```
library(car)
library(dplyr)
library(ggpubr)
library(ggplot2)
library(lme4)
library(patchwork)
library(tidyverse)
library(lme4)
library(ggpmisc)
library(emmeans)
library(multcomp)
library(ggbeeswarm)
# Mothers' life history traits -----------------------------------------------
mum_df<-read.csv('f0.csv', stringsAsFactors = TRUE)

# means and SEMs for life history traits
summary_table <- mum_df %>%
  group_by(treat) %>%
  summarise(across(
    .cols = -c(no),
    .fns = list(
      mean = ~mean(.x, na.rm = TRUE),
      sem  = ~sd(.x, na.rm = TRUE) / sqrt(n())
    ),
    .names = "{.col}_{.fn}"
  ))

summary_table

# Mothers' individual traits (GLM) ---------------------------------------------

#1. Developmental prey consumption
hist(mum_df$con)
con_model <- glm(con ~ treat, data = mum_df, family = poisson(link = "log"))
summary (con_model)
Anova(con_model)
dispersion <- sum(residuals(con_model, type = "pearson")^2) / df.residual(con_model)
dispersion # check for overdispersion

#2. Adult prey consumption Gamma(link = "log")
hist(mum_df$adcon)
adcon_model <- glm(adcon ~ treat, data = mum_df, family = quasipoisson(link = "log"))
summary (adcon_model)
Anova(adcon_model)

#3. Adulthood daily
hist(mum_df$adc)
adc_model <- glm(adc ~ treat, data = mum_df, family = quasipoisson(link = "log"))
summary (adc_model)
Anova(adc_model)

#4. Developmental time
hist(mum_df$ea)
ea_model <- glm(ea ~ treat, data = mum_df, family = quasipoisson(link = "log"))
summary (ea_model)
Anova(ea_model)

#5. Pre-oviposition period
hist(mum_df$pre)
pre_model <- glm(pre ~ treat, data = mum_df, family = quasipoisson(link = "log"))
summary (pre_model)
Anova(pre_model)
dispersion <- sum(residuals(pre_model, type = "pearson")^2) / df.residual(pre_model)
dispersion

#6. Oviposition period
hist(mum_df$ovi)
ovi_model <- glm(ovi ~ treat, data = mum_df, family = quasipoisson(link = "log"))
summary (ovi_model)
```

```
Anova(ovi_model)

#7. Post-oviposition period
hist(mum_df$post)
post_model <- glm(post ~ treat, data = mum_df, family = quasipoisson(link = "log"))
summary (post_model)
Anova(post_model)

#8. Lifespan
hist(mum_df$ls)
ls_model <- glm(ls ~ treat, data = mum_df, family = quasipoisson(link = "log"))
summary (ls_model)
Anova(ls_model)
dispersion <- sum(residuals(ls_model, type = "pearson")^2) / df.residual(ls_model)
dispersion

#9. Fecundity
hist(mum_df$fec)
fec_model <- glm(fec ~ treat, data = mum_df, family = quasipoisson(link = "log"))
summary (fec_model)
Anova(fec_model)

#10. Daily oviposition
hist(mum_df$daily)
daily_model <- glm(daily ~ treat, data = mum_df, family = quasipoisson(link = "log"))
summary (daily_model)
Anova(daily_model)

#11. Max. daily oviposition
hist(mum_df$max)
max_model <- glm(max ~ treat, data = mum_df, family = quasipoisson(link = "log"))
summary (max_model)
Anova(max_model)

#12. Size
hist(mum_df$size)
size_model <- glm(size ~ treat, data = mum_df, family = quasipoisson(link = "log"))
summary (size_model)
Anova(size_model)

# Mothers' age and prey consumption ------------------------------------------
con_df <- read.csv('conovi.csv', stringsAsFactors = TRUE)
con_df$treat <- factor(con_df$treat, levels = c("Restricted", "Full"))
re_con_df <- subset(con_df, treat == "Restricted")
ab_con_df <- subset(con_df, treat == "Full")
hist(re_con$con)
hist(ab_con$con)

con <- ggscatter(con_df, x = "day", y = "con",
                 add = "reg.line", conf.int = TRUE,
                 add.params = list(color = "#707D99"),
                 conf.int.fill = "#707D99",
                 conf.int.alpha = 0.2,
                 cor.coef = FALSE,
                 cor.coef.size = 6,
                 ylab = "Prey consumption (number of eggs)",
                 xlab = "Adult age (day)") +
  theme_classic2() +
  stat_cor(aes(label = paste(..rr.label.., gsub("p", "P", ..p.label..), sep =
"~`,`~")),
           method = "spearman",
           size = 6,
           p.accuracy = 0.001,
           r.accuracy = 0.01,
           label.sep = ", ") +
  stat_regline_equation(label.x = 1, label.y = 61, aes(label = after_stat(eq.label)),
                        vjust = 0, formula = y ~ x, size = 6) +
  theme(text = element_text(family = "Helvetica", size = 26),
        plot.margin = margin(1, 0.5, 1, 1, "cm"),
```

```
        axis.title.x = element_text(margin = margin(t = 10)),
        axis.title.y = element_text(margin = margin(r = 10)),
        panel.spacing = unit(1, "cm")) +
  facet_wrap(~treat, labeller = as_labeller(c('Restricted' = "Restricted", 'Full' =
"Abundant"))) +
  ylim(NA, 70) +
  scale_x_continuous(breaks = c(1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60))+
  geom_hline(data = subset(con_df, treat == "Restricted"), aes(yintercept = 20), color
= "black", linetype = "dashed") +
  geom_hline(data = subset(con_df, treat == "Full"), aes(yintercept = 60), color =
"black", linetype = "dashed")

print(con)

# Mother's age and oviposition -------------------------------------------------

ovi <- ggscatter(con_df, x = "day", y = "fec",
                 add = "reg.line", conf.int = TRUE,
                 add.params = list(color = "#707D99"),
                 conf.int.fill = "#707D99",
                 conf.int.alpha = 0.2,
                 cor.coef = FALSE,
                 cor.coef.size = 6,
                 ylab = "Daily oviposition (eggs/day)",
                 xlab = "Adult age (day)") +
  theme_classic2() +
  stat_cor(aes(label = paste(..rr.label.., gsub("p", "P", ..p.label..), sep =
"~`,`~")),
           method = "spearman",
           size = 6,
           p.accuracy = 0.001,
           r.accuracy = 0.01,
           label.sep = ", ") +
  stat_regline_equation(label.x = 1, label.y = 4, aes(label = after_stat(eq.label)),
                        vjust = 0, formula = y ~ x, size = 6) +
  theme(text = element_text(family = "Helvetica", size = 26),
        plot.margin = margin(1, 0.5, 1, 1, "cm"),
        axis.title.x = element_text(margin = margin(t = 10)),
        axis.title.y = element_text(margin = margin(r = 10)),
        panel.spacing = unit(1, "cm")) +  # Increase space between facets) +
  facet_wrap(~treat, labeller = as_labeller(c('Restricted' = "Restricted", 'Full' =
"Abundant"))) +
  ylim(NA, 5)
print(ovi)

# Mothers' age and egg volume -------------------------------------------------
egg_df<-read.csv('eggv.csv', stringsAsFactors = TRUE)
hist(egg_df$volume)

eggv_model <- lmer(volume ~ day * treat  + (1|mum), data = egg_df)
summary(eggv_model)
Anova(eggv_model, type = "III")

cld(emmeans(eggv_model, pairwise ~ day * treat, adjust = "tukey"),
    Letters = letters)

###Effect size###
emm_egg <- emmeans(eggv_model, ~ treat)
pairs(emm_egg)
eff_size(emm_egg,
         sigma = sigma(eggv_model),
         edf = df.residual(eggv_model))

###Plot###
egg_df$treat <- factor(egg_df$treat, levels = c("rest", "full"))
eggv <- ggscatter(egg_df, x = "day", y = "volume",
                  add = "reg.line", conf.int = TRUE,
                  add.params = list(color = "#707D99"),
                  conf.int.fill = "#707D99",
```

```
                  conf.int.alpha = 0.2,
                  cor.coef = FALSE,
                  cor.coef.size = 6,
                  xlab = "Maternal age at oviposition (day)",
                  ylab = "Egg size (mm³)",
                  palette = c("darkgrey", "lightgrey")) +
  theme_classic2() +
  stat_regline_equation(label.x = 1, label.y = 0.00161, aes(label =
after_stat(eq.label)),
                        vjust = 0, formula = y ~ x, size = 6) +
  theme(text = element_text(family = "Helvetica", size = 26),
        plot.margin = margin(1, 1, 1, 0.5, "cm"),
        axis.title.x = element_text(margin = margin(t = 10)),
        axis.title.y = element_text(margin = margin(r = 10)),
        panel.spacing = unit(1, "cm")) +
  facet_wrap(~treat, labeller = as_labeller(c('full' = "Abundant", 'rest' =
"Restricted"))) +
  scale_x_continuous(breaks = c(1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50)) +
  ylim(0.00095, 0.00167)

print(eggv)

# Offspring survival and hating -------------------------------------------------------
--------
# Hatching rate
hatch_df<-read.csv('f1.csv', stringsAsFactors = TRUE)

hatch_model <- glm(hatch ~ diet * treat * age, data = hatch_df, family = binomial)
summary(hatch_model)
Anova(hatch_model, type = "III")

# Survival rate to adulthood
sur_df <- subset(hatch_df, !is.na(adult) & adult != "")

sur_model <- glm(adult ~ diet * treat * age, data = sur_df, family = binomial)
summary(sur_model)
Anova(sur_model, type = "III")

###Effect size###
emm_sur <- emmeans(sur_model, ~  age)
pairs(emm_sur, type = "response")

# Graphic presentation for hatching
hatch_df$hatch <- factor(hatch_df$hatch, levels = c("N", "Y"))

hatch_summary <- hatch_df %>%
  group_by(treat, age, diet) %>%
  summarise(hatch_rate = mean(hatch == "Y") * 100, .groups = "drop")
hatch_summary$age <- factor(hatch_summary$age, levels = c("y", "o"))
hatch_summary$treat <- factor(hatch_summary$treat, levels = c('r', 'f'))

hatching_plot <- ggplot(hatch_summary, aes(x = treat, y = hatch_rate, fill = age)) +
  geom_bar(stat = "identity", position = "dodge", width = 0.6, size = 1.5, show.legend
= TRUE) +
  scale_y_continuous(limits = c(0, 100), labels = scales::percent_format(scale = 1)) +
  facet_wrap(~diet, labeller = as_labeller(c('20' = '20 eggs', '30' = '30 eggs', '40' =
'40 eggs',
                                             '50' = '50 eggs', '60' = '60 eggs'))) +
  labs(x = "Maternal dietary treatment", y = "Hatch rate (%)", fill = "Maternal age") +
  theme_classic2() +
  theme(text = element_text(family = "Helvetica", size = 22),
        plot.margin = margin(1, 1, 1, 0.5, "cm"),
        axis.title.x = element_text(margin = margin(t = 10)),
        axis.title.y = element_text(margin = margin(r = 10)),
        axis.text.x = element_text(angle = 45, hjust = 1),
        panel.spacing = unit(1, "cm"),
        legend.position = c(1, 0.1),
        legend.justification = c("right", "bottom")) +
  scale_fill_manual(values = c("y" = "#6A9CAF", "o" = "#DD7927"),
```

```
                  labels = c("y" = "Young", "o" = "Old")) +
  scale_x_discrete(labels = c('r' = 'Restricted', 'f' = 'Abundant'))

print(hatching_plot)

# Graphic presentation for survial to adulthood
sur_summary <- sur_df %>%
  group_by(treat, age, diet) %>%
  summarise(sur_rate = mean(adult == "Y") * 100, .groups = "drop")
sur_summary$age <- factor(hatch_summary$age, levels = c("y", "o"))
sur_summary$treat <- factor(hatch_summary$treat, levels = c('r', 'f'))
sur_summary$diet <- factor(sur_summary$diet)

sur_plot <- ggplot(sur_summary, aes(x = treat, y = sur_rate, fill = age)) +
  geom_bar(stat = "identity", position = "dodge", width = 0.6, size = 1.5, show.legend
= TRUE) +
  scale_y_continuous(limits = c(0, 100), labels = scales::percent_format(scale = 1)) +
  facet_wrap(~diet, labeller = as_labeller(c('20' = '20 eggs', '30' = '30 eggs', '40' =
'40 eggs',
                                             '50' = '50 eggs', '60' = '60 eggs'))) +
  labs(x = "Maternal dietary treatment", y = "Survival to adulthood (%)", fill =
"Maternal age") +
  theme_classic2() +
  theme(text = element_text(family = "Helvetica", size = 22),
        plot.margin = margin(1, 1, 1, 0.5, "cm"),
        axis.title.x = element_text(margin = margin(t = 10)),
        axis.title.y = element_text(margin = margin(r = 10)),
        axis.text.x = element_text(angle = 45, hjust = 1),
        panel.spacing = unit(1, "cm"),
        legend.position = c(1, 0.1),
        legend.justification = c("right", "bottom")) +
  scale_fill_manual(values = c("y" = "#6A9CAF", "o" = "#DD7927"),
                    labels = c("y" = "Young", "o" = "Old")) +
  scale_x_discrete(labels = c('r' = 'Restricted', 'f' = 'Abundant'))

print(sur_plot)

# Merge the two plots side by side
merged_plot <- hatching_plot + sur_plot +
  plot_annotation(tag_levels = 'a', tag_prefix = "(", tag_suffix = ")") &
  theme(plot.tag = element_text(size = 20, face = "plain"))

print(merged_plot)


# Offspring development and size ------------------------------------------

f1_df <-read.csv('f1.csv', stringsAsFactors = TRUE)
#development
f1_df_ea <- f1_df %>%
  filter(adult == "Y")
f1_df_ea$age <- as.factor(f1_df_ea$age)
f1_df_ea$treat <- as.factor(f1_df_ea$treat)

hist(f1_df_ea$con)
hist(f1_df_ea$ea)
hist(f1_df_ea$size)

oea_model <- lmer(log(ea) ~ diet * treat * age + con + (1|mum), data = f1_df_ea)
summary(oea_model)
Anova(oea_model, type = 'III')

oea_reduced_model <- lmer(log(ea) ~ treat * age + con + (1|mum), data = f1_df_ea)
anova(oea_model, oea_reduced_model)
Anova(oea_reduced_model, type = 'III')

emm <- emmeans(oea_reduced_model, ~ treat * age)
emm_treat <- emmeans(oea_reduced_model, ~ treat)
emm_age   <- emmeans(oea_reduced_model, ~ age)
```

```
pairs(emm, adjust = "tukey")
pairs(emm_treat)
pairs(emm_age)
cld(emmeans(oea_reduced_model, pairwise ~ treat * age, adjust = "tukey"),
    Letters = letters)

###Effect size###
emm_dev <- emmeans(oea_reduced_model, ~ age)
pairs(emm_dev)
eff_size(emm_dev,
         sigma = sigma(oea_reduced_model),
         edf = df.residual(oea_reduced_model))

# plot
f1_df_ea$age <- factor(f1_df_ea$age, levels = c("y", "o"), labels = c("Young", "Old"))
f1_df_ea$treat <- factor(f1_df_ea$treat, levels = c("r", "f"))
fea <- ggscatter(f1_df_ea, x = "con", y = "ea",
                 color = "age", fill = "age",
                 add = "reg.line",
                 cor.coef = FALSE,  # Remove default correlation text
                 xlab = "Offspring prey consumption (eggs)",
                 ylab = "Developmental duration (day)",
                 palette = c("#6A9CAF", "#DD7927")) +
  geom_smooth(aes(color = age), method = "lm", se = TRUE,
              linetype = "solid", linewidth = 1.5) +
  stat_regline_equation(
    aes(color = age, label = paste(..eq.label.., sep = "~~~")),
    label.x = 20, label.y = c(12.5, 11.8), size = 8
  ) +
  theme_classic2() +
  theme(text = element_text(family = "Helvetica", size = 26),
        plot.margin = margin(1, 1, 1, 0.5, "cm"),
        axis.title.x = element_text(margin = margin(t = 10)),
        axis.title.y = element_text(margin = margin(r = 10)),
        panel.spacing = unit(1, "cm")) +
  ylim(NA, 13) +
  facet_wrap(~ treat, labeller = labeller(treat = c("r" = "Restricted", "f" =
"Abundant"))) +
  labs(color = "Maternal age", fill = "Maternal age")

print(fea)

#size
f1_df_size <- f1_df %>%
  filter(!is.na(size))

osize_model <- lmer(size ~ diet * treat * age + con  + (1|mum), data = f1_df_size)
summary(osize_model)
Anova(osize_model, type = 'III')
osize_reduced_model <- lmer(size ~ treat * age + con + (1|mum), data = f1_df_size)
anova(osize_model, osize_reduced_model)
summary(osize_reduced_model)
Anova(osize_reduced_model, type = 'III')

emm <- emmeans(osize_reduced_model, ~ treat * age)
emm_treat <- emmeans(osize_reduced_model, ~ treat)
emm_age   <- emmeans(osize_reduced_model, ~ age)
pairs(emm, adjust = "tukey")
pairs(emm_treat)
pairs(emm_age)
cld(emmeans(osize_reduced_model, pairwise ~ treat * age, adjust = "tukey"),
    Letters = letters)

###Effect size###
emm_size <- emmeans(osize_reduced_model, ~ age)
pairs(emm_size)
eff_size(emm_size,
         sigma = sigma(osize_reduced_model),
         edf = df.residual(osize_reduced_model))
```

```
###Plot###
f1_df_size <- f1_df_size %>%
  mutate(age = case_when(
    age == "o" ~ "Old",
    age == "y" ~ "Young",
    TRUE ~ as.character(age)
  )) %>%
  mutate(age = factor(age, levels = c("Young", "Old")))

f1_df_size$age <- as.factor(f1_df_size$age)
f1_df_size$treat <- as.factor(f1_df_size$treat)

f1_df_size$treat <- factor(f1_df_size$treat, levels = c("r", "f"))  # Ensure "r"
appears first
fsize <- ggscatter(f1_df_size, x = "con", y = "size",
                   color = "age", fill = "age",
                   add = "reg.line",
                   cor.coef = FALSE,  # Remove default correlation text
                   xlab = "Offspring prey consumption (eggs)",
                   ylab = "Dorsal shield length (µm)",
                   palette = c("#6A9CAF", "#DD7927")) +
  geom_smooth(aes(color = age), method = "lm", se = TRUE,
              linetype = "solid", size = 1.5) +
  stat_regline_equation(
    aes(color = age, label = paste(..eq.label.., sep = "~~~")),
    label.x = 20, label.y = c(390, 382), size = 8
  ) +
  theme_classic2() +
  theme(text = element_text(family = "Helvetica", size = 26),
        plot.margin = margin(1, 1, 1, 0.5, "cm"),
        axis.title.x = element_text(margin = margin(t = 10)),
        axis.title.y = element_text(margin = margin(r = 10)),
        panel.spacing = unit(1, "cm")) +
  ylim(NA, 396) +
  facet_wrap(~ treat, labeller = labeller(treat = c("f" = "Abundant", "r" =
"Restricted"))) +
  labs(color = "Maternal age", fill = "Maternal age")

print(fsize)


# Merge the four plots side by side

merged_plot4 <- ggarrange(
  hatching_plot, sur_plot, fea, fsize,
  labels = c("(a)", "(b)", "(c)", "(d)"),
  ncol = 2, nrow = 2,
  font.label = list(size = 26, face = "plain")  # Increase font size and make bold
)

merged_plot4

# Offspring prey consumption ----------------------------------------------

f1_df_con <- f1_df %>%
  filter(!is.na(con))
hist(f1_df_con$con)
fcon_model <- glm(con ~ treat * age + diet, family = poisson(link = "log"), data =
f1_df_con)
summary(fcon_model)
Anova(fcon_model, type = 'III')

###Effect size###
emm_con <- emmeans(fcon_model, ~ age)
pairs(emm_con, type = "response")

# Extract the Chi-square values
anova_out <- Anova(fcon_model, type = "III")
```

```
chisq_values <- anova_out$"LR Chisq"
chisq_values_3dec <- round(chisq_values, 3)
chisq_values_3dec

dispersion <- sum(residuals(fcon_model, type = "pearson")^2) / df.residual(fcon_model)
dispersion # check for overdispersion

# Plot
f1_df_con <- f1_df_con %>%
  mutate(age = case_when(
    age == "o" ~ "Old",
    age == "y" ~ "Young",
    TRUE ~ as.character(age)
  )) %>%
  mutate(age = factor(age, levels = c("Young", "Old")))

f1_df_con$age <- as.factor(f1_df_con$age)
f1_df_con$treat <- as.factor(f1_df_con$treat)
f1_df_con$treat <- factor(f1_df_con$treat, levels = c("r", "f"))  # Ensure "r" appears
first

n_df <- f1_df_con %>%
  count(treat, age, factor(diet))
n_labels <- data.frame(
  treat = factor(c(
    "r","r","r","r","r",
    "r","r","r","r","r",
    "f","f","f","f","f",
    "f","f","f","f","f"
  )),
  age = factor(c(
    "Young","Young","Young","Young","Young",
    "Old","Old","Old","Old","Old",
    "Young","Young","Young","Young","Young",
    "Old","Old","Old","Old","Old"
  ), levels = c("Young", "Old")),
  diet = factor(c(
    20,30,40,50,60,
    20,30,40,50,60,
    20,30,40,50,60,
    20,30,40,50,60
  )),
  n = c(
    3,25,30,33,32,
    11,34,37,35,39,
    5,26,39,28,36,
    4,22,22,24,25
  ),
  y_pos = min(f1_df_con$con, na.rm = TRUE) - 6
)

n_labels$label <- paste0("italic(n)==", n_labels$n)

fcon <- ggplot(f1_df_con, aes(x = factor(diet), y = con,
                              fill = age, color = age)) +
  geom_beeswarm(dodge.width = 1, size = 2, alpha = 0.6, cex = 0.3) +
  geom_boxplot(color = "black", width = 0.5, position = position_dodge(width = 1),
               outlier.shape = NA, alpha = 0.8) +
  facet_wrap(~ treat,
             labeller = labeller(treat = c("r" = "Restricted", "f" = "Abundant"))) +
  xlab("Prey availability (eggs)") +
  ylab("Prey consumption (eggs)") +
  scale_fill_manual(values = c("#6A9CAF", "#DD7927")) +
  scale_color_manual(values = c("#6A9CAF", "#DD7927")) +
  geom_text(
    data = n_labels,
    aes(x = factor(diet), y = y_pos, label = label, group = age),
    position = position_dodge(width = 1),
    color = "black",
```

```
    size = 6,
    parse = TRUE,
    angle = 90,
    hjust = 0.5,
    vjust = 0.5,
    inherit.aes = FALSE
  ) +
  theme_classic2() +
  theme(
    text = element_text(family = "Helvetica", size = 26),
    plot.margin = margin(1, 1, 1, 0.5, "cm"),
    axis.title.x = element_text(margin = margin(t = 10)),
    axis.title.y = element_text(margin = margin(r = 10)),
    panel.spacing = unit(1, "cm")
  ) +
  labs(fill = "Maternal age", color = "Maternal age") +
  scale_y_continuous(limits = c(10, 70))

print(fcon)
```