Havi Fecundity Analysis

Contents

Load Libraries **1**

Load Data **1**

Calculations **2**

survival 2

fecundity 2

Plot **3**

Plot aphid survival 3

Plot aphid fecundity 6

Statistics **15**

Prepare the data and define helper function 15

Stats 16

Load Libraries

```
pacman::p_load(cowplot, broom, dplyr, devtools, emmeans, ggbeeswarm, ggpmisc, ggplot2,
    knitr, lme4, lmerTest, readr, readxl, tidyr, tidyverse, install = FALSE)
```

Load Data

```
aphid_count <- read_excel("data/fecundity_assay_count.xlsx") %>%
    filter(alate_alive_r1 != "control") %>%
    filter(block != 1) %>%
    mutate(nymphs_r1 = as.numeric(nymphs_r1), nymphs_r2 = as.numeric(nymphs_r2))
```

```
## Warning: There was 1 warning in `mutate()`.
## i In argument: `nymphs_r2 = as.numeric(nymphs_r2)`.
## Caused by warning:
## ! NAs introduced by coercion
```

```r
# filter by block
aphid_count_block2 <- aphid_count %>%
    filter(block == 2)
aphid_count_block3 <- aphid_count %>%
    filter(block == 3)

# === Pivot to long format ===
aphid_long <- aphid_count %>%
    pivot_longer(cols = c(starts_with("nymphs_r"), starts_with("alate_alive_r")),
        names_to = c(".value", "round"), names_pattern = "(.*)_r(\\d)")
```

Calculations

Calculating how many aphids are in each group as a new data frame

survival

```r
# === Survival summary by block and round ===
survival_summary <- aphid_long %>%
  group_by(treatment, block, round) %>%  # Group data by treatment condition, experimental block, and r
  summarise(
    # Count how many alates were alive in each group (handling NAs just in case)
    alive_n = sum(alate_alive == "Yes", na.rm = TRUE),
    # Count how many alates were dead in each group
    dead_n  = sum(alate_alive == "No",  na.rm = TRUE),
    # Compute total number of alates observed (alive + dead)
    total   = alive_n + dead_n,
    # Calculate percent survival per block per round (0-100%)
    survival_pct = 100 * alive_n / total,
    # Drop grouping structure after summarising (avoids nested data frames in later steps)
    .groups = "drop"
  )

# === Average survival across blocks ===
survival_summary_avg <- survival_summary %>%
  group_by(treatment, round) %>%  # Now group just by treatment and round (collapsed across blocks)
  summarise(
    # Compute the mean survival percentage across all blocks in each treatment/round
    mean_survival = mean(survival_pct, na.rm = TRUE),
    # Calculate standard error: standard deviation divided by square root of the number of blocks
    se_survival   = sd(survival_pct, na.rm = TRUE) / sqrt(n()),
    # Drop grouping again for a clean summary table
    .groups = "drop"
  )
```

fecundity

```r
# === block level ===
fecundity_by_block <- aphid_long %>%
  filter(!is.na(nymphs)) %>%  # Remove missing nymph count entries

  # Group by treatment, round, and block to calculate within-block variation
  group_by(treatment, block, round) %>%
  summarise(
    mean_fecundity = mean(nymphs, na.rm = TRUE),              # Mean number of nymphs per alate in that
    se_fecundity   = sd(nymphs, na.rm = TRUE) / sqrt(n()),    # Standard error of nymph counts in that
    n              = n(),                                     # Number of alates (i.e., observations)
    .groups = "drop"
  )

# === treatment level ===
fecundity_by_treatment <- aphid_long %>%
  filter(!is.na(nymphs)) %>%  # Exclude missing nymph counts

  # Step 1: Group by treatment, round, and block to compute block-level means
  group_by(treatment, block, round) %>%
  # Step 2: Group by treatment and round to compute treatment-level summaries
  group_by(treatment, round) %>%
  summarise(
    mean_fecundity = mean(nymphs, na.rm = TRUE),          # Mean of block means
    se_fecundity   = sd(nymphs, na.rm = TRUE) / sqrt(n()), # Standard error across blocks
        n              = n(),                                     # Number of alates (i.e., observation
    .groups = "drop"
  )
```

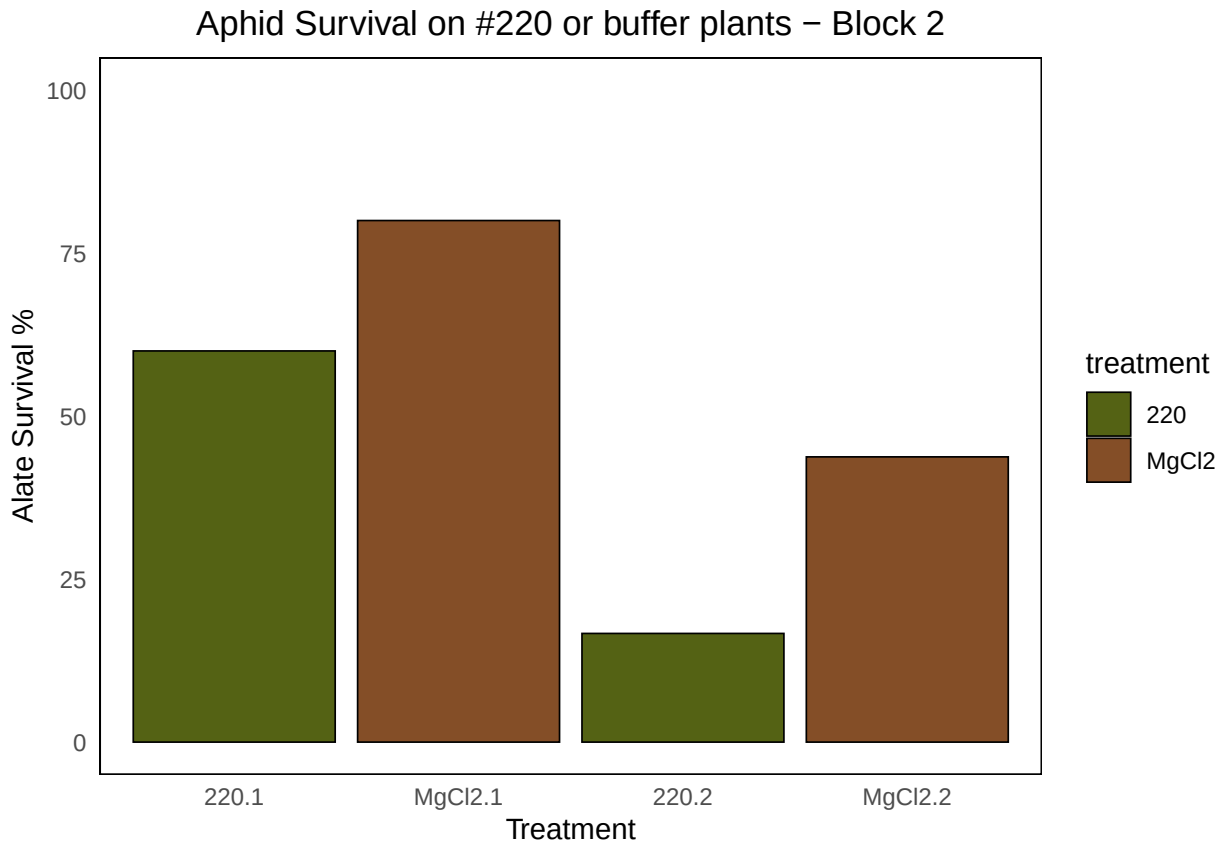
Plot

Plot aphid survival

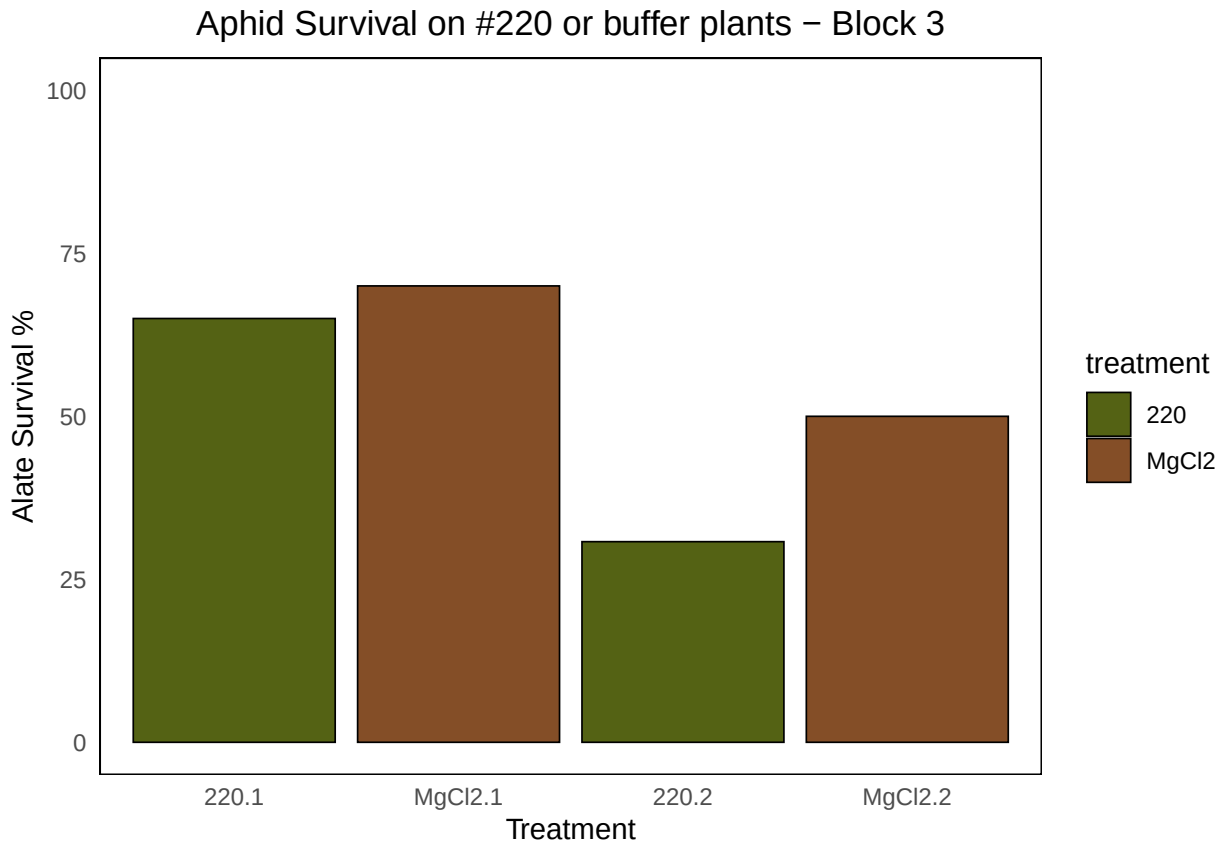
```r
# Filter by block
survival_summary_block2 <- survival_summary %>%
    filter(block == 2)
survival_summary_block3 <- survival_summary %>%
    filter(block == 3)

# === Block 2 ===
ggplot(data = survival_summary_block2, aes(x = interaction(treatment, round), y = survival_pct,
    fill = treatment)) + geom_col(color = "black", size = 0.3) + labs(x = "Treatment",
    y = "Alate Survival %", title = "Aphid Survival on #220 or buffer plants - Block 2") +
    scale_fill_manual(values = c("#546214", "#844e27")) + ylim(0, 100) + theme_minimal() +
    theme(legend.position = "right", panel.background = element_rect(fill = "white"),
        panel.grid = element_blank(), panel.grid.minor.x = element_blank(), plot.title = element_text(h
```

```
## 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
```

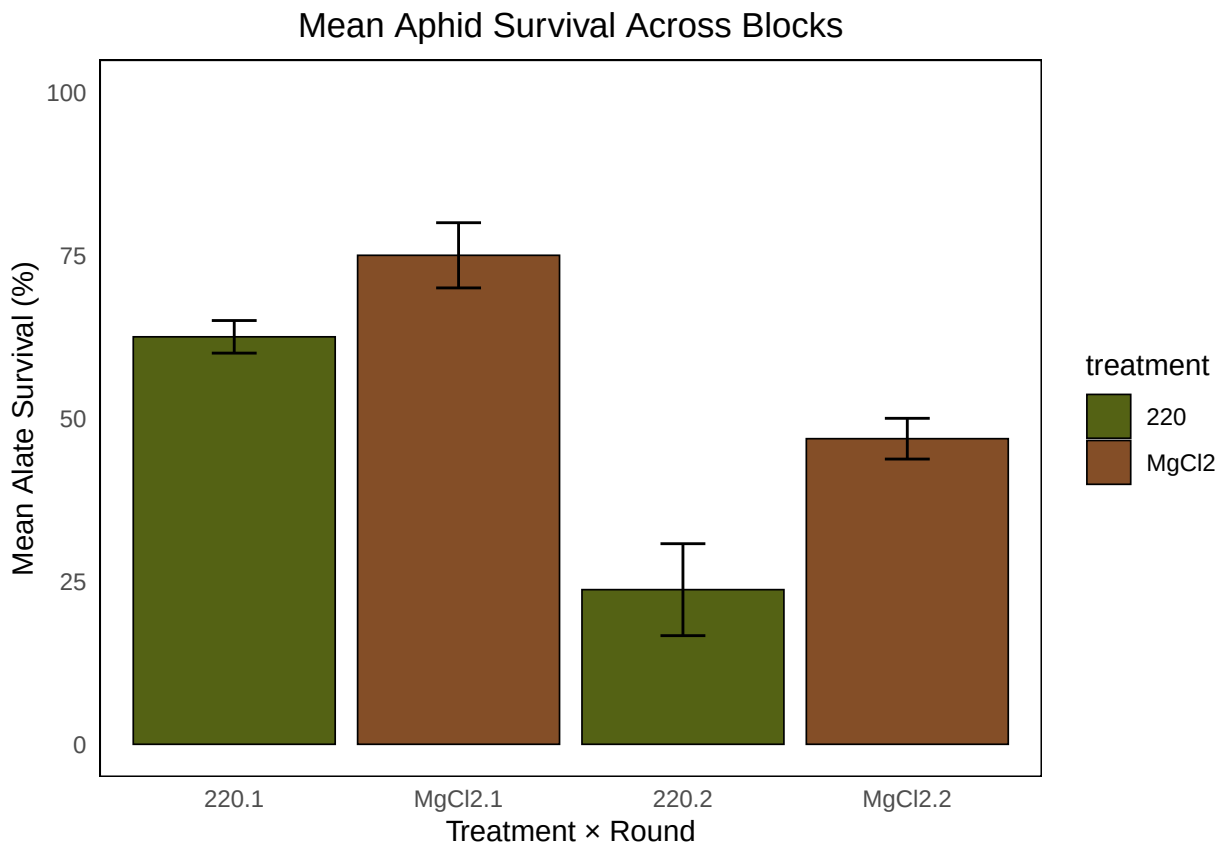
```
## generated.
```




```
# === Block 3 ===
ggplot(data = survival_summary_block3, aes(x = interaction(treatment, round), y = survival_pct,
    fill = treatment)) + geom_col(color = "black", size = 0.3) + labs(x = "Treatment",
    y = "Alate Survival %", title = "Aphid Survival on #220 or buffer plants - Block 3") +
    scale_fill_manual(values = c("#546214", "#844e27")) + ylim(0, 100) + theme_minimal() +
    theme(legend.position = "right", panel.background = element_rect(fill = "white"),
        panel.grid = element_blank(), panel.grid.minor.x = element_blank(), plot.title = element_text(h
```



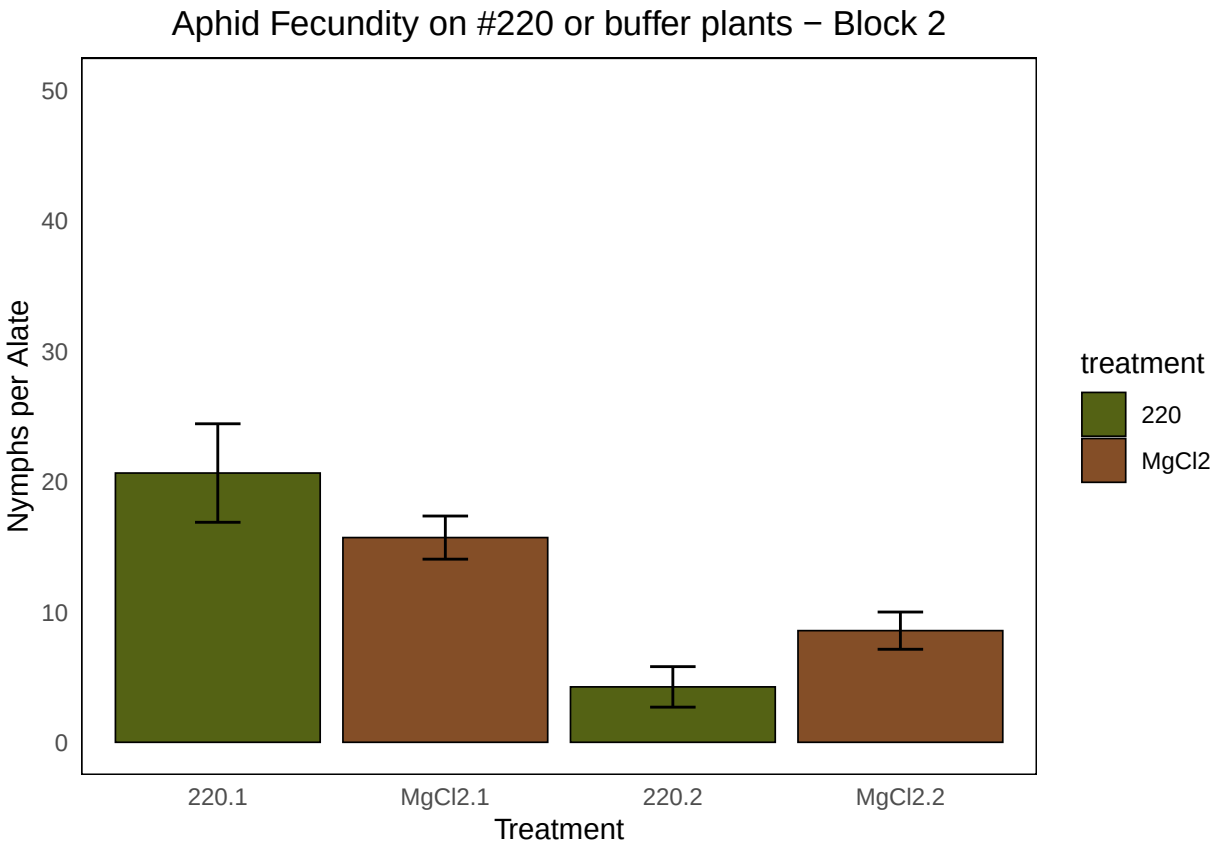

```
# === All Blocks ===
ggplot(survival_summary_avg, aes(x = interaction(treatment, round), y = mean_survival,
    fill = treatment)) + geom_col(color = "black", size = 0.3, position = position_dodge(width = 0.9)) +
    geom_errorbar(aes(ymin = mean_survival - se_survival, ymax = mean_survival +
        se_survival), width = 0.2, color = "black", position = position_dodge(width = 0.9)) +
    labs(x = "Treatment × Round", y = "Mean Alate Survival (%)", title = "Mean Aphid Survival Across Bl
    scale_fill_manual(values = c("#546214", "#844e27")) + ylim(0, 100) + theme_minimal() +
    theme(legend.position = "right", panel.background = element_rect(fill = "white"),
        panel.grid = element_blank(), plot.title = element_text(hjust = 0.5))
```



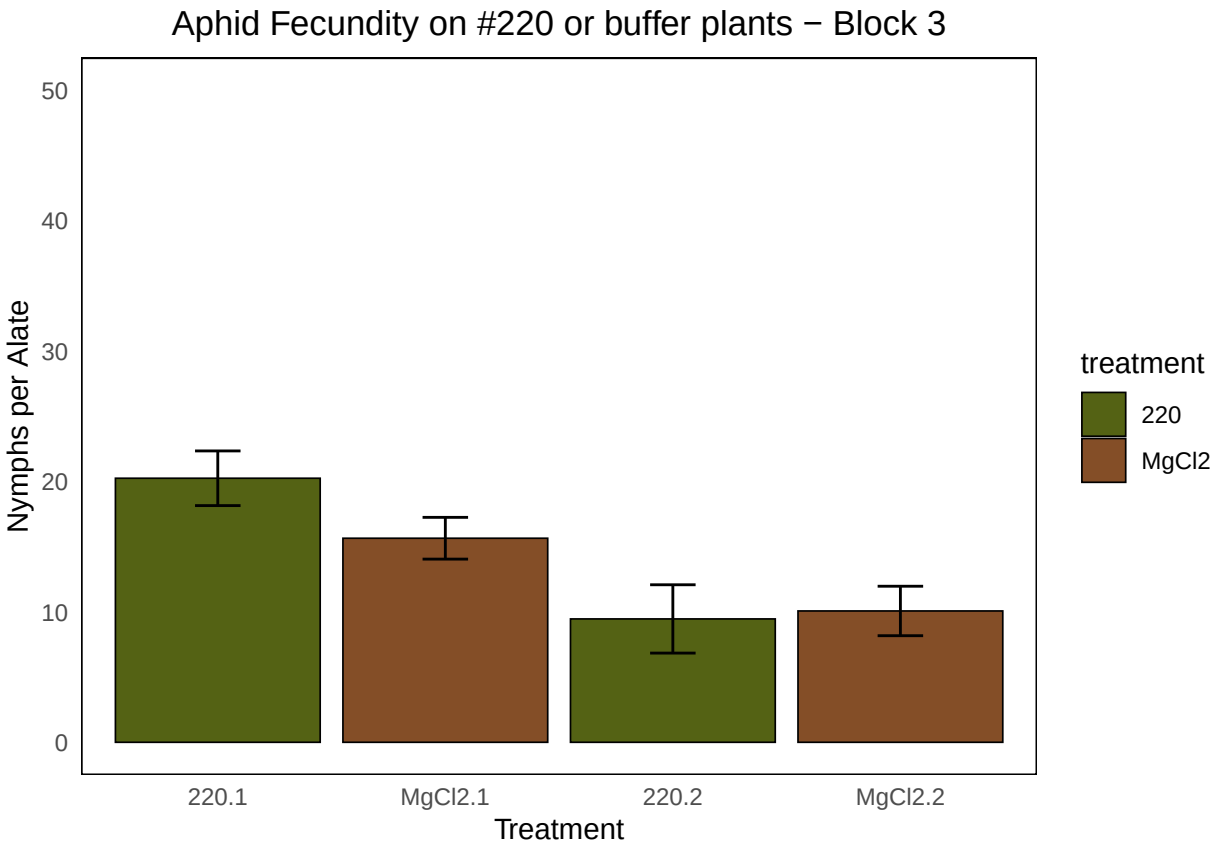
Plot aphid fecundity

Column Plots

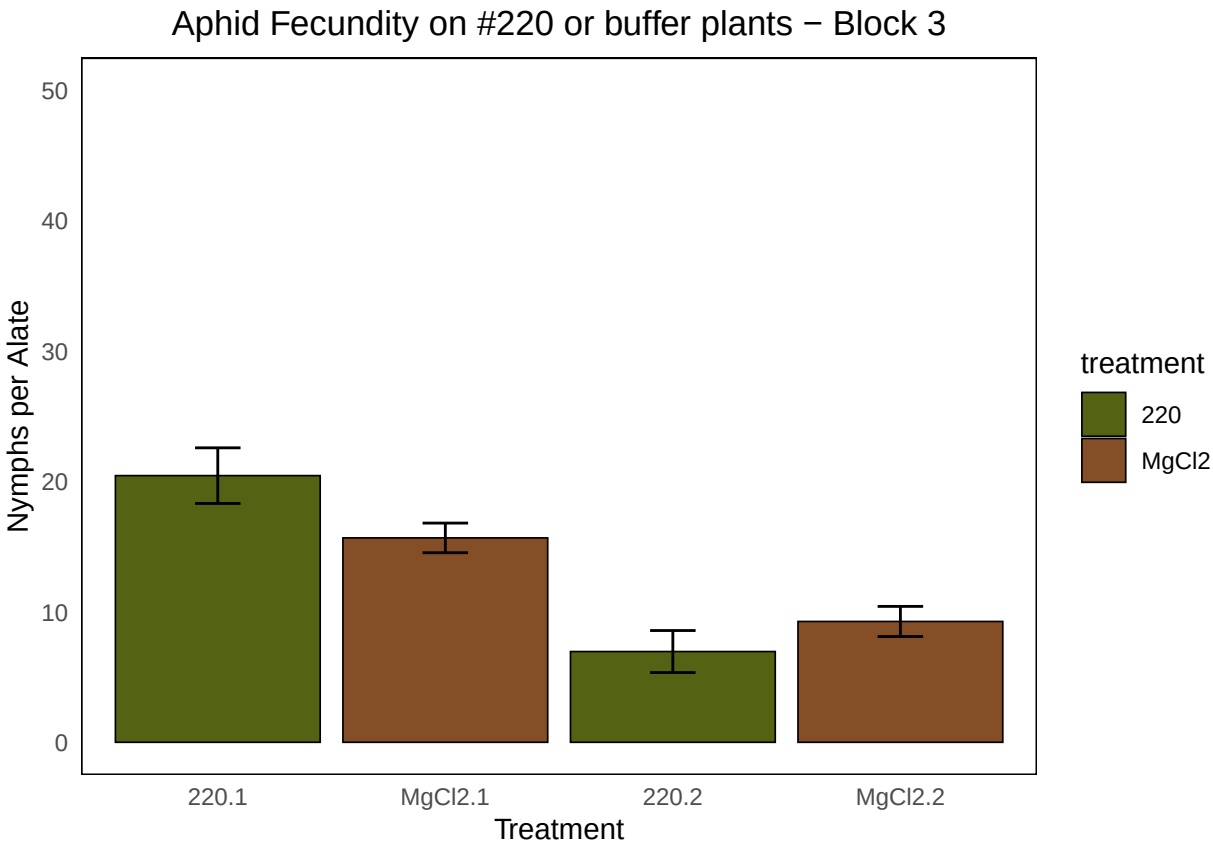
```
# === Block 2 ===
fecundity_by_block_block2 <- fecundity_by_block %>%
    filter(block == 2)
ggplot(data = fecundity_by_block_block2, aes(x = interaction(treatment, round), y = mean_fecundity,
    fill = treatment)) + geom_col(color = "black", size = 0.3) + geom_errorbar(aes(ymin = mean_fecundit
    se_fecundity, ymax = mean_fecundity + se_fecundity), width = 0.2, color = "black",
    position = position_dodge(width = 0.8)) + labs(x = "Treatment", y = "Nymphs per Alate",
    title = "Aphid Fecundity on #220 or buffer plants - Block 2") + scale_fill_manual(values = c("#5462
    "#844e27")) + ylim(0, 50) + theme_minimal() + theme(legend.position = "right",
    panel.background = element_rect(fill = "white"), panel.grid = element_blank(),
    panel.grid.minor.x = element_blank(), plot.title = element_text(hjust = 0.5))
```




```
# === Block 3 ===
fecundity_by_block_block3 <- fecundity_by_block %>%
    filter(block == 3)
ggplot(data = fecundity_by_block_block3, aes(x = interaction(treatment, round), y = mean_fecundity,
    fill = treatment)) + geom_col(color = "black", size = 0.3) + geom_errorbar(aes(ymin = mean_fecundity
    se_fecundity, ymax = mean_fecundity + se_fecundity), width = 0.2, color = "black",
    position = position_dodge(width = 0.8)) + labs(x = "Treatment", y = "Nymphs per Alate",
    title = "Aphid Fecundity on #220 or buffer plants - Block 3") + scale_fill_manual(values = c("#5462
    "#844e27")) + ylim(0, 50) + theme_minimal() + theme(legend.position = "right",
    panel.background = element_rect(fill = "white"), panel.grid = element_blank(),
    panel.grid.minor.x = element_blank(), plot.title = element_text(hjust = 0.5))
```




```
# === All Blocks ===
ggplot(data = fecundity_by_treatment, aes(x = interaction(treatment, round), y = mean_fecundity,
    fill = treatment)) + geom_col(color = "black", size = 0.3) + geom_errorbar(aes(ymin = mean_fecundity -
    se_fecundity, ymax = mean_fecundity + se_fecundity), width = 0.2, color = "black",
    position = position_dodge(width = 0.8)) + labs(x = "Treatment", y = "Nymphs per Alate",
    title = "Aphid Fecundity on #220 or buffer plants - Block 3") + scale_fill_manual(values = c("#5462
    "#844e27")) + ylim(0, 50) + theme_minimal() + theme(legend.position = "right",
    panel.background = element_rect(fill = "white"), panel.grid = element_blank(),
    panel.grid.minor.x = element_blank(), plot.title = element_text(hjust = 0.5))
```



Violin plots

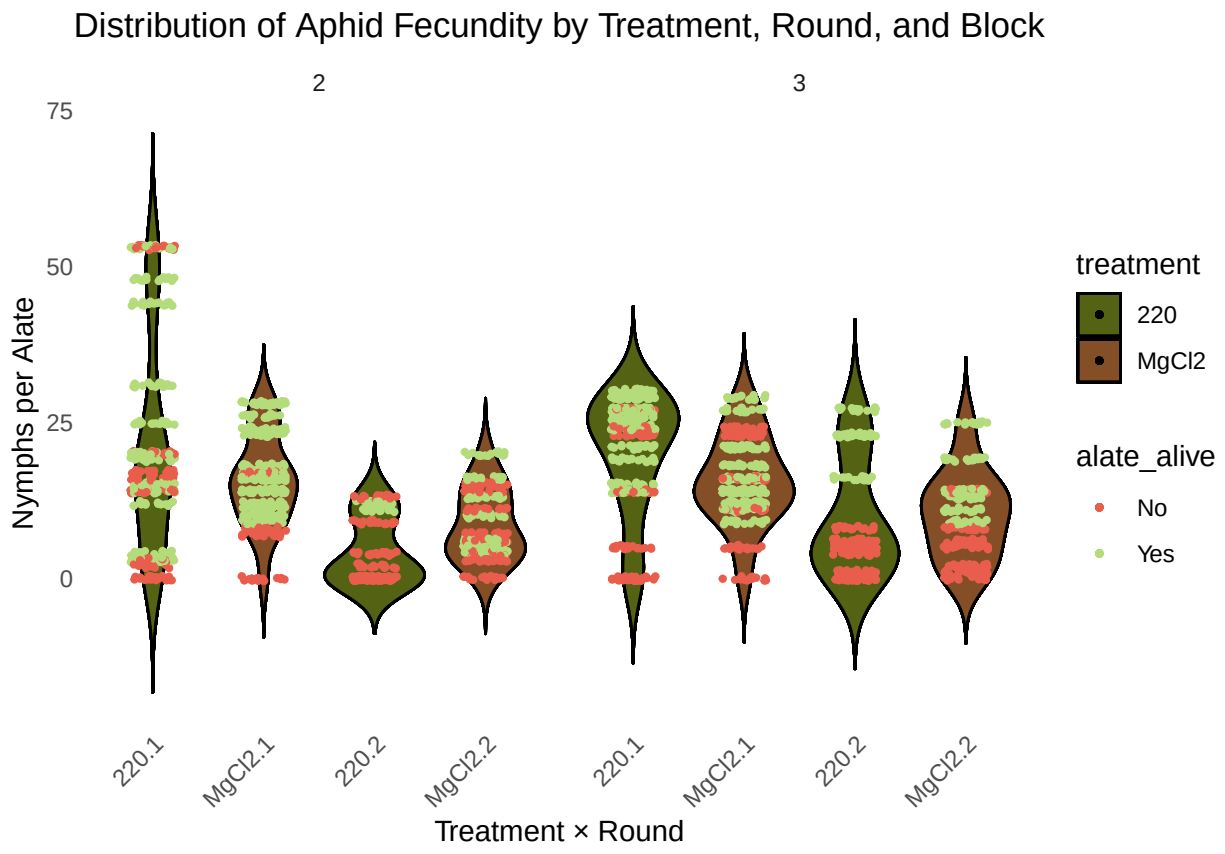
```
# === Violin Plot per block ===
ggplot(aphid_long, aes(x = interaction(treatment, round), y = nymphs, fill = treatment)) +
    # Violin geometry: distribution shape
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_violin(trim = FALSE, alpha = 0.6, color = "black") + # Overlay individual data points, jittered fo
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Facet by block to compare spatial re
```

```
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Facet by block to compare spatial re
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Facet by block to compare spatial re
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Facet by block to compare spatial re
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Facet by block to compare spatial re
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Facet by block to compare spatial re
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Facet by block to compare spatial re
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Facet by block to compare spatial re
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Facet by block to compare spatial re
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Facet by block to compare spatial re
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Facet by block to compare spatial re
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Facet by block to compare spatial re
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Facet by block to compare spatial re
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Facet by block to compare spatial re
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Facet by block to compare spatial re
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Facet by block to compare spatial re
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Facet by block to compare spatial re
facet_wrap(~block, nrow = 1) + # Axis labels and plot title facet_wrap(~block,
facet_wrap(~block, nrow = 1) + # Axis labels and plot title nrow = 1) + # Axis
facet_wrap(~block, nrow = 1) + # Axis labels and plot title labels and plot
facet_wrap(~block, nrow = 1) + # Axis labels and plot title title
labs(x = "Treatment × Round", y = "Nymphs per Alate", title = "Distribution of Aphid Fecundity by Treatm
    # Consistent fill and point colors
scale_fill_manual(values = c(`220` = "#546214", MgCl2 = "#844e27")) + scale_color_manual(values = c(Yes
    No = "#e95d4d")) + # Theme cleanup No = "#e95d4d")) + # Theme cleanup
theme_minimal() + theme(legend.position = "right", panel.grid = element_blank(),
    plot.title = element_text(hjust = 0.5), axis.text.x = element_text(angle = 45,
        hjust = 1))
```

```
## Warning: Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
```

```
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
```

```
## Warning: Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
```



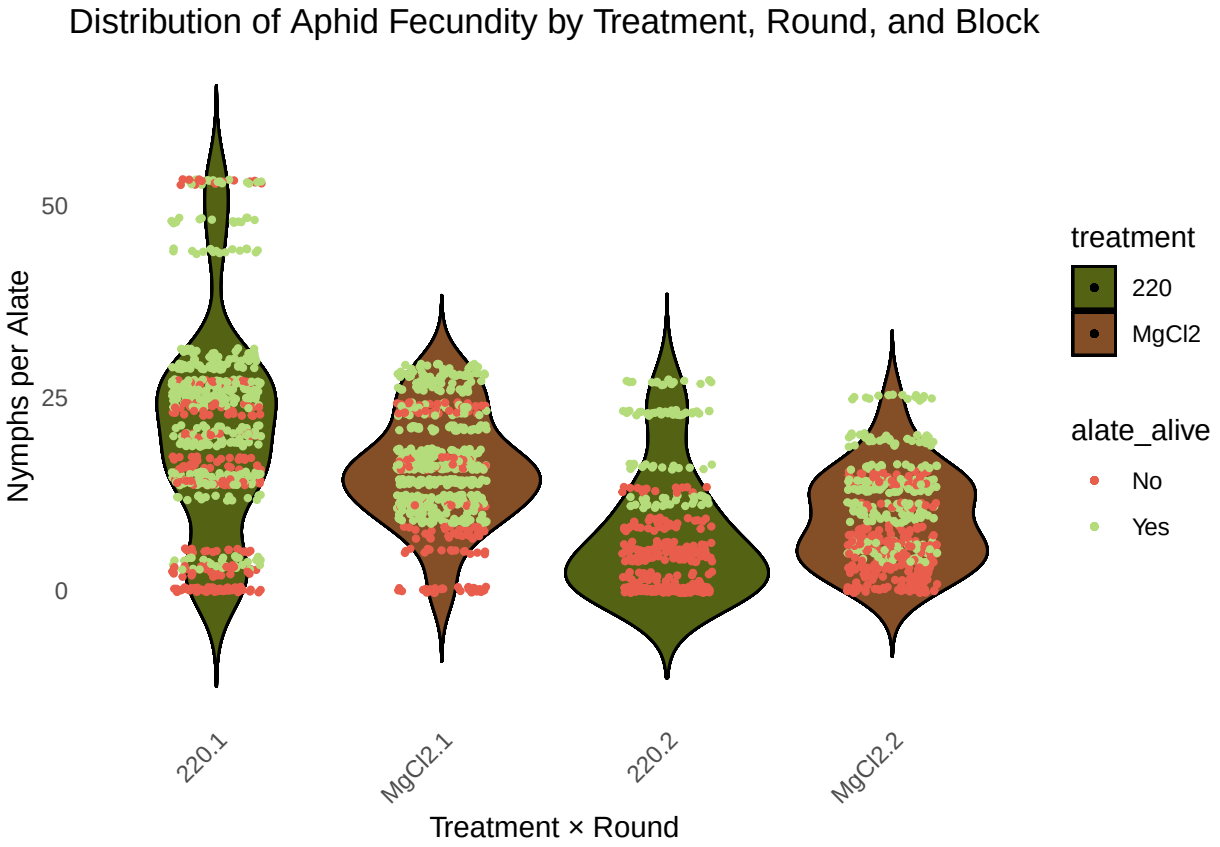

```
# === Violin Plot overall ===
ggplot(aphid_long, aes(x = interaction(treatment, round), y = nymphs, fill = treatment)) +
    # Violin geometry: distribution shape
geom_violin(trim = FALSE, alpha = 1, color = "black") + # Overlay individual data points, jittered for
geom_violin(trim = FALSE, alpha = 1, color = "black") + # Overlay individual data points, jittered for
geom_violin(trim = FALSE, alpha = 1, color = "black") + # Overlay individual data points, jittered for
geom_violin(trim = FALSE, alpha = 1, color = "black") + # Overlay individual data points, jittered for
geom_violin(trim = FALSE, alpha = 1, color = "black") + # Overlay individual data points, jittered for
geom_violin(trim = FALSE, alpha = 1, color = "black") + # Overlay individual data points, jittered for
geom_violin(trim = FALSE, alpha = 1, color = "black") + # Overlay individual data points, jittered for
geom_violin(trim = FALSE, alpha = 1, color = "black") + # Overlay individual data points, jittered for
geom_violin(trim = FALSE, alpha = 1, color = "black") + # Overlay individual data points, jittered for
geom_violin(trim = FALSE, alpha = 1, color = "black") + # Overlay individual data points, jittered for
geom_violin(trim = FALSE, alpha = 1, color = "black") + # Overlay individual data points, jittered for
geom_violin(trim = FALSE, alpha = 1, color = "black") + # Overlay individual data points, jittered for
geom_violin(trim = FALSE, alpha = 1, color = "black") + # Overlay individual data points, jittered for
geom_violin(trim = FALSE, alpha = 1, color = "black") + # Overlay individual data points, jittered for
geom_violin(trim = FALSE, alpha = 1, color = "black") + # Overlay individual data points, jittered for
geom_violin(trim = FALSE, alpha = 1, color = "black") + # Overlay individual data points, jittered for
geom_violin(trim = FALSE, alpha = 1, color = "black") + # Overlay individual data points, jittered for
geom_violin(trim = FALSE, alpha = 1, color = "black") + # Overlay individual data points, jittered for
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Axis labels and plot title geom_jitt
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Axis labels and plot title =
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Axis labels and plot title alate_ali
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Axis labels and plot title width
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Axis labels and plot title =
```

```
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Axis labels and plot title 0.2,
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Axis labels and plot title size
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Axis labels and plot title =
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Axis labels and plot title 0.8)
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Axis labels and plot title +
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Axis labels and plot title #
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Axis labels and plot title Axis
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Axis labels and plot title labels
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Axis labels and plot title and
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Axis labels and plot title plot
geom_jitter(aes(color = alate_alive), width = 0.2, size = 0.8) + # Axis labels and plot title title
labs(x = "Treatment × Round", y = "Nymphs per Alate", title = "Distribution of Aphid Fecundity by Treatr
    # Consistent fill and point colors
scale_fill_manual(values = c(`220` = "#546214", MgCl2 = "#844e27")) + scale_color_manual(values = c(Yes
    No = "#e95d4d")) + # Theme cleanup No = "#e95d4d")) + # Theme cleanup
theme_minimal() + theme(legend.position = "right", panel.grid = element_blank(),
    plot.title = element_text(hjust = 0.5), axis.text.x = element_text(angle = 45,
        hjust = 1))
```

```
## Warning: Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
```

```
## Warning: Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).
##
```

```
## (`stat_ydensity()`).
## Removed 25 rows containing non-finite outside the scale range
## (`stat_ydensity()`).

## Warning: Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
## Removed 25 rows containing missing values or values outside the scale range
## (`geom_point()`).
```



Statistics

Prepare the data and define helper function

```
# Identify unique blocks in your dataset
blocks <- unique(aphid_count$block)

# This function takes a subset of the data (e.g., one block or full data) and
# prints model summaries for survival and fecundity across both rounds
analyze_block <- function(df, label = "All Blocks") {
    cat("\n==============================", label, "==============================\n")

    # -------------------- Survival: Round 1 --------------------
    cat("\n--- Survival Round 1 ---\n")
    surv_r1 <- df %>%
        group_by(treatment) %>%
        summarise(alive_n = sum(alate_alive_r1 == "Yes", na.rm = TRUE), dead_n = sum(alate_alive_r1 ==
            "No", na.rm = TRUE), .groups = "drop")
    ch_r1 <- glm(cbind(alive_n, dead_n) ~ treatment, family = binomial, data = surv_r1)
    print(summary(ch_r1))
    print(emmeans(ch_r1, ~treatment, type = "response"))

    # -------------------- Survival: Round 2 --------------------
```

```
    cat("\n--- Survival Round 2 ---\n")
    surv_r2 <- df %>%
        group_by(treatment) %>%
        summarise(alive_n = sum(alate_alive_r2 == "Yes", na.rm = TRUE), dead_n = sum(alate_alive_r2 ==
            "No", na.rm = TRUE), .groups = "drop")
    ch_r2 <- glm(cbind(alive_n, dead_n) ~ treatment, family = binomial, data = surv_r2)
    print(summary(ch_r2))
    print(emmeans(ch_r2, ~treatment, type = "response"))

    # -------------------- Fecundity: Round 1 --------------------
    cat("\n--- Fecundity Round 1 (Alive Only) ---\n")
    fec_r1_alive <- df %>%
        filter(alate_alive_r1 == "Yes")
    ch_fec_r1_alive <- lm(nymphs_r1 ~ treatment, data = fec_r1_alive)
    print(summary(ch_fec_r1_alive))
    print(emmeans(ch_fec_r1_alive, ~treatment))

    cat("\n--- Fecundity Round 1 (All Alates) ---\n")
    ch_fec_r1 <- lm(nymphs_r1 ~ treatment, data = df)
    print(summary(ch_fec_r1))
    print(emmeans(ch_fec_r1, ~treatment))

    # -------------------- Fecundity: Round 2 --------------------
    cat("\n--- Fecundity Round 2 (Alive Only) ---\n")
    fec_r2_alive <- df %>%
        filter(alate_alive_r2 == "Yes")
    ch_fec_r2_alive <- lm(nymphs_r2 ~ treatment, data = fec_r2_alive)
    print(summary(ch_fec_r2_alive))
    print(emmeans(ch_fec_r2_alive, ~treatment))

    cat("\n--- Fecundity Round 2 (All Alates) ---\n")
    ch_fec_r2 <- lm(nymphs_r2 ~ treatment, data = df)
    print(summary(ch_fec_r2))
    print(emmeans(ch_fec_r2, ~treatment))
}
```

Stats

Individual blocks

```
# Loop through each block and run the full analysis
for (blk in blocks) {
    df_blk <- aphid_count %>%
        filter(block == blk)
    analyze_block(df_blk, paste("Block", blk))
}
```

```
##
## ================================ Block 2 ================================
##
## --- Survival Round 1 ---
```

```
##
## Call:
## glm(formula = cbind(alive_n, dead_n) ~ treatment, family = binomial,
##     data = surv_r1)
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.4055     0.4564   0.888    0.374
## treatmentMgCl2   0.9808     0.7217   1.359    0.174
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance:  1.9326e+00  on 1  degrees of freedom
## Residual deviance: -3.5527e-15  on 0  degrees of freedom
## AIC: 10.478
##
## Number of Fisher Scoring iterations: 3
##
##  treatment prob     SE  df asymp.LCL asymp.UCL
##  220        0.6 0.1100 Inf     0.380     0.786
##  MgCl2      0.8 0.0894 Inf     0.572     0.923
##
## Confidence level used: 0.95
## Intervals are back-transformed from the logit scale
##
## --- Survival Round 2 ---
##
## Call:
## glm(formula = cbind(alive_n, dead_n) ~ treatment, family = binomial,
##     data = surv_r2)
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)     -1.6094     0.7746  -2.078   0.0377 *
## treatmentMgCl2   1.3581     0.9241   1.470   0.1417
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance:  2.4212e+00  on 1  degrees of freedom
## Residual deviance: -8.8818e-16  on 0  degrees of freedom
## AIC: 9.6745
##
## Number of Fisher Scoring iterations: 4
##
##  treatment  prob    SE  df asymp.LCL asymp.UCL
##  220       0.167 0.108 Inf     0.042     0.477
##  MgCl2     0.438 0.124 Inf     0.225     0.676
##
## Confidence level used: 0.95
## Intervals are back-transformed from the logit scale
##
## --- Fecundity Round 1 (Alive Only) ---
```

```
##
## Call:
## lm(formula = nymphs_r1 ~ treatment, data = fec_r1_alive)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -21.000  -6.875  -1.625   6.531  29.000
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)      24.000      3.431   6.996 1.99e-07 ***
## treatmentMgCl2   -6.375      4.538  -1.405    0.172
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.88 on 26 degrees of freedom
## Multiple R-squared:  0.07054,    Adjusted R-squared:  0.0348
## F-statistic: 1.973 on 1 and 26 DF,  p-value: 0.1719
##
##  treatment emmean   SE df lower.CL upper.CL
##  220         24.0 3.43 26     16.9     31.1
##  MgCl2       17.6 2.97 26     11.5     23.7
##
## Confidence level used: 0.95
##
## --- Fecundity Round 1 (All Alates) ---
##
## Call:
## lm(formula = nymphs_r1 ~ treatment, data = df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -20.650  -6.662  -1.675   5.088  32.350
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)      20.650      2.916   7.082  1.9e-08 ***
## treatmentMgCl2   -4.950      4.123  -1.200    0.237
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 13.04 on 38 degrees of freedom
## Multiple R-squared:  0.03654,    Adjusted R-squared:  0.01119
## F-statistic: 1.441 on 1 and 38 DF,  p-value: 0.2374
##
##  treatment emmean   SE df lower.CL upper.CL
##  220         20.6 2.92 38     14.7     26.6
##  MgCl2       15.7 2.92 38      9.8     21.6
##
## Confidence level used: 0.95
##
## --- Fecundity Round 2 (Alive Only) ---
##
## Call:
```

```
## lm(formula = nymphs_r2 ~ treatment, data = fec_r2_alive)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -6.571 -4.571 -0.500  2.429  9.429
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)     11.5000     3.9661   2.900    0.023 *
## treatmentMgCl2  -0.9286     4.4971  -0.206    0.842
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.609 on 7 degrees of freedom
## Multiple R-squared:  0.006054,   Adjusted R-squared:  -0.1359
## F-statistic: 0.04264 on 1 and 7 DF,  p-value: 0.8423
##
##  treatment emmean   SE df lower.CL upper.CL
##  220         11.5 3.97  7     2.12     20.9
##  MgCl2       10.6 2.12  7     5.56     15.6
##
## Confidence level used: 0.95
##
## --- Fecundity Round 2 (All Alates) ---
##
## Call:
## lm(formula = nymphs_r2 ~ treatment, data = df)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -8.562 -4.250 -2.406  4.922 11.438
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)       4.250      1.609   2.641   0.0138 *
## treatmentMgCl2    4.313      2.129   2.025   0.0532 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.575 on 26 degrees of freedom
##   (12 observations deleted due to missingness)
## Multiple R-squared:  0.1363, Adjusted R-squared:  0.1031
## F-statistic: 4.103 on 1 and 26 DF,  p-value: 0.0532
##
##  treatment emmean   SE df lower.CL upper.CL
##  220         4.25 1.61 26    0.942     7.56
##  MgCl2       8.56 1.39 26    5.697    11.43
##
## Confidence level used: 0.95
##
## ============================== Block 3 ==============================
##
## --- Survival Round 1 ---
##
```

```
## Call:
## glm(formula = cbind(alive_n, dead_n) ~ treatment, family = binomial,
##     data = surv_r1)
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.6190     0.4688   1.320    0.187
## treatmentMgCl2   0.2283     0.6767   0.337    0.736
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance:  1.1404e-01  on 1  degrees of freedom
## Residual deviance: -4.4409e-16  on 0  degrees of freedom
## AIC: 10.686
##
## Number of Fisher Scoring iterations: 3
##
##  treatment prob    SE  df asymp.LCL asymp.UCL
##  220       0.65 0.107 Inf     0.426     0.823
##  MgCl2     0.70 0.102 Inf     0.473     0.859
##
## Confidence level used: 0.95
## Intervals are back-transformed from the logit scale
##
## --- Survival Round 2 ---
##
## Call:
## glm(formula = cbind(alive_n, dead_n) ~ treatment, family = binomial,
##     data = surv_r2)
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)     -0.8109     0.6009  -1.349    0.177
## treatmentMgCl2   0.8109     0.8043   1.008    0.313
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1.0422e+00  on 1  degrees of freedom
## Residual deviance: 2.2204e-15  on 0  degrees of freedom
## AIC: 10.03
##
## Number of Fisher Scoring iterations: 3
##
##  treatment  prob    SE  df asymp.LCL asymp.UCL
##  220       0.308 0.128 Inf      0.12     0.591
##  MgCl2     0.500 0.134 Inf      0.26     0.740
##
## Confidence level used: 0.95
## Intervals are back-transformed from the logit scale
##
## --- Fecundity Round 1 (Alive Only) ---
##
## Call:
## lm(formula = nymphs_r1 ~ treatment, data = fec_r1_alive)
```

```
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -10.000  -3.857   0.000   3.643  12.286
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)      24.000      1.552   15.46 2.63e-14 ***
## treatmentMgCl2   -7.286      2.155   -3.38  0.00238 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.596 on 25 degrees of freedom
## Multiple R-squared:  0.3137, Adjusted R-squared:  0.2862
## F-statistic: 11.43 on 1 and 25 DF,  p-value: 0.002381
##
##  treatment emmean   SE df lower.CL upper.CL
##  220         24.0 1.55 25     20.8     27.2
##  MgCl2       16.7 1.50 25     13.6     19.8
##
## Confidence level used: 0.95
##
## --- Fecundity Round 1 (All Alates) ---
##
## Call:
## lm(formula = nymphs_r1 ~ treatment, data = df)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -20.25  -4.65   0.55   6.00  13.35
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)      20.250      1.865  10.856 3.32e-13 ***
## treatmentMgCl2   -4.600      2.638  -1.744   0.0893 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.342 on 38 degrees of freedom
## Multiple R-squared:  0.07409,    Adjusted R-squared:  0.04973
## F-statistic: 3.041 on 1 and 38 DF,  p-value: 0.08928
##
##  treatment emmean   SE df lower.CL upper.CL
##  220         20.2 1.87 38     16.5     24.0
##  MgCl2       15.7 1.87 38     11.9     19.4
##
## Confidence level used: 0.95
##
## --- Fecundity Round 2 (Alive Only) ---
##
## Call:
## lm(formula = nymphs_r2 ~ treatment, data = fec_r2_alive)
##
## Residuals:
```

```
##    Min     1Q Median     3Q    Max
## -6.250 -3.000 -1.000  2.375 10.000
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)     22.250      2.564   8.676 1.15e-05 ***
## treatmentMgCl2  -7.250      3.215  -2.255   0.0506 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.129 on 9 degrees of freedom
## Multiple R-squared:  0.3611, Adjusted R-squared:  0.2901
## F-statistic: 5.086 on 1 and 9 DF,  p-value: 0.05057
##
##  treatment emmean   SE df lower.CL upper.CL
##  220         22.2 2.56  9     16.4     28.1
##  MgCl2       15.0 1.94  9     10.6     19.4
##
## Confidence level used: 0.95
##
## --- Fecundity Round 2 (All Alates) ---
##
## Call:
## lm(formula = nymphs_r2 ~ treatment, data = df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -10.071  -5.266  -2.071   3.929  17.538
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)     9.4615     2.3046   4.105 0.000378 ***
## treatmentMgCl2  0.6099     3.2005   0.191 0.850408
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.309 on 25 degrees of freedom
##   (13 observations deleted due to missingness)
## Multiple R-squared:  0.00145,    Adjusted R-squared:  -0.03849
## F-statistic: 0.03631 on 1 and 25 DF,  p-value: 0.8504
##
##  treatment emmean   SE df lower.CL upper.CL
##  220         9.46 2.30 25     4.72     14.2
##  MgCl2      10.07 2.22 25     5.50     14.6
##
## Confidence level used: 0.95
```

All blocks combines

```
# Run the same analysis on the entire dataset (all blocks together)
analyze_block(aphid_count, "All Blocks Combined")
```

```
##
## ============================== All Blocks Combined ================================
##
## --- Survival Round 1 ---
##
## Call:
## glm(formula = cbind(alive_n, dead_n) ~ treatment, family = binomial,
##     data = surv_r1)
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.5108     0.3266   1.564    0.118
## treatmentMgCl2   0.5878     0.4899   1.200    0.230
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1.4619  on 1  degrees of freedom
## Residual deviance: 0.0000  on 0  degrees of freedom
## AIC: 11.96
##
## Number of Fisher Scoring iterations: 3
##
##  treatment  prob     SE  df asymp.LCL asymp.UCL
##  220       0.625 0.0765 Inf     0.468      0.76
##  MgCl2     0.750 0.0685 Inf     0.595      0.86
##
## Confidence level used: 0.95
## Intervals are back-transformed from the logit scale
##
## --- Survival Round 2 ---
##
## Call:
## glm(formula = cbind(alive_n, dead_n) ~ treatment, family = binomial,
##     data = surv_r2)
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)     -1.1527     0.4683  -2.461   0.0138 *
## treatmentMgCl2   1.0191     0.5943   1.715   0.0864 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance:  3.0936e+00  on 1  degrees of freedom
## Residual deviance: -3.9968e-15  on 0  degrees of freedom
## AIC: 11.25
##
## Number of Fisher Scoring iterations: 3
##
##  treatment  prob     SE  df asymp.LCL asymp.UCL
##  220       0.240 0.0854 Inf     0.112     0.442
##  MgCl2     0.467 0.0911 Inf     0.299     0.642
##
```

```
## Confidence level used: 0.95
## Intervals are back-transformed from the logit scale
##
## --- Fecundity Round 1 (Alive Only) ---
##
## Call:
## lm(formula = nymphs_r1 ~ treatment, data = fec_r1_alive)
##
## Residuals:
##    Min     1Q Median     3Q    Max
##  -21.0   -5.2   -1.2    4.4   29.0
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)      24.000      1.835  13.080  < 2e-16 ***
## treatmentMgCl2   -6.800      2.484  -2.737  0.00842 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.174 on 53 degrees of freedom
## Multiple R-squared:  0.1238, Adjusted R-squared:  0.1073
## F-statistic: 7.492 on 1 and 53 DF,  p-value: 0.008418
##
##  treatment emmean   SE df lower.CL upper.CL
##  220         24.0 1.83 53     20.3     27.7
##  MgCl2       17.2 1.67 53     13.8     20.6
##
## Confidence level used: 0.95
##
## --- Fecundity Round 1 (All Alates) ---
##
## Call:
## lm(formula = nymphs_r1 ~ treatment, data = df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -20.450  -5.869  -0.062   5.800  32.550
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)      20.450      1.708  11.970   <2e-16 ***
## treatmentMgCl2   -4.775      2.416  -1.976   0.0517 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.81 on 78 degrees of freedom
## Multiple R-squared:  0.04769,    Adjusted R-squared:  0.03548
## F-statistic: 3.906 on 1 and 78 DF,  p-value: 0.05165
##
##  treatment emmean   SE df lower.CL upper.CL
##  220         20.4 1.71 78     17.0     23.9
##  MgCl2       15.7 1.71 78     12.3     19.1
##
## Confidence level used: 0.95
```

```
##
## --- Fecundity Round 2 (Alive Only) ---
##
## Call:
## lm(formula = nymphs_r2 ~ treatment, data = fec_r2_alive)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -8.7857 -4.5060  0.2143  4.3333 12.2143
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)      18.667      2.509   7.441 6.77e-07 ***
## treatmentMgCl2   -5.881      2.998  -1.961   0.0655 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.145 on 18 degrees of freedom
## Multiple R-squared:  0.1761, Adjusted R-squared:  0.1303
## F-statistic: 3.847 on 1 and 18 DF,  p-value: 0.0655
##
##  treatment emmean   SE df lower.CL upper.CL
##  220         18.7 2.51 18    13.40     23.9
##  MgCl2       12.8 1.64 18     9.34     16.2
##
## Confidence level used: 0.95
##
## --- Fecundity Round 2 (All Alates) ---
##
## Call:
## lm(formula = nymphs_r2 ~ treatment, data = df)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -9.267 -6.113 -1.960  4.733 20.040
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)       6.960      1.433   4.857  1.1e-05 ***
## treatmentMgCl2    2.307      1.940   1.189     0.24
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.165 on 53 degrees of freedom
##   (25 observations deleted due to missingness)
## Multiple R-squared:  0.02597,    Adjusted R-squared:  0.007596
## F-statistic: 1.413 on 1 and 53 DF,  p-value: 0.2398
##
##  treatment emmean   SE df lower.CL upper.CL
##  220         6.96 1.43 53     4.09     9.83
##  MgCl2       9.27 1.31 53     6.64    11.89
##
## Confidence level used: 0.95
```