

# DS 2021 Jelly Figures

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```
knitr::opts_chunk$set(tidy.opts=list(width.cutoff=70), tidy=TRUE)
# code above ensures no text is cut off when knit
```

## Loading In Packages and Data

```
library(patchwork)
library(car)
library(performance)
library(DHARMA)
library(fitdistrplus)
library(gamlss)
library(tidyverse)

polyp_data <- read_csv("/Users/marabohm/Github/Jelly-Data/data/ds2021_polyp_data.csv")
```

## Cleaning the Data

```
polyp_clean <- polyp_data %>%
  rename(collection_day = "Data collection day", jar_code = "Jar Code (ex. E1)",
    treatment = Chemical, num_elongated = "Elongation?", num_ruffled = "Ruffled?",
    num_aseexual_buds = "Asexual Repro?", total_num = Total, time_in_days = days_after) %>%
  mutate(jar_code = as.factor(jar_code), treatment = as.factor(treatment),
    treatment = fct_relevel(treatment, "Control", "Caffeine", "Estradiol",
      "Combo")) %>%
  dplyr::select(collection_day, jar_code, treatment, num_elongated, num_ruffled,
    num_aseexual_buds, total_num, time_in_days)
```

## Making Single Treatment Data Frames for Later Analyses

```
# data frame with only control
only_control <- polyp_clean %>%
  filter(treatment == "Control")
```

```

# data frame with only caffeine
only_caf <- polyp_clean %>%
  filter(treatment == "Caffeine")

# data frame with only estradiol
only_est <- polyp_clean %>%
  filter(treatment == "Estradiol")

# data frame with only combination
only_combo <- polyp_clean %>%
  filter(treatment == "Combination")

# data frame with caffeine and control
just_caf <- polyp_clean %>%
  filter(treatment == "Caffeine" | treatment == "Control")

# data frame with combination and control
just_combo <- polyp_clean %>%
  filter(treatment == "Combination" | treatment == "Control")

# data frame with caffeine, combination, and control
just_caf_combo <- polyp_clean %>%
  filter(treatment == "Combination" | treatment == "Control" | treatment ==
    "Caffeine")

```

## Figure 1: Response Variables Over Time

Figure 1A: Ruffled Polyps Over Time

```

ruffles_time <- ggplot(polyp_clean, aes(x = time_in_days, y = num_ruffled)) +
  geom_point(colour = "#fb9b06") + geom_smooth(method = "lm", se = FALSE,
  colour = "black", show.legend = FALSE) + labs(x = "Time (days)", y = "Number of Ruffled Polyps") +
  scale_x_continuous(breaks = c(0, 3, 6, 9, 12)) + theme_classic() +
  theme(legend.position = "none") + ggtitle("A. Ruffling")

# Spearman's rank correlation coefficient for the correlation between
# the number of ruffled polyps and time
cor(polyp_clean$time_in_days, polyp_clean$num_ruffled, method = "spearman")

## [1] 0.9104122

```

Figure 1B: Elongated Polyps Over Time

```

elo_time <- ggplot(polyp_clean, aes(x = time_in_days, y = num_elongated)) +
  geom_point(colour = "#e55c30") + geom_smooth(method = "lm", se = FALSE,
  colour = "black", show.legend = FALSE) + labs(x = "Time (days)", y = "Number of Elongated Polyps") +
  scale_x_continuous(breaks = c(0, 3, 6, 9, 12)) + theme_classic() +
  theme(legend.position = "none") + ggtitle("B. Elongation")

```

```
# Spearman's rank correlation coefficient for the correlation between
# the number of elongated polyps and time
cor(polyp_clean$time_in_days, polyp_clean$num_elongated, method = "spearman")
```

```
## [1] 0.8303654
```

**Figure 1C: Asexual Buds Over Time**

```
buds_time <- ggplot(polyp_clean, aes(x = time_in_days, y = num_asexual_buds)) +
  geom_point(colour = "#450a69") + geom_smooth(method = "lm", se = FALSE,
  colour = "black", show.legend = FALSE) + labs(x = "Time (days)", y = "Number of Asexual Buds") +
  scale_x_continuous(breaks = c(0, 3, 6, 9, 12)) + theme_classic() +
  theme(legend.position = "none") + ggtitle("C. Budding")

# Spearman's rank correlation coefficient for the correlation between
# number of asexual buds and time
cor(polyp_clean$time_in_days, polyp_clean$num_asexual_buds, method = "spearman")
```

```
## [1] 0.8452308
```

**Figure 1D: Total Number of Polyps Over Time**

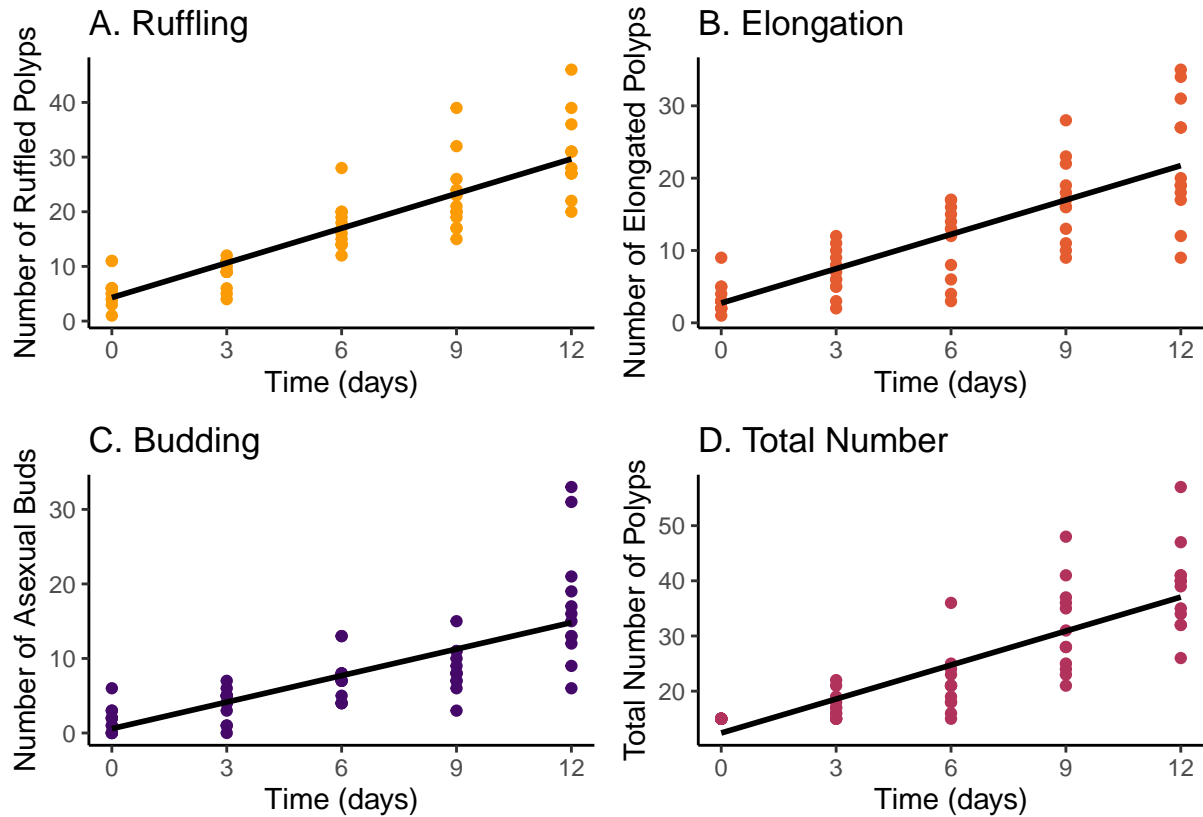
```
total_time <- ggplot(polyp_clean, aes(x = time_in_days, y = total_num)) +
  geom_point(colour = "#b1325a") + geom_smooth(method = "lm", se = FALSE,
  colour = "black", show.legend = FALSE) + labs(x = "Time (days)", y = "Total Number of Polyps") +
  scale_x_continuous(breaks = c(0, 3, 6, 9, 12)) + theme_classic() +
  theme(legend.position = "none") + ggtitle("D. Total Number")

# Spearman's rank correlation coefficient for the correlation between
# total number of polyps and time
cor(polyp_clean$time_in_days, polyp_clean$total_num, method = "spearman")
```

```
## [1] 0.8988422
```

## Merging The Four Graphs Into One Figure Through Patchwork

```
(ruffles_time | elo_time)/(buds_time | total_time)
```



**Figure 2: Ruffling In Each Treatment**

Building a Box Plot For Control, Caffeine, Estradiol and Combination with Time as a Factor

```
box_caf_combo <- ggplot(just_caf_combo, aes(x = as.factor(time_in_days),
  y = num_ruffled, fill = treatment)) + geom_boxplot() + theme_classic() +
  scale_fill_manual(values = c("#404788FF", "#238A8DFF", "#55C667FF")) +
  labs(x = "Time (days)", y = "Number of Ruffled Polyps", fill = "Treatment")
box_caf_combo
```

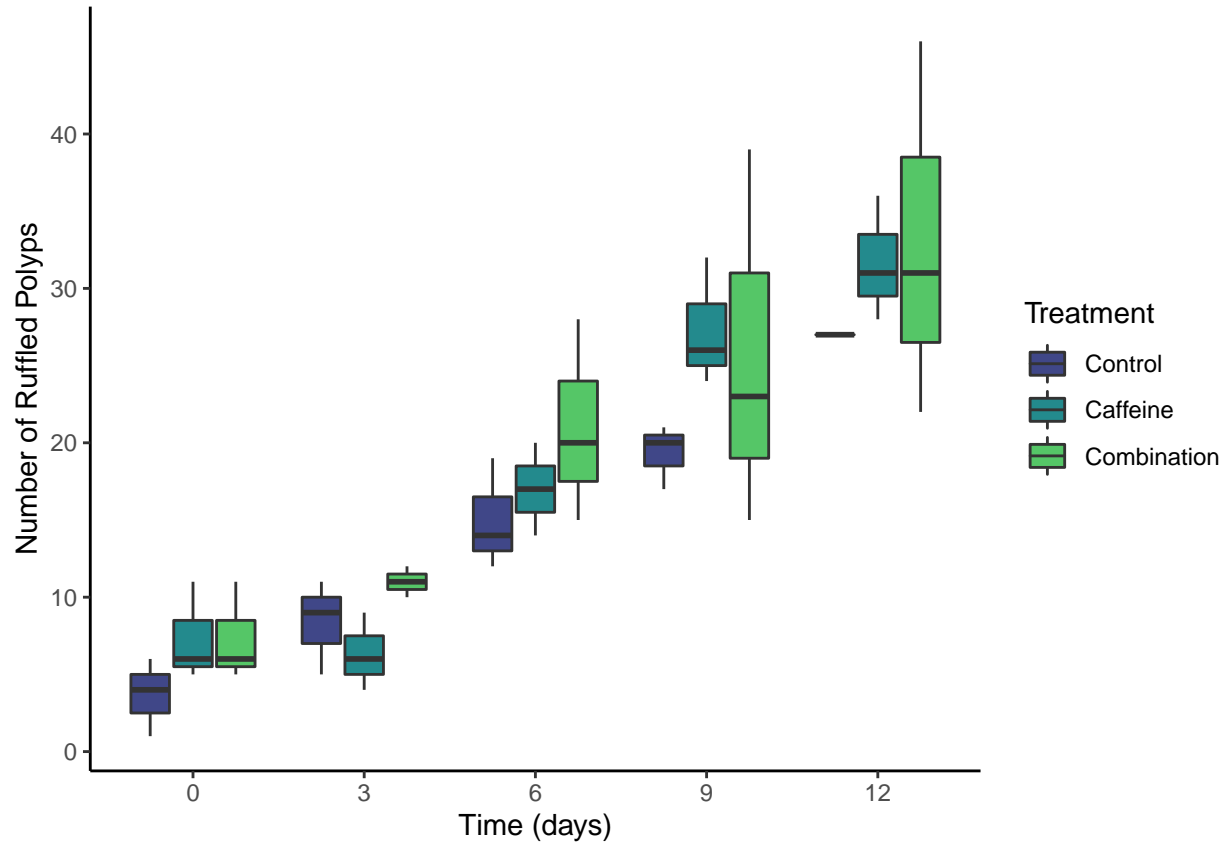


Figure 3: Elongation per treatment and over time

Figure 3A: Box Plot of Overall Elongation per Treatment

```
box_elongation <- ggplot(polyp_clean, aes(x = treatment, y = num_elongated,
  fill = treatment)) + geom_boxplot() + theme_classic() + scale_fill_manual(values = c("#404788FF",
  "#238A8DFF", "#FDE725FF", "#55C667FF")) + labs(x = "Treatment", y = "Number of Elongated Polyps") +
  theme(legend.position = "none", axis.text.x = element_text(angle = 30,
    vjust = 0.8, hjust = 0.7)) + ggtitle("A")
box_elongation
```

Figure 3B: Scatter/Line Plot of the Number of Elongated Polyps over Time, Per Treatment

```
plot_elongation <- ggplot(polyp_clean, aes(x = time_in_days, y = num_elongated,
  colour = treatment, shape = treatment)) + geom_point(aes(x = time_in_days,
  y = num_elongated, colour = treatment, shape = treatment)) + theme_classic() +
  geom_smooth(se = FALSE, method = "lm") + labs(x = "Time (days)", y = "Number of Elongated Polyps",
  colour = "Treatment", shape = NULL) + scale_colour_manual(name = "Treatment",
  labels = c("Control", "Caffeine", "Estradiol", "Combination"), values = c("#404788FF",
  "#238A8DFF", "#FDE725FF", "#55C667FF")) + scale_shape_manual(name = "Treatment",
```

```
labels = c("Control", "Caffeine", "Estradiol", "Combination"), values = c(15,
  19, 17, 8)) + scale_x_continuous(breaks = c(0, 3, 6, 9, 12)) +
ggtitle("B")
```

```
# Spearman's Rank Correlation Coefficient for Correlation Between
# Number of Elongated Polyps and Time in Each Treatment
```

```
# control:
cor(only_control$time_in_days, only_control$num_elongated, method = "spearman")
```

```
## [1] 0.7446049
```

```
# caffeine:
cor(only_caf$time_in_days, only_caf$num_elongated, method = "spearman")
```

```
## [1] 0.82348
```

```
# estradiol:
cor(only_est$time_in_days, only_est$num_elongated, method = "spearman")
```

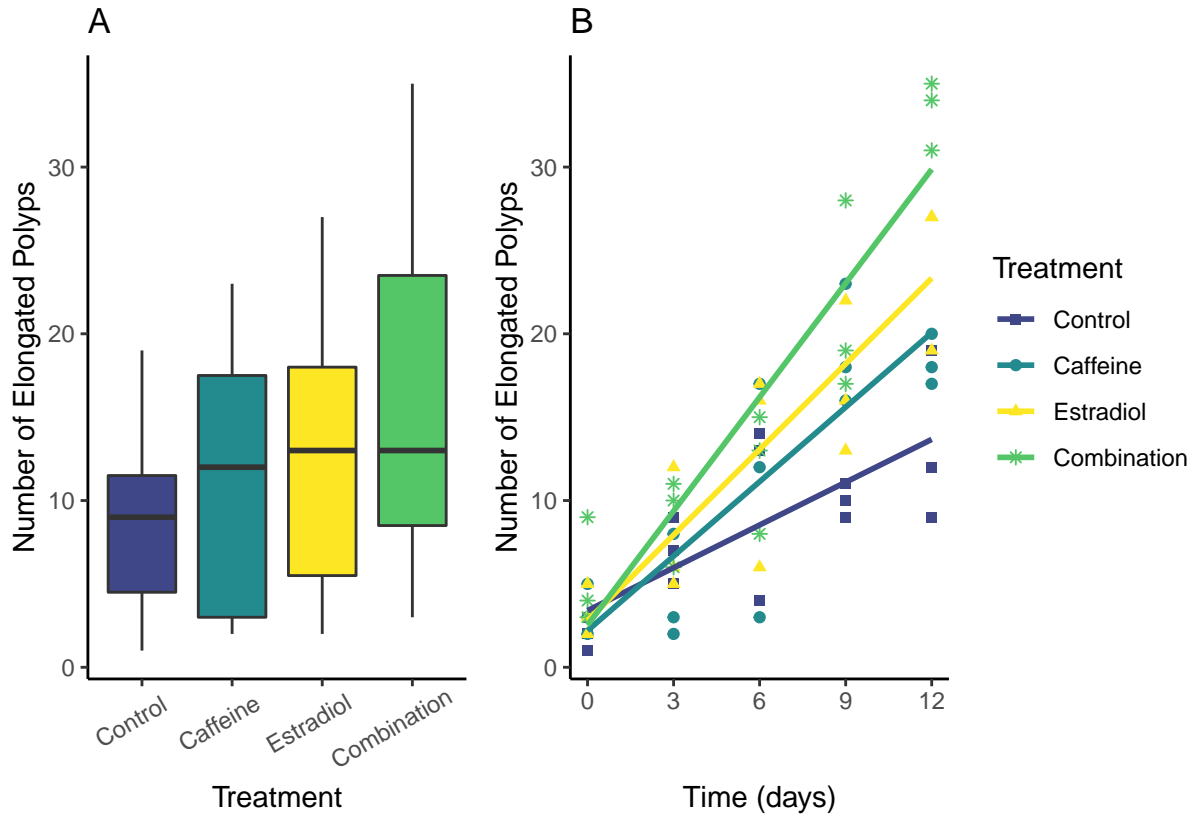
```
## [1] 0.914331
```

```
# combination:
cor(only_combo$time_in_days, only_combo$num_elongated, method = "spearman")
```

```
## [1] 0.927426
```

Merging The Two Graphs Into One Figure Through Patchwork

```
(box_elongation | plot_elongation)
```



**Figure 4: Budding in the Control and Combination Treatments**

**Figure 4A: Box Plot of Overall Budding in Control and Combo**

```
box_buds <- ggplot(just_combo, aes(x = treatment, y = num_asexual_buds,
  fill = treatment)) + geom_boxplot() + theme_classic() + scale_fill_manual(values = c("#404788FF",
  "#55C667FF")) + labs(x = "Treatment", y = "Number of Asexual Buds") +
  theme(legend.position = "none") + ggtitle("A")
```

**Figure 4B: Scatter/Line Plot of Budding in Control and Combination over Time**

```
plot_buds <- ggplot(just_combo, aes(x = time_in_days, y = num_asexual_buds,
  colour = treatment, shape = treatment)) + geom_point() + theme_classic() +
  labs(x = "Time (days)", y = "Number of Asexual Buds", colour = "Treatment") +
  geom_smooth(se = FALSE, method = "lm") + scale_colour_manual(name = "Treatment",
  labels = c("Control", "Combination"), values = c("#404788FF", "#55C667FF")) +
  scale_shape_manual(name = "Treatment", labels = c("Control", "Combination"),
  values = c(15, 8)) + scale_x_continuous(breaks = c(0, 3, 6, 9,
  12)) + ggtitle("B")
```

*# Spearman's rank correlation coefficient for the correlation between*

```
# number of asexual buds and time in each treatment
```

```
# control:
```

```
cor(only_control$time_in_days, only_control$num_asexual_buds, method = "spearman")
```

```
## [1] 0.9168078
```

```
# combination:
```

```
cor(only_combo$time_in_days, only_combo$num_asexual_buds, method = "spearman")
```

```
## [1] 0.914331
```

Merging The Two Graphs Into One Figure Through Patchwork

```
(box_buds | plot_buds)
```

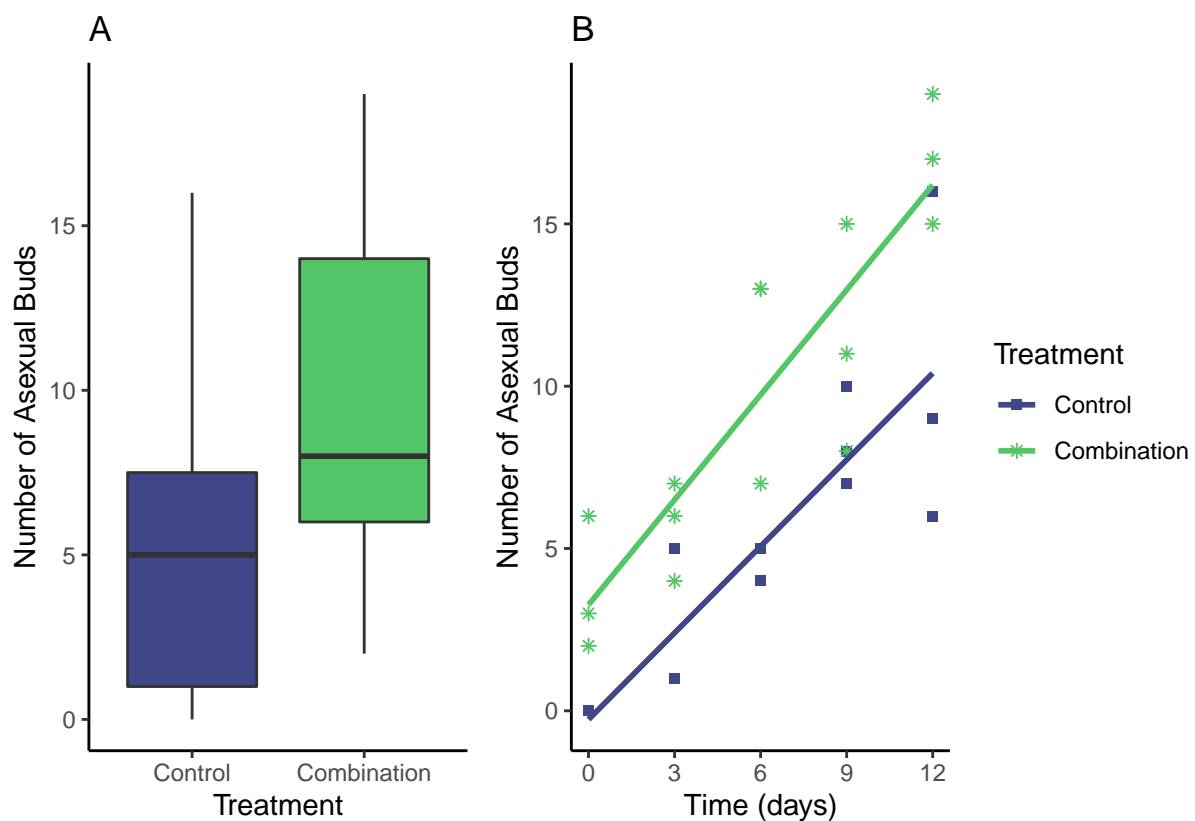


Figure 4: Total Number of Polyps

Figure 4A: Box Plot for Overall Total Number of Polyps by Treatment



```
box_total <- ggplot(polyp_clean, aes(x = treatment, y = total_num, fill = treatment)) +
  geom_boxplot() + theme_classic() + scale_fill_manual(values = c("#404788FF",
    "#238A8DFF", "#FDE725FF", "#55C667FF")) + labs(x = "Treatment", y = "Total Number of Polyps") +
  theme(legend.position = "none", axis.text.x = element_text(angle = 30,
    vjust = 0.8, hjust = 0.7)) + ggtitle("A")
```

Figure 4B: Scatter/Line Plot of Total Number of Polyps Over Time, Broken Up By Treatment

```
plot_total <- ggplot(polyp_clean, aes(x = time_in_days, y = total_num,
  colour = treatment, shape = treatment)) + geom_point(aes(colour = treatment)) +
  theme_classic() + geom_smooth(se = FALSE, method = "lm") + labs(x = "Time (days)",
  y = "Total Number of Polyps", colour = "Treatment") + scale_colour_manual(name = "Treatment",
  labels = c("Control", "Caffeine", "Estradiol", "Combination"), values = c("#404788FF",
    "#238A8DFF", "#FDE725FF", "#55C667FF")) + scale_shape_manual(name = "Treatment",
  labels = c("Control", "Caffeine", "Estradiol", "Combination"), values = c(15,
    19, 17, 8)) + scale_x_continuous(breaks = c(0, 3, 6, 9, 12)) +
  ggtitle("B")
```

```
# Spearman's rank correlation coefficient for the correlation between
# total number of polyps and time in each treatment control:
cor(only_control$time_in_days, only_control$total_num, method = "spearman")
```

```
## [1] 0.9600104
```

```
# caffeine:
cor(only_caf$time_in_days, only_caf$total_num, method = "spearman")
```

```
## [1] 0.9540699
```

```
# estradiol:
cor(only_est$time_in_days, only_est$total_num, method = "spearman")
```

```
## [1] 0.9063952
```

```
# combination:
cor(only_combo$time_in_days, only_combo$total_num, method = "spearman")
```

```
## [1] 0.9168078
```

## Merging The Two Graphs Into One Figure Through Patchwork

```
(box_total | plot_total)
```

