conditionTH_inh_10nM:rodPO:litLD  1.00      859     1635
## sigma_conditionTH_inh_10nM:rodALA:litLD 1.00      906     1707
##
## 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).
```

```
plot(Sp_rod_lit_mod, ask=FALSE, variable = "^b_", regex = TRUE)
```




b_litLD
b_litLD
b_conditionTH_inh_10nM:rodPO
_conditionTH_inh_10nM:rodP(
b_conditionTH_inh_10nM:rodALA
_conditionTH_inh_10nM:rodAL
b_conditionTH_inh_10nM:litLD
_conditionTH_inh_10nM:litLD
b_rodPO:litLD
b_rodPO:litLD
b_rodALA:litLD
b_rodALA:litLD
b_conditionTH_inh_10nM:rodPO:litLD
nditionTH_inh_10nM:rodPO:li
b_conditionTH_inh_10nM:rodALA:litLD
nditionTH_inh_10nM:rodALA:
b_sigma_conditionTH_inh_10nM
_sigma_conditionTH_inh_10nM
b_sigma_rodPO
b_sigma_rodPO
Chain
1
2
3
4
Chain
1
2
3
4


b_sigma_rodALA
b_sigma_litLD
b_sigma_conditionTH_inh_10nM:rodPO
b_sigma_conditionTH_inh_10nM:rodALA
b_sigma_conditionTH_inh_10nM:litLD
b_sigma_rodPO:litLD
b_sigma_rodALA:litLD
Chain
1
2
3
4

M4 condition Rod Fed Lit model

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

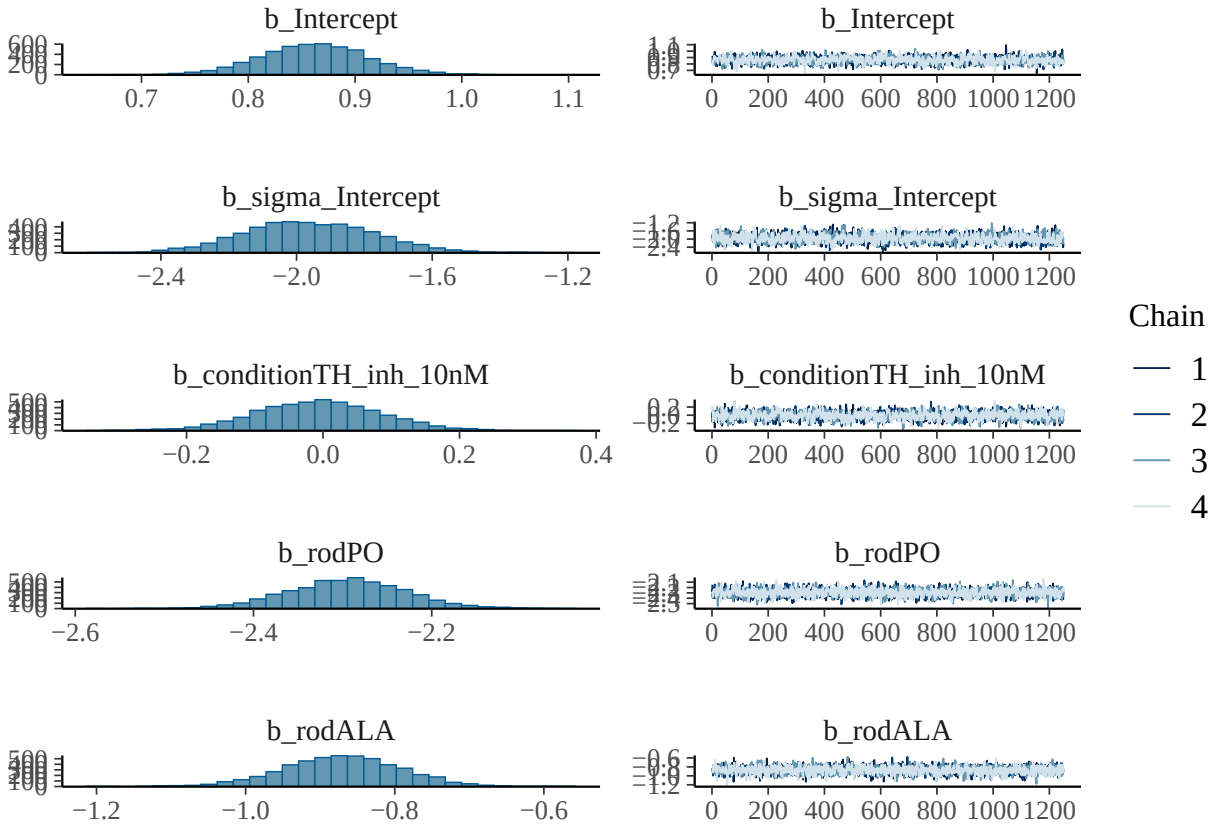
```
##  Family: gaussian
##   Links: mu = identity; sigma = log
## Formula: L ~ condition * rod * fed * lit + (1 | larva)
##          sigma ~ condition * rod * fed * lit
##    Data: Sp_df (Number of observations: 573)
##   Draws: 4 chains, each with iter = 2500; warmup = 1250; thin = 1;
##          total post-warmup draws = 5000
##
## Multilevel Hyperparameters:
## ~larva (Number of levels: 111)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.15      0.02     0.12     0.19 1.00     1430     2983
##
## Regression Coefficients:
##                                                  Estimate Est.Error l-95% CI
## Intercept                                            0.86      0.05     0.76
## sigma_Intercept                                     -1.96      0.19    -2.33
## conditionTH_inh_10nM                                -0.01      0.09    -0.19
## rodPO                                               -2.29      0.07    -2.43
## rodALA                                              -0.87      0.08    -1.03
## fedStarved                                           0.07      0.07    -0.07
## litLD                                                0.20      0.07     0.06
## conditionTH_inh_10nM:rodPO                           0.04      0.13    -0.22
## conditionTH_inh_10nM:rodALA                         -0.05      0.21    -0.45
## conditionTH_inh_10nM:fedStarved                     -0.26      0.19    -0.64
## rodPO:fedStarved                                    -0.09      0.09    -0.27
## rodALA:fedStarved                                   -0.04      0.11    -0.27
## conditionTH_inh_10nM:litLD                          -0.05      0.12    -0.28
## rodPO:litLD                                          0.12      0.09    -0.06
## rodALA:litLD                                         0.09      0.11    -0.14
## fedStarved:litLD                                    -0.18      0.10    -0.38
## conditionTH_inh_10nM:rodPO:fedStarved                0.33      0.21    -0.08
## conditionTH_inh_10nM:rodALA:fedStarved               0.46      0.27    -0.09
## conditionTH_inh_10nM:rodPO:litLD                     0.24      0.16    -0.07
## conditionTH_inh_10nM:rodALA:litLD                    0.28      0.24    -0.19
## conditionTH_inh_10nM:fedStarved:litLD                0.42      0.22    -0.01
## rodPO:fedStarved:litLD                               0.65      0.14     0.38
## rodALA:fedStarved:litLD                              0.52      0.18     0.17
## conditionTH_inh_10nM:rodPO:fedStarved:litLD         -1.04      0.26    -1.55
## conditionTH_inh_10nM:rodALA:fedStarved:litLD        -0.97      0.34    -1.65
## sigma_conditionTH_inh_10nM                           0.36      0.31    -0.26
## sigma_rodPO                                          0.78      0.26     0.28
```

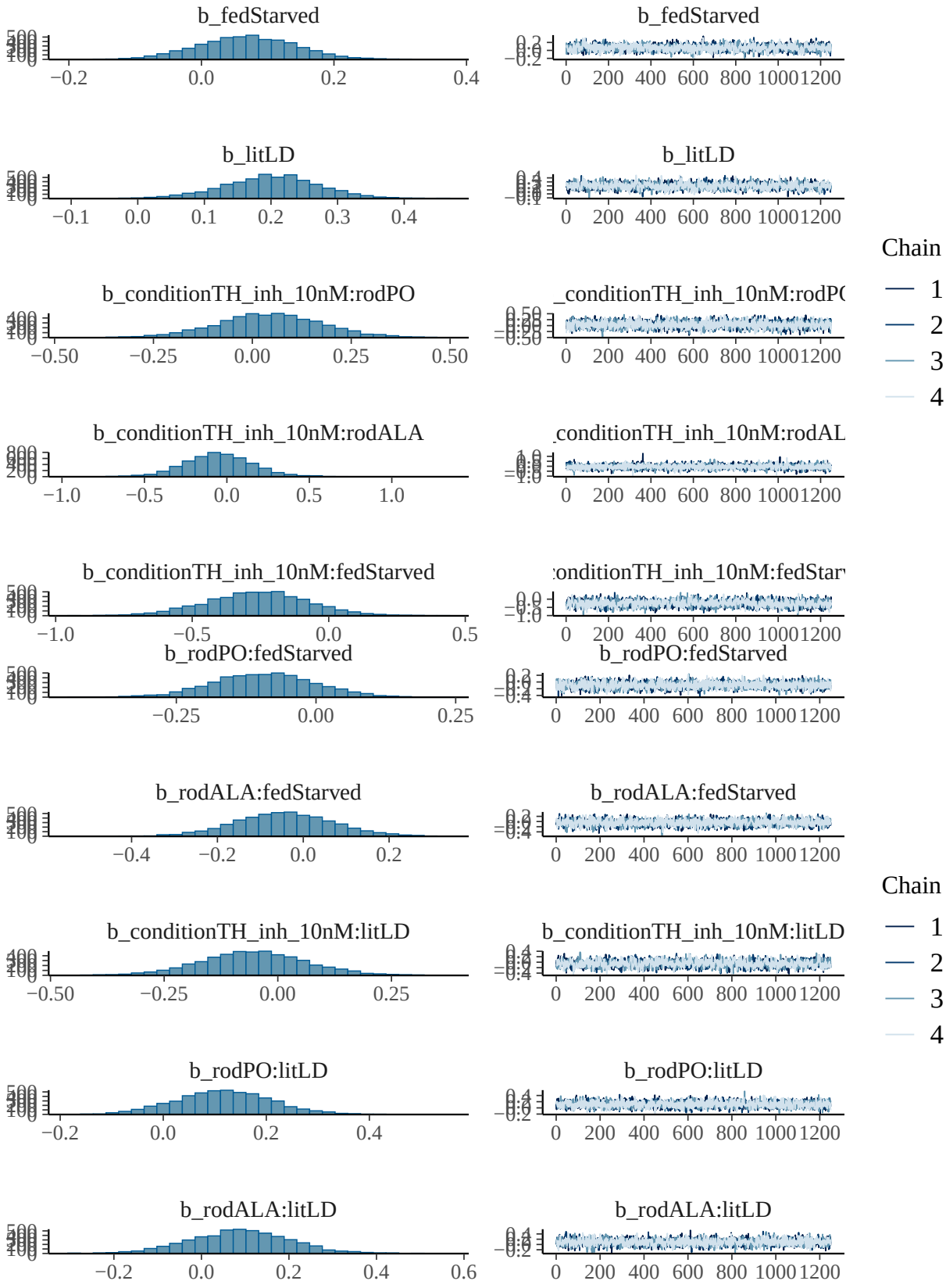
```
## sigma_rodALA                                          0.76      0.28     0.21
## sigma_fedStarved                                      0.45      0.26    -0.09
## sigma_litLD                                           0.32      0.27    -0.23
## sigma_conditionTH_inh_10nM:rodPO                     -0.14      0.42    -0.96
## sigma_conditionTH_inh_10nM:rodALA                     0.18      0.45    -0.68
## sigma_conditionTH_inh_10nM:fedStarved                 0.75      0.37     0.02
## sigma_rodPO:fedStarved                               -0.61      0.38    -1.34
## sigma_rodALA:fedStarved                              -0.51      0.40    -1.27
## sigma_conditionTH_inh_10nM:litLD                     -0.52      0.40    -1.29
## sigma_rodPO:litLD                                    -0.28      0.38    -1.00
## sigma_rodALA:litLD                                   -0.15      0.39    -0.89
## sigma_fedStarved:litLD                               -0.61      0.37    -1.33
## sigma_conditionTH_inh_10nM:rodPO:fedStarved          -1.41      0.54    -2.46
## sigma_conditionTH_inh_10nM:rodALA:fedStarved         -1.46      0.58    -2.60
## sigma_conditionTH_inh_10nM:rodPO:litLD                0.21      0.55    -0.89
## sigma_conditionTH_inh_10nM:rodALA:litLD               0.22      0.56    -0.87
## sigma_conditionTH_inh_10nM:fedStarved:litLD          -0.47      0.50    -1.46
## sigma_rodPO:fedStarved:litLD                          1.13      0.53     0.07
## sigma_rodALA:fedStarved:litLD                         1.04      0.53    -0.02
## sigma_conditionTH_inh_10nM:rodPO:fedStarved:litLD     1.19      0.73    -0.21
## sigma_conditionTH_inh_10nM:rodALA:fedStarved:litLD    0.62      0.74    -0.81
##                                                   u-95% CI Rhat Bulk_ESS
## Intercept                                            0.96 1.00     1706
## sigma_Intercept                                     -1.59 1.00     1581
## conditionTH_inh_10nM                                 0.17 1.00     1807
## rodPO                                               -2.16 1.00     2675
## rodALA                                              -0.72 1.00     2825
## fedStarved                                           0.21 1.00     1587
## litLD                                                0.34 1.00     1634
## conditionTH_inh_10nM:rodPO                           0.31 1.00     2584
## conditionTH_inh_10nM:rodALA                          0.36 1.00     2709
## conditionTH_inh_10nM:fedStarved                      0.11 1.00     1748
## rodPO:fedStarved                                     0.08 1.00     2684
## rodALA:fedStarved                                    0.19 1.00     2624
## conditionTH_inh_10nM:litLD                           0.18 1.00     1590
## rodPO:litLD                                          0.30 1.00     2489
## rodALA:litLD                                         0.32 1.00     2640
## fedStarved:litLD                                     0.02 1.00     1674
## conditionTH_inh_10nM:rodPO:fedStarved                0.74 1.00     1913
## conditionTH_inh_10nM:rodALA:fedStarved               1.00 1.00     2076
## conditionTH_inh_10nM:rodPO:litLD                     0.56 1.00     2359
## conditionTH_inh_10nM:rodALA:litLD                    0.76 1.00     2624
## conditionTH_inh_10nM:fedStarved:litLD                0.83 1.00     1597
## rodPO:fedStarved:litLD                               0.93 1.00     2703
## rodALA:fedStarved:litLD                              0.87 1.00     2798
## conditionTH_inh_10nM:rodPO:fedStarved:litLD         -0.52 1.00     2109
## conditionTH_inh_10nM:rodALA:fedStarved:litLD        -0.30 1.00     2296
## sigma_conditionTH_inh_10nM                           0.96 1.01     1085
## sigma_rodPO                                          1.27 1.00     1697
## sigma_rodALA                                         1.30 1.00     1788
## sigma_fedStarved                                     0.95 1.00     1382
## sigma_litLD                                          0.83 1.00     1074
## sigma_conditionTH_inh_10nM:rodPO                     0.68 1.00     1128
## sigma_conditionTH_inh_10nM:rodALA                    1.07 1.00     1437
```

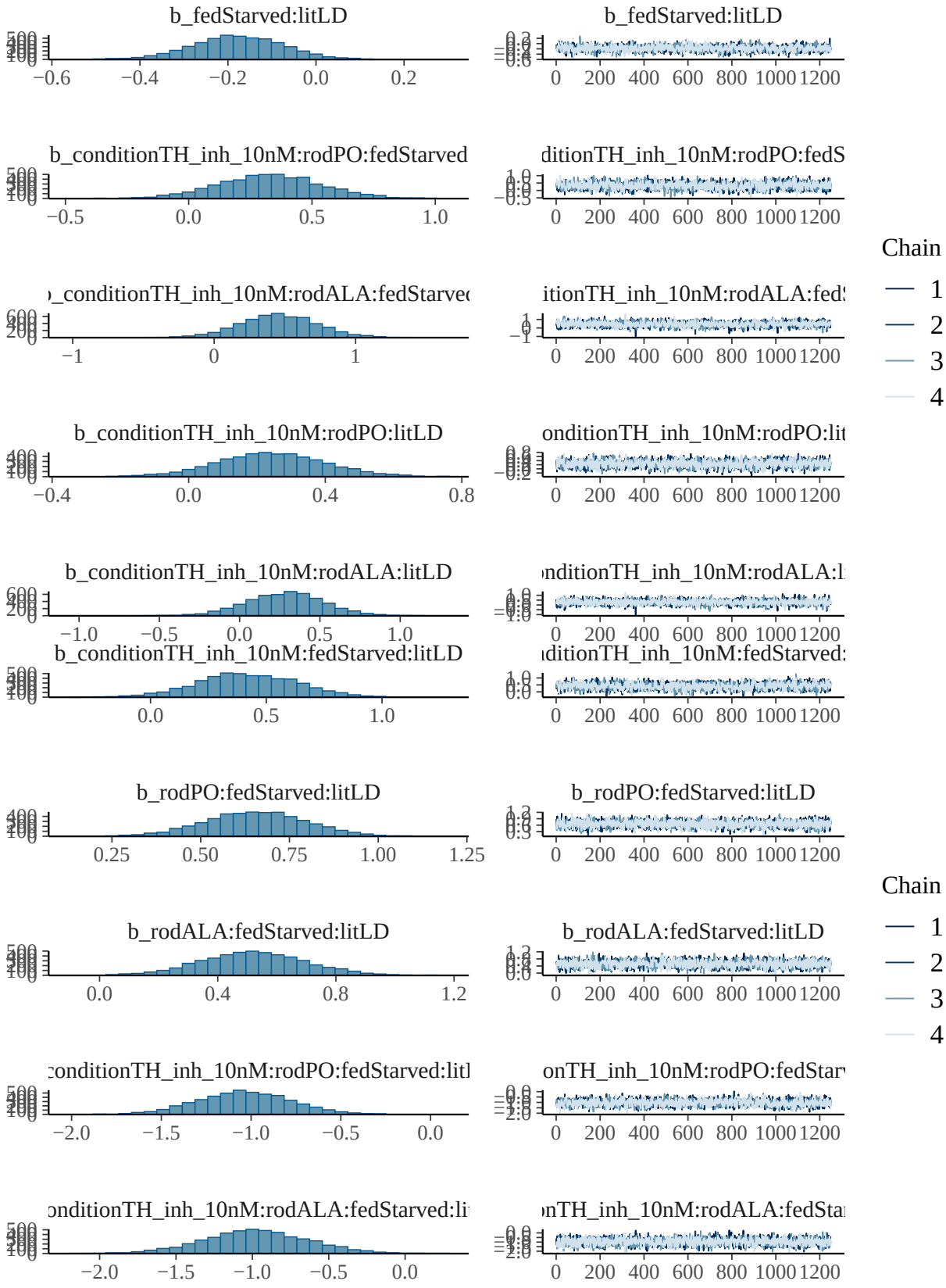
```
## sigma_conditionTH_inh_10nM:fedStarved                  1.47 1.01     1064
## sigma_rodPO:fedStarved                                 0.14 1.00     1488
## sigma_rodALA:fedStarved                                0.30 1.00     1671
## sigma_conditionTH_inh_10nM:litLD                       0.26 1.00      959
## sigma_rodPO:litLD                                      0.48 1.00     1111
## sigma_rodALA:litLD                                     0.63 1.00     1255
## sigma_fedStarved:litLD                                 0.12 1.00     1267
## sigma_conditionTH_inh_10nM:rodPO:fedStarved           -0.34 1.01     1255
## sigma_conditionTH_inh_10nM:rodALA:fedStarved          -0.35 1.00     1460
## sigma_conditionTH_inh_10nM:rodPO:litLD                 1.27 1.00     1037
## sigma_conditionTH_inh_10nM:rodALA:litLD                1.31 1.00     1356
## sigma_conditionTH_inh_10nM:fedStarved:litLD            0.51 1.00     1174
## sigma_rodPO:fedStarved:litLD                           2.16 1.00     1377
## sigma_rodALA:fedStarved:litLD                          2.08 1.00     1440
## sigma_conditionTH_inh_10nM:rodPO:fedStarved:litLD      2.59 1.00     1396
## sigma_conditionTH_inh_10nM:rodALA:fedStarved:litLD     2.07 1.00     1596
##                                                    Tail_ESS
## Intercept                                              2705
## sigma_Intercept                                        3270
## conditionTH_inh_10nM                                   2965
## rodPO                                                  3457
## rodALA                                                 3077
## fedStarved                                             2756
## litLD                                                  2604
## conditionTH_inh_10nM:rodPO                             3175
## conditionTH_inh_10nM:rodALA                            2856
## conditionTH_inh_10nM:fedStarved                        2678
## rodPO:fedStarved                                       3514
## rodALA:fedStarved                                      3402
## conditionTH_inh_10nM:litLD                             2884
## rodPO:litLD                                            3659
## rodALA:litLD                                           3570
## fedStarved:litLD                                       2551
## conditionTH_inh_10nM:rodPO:fedStarved                  2864
## conditionTH_inh_10nM:rodALA:fedStarved                 2900
## conditionTH_inh_10nM:rodPO:litLD                       3243
## conditionTH_inh_10nM:rodALA:litLD                      3118
## conditionTH_inh_10nM:fedStarved:litLD                  2612
## rodPO:fedStarved:litLD                                 3399
## rodALA:fedStarved:litLD                                3128
## conditionTH_inh_10nM:rodPO:fedStarved:litLD            3069
## conditionTH_inh_10nM:rodALA:fedStarved:litLD           3184
## sigma_conditionTH_inh_10nM                             2243
## sigma_rodPO                                            3187
## sigma_rodALA                                           3269
## sigma_fedStarved                                       2521
## sigma_litLD                                            2323
## sigma_conditionTH_inh_10nM:rodPO                       2305
## sigma_conditionTH_inh_10nM:rodALA                      2587
## sigma_conditionTH_inh_10nM:fedStarved                  2322
## sigma_rodPO:fedStarved                                 2704
## sigma_rodALA:fedStarved                                2917
## sigma_conditionTH_inh_10nM:litLD                       1785
## sigma_rodPO:litLD                                      2046
```

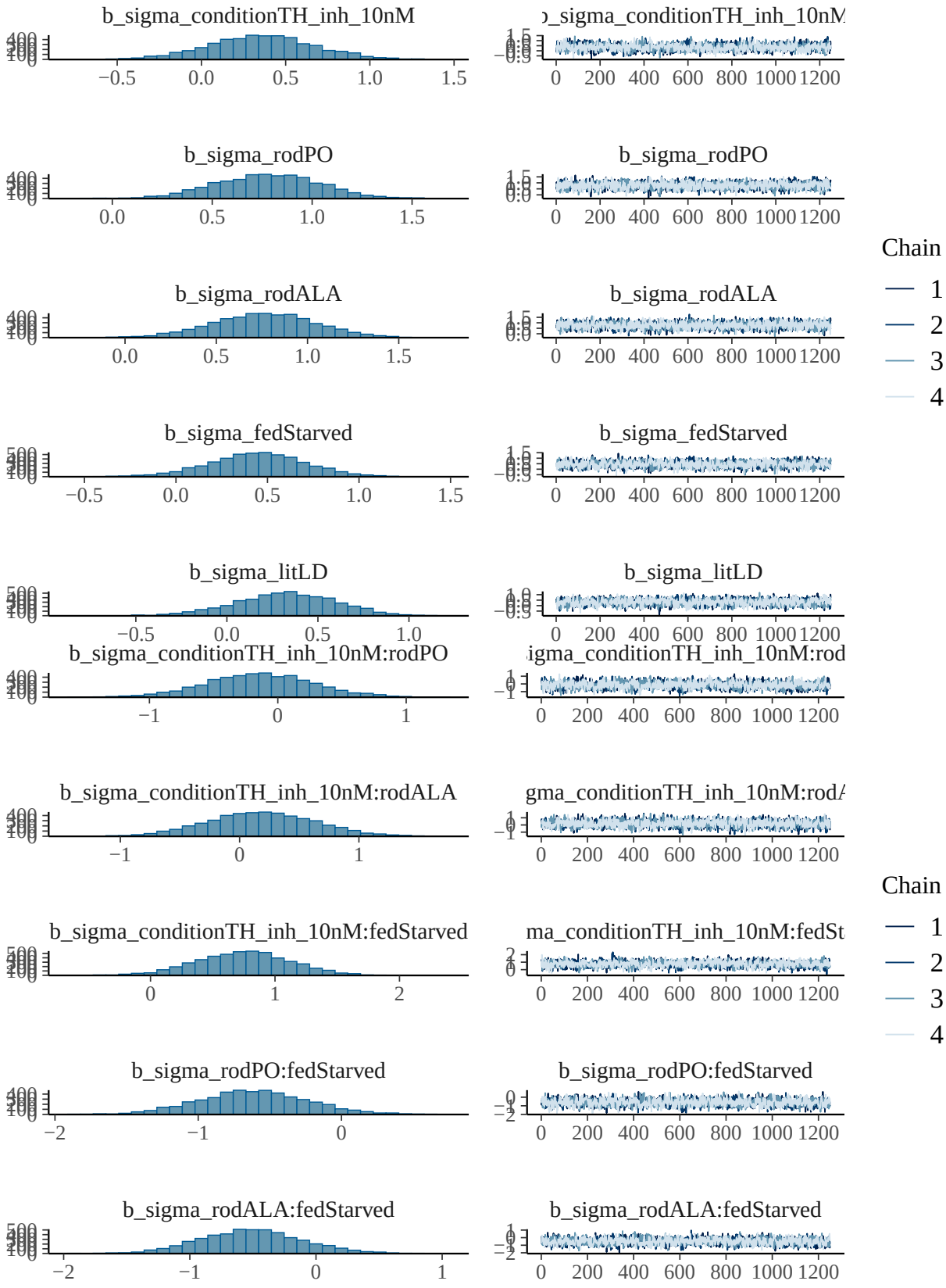
```
## sigma_rodALA:litLD                                    2432
## sigma_fedStarved:litLD                                2294
## sigma_conditionTH_inh_10nM:rodPO:fedStarved           2651
## sigma_conditionTH_inh_10nM:rodALA:fedStarved          2750
## sigma_conditionTH_inh_10nM:rodPO:litLD                2212
## sigma_conditionTH_inh_10nM:rodALA:litLD               2573
## sigma_conditionTH_inh_10nM:fedStarved:litLD           2257
## sigma_rodPO:fedStarved:litLD                          2668
## sigma_rodALA:fedStarved:litLD                         2783
## sigma_conditionTH_inh_10nM:rodPO:fedStarved:litLD     2613
## sigma_conditionTH_inh_10nM:rodALA:fedStarved:litLD    2745
##
## 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).
```

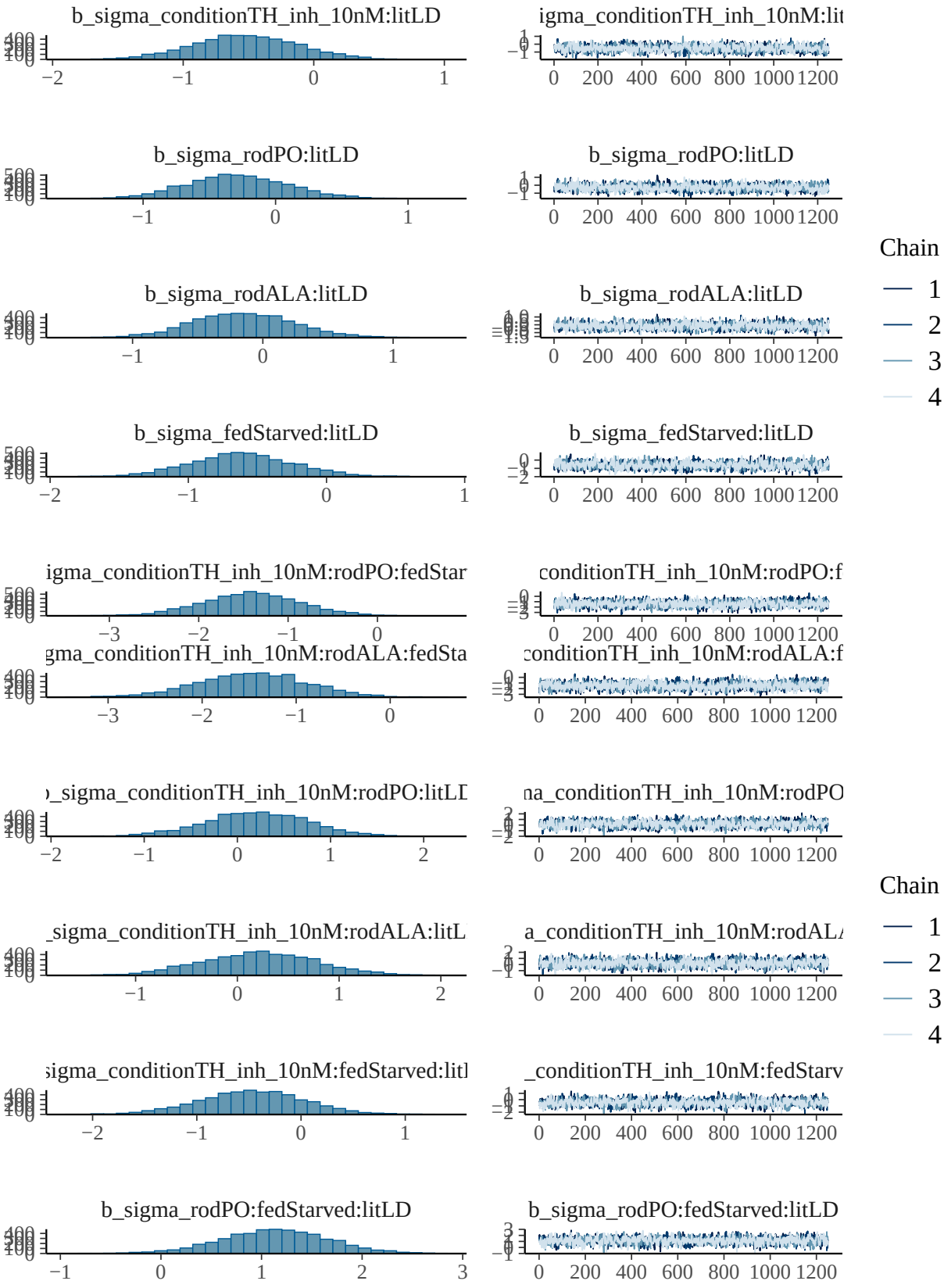
```
plot(Sp_rod_fed_lit_mod, ask=FALSE, variable = "^b_", regex = TRUE)
```

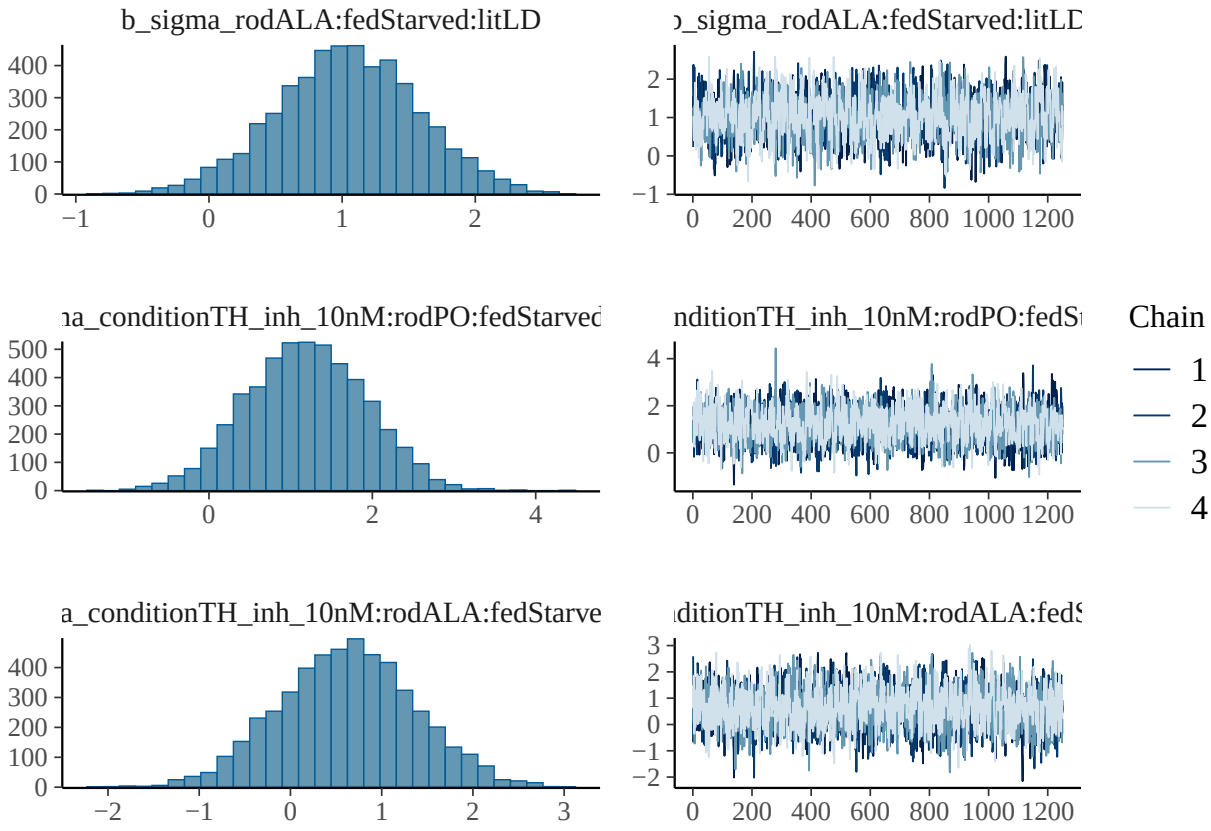



b_fedStarved
b_litLD
b_conditionTH_inh_10nM:rodPO
b_conditionTH_inh_10nM:rodALA
b_conditionTH_inh_10nM:fedStarved
b_rodPO:fedStarved
b_rodALA:fedStarved
b_conditionTH_inh_10nM:litLD
b_rodPO:litLD
b_rodALA:litLD
Chain
1
2
3
4


b_fedStarved:litLD
b_fedStarved:litLD
b_conditionTH_inh_10nM:rodPO:fedStarved
ditionTH_inh_10nM:rodPO:fedS
_conditionTH_inh_10nM:rodALA:fedStarve
itionTH_inh_10nM:rodALA:fed
b_conditionTH_inh_10nM:rodPO:litLD
onditionTH_inh_10nM:rodPO:lit
b_conditionTH_inh_10nM:rodALA:litLD
nditionTH_inh_10nM:rodALA:l
b_conditionTH_inh_10nM:fedStarved:litLD
ditionTH_inh_10nM:fedStarved:
b_rodPO:fedStarved:litLD
b_rodPO:fedStarved:litLD
b_rodALA:fedStarved:litLD
b_rodALA:fedStarved:litLD
conditionTH_inh_10nM:rodPO:fedStarved:litl
onTH_inh_10nM:rodPO:fedStar
onditionTH_inh_10nM:rodALA:fedStarved:li
nTH_inh_10nM:rodALA:fedSta
Chain
1
2
3
4
Chain
1
2
3
4


b_sigma_conditionTH_inh_10nM
b_sigma_rodPO
b_sigma_rodALA
b_sigma_fedStarved
b_sigma_litLD
b_sigma_conditionTH_inh_10nM:rodPO
b_sigma_conditionTH_inh_10nM:rodALA
b_sigma_conditionTH_inh_10nM:fedStarved
b_sigma_rodPO:fedStarved
b_sigma_rodALA:fedStarved
Chain
1
2
3
4


b_sigma_conditionTH_inh_10nM:litLD
b_sigma_rodPO:litLD
b_sigma_rodALA:litLD
b_sigma_fedStarved:litLD
igma_conditionTH_inh_10nM:rodPO:fedStar
conditionTH_inh_10nM:rodPO:f
gma_conditionTH_inh_10nM:rodALA:fedSta
conditionTH_inh_10nM:rodALA:f
_sigma_conditionTH_inh_10nM:rodPO:litLI
na_conditionTH_inh_10nM:rodPO
_sigma_conditionTH_inh_10nM:rodALA:litL
a_conditionTH_inh_10nM:rodALA
sigma_conditionTH_inh_10nM:fedStarved:litl
_conditionTH_inh_10nM:fedStarv
b_sigma_rodPO:fedStarved:litLD
Chain
1
2
3
4



3. Models evaluation using LOO

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

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

```
Sp_rod_mod = add_criterion(Sp_rod_mod,
                         criterion = "loo", moment_match = moment_match, 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 545)
```

```
## Start sampling
```

```
Sp_rod_lit_mod = add_criterion(Sp_rod_lit_mod,
                         criterion = "loo", moment_match = moment_match, 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 545)
```

```
## Start sampling
```

```
Sp_rod_fed_mod = add_criterion(Sp_rod_fed_mod,
                         criterion = "loo", moment_match = moment_match, 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 545)
```

```
## Start sampling
```

```
Sp_rod_fed_lit_mod = add_criterion(Sp_rod_fed_lit_mod,
                         criterion = "loo", moment_match = moment_match, 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 334)
```

```
## Start sampling
```

```
##
## Fitting model 2 out of 3 (leaving out observation 359)
```

```
## Start sampling
```

```
##
## Fitting model 3 out of 3 (leaving out observation 545)
```

```
## Start sampling
```

```
# Perform LOO comparison
loo_results <- loo_compare(Sp_intercept_mod,
                           Sp_rod_mod,
                           Sp_rod_fed_mod,
                           Sp_rod_lit_mod,
                           Sp_rod_fed_lit_mod)
loo_results
```

```
##                     elpd_diff se_diff
## Sp_rod_fed_lit_mod    0.0       0.0
## Sp_rod_lit_mod      -22.8      13.4
## Sp_rod_fed_mod      -42.5      20.1
## Sp_rod_mod          -85.9      48.0
## Sp_intercept_mod   -639.7      38.9
```

```
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: Sp_rod_fed_lit_mod"
```

Model Equation

The response variable follows a normal distribution:

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

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 model estimates both the mean and variance of the response variable (Y), incorporating fixed and random effects while allowing for hierarchical structure in the data.

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