

# Impact of food availability, larval concentration and light on *P. lividus* larval growth - model visualization

```
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')
```

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

## 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$species == "P1",]
Pl_df <- Pl_df[Pl_df$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 larvae.'))

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

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>
```

## 2. Load best model

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

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

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

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

Pl_rod_C_fed_lit_mod <- readRDS('model_objects/Pl_rod_C_fed_lit_mod.rds')
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 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    0.40      0.03    0.34    0.46 1.00     612     1185
##
## Regression Coefficients:
##          Estimate Est.Error 1-95% CI u-95% CI Rhat
## Intercept         0.21      0.07    0.07    0.35 1.00
## sigma_Intercept   -0.87      0.10   -1.06   -0.68 1.00
## rodPO             -1.76      0.08   -1.92   -1.61 1.00
## rodALA            -0.28      0.06   -0.39   -0.16 1.00
## C                 -0.01      0.07   -0.16    0.13 1.00
## fedStarved        -0.26      0.10   -0.44   -0.07 1.00
```

## litLD	0.47	0.09	0.29	0.65	1.00
## rodPO:C	0.02	0.08	-0.12	0.17	1.00
## rodALA:C	-0.10	0.06	-0.22	0.02	1.00
## rodPO:fedStarved	0.47	0.11	0.27	0.69	1.00
## rodALA:fedStarved	0.48	0.09	0.31	0.65	1.00
## C:fedStarved	-0.06	0.10	-0.26	0.13	1.00
## rodPO:litLD	0.34	0.11	0.12	0.55	1.00
## rodALA:litLD	0.24	0.08	0.09	0.40	1.00
## C:litLD	0.07	0.09	-0.12	0.25	1.00
## fedStarved:litLD	0.47	0.13	0.20	0.72	1.00
## rodPO:C:fedStarved	-0.04	0.10	-0.24	0.16	1.00
## rodALA:C:fedStarved	0.26	0.09	0.09	0.43	1.00
## rodPO:C:litLD	0.27	0.11	0.05	0.49	1.00
## rodALA:C:litLD	0.18	0.08	0.02	0.33	1.00
## rodPO:fedStarved:litLD	0.24	0.17	-0.09	0.58	1.00
## rodALA:fedStarved:litLD	-0.31	0.13	-0.56	-0.07	1.00
## C:fedStarved:litLD	0.15	0.13	-0.11	0.39	1.00
## rodPO:C:fedStarved:litLD	-0.60	0.17	-0.94	-0.26	1.00
## rodALA:C:fedStarved:litLD	-0.40	0.13	-0.65	-0.15	1.00
## sigma_rodPO	0.32	0.13	0.06	0.58	1.00
## sigma_rodALA	-0.19	0.14	-0.47	0.09	1.00
## sigma_fedStarved	-0.14	0.16	-0.47	0.17	1.00
## sigma_litLD	-0.25	0.16	-0.58	0.05	1.00
## sigma_rodPO:fedStarved	0.20	0.21	-0.20	0.61	1.01
## sigma_rodALA:fedStarved	0.53	0.23	0.05	0.99	1.00
## sigma_rodPO:litLD	0.57	0.20	0.19	0.99	1.00
## sigma_rodALA:litLD	0.46	0.24	0.01	0.94	1.00
## sigma_fedStarved:litLD	-0.62	0.27	-1.12	-0.07	1.00
## sigma_rodPO:fedStarved:litLD	0.70	0.32	0.05	1.31	1.00
## sigma_rodALA:fedStarved:litLD	0.68	0.36	-0.05	1.36	1.00
##	Bulk_ESS	Tail_ESS			
## Intercept	1346	2256			
## sigma_Intercept	1979	2981			
## rodPO	2224	3178			
## rodALA	1959	2998			
## C	1067	1767			
## fedStarved	1244	1978			
## litLD	1295	2016			
## rodPO:C	2274	3361			
## rodALA:C	1820	2693			
## rodPO:fedStarved	2428	3442			
## rodALA:fedStarved	2114	2580			
## C:fedStarved	1136	1958			
## rodPO:litLD	2485	3264			
## rodALA:litLD	2177	2982			
## C:litLD	1117	2172			
## fedStarved:litLD	1157	1937			
## rodPO:C:fedStarved	2606	3214			
## rodALA:C:fedStarved	2246	3093			
## rodPO:C:litLD	2825	3438			
## rodALA:C:litLD	2224	2936			
## rodPO:fedStarved:litLD	2661	3151			
## rodALA:fedStarved:litLD	2683	3396			
## C:fedStarved:litLD	1101	1583			

```
## rodPO:C:fedStarved:litLD      3332      3541
## rodALA:C:fedStarved:litLD     2837      3558
## sigma_rodPO                  2178      3113
## sigma_rodALA                 2030      2841
## sigma_fedStarved              800      1777
## sigma_litLD                  929      1845
## sigma_rodPO:fedStarved        876      1794
## sigma_rodALA:fedStarved       863      2023
## sigma_rodPO:litLD            1070      1977
## sigma_rodALA:litLD           992      1700
## sigma_fedStarved:litLD       731      943
## sigma_rodPO:fedStarved:litLD  847      1213
## sigma_rodALA:fedStarved:litLD 791      1128
##
## 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. Marginal effects plot with avg\_predictions

```
preds_df <- marginalesffects::avg_predictions(Pl_rod_C_fed_lit_mod,
  newdata = datagrid(fed = unique(Pl_df$fed),
    lit = unique(Pl_df$lit),
    rod = unique(Pl_df$rod),
    C = unique(Pl_df$C)
  ),
  by = c("C", "lit", "rod", "fed"),
  transform = unscale_outcome,
  re_formula = NA
)
preds_df$lar_ml <- (preds_df$C * sdC) + meanC
preds_df$lar_ml <- (preds_df$C * sdC) + meanC

head(preds_df, 10)
```

```
##
##      fed lit rod      C Estimate 2.5 % 97.5 % larva
## Fed      DD BR  -1.66      189   182   197   P11
## Starved  DD BR  -1.66      185   177   192   P11
## Fed      DD PO  -1.66      136   127   145   P11
## Starved  DD PO  -1.66      148   138   157   P11
## Fed      DD ALA -1.66      186   179   193   P11
## Starved  DD ALA -1.66      183   174   192   P11
## Fed      LD BR  -1.66      200   193   206   P11
## Starved  LD BR  -1.66      202   195   209   P11
## Fed      LD PO  -1.66      143   133   153   P11
## Starved  LD PO  -1.66      198   184   212   P11
##
## Type: response
## Columns: rowid, C, lit, rod, fed, estimate, conf.low, conf.high, larva, L, lar_ml
Check levels for lar_ml
```

```
unique(preds_df$lar_ml)
```

```
## [1] 12.5 25.0 50.0
```

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.

```
ggplot() +  
  # Add original data points  
  geom_jitter(data = Pl_df, aes(x = C, 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 = C, y = estimate, fill = fed), # Use "response" column  
            size = 2, position = position_dodge(width = 0.5)) +  
  geom_errorbar(data = preds_df, aes(x = C, 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 = "Average predictions for fed, conditioned on lit and rod",  
       y = "Length in um", x = "larvae/mL") +  
  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.
```

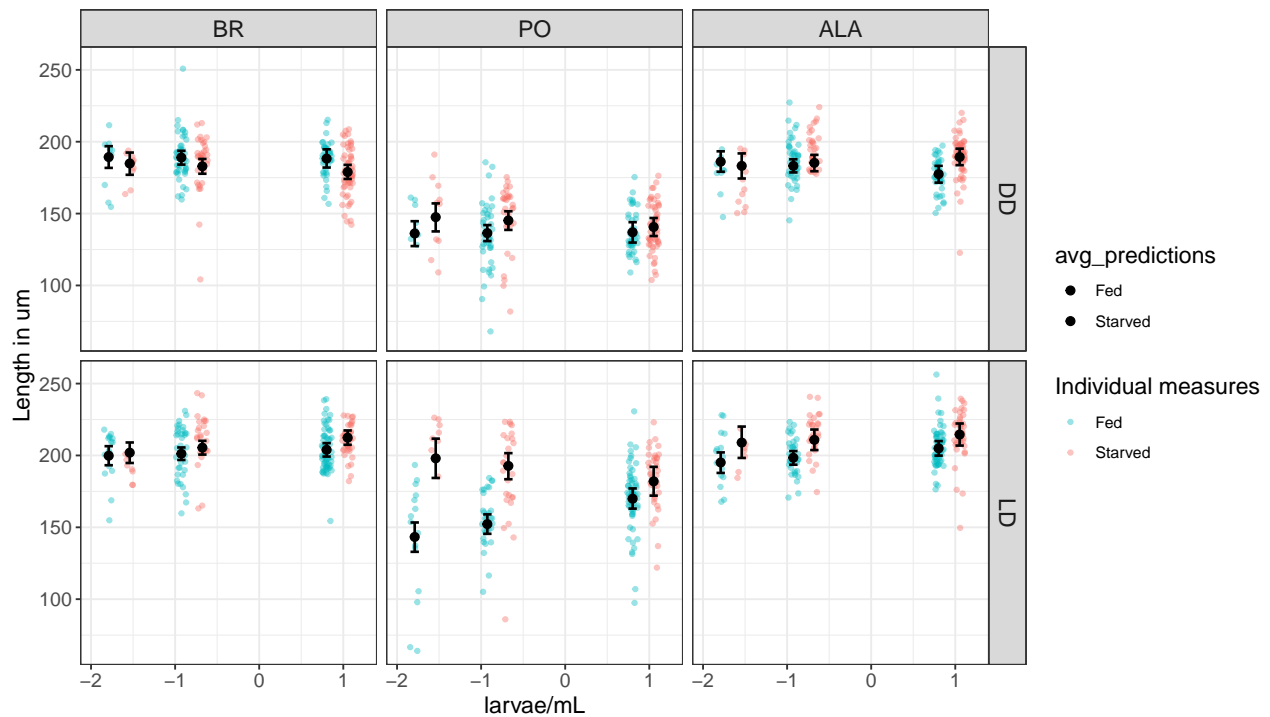
```
## This warning is displayed once every 8 hours.
```

```
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was  
## generated.
```

```
## Warning in geom_errorbar(data = preds_df, aes(x = C, ymin = conf.low, ymax =
```

```
## conf.high, : Ignoring unknown aesthetics: fill
```

### Average predictions for fed, conditioned on lit and rod



```
ggplot() +
  # Add original data points
  geom_jitter(data = Pl_df, aes(x = lar_ml, y = length, color = fed),
    position = position_jitterdodge(jitter.width = 2, dodge.width = 0),
    size = 0.8, alpha = 0.5) +
  scale_colour_manual(values = c("#00BBC1", "#F86D63"), name = "Individual measures") +

  # Add the avg_predictions and error bars (95% CI)
  geom_smooth(data = preds_df, aes(x = lar_ml, y = estimate, color = fed),
    size = 1, method = "lm")+
    scale_fill_manual(values = c("#00BBC1", "#F86D63"), name = "avg_predictions") +

  geom_ribbon(data = preds_df, aes(x = lar_ml, ymin = conf.low, ymax = conf.high, fill = fed),
    alpha = 0.3) +
    scale_fill_manual(values = c("#00BBC1", "#F86D63"), name = "avg_predictions") +

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

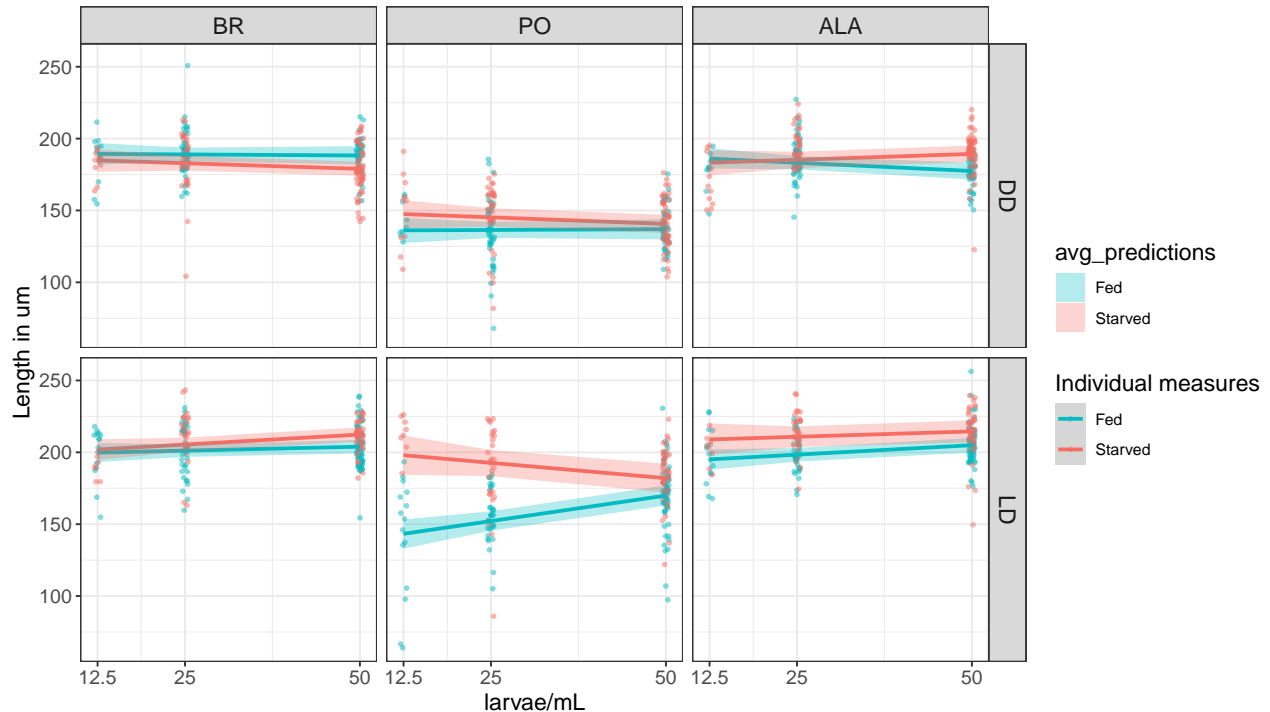
  # Customize x-axis values
  scale_x_continuous(breaks = c(12.5, 25, 50), labels = c("12.5", "25", "50")) +

  # Customize plot
  labs(title = "Average predictions for fed, conditioned on lit, larval concentration and rod",
    y = "Length in um", x = "larvae/mL") +
  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"))
```

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
## `geom_smooth()` using formula = 'y ~ x'
```

### Average predictions for fed, conditioned on lit, larval concentration and rod



```
ggplot() +
  # Add original data points
  geom_jitter(data = Pl_df, aes(x = C, y = length, color = lit),
    position = position_jitterdodge(jitter.width = 0.25, dodge.width = 0.5),
    size = 1, alpha = 0.4) +
  scale_colour_manual(values = c( "#7473d1", "#f5b905"), name = "Individual measures") +

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

  # Add the avg_predictions and error bars (95% CI)
  geom_point(data = preds_df, aes(x = C, y = estimate, fill = lit), # Use "response" column
    size = 2, position = position_dodge(width = 0.5)) +
  geom_errorbar(data = preds_df, aes(x = C, 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"), name = "avg_predictions") +

  # Customize plot
  labs(title = "Average predictions for lit, conditioned on fed, larval concentration and rod",
    y = "Length in um", x = "larvae/mL") +
  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"))

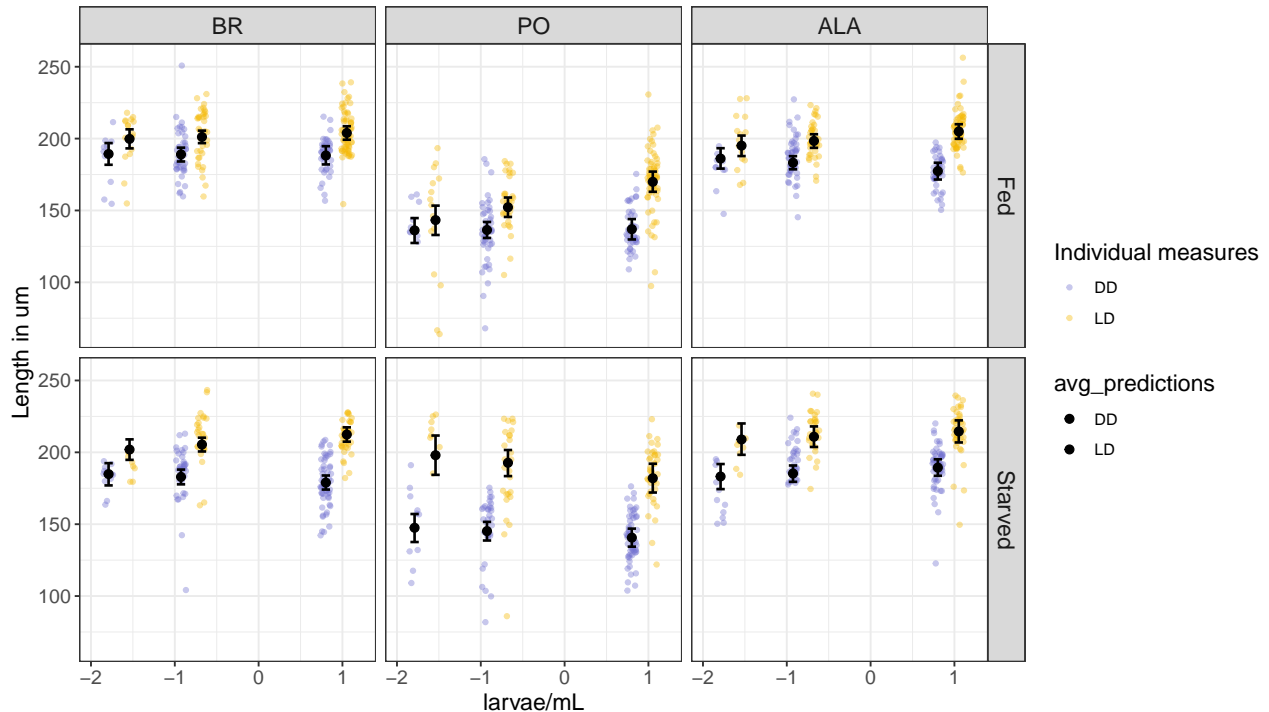
```

```

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

```

### Average predictions for lit, conditioned on fed, larval concentration and rod



```

ggplot() +
  # Add original data points
  geom_jitter(data = Pl_df, aes(x = rod, y = length, color = lit),
    position = position_jitterdodge(jitter.width = 0.25, dodge.width = 0.5),
    size = 1, alpha = 0.4) +
  scale_colour_manual(values = c("#7473d1", "#f5b905"), name = "Individual measures") +

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

  # Add the avg_predictions and error bars (95% CI)
  geom_point(data = preds_df, aes(x = rod, y = estimate, fill = lit), # 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 = lit),
    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 = "Average predictions for lit, conditioned on fed, larval concentration 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")) #, panel.grid = element_line(color="gray80")

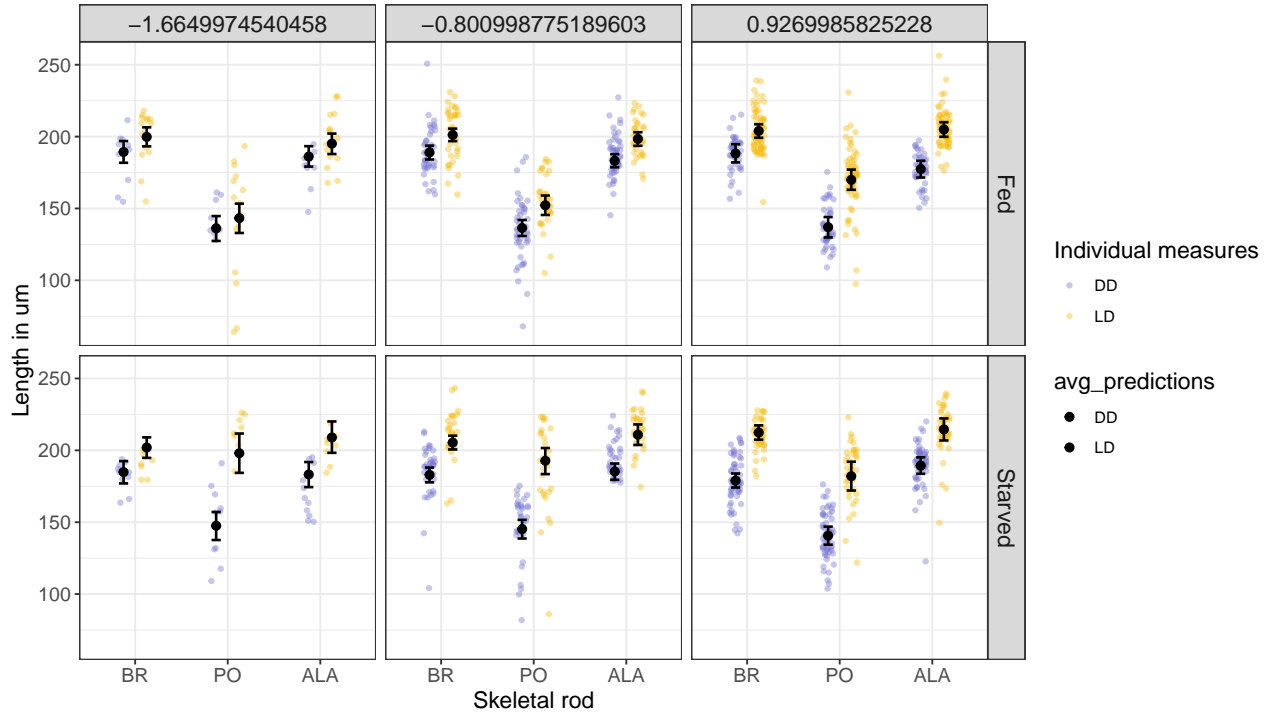
```

```

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

```

### Average predictions for lit, conditioned on fed, larval concentration and rod



```

ggplot() +
  # Add original data points
  geom_jitter(data = Pl_df, aes(x = rod, y = length, color = lit),
    position = position_jitterdodge(jitter.width = 0.25, dodge.width = 0.5),
    size = 1, alpha = 0.4) +
  scale_colour_manual(values = c("#7473d1", "#f5b905"), name = "Individual measures") +

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

  # Add the avg_predictions and error bars (95% CI)
  geom_point(data = preds_df, aes(x = rod, y = estimate, fill = lit), # 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 = lit),
    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 = "Average predictions for lit, conditioned on fed, larval concentration 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"))

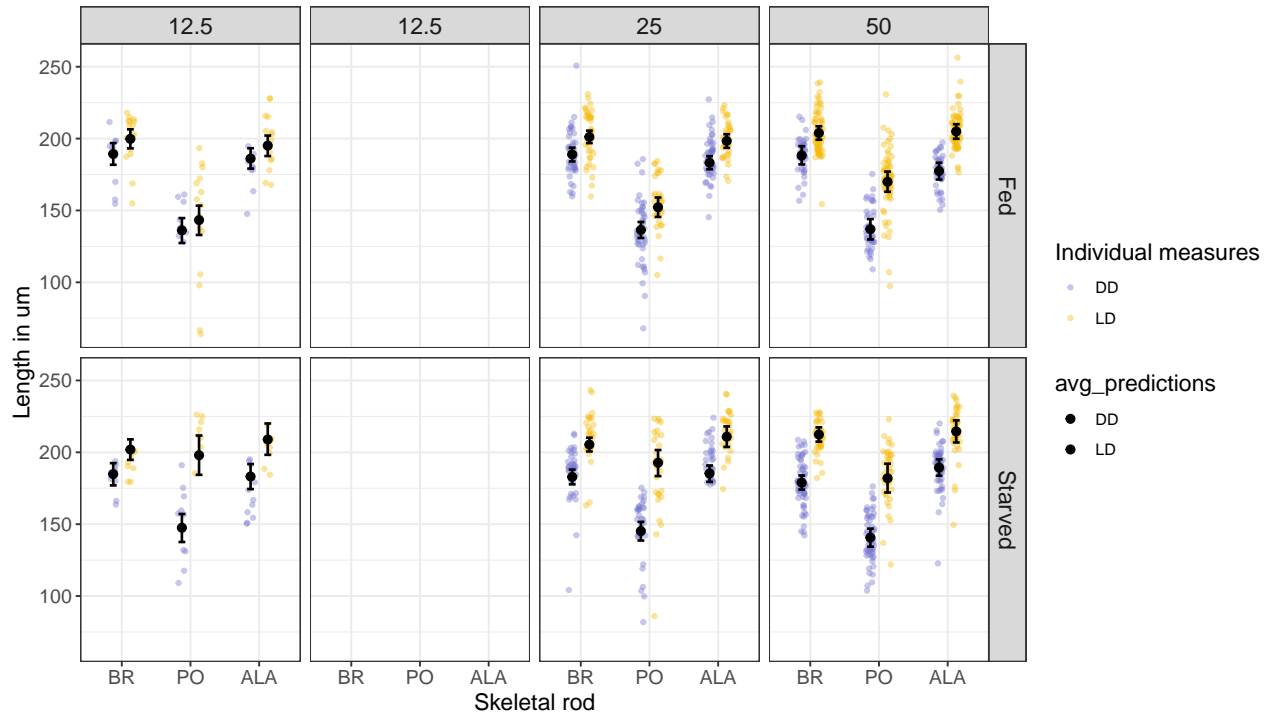
```

```

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

```

### Average predictions for lit, conditioned on fed, larval concentration and rod



### using C\_vals

```

C_vals = seq(from = min(Pl_df$C), to = max(Pl_df$C), length.out=100)

```

```

preds_df <- marginalesffects::avg_predictions(Pl_rod_C_fed_lit_mod,
  newdata = datagrid(fed = unique(Pl_df$fed),
    C = C_vals, #unique(Pl_df$C),
    lit = unique(Pl_df$lit),
    rod = unique(Pl_df$rod)
  ),
  by = c("C", "fed", "rod", "lit"),
  transform = unscale_outcome,
  re_formula = NA
)

```

```

preds_df$lar_ml <- (preds_df$C * sdC) + meanC
preds_df$lar_ml <- (preds_df$C * sdC) + meanC
preds_df

```

```

##
##      fed      C lit rod Estimate 2.5 % 97.5 % larva
## Fed    -1.665 DD BR      189   182   197   P11

```

```
## Fed      -1.665 LD BR      200  193   206   P11
## Fed      -1.665 DD PO      136  127   145   P11
## Fed      -1.665 LD PO      143  133   153   P11
## Fed      -1.665 DD ALA     186  179   193   P11
## --- 1190 rows omitted. See ?print.marginaleffects ---
## Starved  0.927 LD BR      212  207   217   P11
## Starved  0.927 DD PO      141  134   147   P11
## Starved  0.927 LD PO      182  172   192   P11
## Starved  0.927 DD ALA     189  184   195   P11
## Starved  0.927 LD ALA     215  207   222   P11
## Type: response
## Columns: rowid, C, fed, rod, lit, estimate, conf.low, conf.high, larva, L, lar_ml

preds_df %>%
  ggplot(aes(x = lar_ml, y = estimate, color = fed)) +
  # Add original data points
  geom_point(data = Pl_df, aes(x = lar_ml, y = length, color = fed),
    position = position_jitter(width = 2), size = 0.9, alpha = 0.6) +
    scale_colour_manual(values = c("#00BBC1", "#F86D63"), name="Individual measures") +

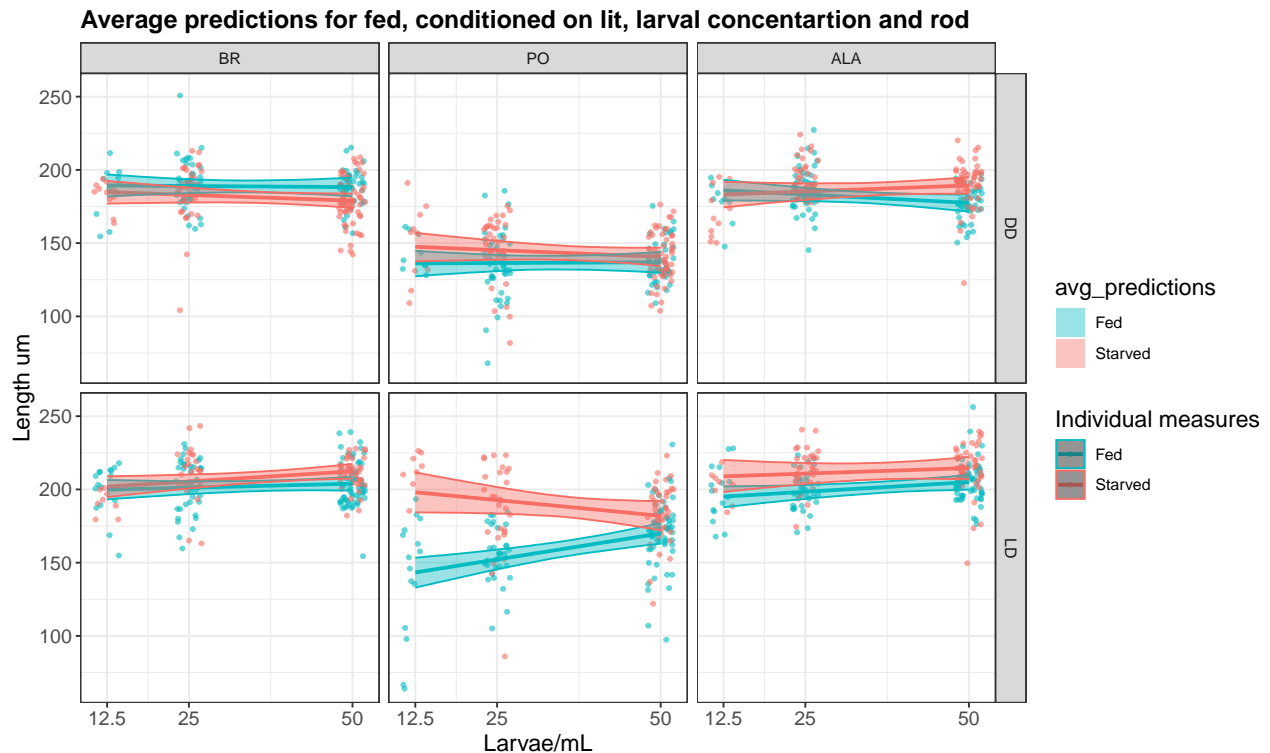
  geom_smooth(data = preds_df, aes(x = lar_ml, y = estimate, color = fed),
    size = 1, method = "lm") +
  scale_fill_manual(values = c("#00BBC1", "#F86D63"), name = "avg_predictions") +
  geom_ribbon(data = preds_df,
    aes(x = lar_ml, ymin = conf.low, ymax = conf.high, fill = fed),
    alpha = 0.4) +
  scale_fill_manual(values = c("#00BBC1", "#F86D63"), name = "avg_predictions") +

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

  # Customize x-axis values
  scale_x_continuous(breaks = c(12.5, 25, 50), labels = c("12.5", "25", "50")) +

  # Customize plot
  labs(title = "Average predictions for fed, conditioned on lit, larval concentration and rod",
    y = "Length um", x = "Larvae/mL") +
  theme_bw() +
  theme(axis.text = element_text(size = 11),
    axis.title = element_text(size = 13),
    legend.title = element_text(size = 13),
    plot.title = element_text(size = 14, face = "bold"))

## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
## `geom_smooth()` using formula = 'y ~ x'
```



```

preds_df %>%
  ggplot(aes(x = lar_ml, y = estimate, color = lit)) +
  # Add original data points
  geom_point(data = Pl_df, aes(x = lar_ml, y = length, color = lit),
            position = position_jitter(width = 2), size = 0.9, alpha = 0.6) +
  scale_colour_manual(values = c("#7473d1", "#FFB74D"), name = "Individual measures") +

  geom_smooth(data = preds_df, aes(x = lar_ml, y = estimate, color = lit),
            size = 1, method = "lm") +
  scale_fill_manual(values = c("#7473d1", "#FFB74D"), name = "avg_predictions") +
  geom_ribbon(data = preds_df,
            aes(x = lar_ml, ymin = conf.low, ymax = conf.high, fill = lit),
            alpha = 0.4) +
  scale_fill_manual(values = c("#7473d1", "#FFB74D"), name = "avg_predictions") +

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

  # Customize x-axis values
  scale_x_continuous(breaks = c(12.5, 25, 50), labels = c("12.5", "25", "50")) +

  # Customize plot
  labs(title = "Average predictions for lit, conditioned on fed, larval concentration and rod",
       y = "Length um", x = "Larvae/mL") +
  theme_bw() +
  theme(axis.text = element_text(size = 11),
        axis.title = element_text(size = 13),
        legend.title = element_text(size = 13),
        plot.title = element_text(size = 14, face = "bold"))

```

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
## `geom_smooth()` using formula = 'y ~ x'
```

**Average predictions for lit, conditioned on fed, larval concentration and rod**

