Impact of food availability and light on S. purpuratus larval growth - model visualization

```r
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')
```

```r
unscale_outcome <- function(x){
  x = (x * sdL) + meanL
}
```

1. Data overview

Making a dataset containing only the data on **S. purpuratus**

```r
Sp_df <-  read_delim("larval_morphology.csv", delim = ",",
                 col_types = "fffnfifffffiniif")
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")))
```

```r
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."
```

```r
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>
```

```r
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>
```

2. Load best model

We load the model object derived from the predictive model in the S_purpuratus_mixeff_distributional.Rmd document.

```r
dir.create("model_objects", showWarnings = FALSE)

url <- "https://github.com/MariaCoc/Urchin_phenotypic_plasticity/releases/download/v1.0.0/Sp_rod_fed_li

local_file <- file.path("model_objects", "Sp_rod_fed_lit_mod.rds")

if (!file.exists(local_file)) {
  download.file(url, local_file, mode = "wb")
}

Sp_rod_fed_lit_mod <- readRDS('model_objects/Sp_rod_fed_lit_mod.rds')
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     1731     3214
##
## 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    -0.20
## rodPO                                                 -2.30      0.07    -2.43
## rodALA                                                -0.87      0.08    -1.02
## 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      0.20    -0.44
## conditionTH_inh_10nM:fedStarved                       -0.26      0.19    -0.62
## rodPO:fedStarved                                      -0.09      0.09    -0.28
## rodALA:fedStarved                                     -0.05      0.11    -0.27
## conditionTH_inh_10nM:litLD                            -0.06      0.12    -0.29
## rodPO:litLD                                            0.12      0.09    -0.07
## rodALA:litLD                                           0.08      0.11    -0.14
## fedStarved:litLD                                      -0.18      0.10    -0.39
## conditionTH_inh_10nM:rodPO:fedStarved                  0.33      0.21    -0.09
## conditionTH_inh_10nM:rodALA:fedStarved                 0.46      0.27    -0.08
## conditionTH_inh_10nM:rodPO:litLD                       0.24      0.16    -0.08
## conditionTH_inh_10nM:rodALA:litLD                      0.29      0.24    -0.18
## conditionTH_inh_10nM:fedStarved:litLD                  0.43      0.21     0.01
## rodPO:fedStarved:litLD                                 0.66      0.14     0.38
## rodALA:fedStarved:litLD                                0.52      0.18     0.18
## conditionTH_inh_10nM:rodPO:fedStarved:litLD           -1.04      0.27    -1.56
## conditionTH_inh_10nM:rodALA:fedStarved:litLD          -0.98      0.34    -1.64
## sigma_conditionTH_inh_10nM                             0.36      0.31    -0.26
## sigma_rodPO                                            0.77      0.26     0.27
## sigma_rodALA                                           0.76      0.28     0.22
## sigma_fedStarved                                       0.45      0.26    -0.06
## sigma_litLD                                            0.33      0.27    -0.21
## sigma_conditionTH_inh_10nM:rodPO                      -0.14      0.41    -0.93
## sigma_conditionTH_inh_10nM:rodALA                      0.18      0.45    -0.70
## sigma_conditionTH_inh_10nM:fedStarved                  0.75      0.37     0.01
## sigma_rodPO:fedStarved                                -0.61      0.38    -1.33
## sigma_rodALA:fedStarved                               -0.51      0.39    -1.27
## sigma_conditionTH_inh_10nM:litLD                      -0.52      0.39    -1.29
## sigma_rodPO:litLD                                     -0.29      0.38    -1.00
## sigma_rodALA:litLD                                    -0.15      0.38    -0.87
## sigma_fedStarved:litLD                                -0.62      0.37    -1.34
## sigma_conditionTH_inh_10nM:rodPO:fedStarved           -1.41      0.53    -2.44
## sigma_conditionTH_inh_10nM:rodALA:fedStarved          -1.45      0.57    -2.58
## sigma_conditionTH_inh_10nM:rodPO:litLD                 0.20      0.53    -0.83
## sigma_conditionTH_inh_10nM:rodALA:litLD                0.21      0.55    -0.88
## sigma_conditionTH_inh_10nM:fedStarved:litLD           -0.47      0.50    -1.45
## sigma_rodPO:fedStarved:litLD                           1.14      0.53     0.08
## sigma_rodALA:fedStarved:litLD                          1.05      0.53    -0.02
## sigma_conditionTH_inh_10nM:rodPO:fedStarved:litLD      1.18      0.71    -0.21
## sigma_conditionTH_inh_10nM:rodALA:fedStarved:litLD     0.61      0.74    -0.84
##                                                    u-95% CI Rhat Bulk_ESS
```

```
## Intercept                                                   0.96 1.00    1781
## sigma_Intercept                                            -1.58 1.00    1306
## conditionTH_inh_10nM                                         0.18 1.00    1843
## rodPO                                                       -2.17 1.00    2344
## rodALA                                                      -0.72 1.00    2924
## fedStarved                                                   0.22 1.00    1780
## litLD                                                        0.35 1.00    1704
## conditionTH_inh_10nM:rodPO                                   0.31 1.00    2251
## conditionTH_inh_10nM:rodALA                                  0.37 1.00    2810
## conditionTH_inh_10nM:fedStarved                              0.10 1.00    2081
## rodPO:fedStarved                                             0.09 1.00    2462
## rodALA:fedStarved                                            0.17 1.00    2848
## conditionTH_inh_10nM:litLD                                   0.18 1.00    1616
## rodPO:litLD                                                  0.30 1.00    2278
## rodALA:litLD                                                 0.30 1.00    2783
## fedStarved:litLD                                             0.02 1.00    1702
## conditionTH_inh_10nM:rodPO:fedStarved                        0.75 1.00    2134
## conditionTH_inh_10nM:rodALA:fedStarved                       0.98 1.00    2301
## conditionTH_inh_10nM:rodPO:litLD                             0.55 1.00    2097
## conditionTH_inh_10nM:rodALA:litLD                            0.76 1.00    2619
## conditionTH_inh_10nM:fedStarved:litLD                        0.85 1.00    1727
## rodPO:fedStarved:litLD                                       0.94 1.00    2456
## rodALA:fedStarved:litLD                                      0.88 1.00    2996
## conditionTH_inh_10nM:rodPO:fedStarved:litLD                 -0.50 1.00    2144
## conditionTH_inh_10nM:rodALA:fedStarved:litLD               -0.30 1.00    2487
## sigma_conditionTH_inh_10nM                                   1.00 1.00    1339
## sigma_rodPO                                                  1.27 1.00    1396
## sigma_rodALA                                                 1.31 1.00    1585
## sigma_fedStarved                                             0.92 1.00    1124
## sigma_litLD                                                  0.84 1.00    1255
## sigma_conditionTH_inh_10nM:rodPO                             0.67 1.00    1405
## sigma_conditionTH_inh_10nM:rodALA                            1.08 1.00    1583
## sigma_conditionTH_inh_10nM:fedStarved                        1.47 1.00    1060
## sigma_rodPO:fedStarved                                       0.15 1.00    1247
## sigma_rodALA:fedStarved                                      0.27 1.00    1445
## sigma_conditionTH_inh_10nM:litLD                             0.23 1.00    1350
## sigma_rodPO:litLD                                            0.47 1.00    1326
## sigma_rodALA:litLD                                           0.61 1.00    1405
## sigma_fedStarved:litLD                                       0.12 1.00    1167
## sigma_conditionTH_inh_10nM:rodPO:fedStarved                 -0.40 1.00    1147
## sigma_conditionTH_inh_10nM:rodALA:fedStarved                -0.35 1.00    1499
## sigma_conditionTH_inh_10nM:rodPO:litLD                       1.24 1.00    1520
## sigma_conditionTH_inh_10nM:rodALA:litLD                      1.27 1.00    1652
## sigma_conditionTH_inh_10nM:fedStarved:litLD                  0.51 1.00    1284
## sigma_rodPO:fedStarved:litLD                                 2.17 1.00    1282
## sigma_rodALA:fedStarved:litLD                                2.06 1.00    1312
## sigma_conditionTH_inh_10nM:rodPO:fedStarved:litLD            2.56 1.00    1568
## sigma_conditionTH_inh_10nM:rodALA:fedStarved:litLD           2.07 1.00    1711
##                                                         Tail_ESS
## Intercept                                                   3046
## sigma_Intercept                                             2557
## conditionTH_inh_10nM                                        2598
## rodPO                                                       2655
## rodALA                                                      3278
```

```
## fedStarved                                          2906
## litLD                                               2863
## conditionTH_inh_10nM:rodPO                          3136
## conditionTH_inh_10nM:rodALA                         2845
## conditionTH_inh_10nM:fedStarved                     2965
## rodPO:fedStarved                                    3115
## rodALA:fedStarved                                   3540
## conditionTH_inh_10nM:litLD                          2700
## rodPO:litLD                                         3160
## rodALA:litLD                                        3339
## fedStarved:litLD                                    2778
## conditionTH_inh_10nM:rodPO:fedStarved               2771
## conditionTH_inh_10nM:rodALA:fedStarved              2805
## conditionTH_inh_10nM:rodPO:litLD                    2567
## conditionTH_inh_10nM:rodALA:litLD                   3126
## conditionTH_inh_10nM:fedStarved:litLD               2682
## rodPO:fedStarved:litLD                              2795
## rodALA:fedStarved:litLD                             3389
## conditionTH_inh_10nM:rodPO:fedStarved:litLD         2734
## conditionTH_inh_10nM:rodALA:fedStarved:litLD        3073
## sigma_conditionTH_inh_10nM                          2112
## sigma_rodPO                                         2291
## sigma_rodALA                                        3104
## sigma_fedStarved                                    2176
## sigma_litLD                                         2471
## sigma_conditionTH_inh_10nM:rodPO                    2834
## sigma_conditionTH_inh_10nM:rodALA                   2349
## sigma_conditionTH_inh_10nM:fedStarved               1930
## sigma_rodPO:fedStarved                              2533
## sigma_rodALA:fedStarved                             2627
## sigma_conditionTH_inh_10nM:litLD                    2146
## sigma_rodPO:litLD                                   2473
## sigma_rodALA:litLD                                  2644
## sigma_fedStarved:litLD                              2135
## sigma_conditionTH_inh_10nM:rodPO:fedStarved         2833
## sigma_conditionTH_inh_10nM:rodALA:fedStarved        3120
## sigma_conditionTH_inh_10nM:rodPO:litLD              2437
## sigma_conditionTH_inh_10nM:rodALA:litLD             2778
## sigma_conditionTH_inh_10nM:fedStarved:litLD         2395
## sigma_rodPO:fedStarved:litLD                        2539
## sigma_rodALA:fedStarved:litLD                       2890
## sigma_conditionTH_inh_10nM:rodPO:fedStarved:litLD   2576
## sigma_conditionTH_inh_10nM:rodALA:fedStarved:litLD  2753
##
## 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. Marginaleffects plot with avg_predictions

We tabulate average predictions using the marginaleffects package.

```
preds_df <- marginaleffects::avg_predictions(Sp_rod_fed_lit_mod,
                newdata = datagrid(fed = unique(Sp_df$fed),
```

```r
                        lit = unique(Sp_df$lit),
                        rod = unique(Sp_df$rod),
                        condition = unique(Sp_df$condition)
                        ),
              by = c("lit","condition", "rod","fed"),
              transform = unscale_outcome,
              re_formula = NA
              )

head(preds_df, 10)
```

```
##
##  lit   condition rod     fed Estimate 2.5 % 97.5 %
##   DD DMSO        BR  Fed        167.0 163.5  170.5
##   DD DMSO        BR  Starved    169.4 165.8  173.1
##   DD DMSO        PO  Fed         87.7  82.7   92.5
##   DD DMSO        PO  Starved     86.8  82.6   90.9
##   DD DMSO       ALA Fed        137.0 131.1  142.8
##   DD DMSO       ALA Starved    137.6 132.4  143.2
##   DD TH_inh_10nM BR  Fed        166.7 161.4  171.9
##   DD TH_inh_10nM BR  Starved    160.0 149.6  171.0
##   DD TH_inh_10nM PO  Fed         88.9  81.0   96.9
##   DD TH_inh_10nM PO  Starved     90.4  86.3   94.5
##
## Type:  response
## Columns: rowid, lit, condition, rod, fed, estimate, conf.low, conf.high, larva, rowid_dedup
```

We plot model predictions of the mean alongside the original data. The scaling and centering in the model has been reversed to show the predictions in the original scale.

```r
ggplot() +
  # Add original data points
  geom_jitter(data = Sp_df, aes(x = rod, y = length, color = fed),
              position = position_jitterdodge(jitter.width = 0.25, dodge.width = 0.5),
              size = 1, alpha = 0.4) +
  scale_colour_manual(values = c("#00BBC1", "#F86D63"), name = "Individual measures") +

  # Facet by specific variables of interest
  facet_grid(condition~lit) +

  # Add the avg_predictions and error bars (95% CI)
  geom_point(data = preds_df, aes(x = rod, y = estimate, fill = fed),  # Use "response" column
             size = 2, position = position_dodge(width = 0.5)) +
  geom_errorbar(data = preds_df, aes(x = rod, ymin = conf.low, ymax = conf.high, fill = fed),
                width = 0.2, size = 0.7, position = position_dodge(width = 0.5)) +
  scale_fill_manual(values = c("black", "black"), name = "avg_predictions") +

  # Customize plot
  labs(title = "avg_predictions for fed, conditioned on lit, treatment and rod",
       y = "Length in um", x = "Skeletal rod") +
  theme_bw() +
  theme(axis.text = element_text(size = 11),
        axis.title = element_text(size = 13),
        legend.title = element_text(size = 13),
        strip.text = element_text(size = 13),
```
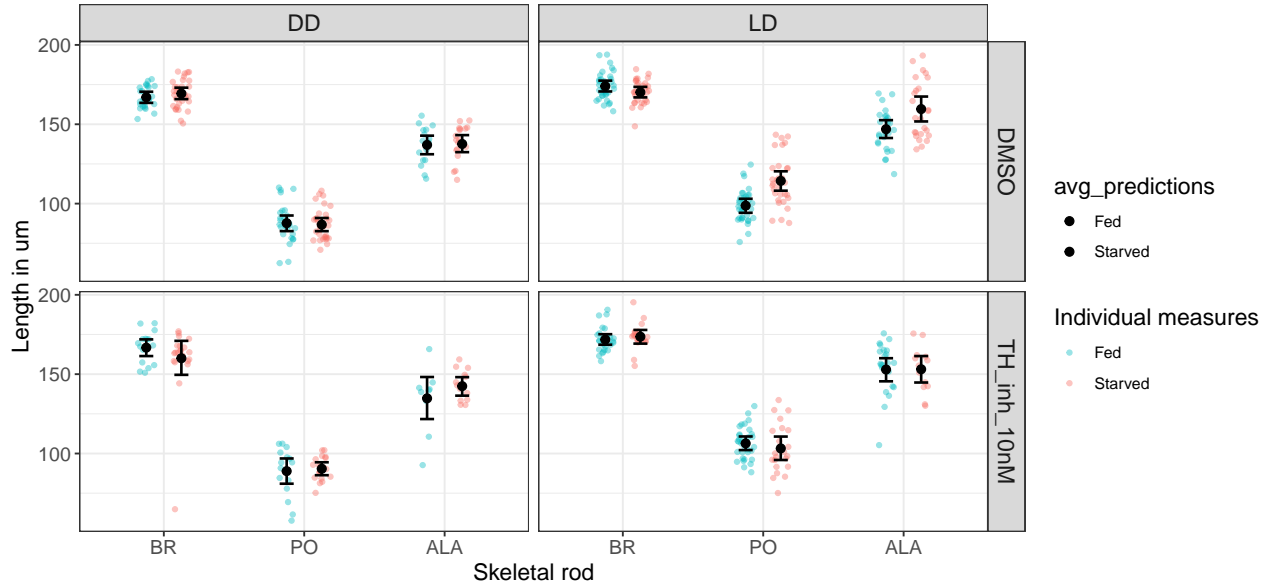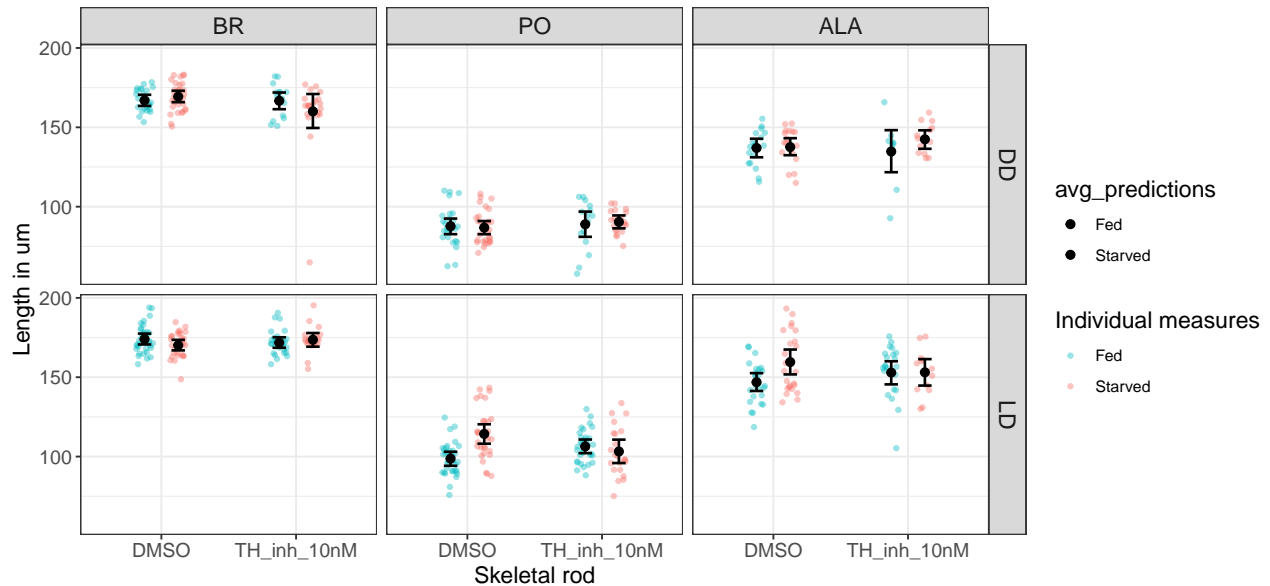
```
        plot.title = element_text(size = 17, face = "bold"))
```

```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
## Warning in geom_errorbar(data = preds_df, aes(x = rod, ymin = conf.low, :
## Ignoring unknown aesthetics: fill
```

avg_predictions for fed, conditioned on lit, treatment and rod

The plot below shows the average predictions for the length of larvae in each condition and light regime. The error bars represent the 95% confidence interval. The scatter points correspond to the original data. The scaling and centering in the model has been reversed to show the predictions in the original scale.

```
ggplot() +
  # Add original data points
  geom_jitter(data = Sp_df, aes(x = condition, y = length, color = fed),
              position = position_jitterdodge(jitter.width = 0.25, dodge.width = 0.5),
              size = 1, alpha = 0.4) +
  scale_colour_manual(values = c("#00BBC1", "#F86D63"), name = "Individual measures") +

  # Facet by specific variables of interest
  facet_grid(lit~rod) +

  # Add the avg_predictions and error bars (95% CI)
  geom_point(data = preds_df, aes(x = condition, y = estimate, fill = fed),   # Use "response" column
             size = 2, position = position_dodge(width = 0.5)) +
  geom_errorbar(data = preds_df, aes(x = condition, ymin = conf.low, ymax = conf.high, fill = fed),
                width = 0.2, size = 0.7, position = position_dodge(width = 0.5)) +
  scale_fill_manual(values = c("black", "black"), name = "avg_predictions") +

  # Customize plot
  labs(title = "avg_predictions for fed, conditioned on lit, treatment and rod",
       y = "Length in um", x = "Skeletal rod") +
```

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```
  theme_bw() +
  theme(axis.text = element_text(size = 11),
        axis.title = element_text(size = 13),
        legend.title = element_text(size = 13),
        strip.text = element_text(size = 13),
        plot.title = element_text(size = 17, face = "bold"))
```

```
## Warning in geom_errorbar(data = preds_df, aes(x = condition, ymin = conf.low, :
## Ignoring unknown aesthetics: fill
```


avg_predictions for fed, conditioned on lit, treatment and rod

The plot below shows the average predictions for the length of larvae in each condition and light regime. The error bars represent the 95% confidence interval.The scatter points correspond to the original data.The scaling and centering in the model has been reversed to show the predictions in the original scale.

```
ggplot() +
  # Add original data points
  geom_jitter(data = Sp_df, aes(x = rod, y = length, color = lit),
              position = position_jitterdodge(jitter.width = 0.25, dodge.width = 0.5),
              size = 1, alpha = 0.6) +
  scale_colour_manual(values = c("#7473d1", "#f5b905","#d62222"), name= "Individual measures") +

  # Add the avg_predictions and error bars (95% CI)
  geom_point(data = preds_df, aes(x = rod, y = estimate, fill = lit),
             size = 2, position = position_dodge(width = 0.5)) +
  geom_errorbar(data = preds_df, aes(x = rod, ymin = conf.low, ymax = conf.high, fill=lit),
                width = 0.2, size = 0.7, position = position_dodge(width = 0.5)) +
  scale_fill_manual(values = c("black", "black", "black"), name="avg_predictions") +

  # Facet by specific variables of interest
  facet_grid(fed~condition ) +

  # Customize plot
  labs(title = "avg_predictions for lit, conditioned on fed, treatment and rod",
       y = "Length um", x = "rod") +
```
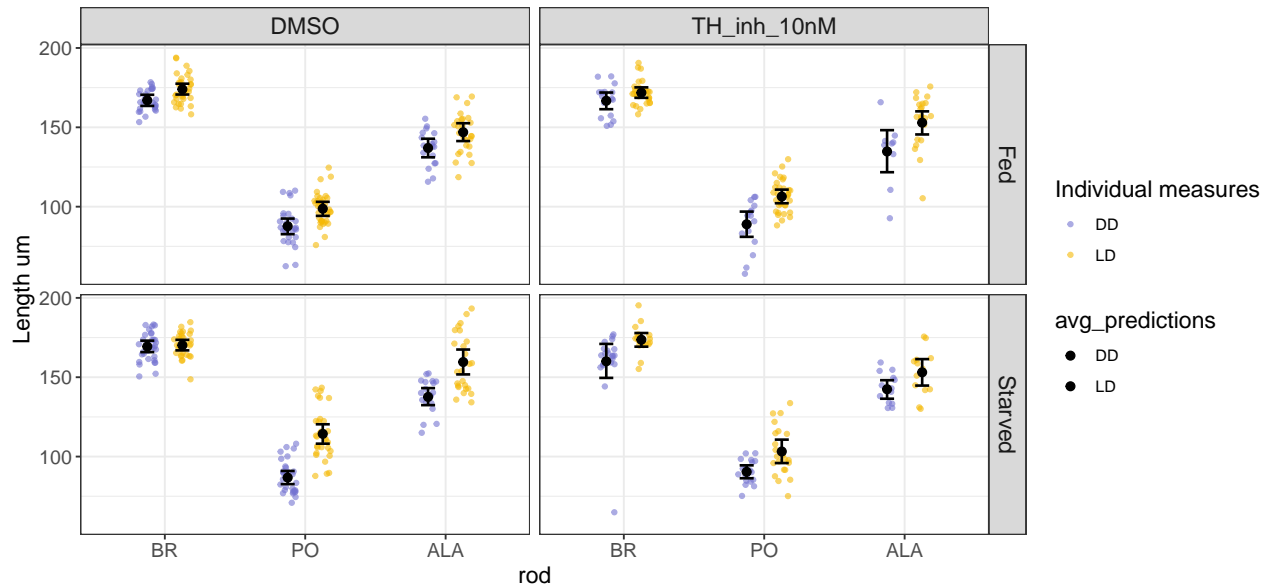
```
theme_bw() +
theme(axis.text = element_text(size = 11),
      axis.title = element_text(size = 13),
      legend.title = element_text(size = 13),
      strip.text = element_text(size = 13),
      plot.title = element_text(size = 17, face = "bold"))
```

```
## Warning in geom_errorbar(data = preds_df, aes(x = rod, ymin = conf.low, :
## Ignoring unknown aesthetics: fill
```


The plot below shows the average predictions for the length of larvae in each condition and light regime. The error bars represent the 95% confidence interval.The scatter points correspond to the original data.The scaling and centering in the model has been reversed to show the predictions in the original scale.

```
ggplot() +
  # Add original data points with jittering
  geom_jitter(data = Sp_df, aes(x = condition, y = length, color = lit),
              position = position_jitterdodge(jitter.width = 0.25, dodge.width = 0.5),
              size = 1, alpha = 0.6) +
  scale_colour_manual(values = c("#7473d1", "#f5b905","#d62222"), name= "Individual measures") +

  # Add the avg_predictions and error bars (95% CI)
  geom_point(data = preds_df, aes(x = condition, y = estimate, fill = lit),
             size = 2, position = position_dodge(width = 0.5)) +
  geom_errorbar(data = preds_df, aes(x = condition, ymin = conf.low, ymax = conf.high, fill=lit),
                width = 0.2, size = 0.7, position = position_dodge(width = 0.5)) +
  scale_fill_manual(values = c("black", "black", "black"), name="avg_predictions") +

  # Facet by specific variables of interest
  facet_grid(fed~rod ) +

  # Customize plot
  labs(title = "avg_predictions for lit, conditioned on fed, treatment and rod",
       y = "Length um", x = "rod") +
```
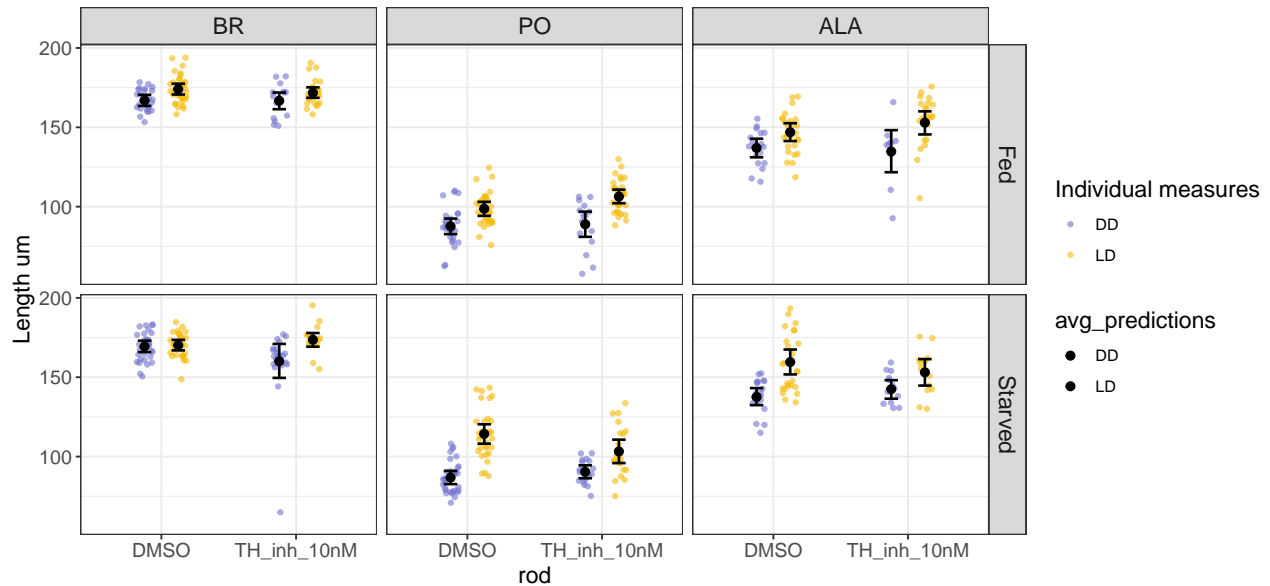
```
    theme_bw() +
    theme(axis.text = element_text(size = 11),
          axis.title = element_text(size = 13),
          legend.title = element_text(size = 13),
          strip.text = element_text(size = 13),
          plot.title = element_text(size = 17, face = "bold"))
```

```
## Warning in geom_errorbar(data = preds_df, aes(x = condition, ymin = conf.low, :
## Ignoring unknown aesthetics: fill
```


avg_predictions for lit, conditioned on fed, treatment and rod

4. Test the hypothesis that longer arms in LD are due too the fact that larvae were feeding more than in DD

The table below shows the proportion of larvae, which having bnen fed, having food in their gut (ate) or otherwise in each condition and light regime (lit). This derives from the raw data, not the predictive model.

```
summary_ate_DD <- Sp_df%>%
  filter(fed=="Fed") %>%
              group_by(lit, condition, fed, ate) %>%
          tally() %>%
          mutate(p = n / sum(n)*100) %>%
          ungroup()

summary_ate_DD
```

```
## # A tibble: 8 x 6
##   lit   condition   fed   ate       n     p
##   <fct> <fct>       <fct> <fct> <int> <dbl>
## 1 DD    DMSO        Fed   NO       51  71.8
## 2 DD    DMSO        Fed   YES      20  28.2
## 3 DD    TH_inh_10nM Fed   NO       26  65
## 4 DD    TH_inh_10nM Fed   YES      14  35
## 5 LD    DMSO        Fed   NO       74  77.1
```

```
## 6 LD      DMSO        Fed   YES       22  22.9
## 7 LD      TH_inh_10nM Fed   NO        66  76.7
## 8 LD      TH_inh_10nM Fed   YES       20  23.3
```

The plots below show the proportion of fed larvae having food in their gut in each condition and light regime. This derives from the raw data, not the predictive model.

```
Sp_df%>%
  filter(fed=="Fed")%>%
  ggplot(aes(condition, fill=ate)) +
  geom_bar(position = 'fill') +
  facet_grid(rows= vars(lit))+
  geom_text(data = . %>%
              group_by(lit, condition, fed, ate) %>%
              tally() %>%
              mutate(p = n / sum(n)) %>%
              ungroup(),
            aes(y = p, label = scales::percent(p)),
            position = position_stack(vjust = 0.5),
            show.legend = FALSE)+
  ggtitle("Larvae having food in gut")+
  theme_bw()+
  theme(plot.title = element_text(hjust = 0.5))
```

Larvae having food in gut