

Stem density by size class

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Packages, data, and functions

```
library(car)
library(tidyverse)

data_stems <- read_csv("data/data_stems.csv") %>%
  mutate(plot_id = as.factor(plot_id),
        size_class = as.factor(size_class),
        harvested = as.factor(harvested),
        vegetation_type = as.factor(vegetation_type),
        milpa = as.factor(milpa))
data_plots <- read_csv("data/data_plots.csv") %>%
  mutate(plot_id = as.factor(plot_id),
        harvested = as.factor(harvested),
        vegetation_type = as.factor(vegetation_type),
        milpa = as.factor(milpa))

compute_bootstrap_interval <- function(var, statistic = mean, num_iters = 50000,
                                         percentiles = c(0.025, 0.975)) {
  boot_samples <- numeric(num_iters)

  for (i in 1:num_iters) {
    boot_samples[i] <- statistic(sample(var, size = length(var), replace = TRUE))
  }

  return(quantile(boot_samples, percentiles))
}

plot_theme <- theme(plot.background = element_rect(fill = "white"),
                     plot.title = element_blank(),
                     plot.subtitle = element_text(family="sans", face="plain"),
                     axis.title.x = element_text(family="sans", face="bold"),
                     axis.title.y = element_text(family="sans", face="bold"),
                     axis.text.x = element_text(family="sans", face="plain"),
                     axis.text.y = element_text(family="sans", face="plain"),
                     panel.background = element_rect(fill="white"),
                     panel.grid.major.x = element_blank(),
                     panel.grid.major.y = element_line(color="gainsboro"),
                     panel.grid.minor = element_blank(),
                     axis.ticks = element_blank(),
```

```

legend.background = element_rect(color="black", fill = "white"),
legend.position = c(0.9, 0.85),
legend.title = element_text(color = "black", face = "bold", hjust = 0.5),
legend.text = element_text(color = "black"))

```

Figures

Average stem density by size class

Compute bootstrap intervals and organize data

```

harvested <- data_plots %>%
  filter(harvested == "yes") %>%
  select(stemden_seedlings, stemden_saplings,
         starts_with("stemden_trees"))

unharvested <- data_plots %>%
  filter(harvested == "no") %>%
  select(stemden_seedlings, stemden_saplings,
         starts_with("stemden_trees"))

set.seed(1)
boot_intervals <- bind_rows(compute_bootstrap_interval(unharvested$stemden_seedlings),
                             compute_bootstrap_interval(unharvested$stemden_saplings),
                             compute_bootstrap_interval(unharvested$stemden_trees05to09),
                             compute_bootstrap_interval(unharvested$stemden_trees10to14),
                             compute_bootstrap_interval(unharvested$stemden_trees15to19),
                             compute_bootstrap_interval(unharvested$stemden_trees20plus),
                             compute_bootstrap_interval(harvested$stemden_seedlings),
                             compute_bootstrap_interval(harvested$stemden_saplings),
                             compute_bootstrap_interval(harvested$stemden_trees05to09),
                             compute_bootstrap_interval(harvested$stemden_trees10to14),
                             compute_bootstrap_interval(harvested$stemden_trees15to19),
                             compute_bootstrap_interval(harvested$stemden_trees20plus))

stemden_mean_data <- data_plots %>%
  select(harvested, stemden_seedlings,
         stemden_saplings, starts_with("stemden_trees")) %>%
  group_by(harvested) %>%
  summarize_all(mean) %>%
  pivot_longer(cols = starts_with("stemden"), names_prefix = "stemden_",
               names_to = "size_class", values_to = "mean") %>%
  bind_cols(boot_intervals) %>%
  select(harvested, size_class, lower = `2.5%`, mean, upper = `97.5%`) %>%
  mutate(size_class = as.factor(size_class)) %>%
  mutate(harvested = fct_recode(harvested,
                                "Harvested" = "yes", "Unharvested" = "no"))

stemden_mean_data_noseedlings <- stemden_mean_data %>%
  filter(size_class != "seedlings") %>%
  mutate(size_class =
        fct_recode(size_class,

```

```

    "Saplings (0-4 cm DBH)" = "saplings",
    "Trees (5-9 cm DBH)" = "trees05to09",
    "Trees (10-14 cm DBH)" = "trees10to14",
    "Trees (15-19 cm DBH)" = "trees15to19",
    "Trees (20+ cm DBH)" = "trees20plus"))

stemden_mean_data_seedlings <- stemden_mean_data %>%
  filter(size_class == "seedlings") %>%
  mutate(size_class = fct_recode(size_class,
    "Seedlings (0 cm DBH)" = "seedlings"))

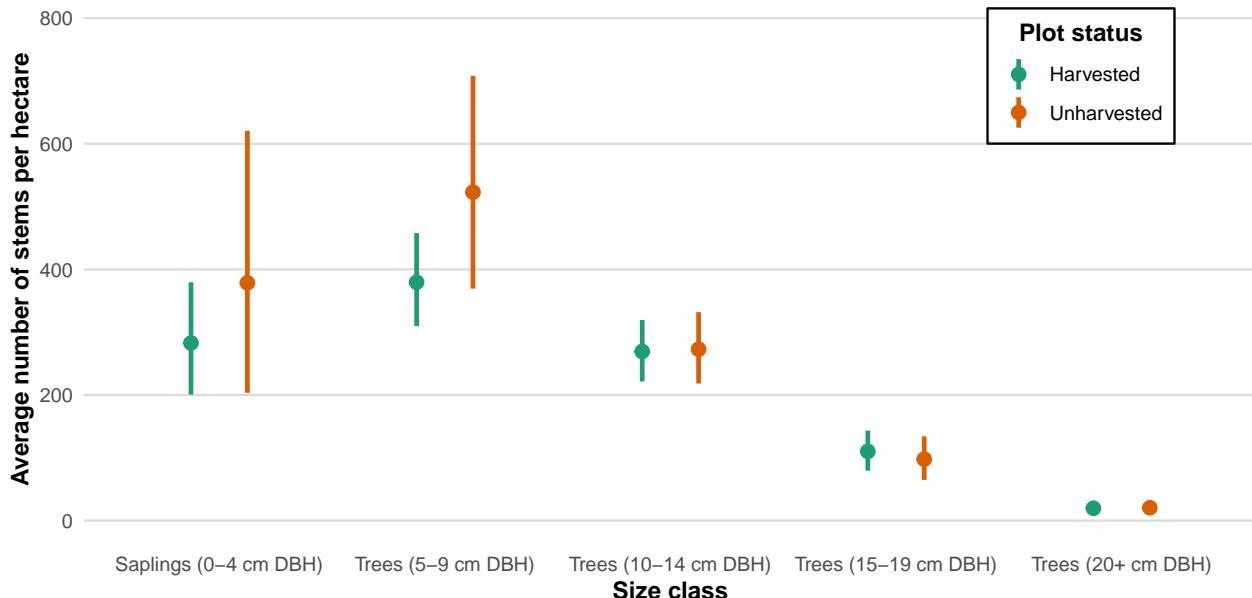
```

Pointrange plots

```

# All size classes except seedlings
stemden_sizeclass_fig1_noseedlings <- stemden_mean_data_noseedlings %>%
  ggplot() +
  geom_pointrange(aes(x = size_class, col = fct_relevel(harvested, "Harvested", "Unharvested"),
    ymin = lower, y = mean, ymax = upper),
    position = position_dodge(width = 0.5), size = 0.5, linewidth = 1) +
  plot_theme + theme(legend.position.inside = c(0.85, 0.85),
    legend.title = element_text(hjust = 0.5)) +
  ylim(0, 800) +
  scale_color_brewer(palette = "Dark2") +
  labs(x = "Size class", y = "Average number of stems per hectare") +
  guides(col=guide_legend(title = "Plot status"))
ggsave("figures/stemden_sizeclass_fig1_noseedlings.png", height = 4, width = 8)
stemden_sizeclass_fig1_noseedlings

```



```

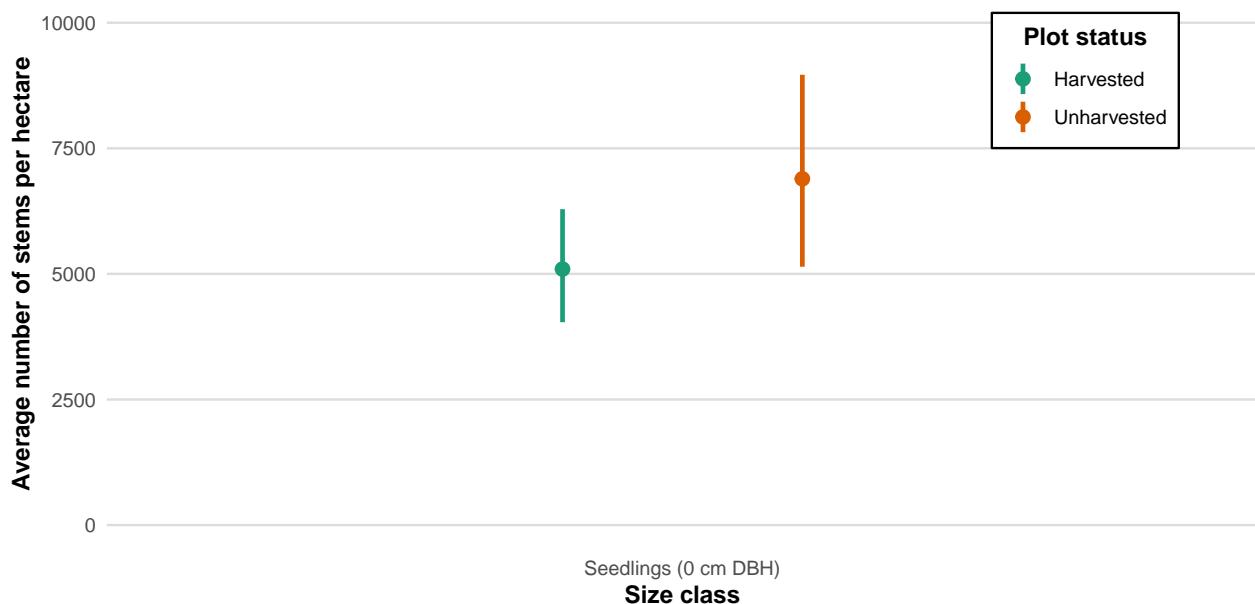
# Seedlings only
stemden_sizeclass_fig1_seedlings <- stemden_mean_data_seedlings %>%
  ggplot() +

```

```

geom_pointrange(aes(x = size_class, col = fct_relevel(harvested, "Harvested", "Unharvested"),
                     ymin = lower, y = mean, ymax = upper),
                 position = position_dodge(width = 0.5), size = 0.5, linewidth = 1) +
plot_theme + theme(legend.position.inside = c(0.85, 0.85),
                   legend.title = element_text(hjust = 0.5)) +
ylim(0, 10000) +
scale_color_brewer(palette = "Dark2") +
labs(x = "Size class", y = "Average number of stems per hectare") +
guides(col=guide_legend(title = "Plot status"))
ggsave("figures/stemden_sizeclass_fig1_seedlings.png", height = 4, width = 8)
stemden_sizeclass_fig1_seedlings

```

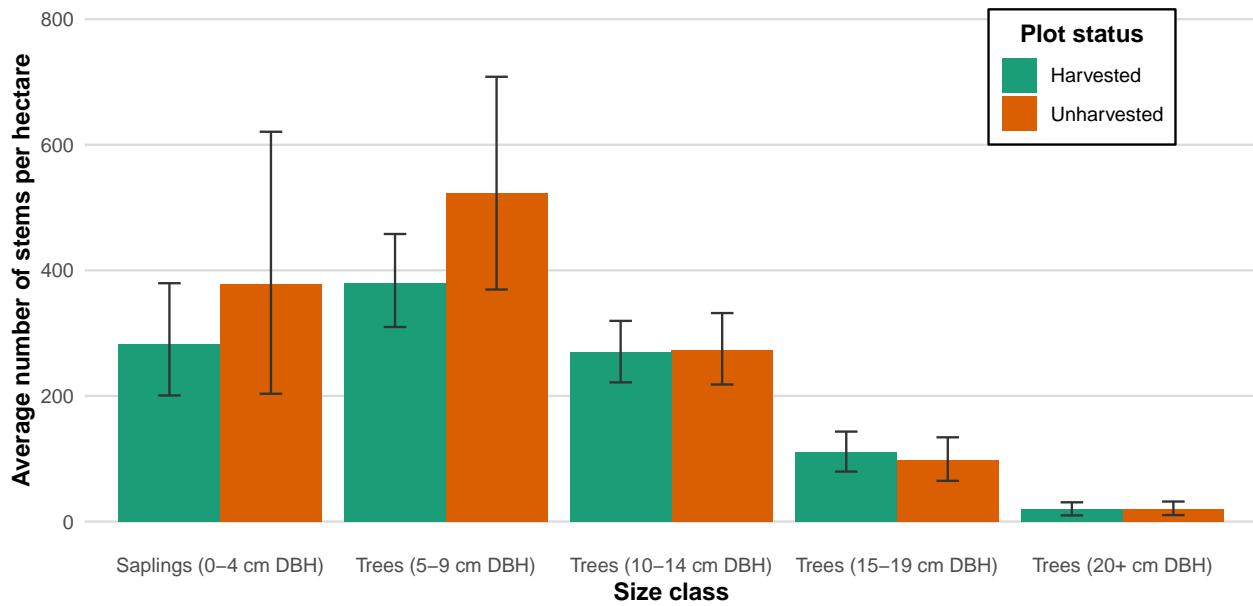


Bar plots

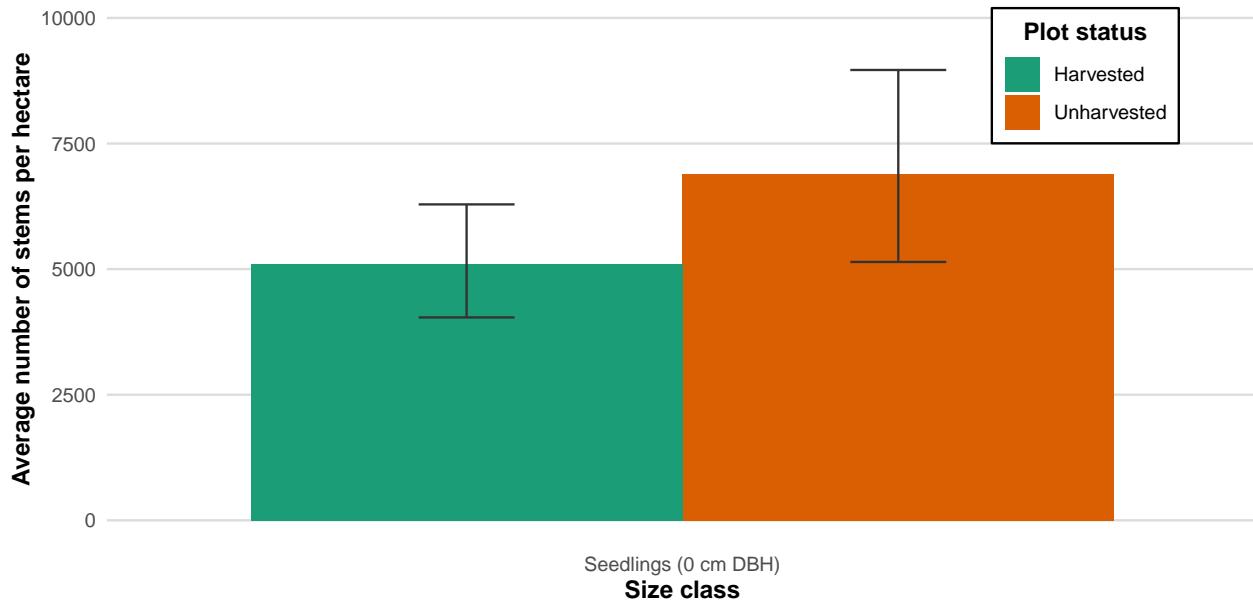
```

# All size classes except seedlings
stemden_sizeclass_fig2_noseedlings <- stemden_mean_data_noseedlings %>%
ggplot(aes(x = size_class,
            fill = fct_relevel(harvested, "Harvested", "Unharvested")) +
  geom_col(aes(y = mean),
           position = "dodge") +
  geom_errorbar(aes(x = size_class, ymin = lower, ymax = upper), col = "gray20",
                position = position_dodge(width = 0.9), width = 0.2, show.legend = FALSE) +
  plot_theme + theme(legend.position.inside = c(0.85, 0.85),
                     legend.title = element_text(hjust = 0.5)) +
  ylim(0, 800) +
  scale_fill_brewer(palette = "Dark2") +
  labs(x = "Size class", y = "Average number of stems per hectare") +
  guides(fill=guide_legend(title = "Plot status"))
ggsave("figures/stemden_sizeclass_fig2_noseedlings.png", height = 4, width = 8)
stemden_sizeclass_fig2_noseedlings

```



```
# Seedlings only
stemden_sizeclass_fig2_seedlings <- stemden_mean_data_seedlings %>%
  ggplot(aes(x = size_class,
             fill = fct_relevel(harvested, "Harvested", "Unharvested"))) +
  geom_col(aes(y = mean),
            position = "dodge") +
  geom_errorbar(aes(x = size_class, ymin = lower, ymax = upper), col = "gray20",
                position = position_dodge(width = 0.9), width = 0.2, show.legend = FALSE) +
  plot_theme + theme(legend.position.inside = c(0.85, 0.85),
                     legend.title = element_text(hjust = 0.5)) +
  ylim(0, 10000) +
  scale_fill_brewer(palette = "Dark2") +
  labs(x = "Size class", y = "Average number of stems per hectare") +
  guides(fill=guide_legend(title = "Plot status"))
ggsave("figures/stemden_sizeclass_fig2_seedlings.png", height = 4, width = 8)
stemden_sizeclass_fig2_seedlings
```



Distribution of stem densities by size class

Organize data

```

stemden_dist_data <- data_plots %>%
  select(harvested, stemden_seedlings,
         stemden_saplings, starts_with("stemden_trees")) %>%
  pivot_longer(cols = starts_with("stemden"),
               names_prefix = "stemden_",
               names_to = "size_class",
               values_to = "num_stems") %>%
  mutate(size_class = as.factor(size_class)) %>%
  mutate(harvested = fct_recode(harvested,
                                "Harvested" = "yes",
                                "Unharvested" = "no"))

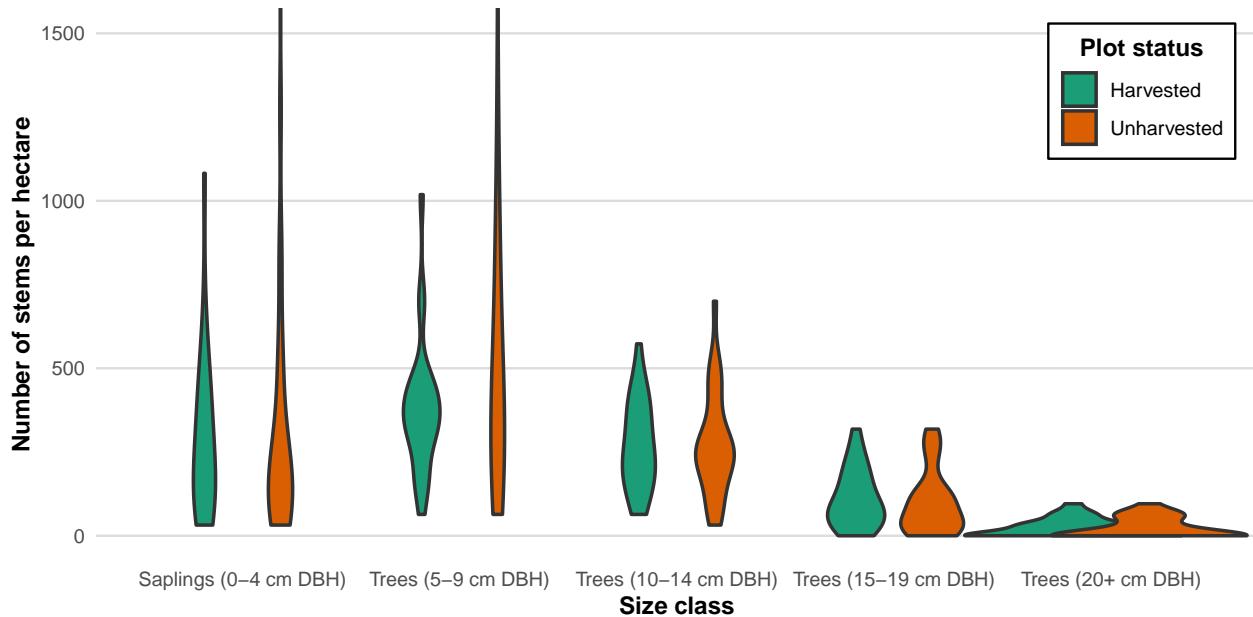
stemden_dist_data_noseedlings <- stemden_dist_data %>%
  filter(size_class != "seedlings") %>%
  mutate(size_class =
    fct_recode(size_class,
              "Saplings (0-4 cm DBH)" = "saplings",
              "Trees (5-9 cm DBH)" = "trees05to09",
              "Trees (10-14 cm DBH)" = "trees10to14",
              "Trees (15-19 cm DBH)" = "trees15to19",
              "Trees (20+ cm DBH)" = "trees20plus"))

stemden_dist_data_seedlings <- stemden_dist_data %>%
  filter(size_class == "seedlings") %>%
  mutate(size_class = fct_recode(size_class,
                                "Seedlings (0 cm DBH)" = "seedlings"))

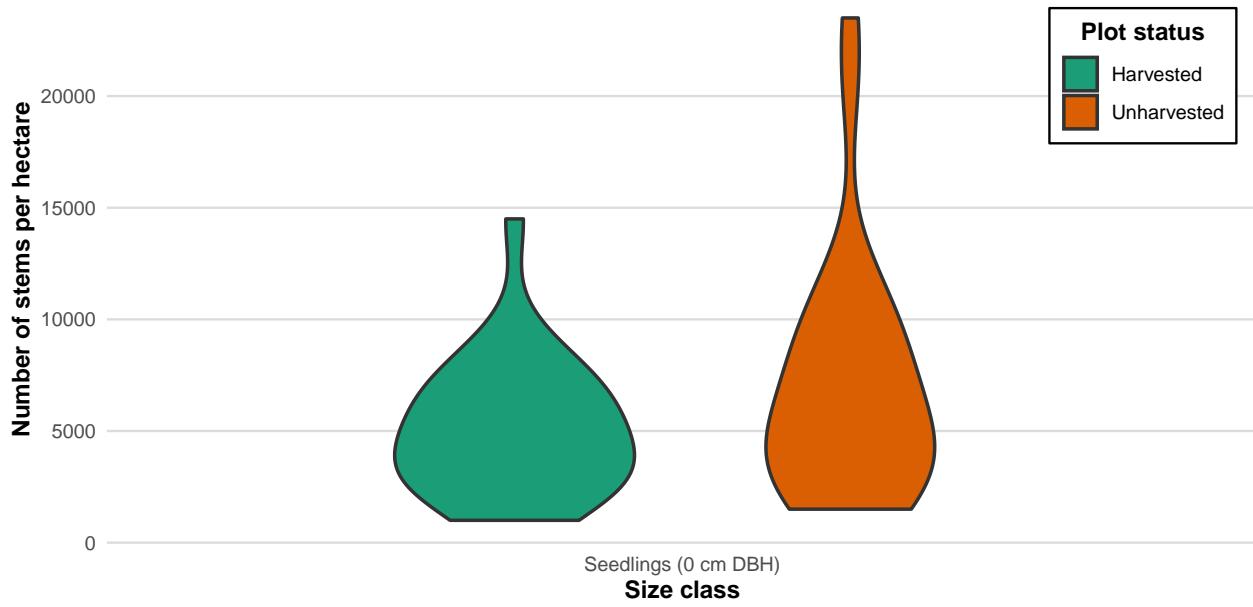
```

Violin plots

```
# All size classes except seedlings
stemden_dist_data_noseedlings %>%
  ggplot() +
  geom_violin(aes(x = size_class, y = num_stems,
                  fill = fct_relevel(harvested, "Harvested", "Unharvested")),
              scale = "area", width = 2, position = position_dodge(width = 0.7),
              lwd = 0.75, kernel = "gaussian", adjust = 1.25) +
  plot_theme +
  scale_fill_brewer(palette = "Dark2") +
  coord_cartesian(ylim = c(0, 1500)) + # 2 outliers not shown
  labs(x = "Size class", y = "Number of stems per hectare") +
  guides(fill = guide_legend(title = "Plot status"))
```

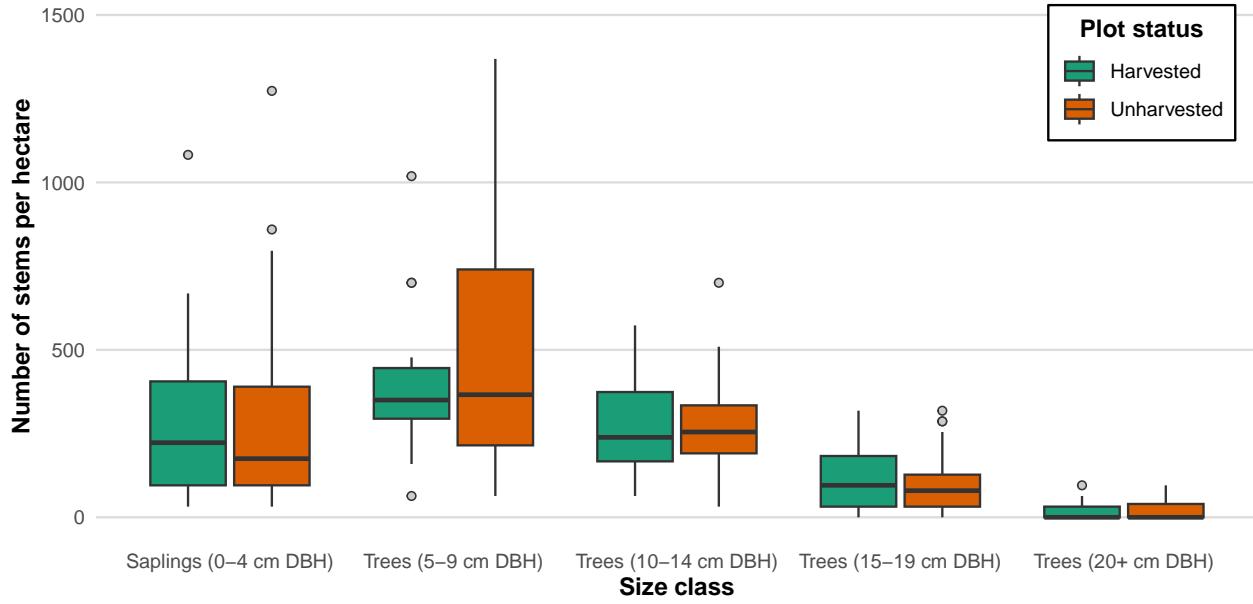


```
# Seedlings only
stemden_dist_data_seedlings %>%
  ggplot() +
  geom_violin(aes(x = size_class, y = num_stems,
                  fill = fct_relevel(harvested, "Harvested", "Unharvested")),
              scale = "area", width = 0.5, position = position_dodge(width = 0.7),
              lwd = 0.75, kernel = "gaussian", adjust = 1.25) +
  plot_theme +
  scale_fill_brewer(palette = "Dark2") +
  labs(x = "Size class", y = "Number of stems per hectare") +
  guides(fill=guide_legend(title = "Plot status"))
```

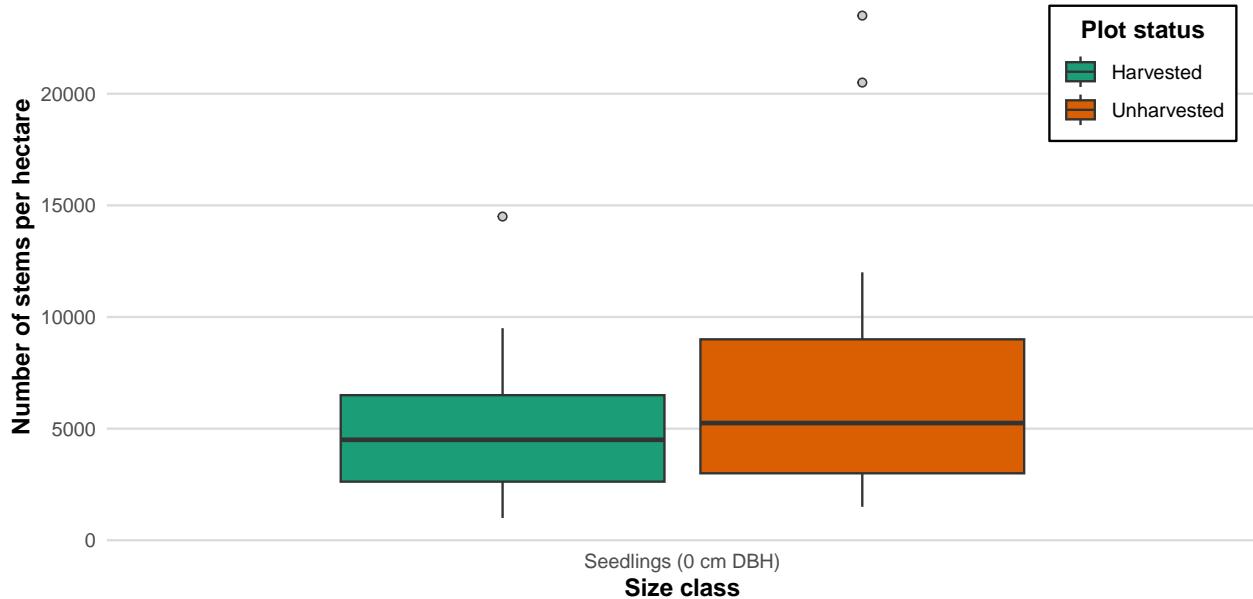


Box plots

```
# All size classes except seedlings
stemden_sizeclass_fig3_noseedlings <- stemden_dist_data_noseedlings %>%
  ggplot() +
  geom_boxplot(aes(x = size_class, y = num_stems,
                    fill = fct_relevel(harvested, "Harvested", "Unharvested")),
                outlier.shape = 21, outlier.color = "gray20",
                outlier.fill = "gray80") +
  plot_theme +
  scale_fill_brewer(palette = "Dark2") +
  coord_cartesian(ylim = c(0, 1500)) + # 2 outliers not shown
  labs(x = "Size class", y = "Number of stems per hectare") +
  guides(fill = guide_legend(title = "Plot status"))
ggsave("figures/stemden_sizeclass_fig3_noseedlings.png", height = 4, width = 8)
stemden_sizeclass_fig3_noseedlings
```



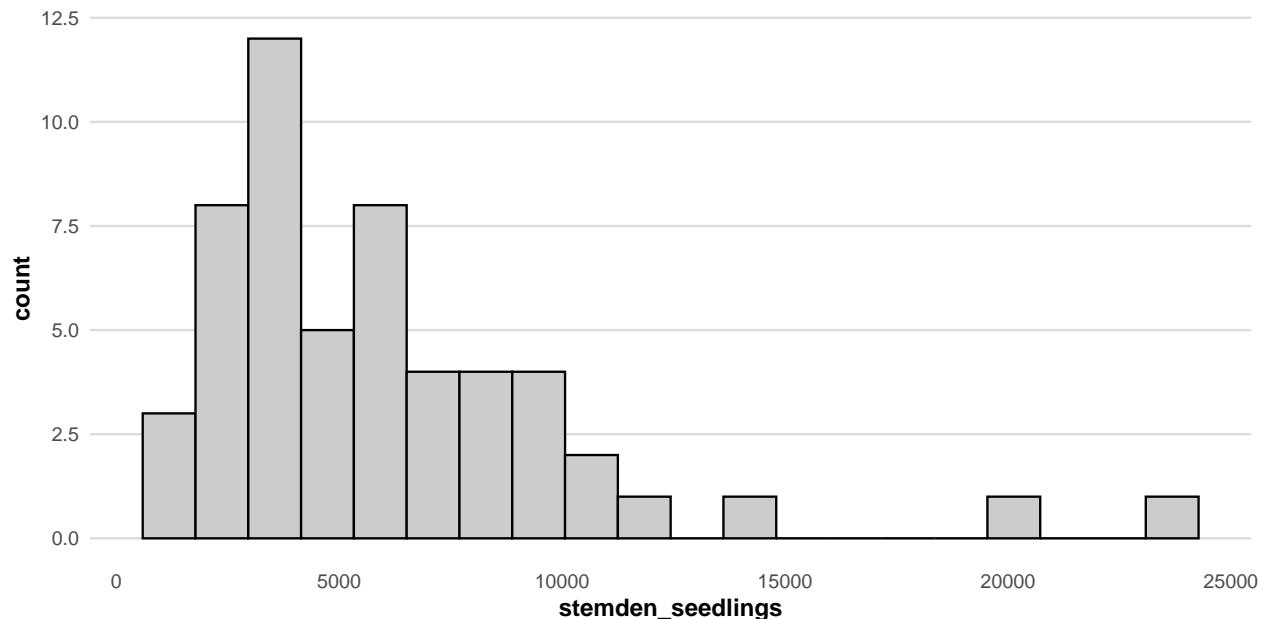
```
# Seedlings only
stemden_sizeclass_fig3_seedlings <- stemden_dist_data_seedlings %>%
  ggplot() +
  geom_boxplot(aes(x = size_class, y = num_stems,
                  fill = fct_relevel(harvested, "Harvested", "Unharvested")),
               outlier.shape = 21, outlier.color = "gray20",
               outlier.fill = "gray80") +
  plot_theme +
  scale_fill_brewer(palette = "Dark2") +
  labs(x = "Size class", y = "Number of stems per hectare") +
  guides(fill = guide_legend(title = "Plot status"))
ggsave("figures/stemden_sizeclass_fig3_seedlings.png", height = 4, width = 8)
stemden_sizeclass_fig3_seedlings
```



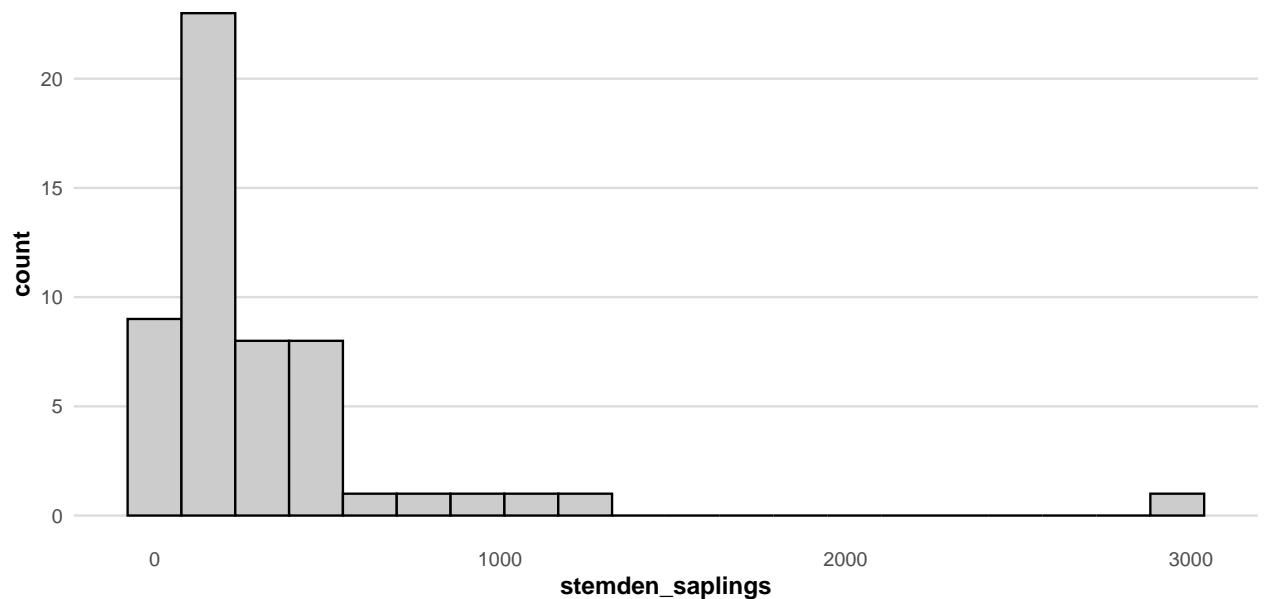
Stem density by size class for different covariates

Histograms, harvesting status

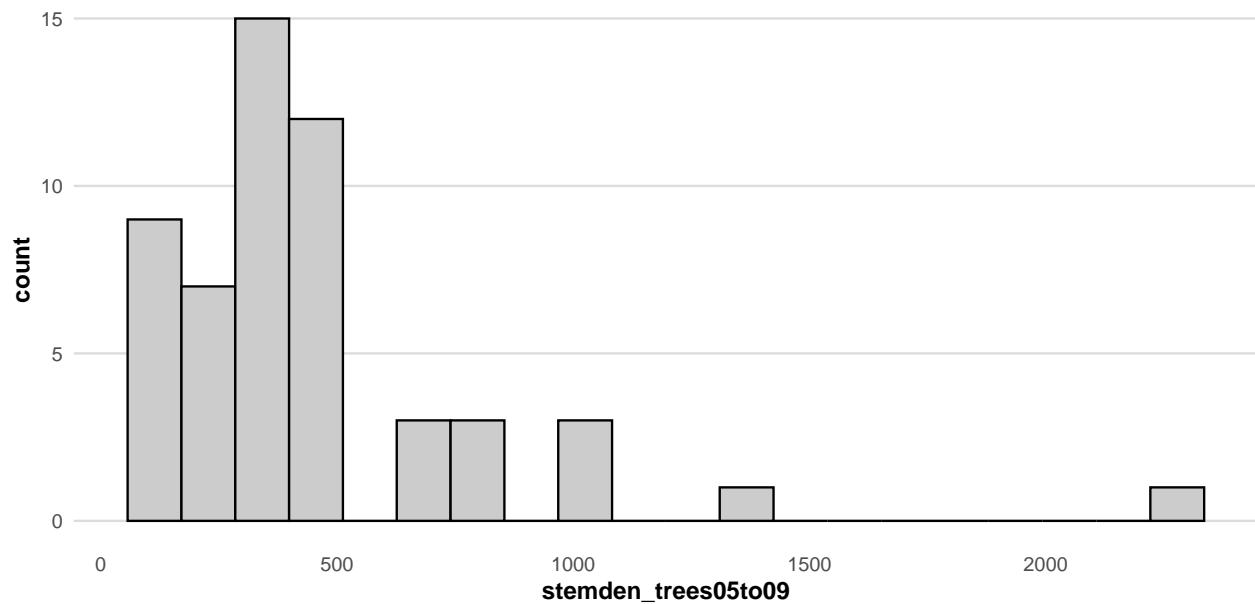
```
data_plots %>%
  ggplot() + geom_histogram(aes(x = stemden_seedlings), bins = 20,
                            col = "black", fill = "gray80") + plot_theme
```



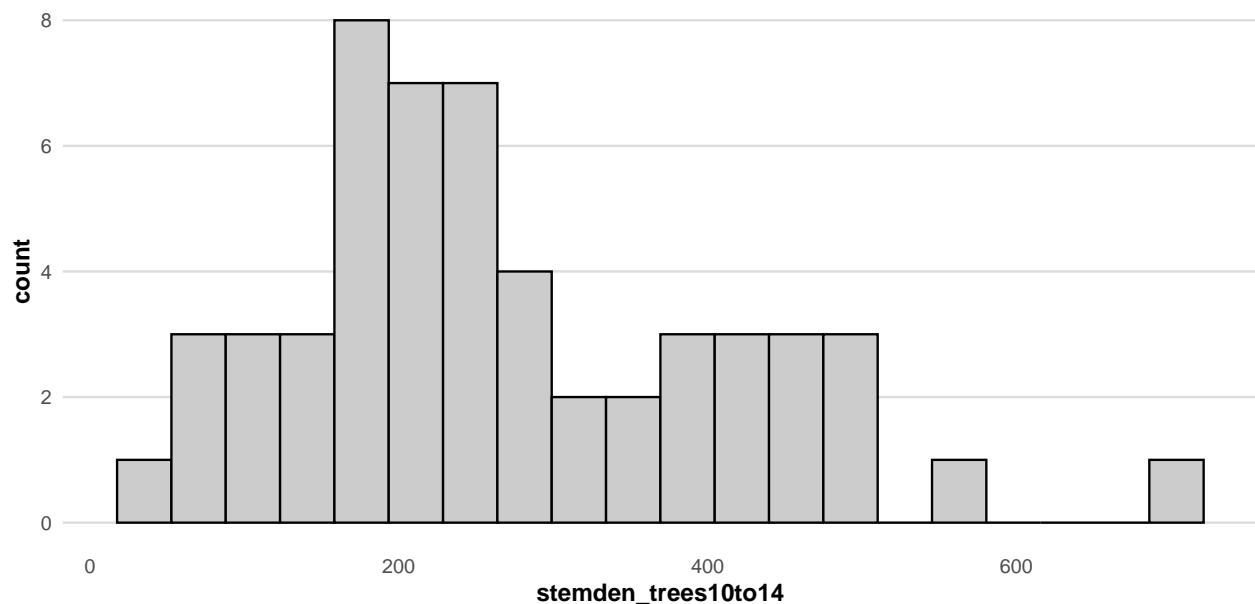
```
data_plots %>%
  ggplot() + geom_histogram(aes(x = stemden_saplings), bins = 20,
                            col = "black", fill = "gray80") + plot_theme
```



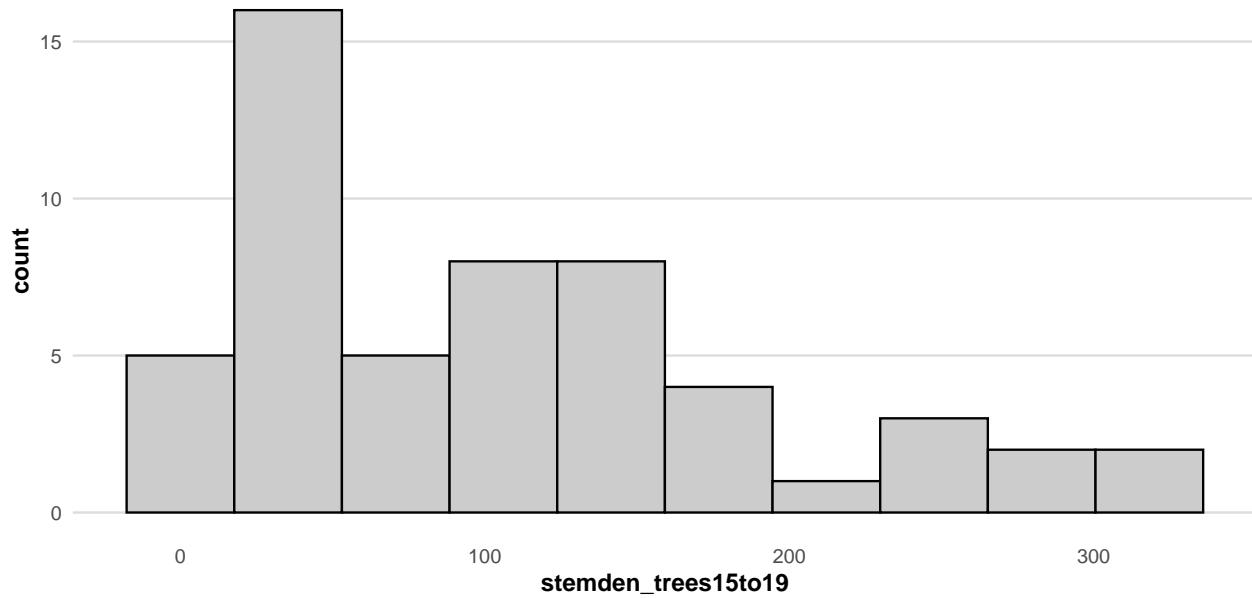
```
data_plots %>%
  ggplot() + geom_histogram(aes(x = stemden_trees05to09), bins = 20,
                            col = "black", fill = "gray80") + plot_theme
```



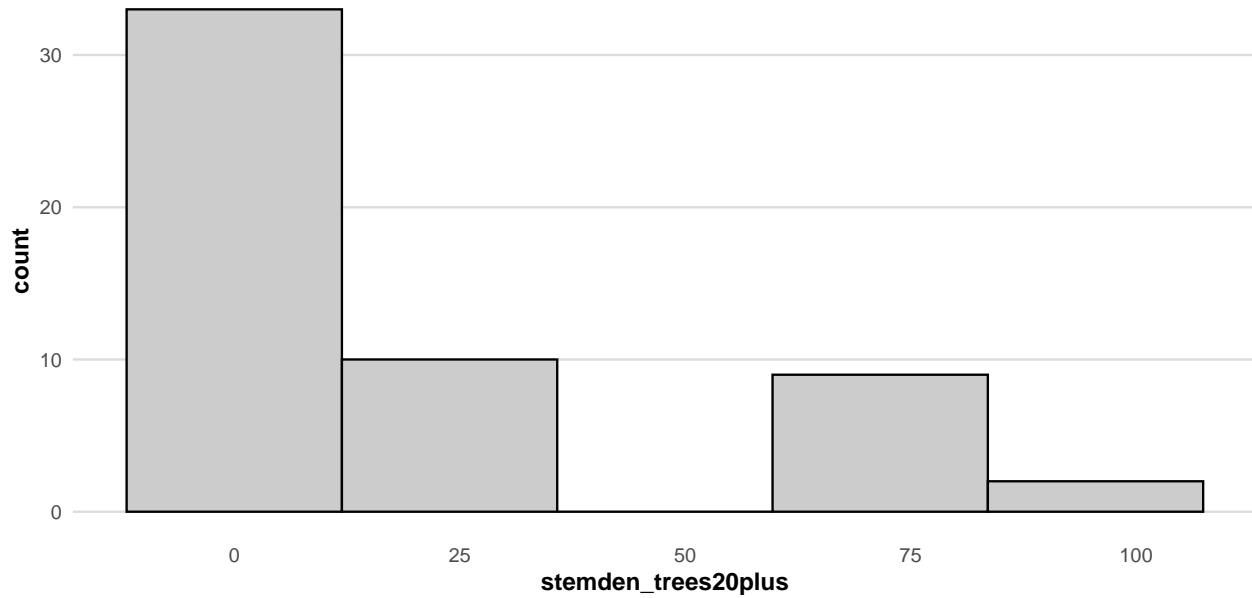
```
data_plots %>%
  ggplot() + geom_histogram(aes(x = stemden_trees10to14), bins = 20,
                            col = "black", fill = "gray80") + plot_theme
```



```
data_plots %>%
  ggplot() + geom_histogram(aes(x = stemden_trees15to19), bins = 10,
                            col = "black", fill = "gray80") + plot_theme
```



```
data_plots %>%
  ggplot() + geom_histogram(aes(x = stemden_trees20plus), bins = 5,
                            col = "black", fill = "gray80") + plot_theme
```



Five-number summaries, harvesting status

```
summary(data_plots$stemden_seedlings)
```

```
##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.
## 1000    3000    4750   6028    7875  23500
```

```
data_plots %>% filter(harvested == "yes") %>% pull(stemden_seedlings) %>% summary()
```

```
##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.  
##   1000    2625    4500    5096    6500  14500
```

```
data_plots %>% filter(harvested == "no") %>% pull(stemden_seedlings) %>% summary()
```

```
##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.  
##   1500    3000    5250    6893    9000  23500
```

```
summary(data_plots$stemden_saplings)
```

```
##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.  
##   31.83   95.49  190.99  332.46  405.85 2992.11
```

```
data_plots %>% filter(harvested == "yes") %>% pull(stemden_saplings) %>% summary()
```

```
##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.  
##   31.83   95.49  222.82  282.81  405.85 1082.25
```

```
data_plots %>% filter(harvested == "no") %>% pull(stemden_saplings) %>% summary()
```

```
##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.  
##   31.83   95.49  175.07  378.56  389.93 2992.11
```

```
summary(data_plots$stemden_trees05to09)
```

```
##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.  
##   63.66  254.65  350.14  453.89  501.34 2228.17
```

```
data_plots %>% filter(harvested == "yes") %>% pull(stemden_trees05to09) %>% summary()
```

```
##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.  
##   63.66  294.44  350.14  379.52  445.63 1018.59
```

```
data_plots %>% filter(harvested == "no") %>% pull(stemden_trees05to09) %>% summary()
```

```
##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.  
##   63.66  214.86  366.06  522.94  740.07 2228.17
```

```
summary(data_plots$stemden_trees10to14)
```

```
##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.  
##   31.83  190.99  254.65  271.15  374.01  700.28
```

```

data_plots %>% filter(harvested == "yes") %>% pull(stemden_trees10to14) %>% summary()

##      Min. 1st Qu. Median     Mean 3rd Qu.    Max.
##    63.66 167.11 238.73 269.34 374.01 572.96

data_plots %>% filter(harvested == "no") %>% pull(stemden_trees10to14) %>% summary()

##      Min. 1st Qu. Median     Mean 3rd Qu.    Max.
##    31.83 190.99 254.65 272.84 334.23 700.28

summary(data_plots$stemden_trees15to19)

##      Min. 1st Qu. Median     Mean 3rd Qu.    Max.
##    0.00  31.83  95.49 103.75 127.32 318.31

data_plots %>% filter(harvested == "yes") %>% pull(stemden_trees15to19) %>% summary()

##      Min. 1st Qu. Median     Mean 3rd Qu.    Max.
##    0.00  31.83  95.49 110.18 183.03 318.31

data_plots %>% filter(harvested == "no") %>% pull(stemden_trees15to19) %>% summary()

##      Min. 1st Qu. Median     Mean 3rd Qu.    Max.
##    0.00  31.83  79.58  97.77 127.32 318.31

summary(data_plots$stemden_trees20plus)

##      Min. 1st Qu. Median     Mean 3rd Qu.    Max.
##    0.00  0.00   0.00   20.04 31.83  95.49

data_plots %>% filter(harvested == "yes") %>% pull(stemden_trees20plus) %>% summary()

##      Min. 1st Qu. Median     Mean 3rd Qu.    Max.
##    0.00  0.00   0.00   19.59 31.83  95.49

data_plots %>% filter(harvested == "no") %>% pull(stemden_trees20plus) %>% summary()

##      Min. 1st Qu. Median     Mean 3rd Qu.    Max.
##    0.00  0.00   0.00   20.46 39.79  95.49

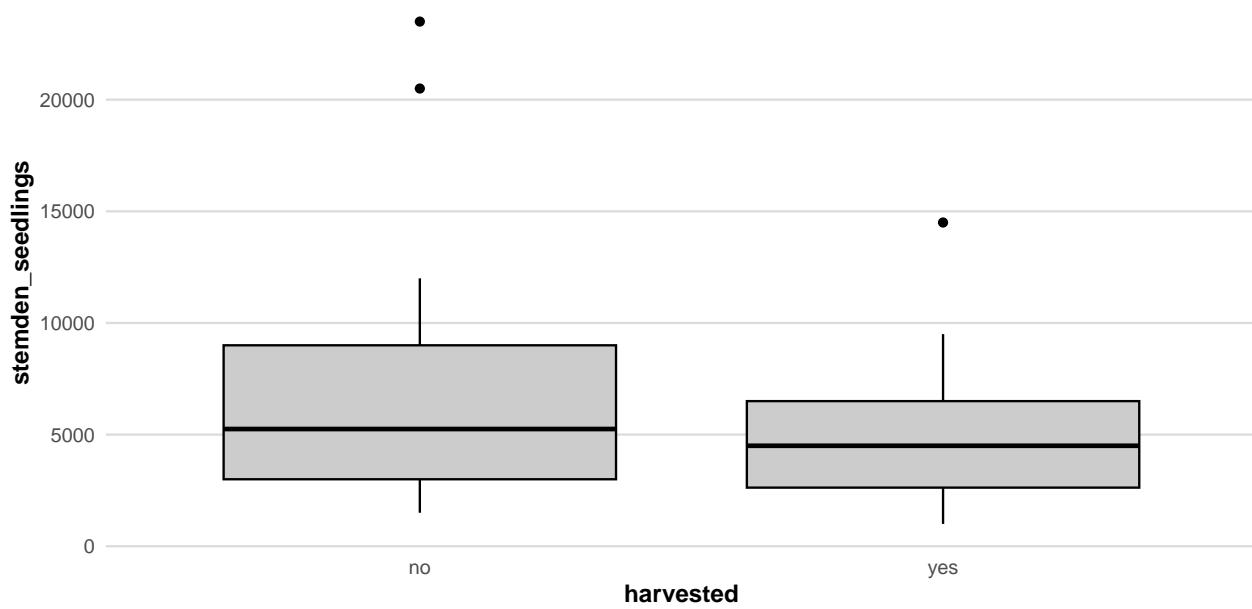
```

Box plots, harvesting status

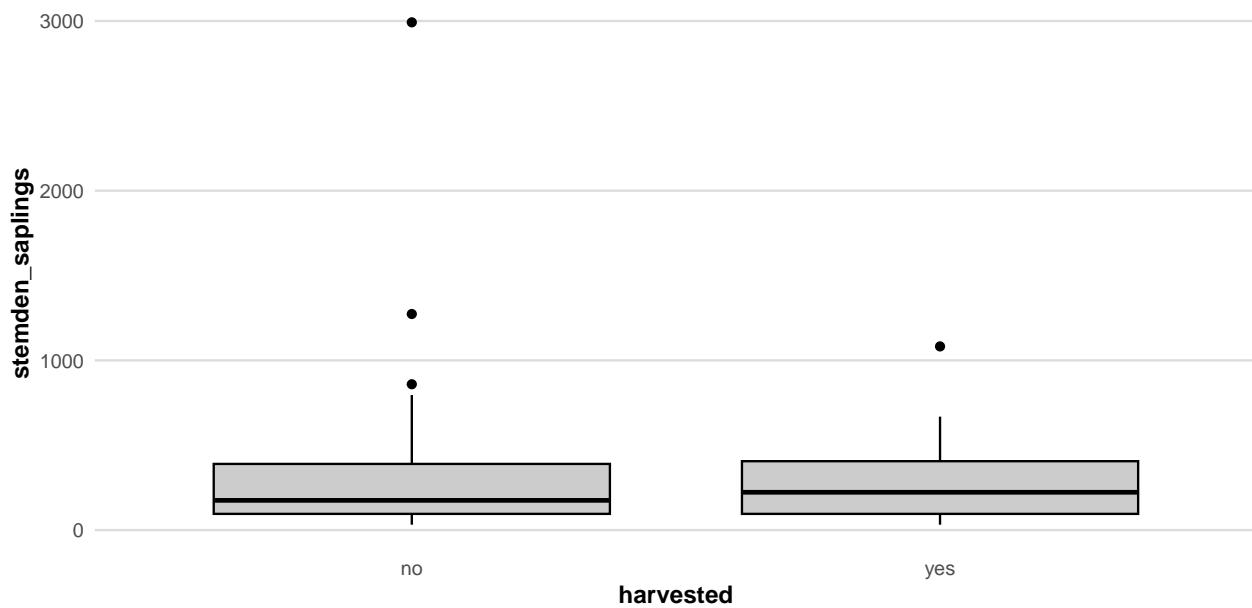
```

data_plots %>% ggplot() +
  geom_boxplot(aes(x = harvested, y = stemden_seedlings),
               col = "black", fill = "gray80") + plot_theme

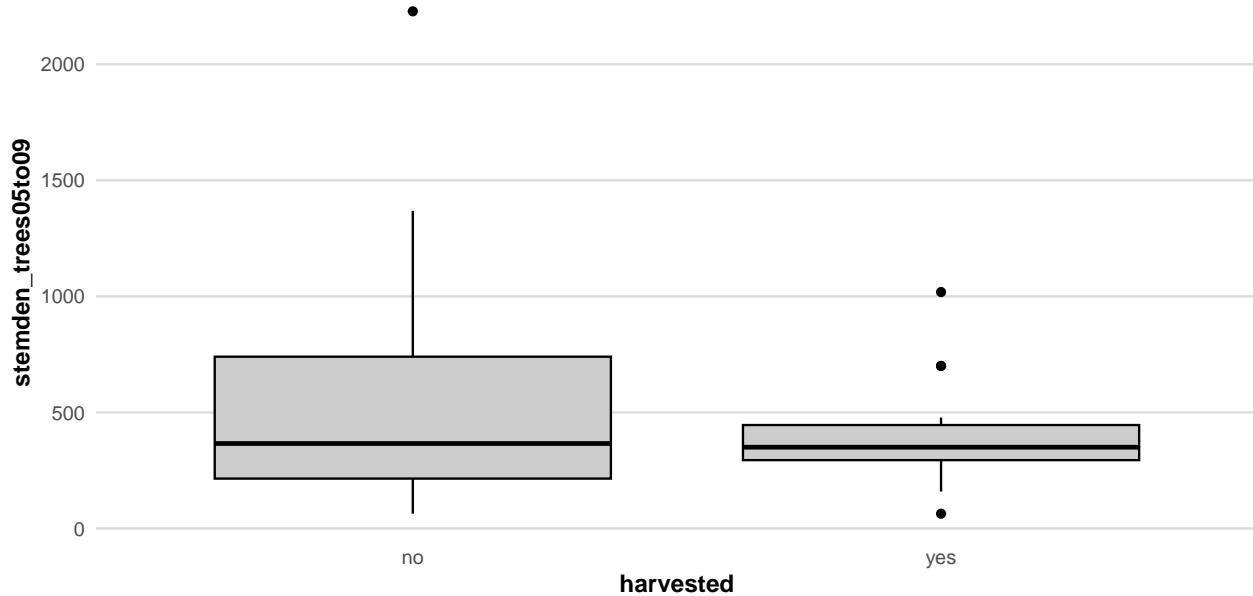
```



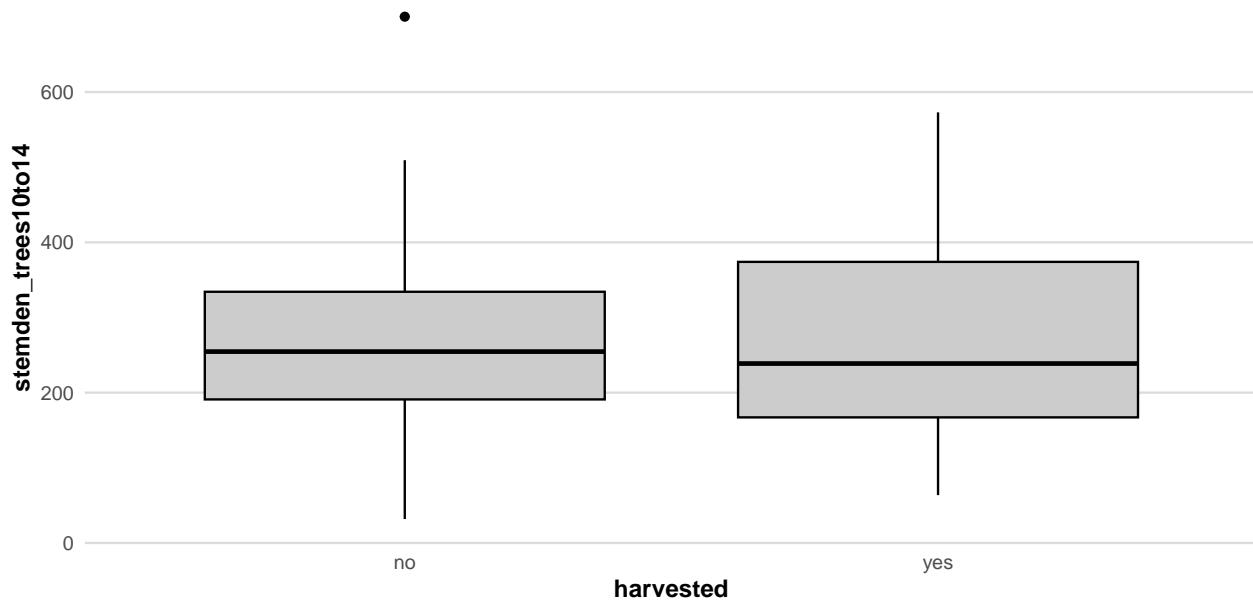
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = harvested, y = stemden_seedlings),
               col = "black", fill = "gray80") + plot_theme
```



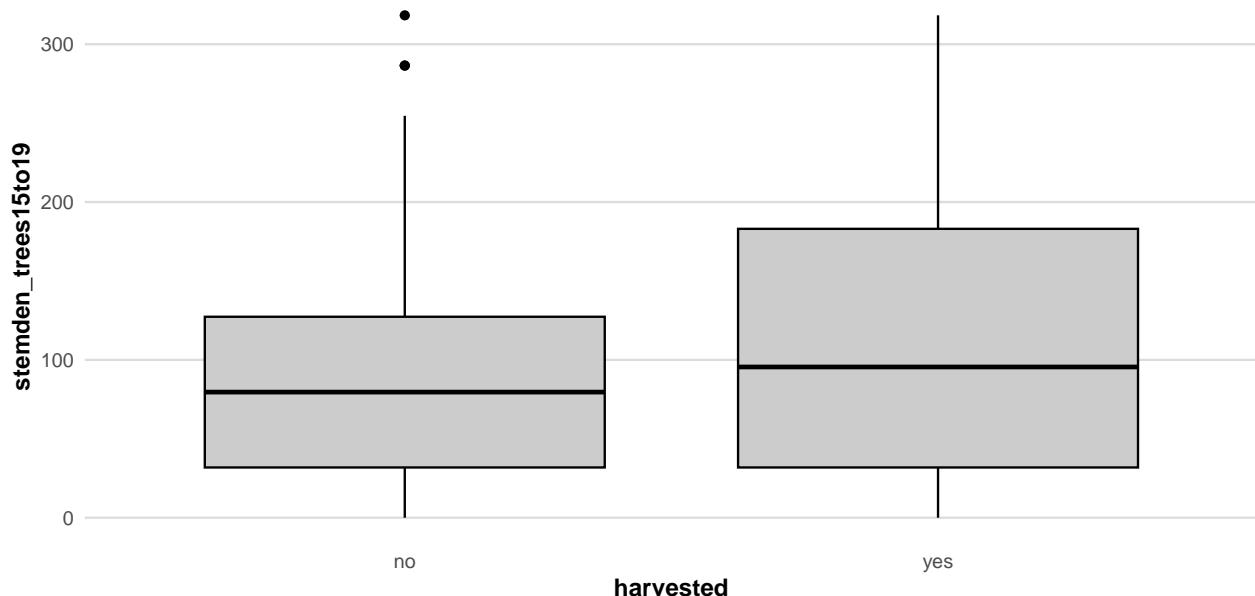
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = harvested, y = stemden_trees05to09),
               col = "black", fill = "gray80") + plot_theme
```



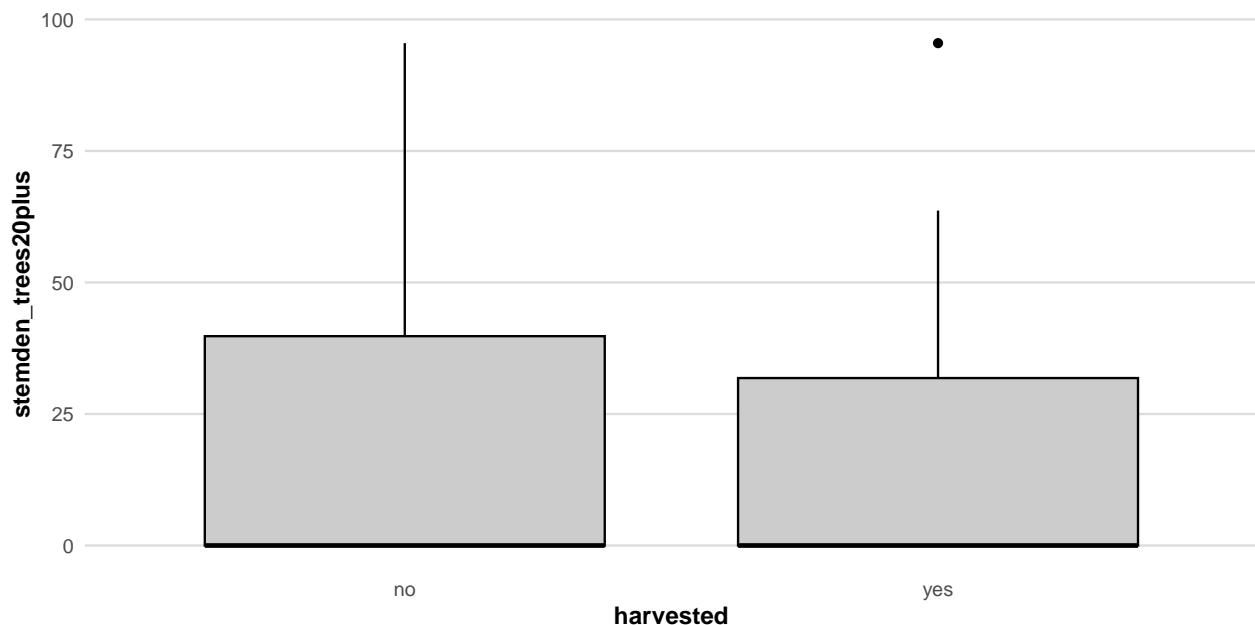
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = harvested, y = stemden_trees10to14),
               col = "black", fill = "gray80") + plot_theme
```



```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = harvested, y = stemden_trees15to19),
               col = "black", fill = "gray80") + plot_theme
```

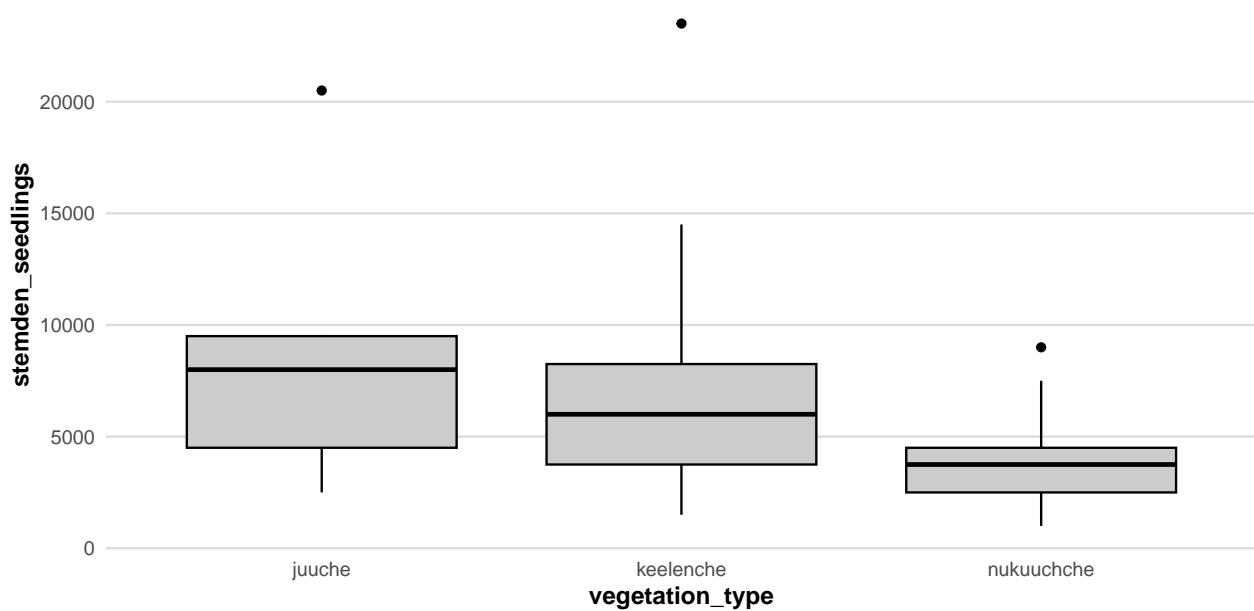


```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = harvested, y = stemden_trees20plus),
               col = "black", fill = "gray80") + plot_theme
```

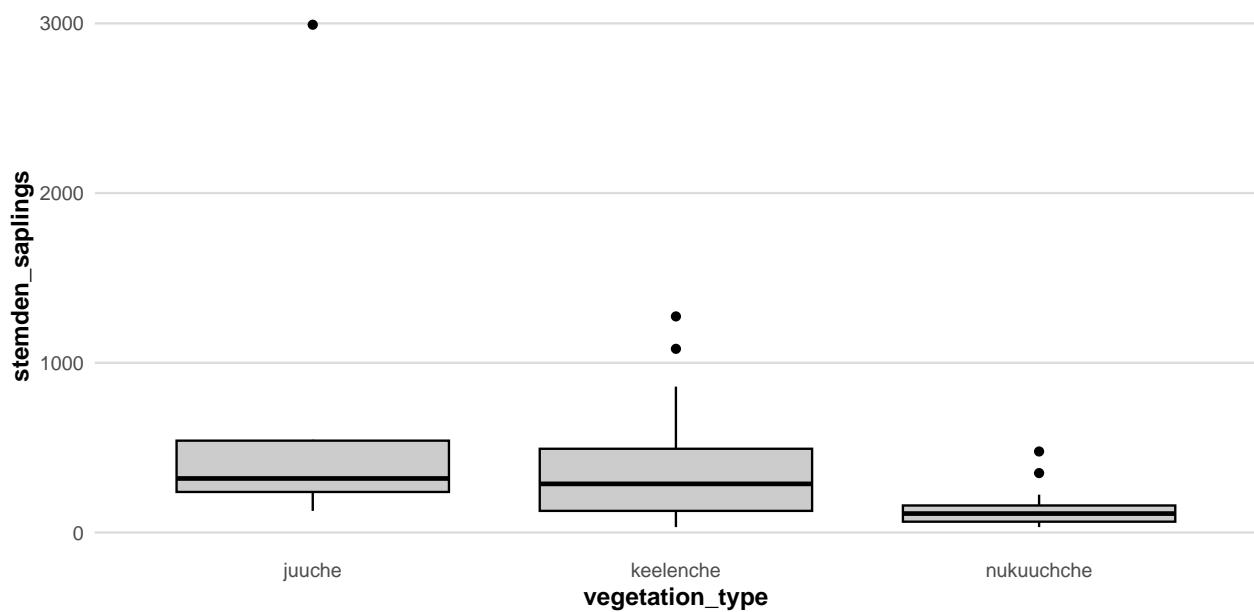


Box plots, vegetation type

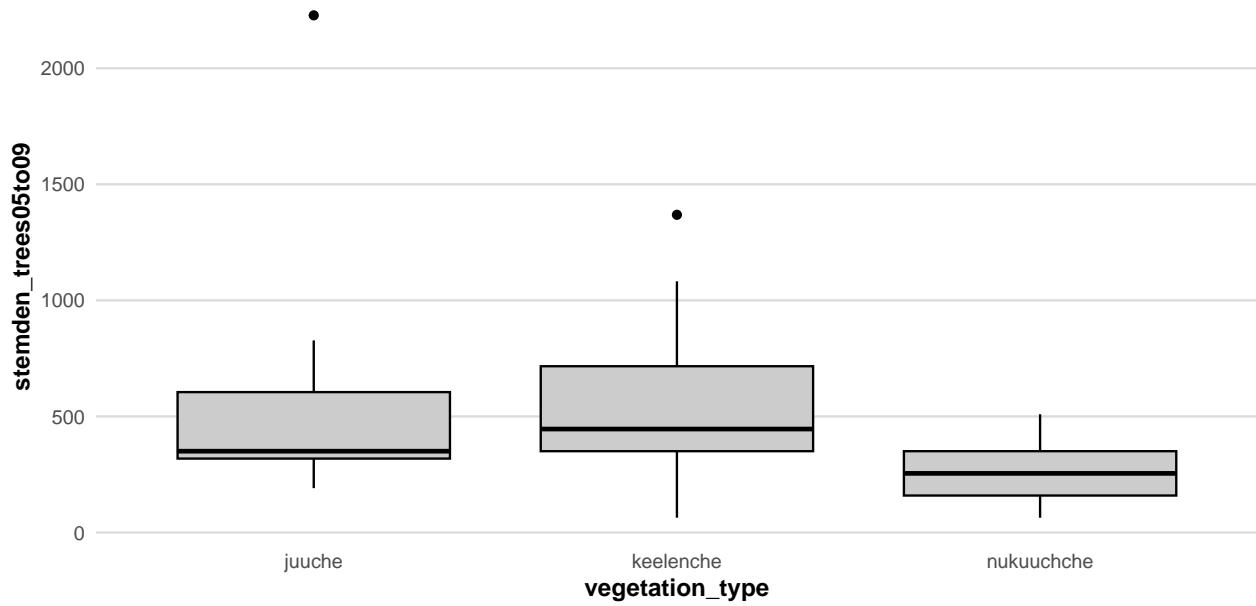
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = vegetation_type, y = stemden_seedlings),
               col = "black", fill = "gray80") + plot_theme
```



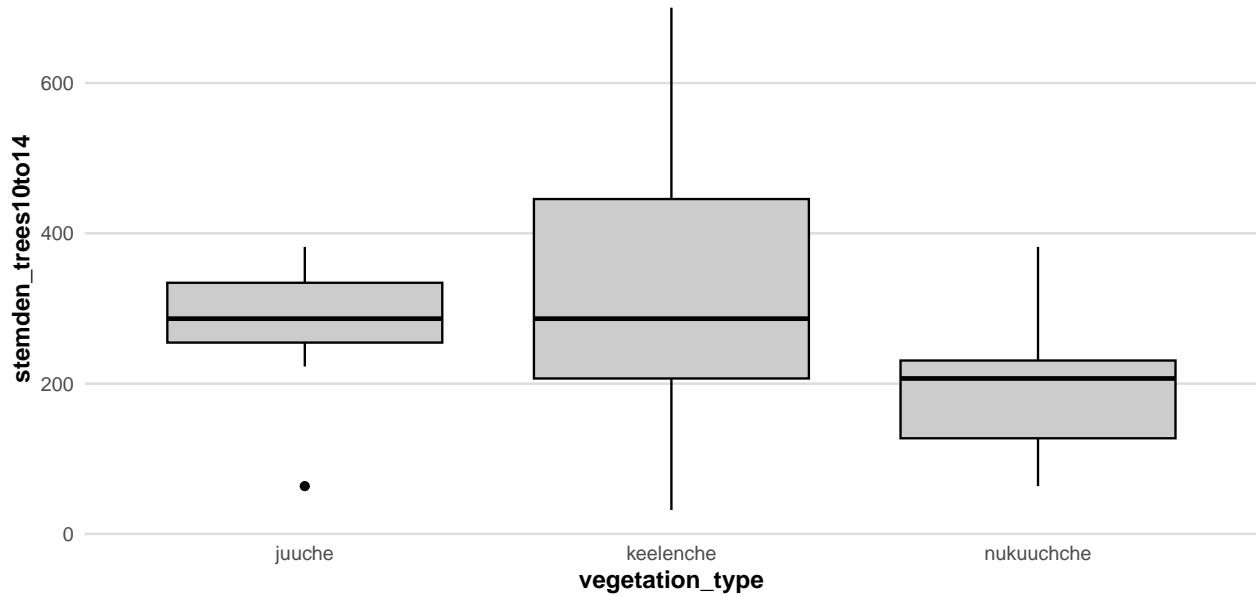
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = vegetation_type, y = stemden_saplings),
               col = "black", fill = "gray80") + plot_theme
```



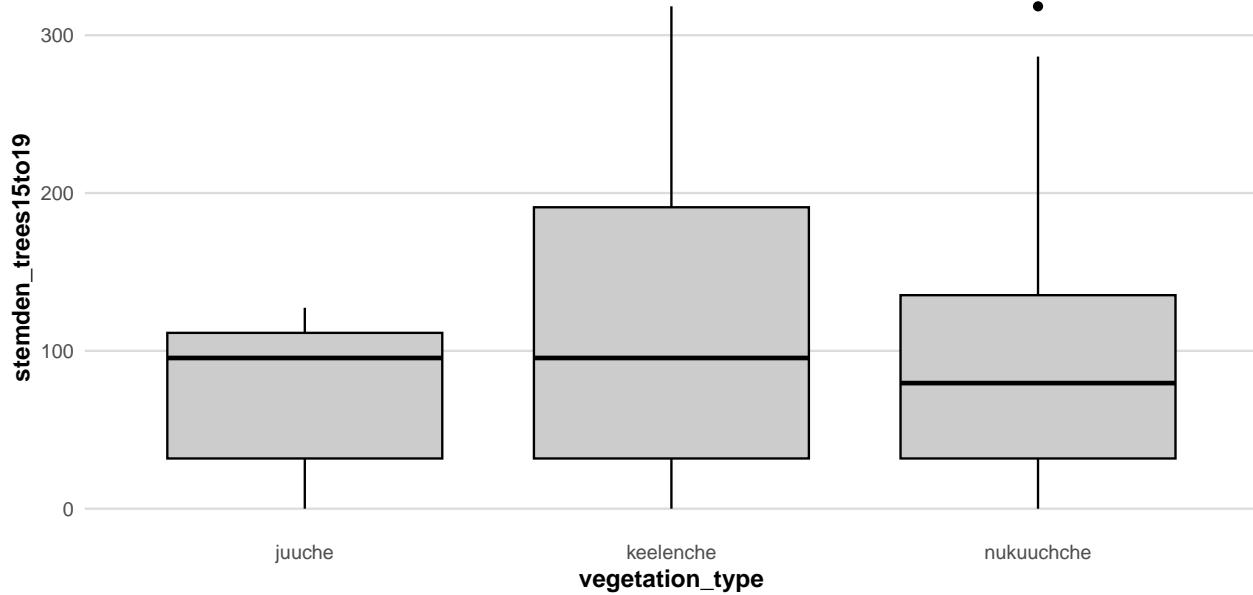
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = vegetation_type, y = stemden_trees05to09),
               col = "black", fill = "gray80") + plot_theme
```



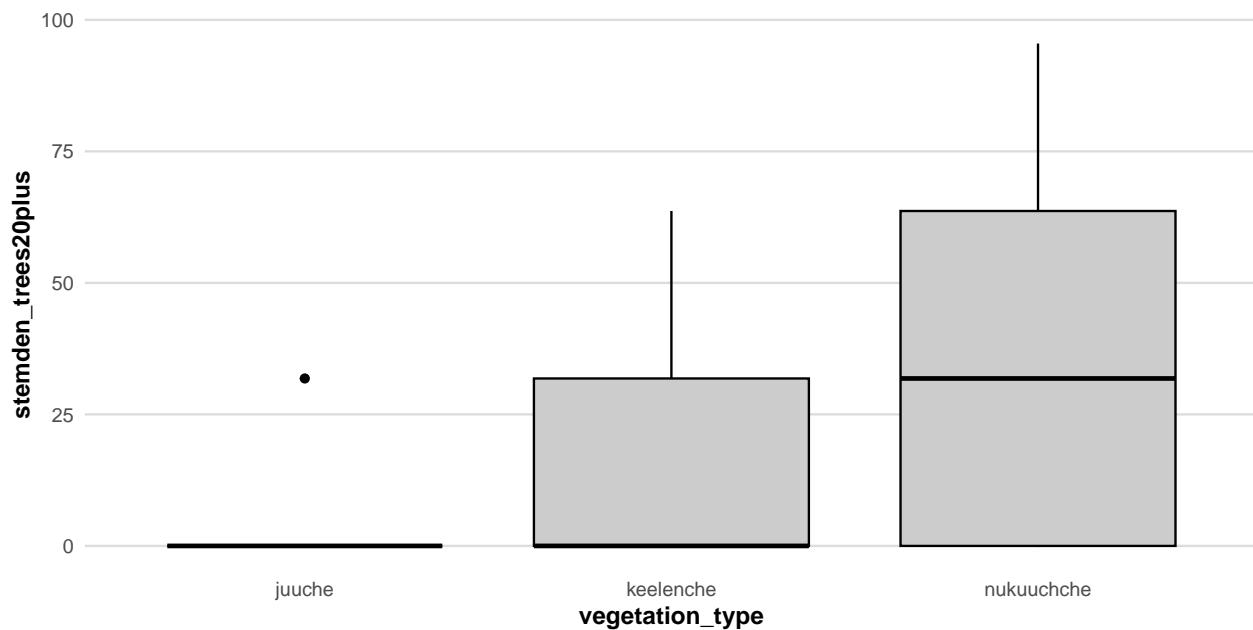
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = vegetation_type, y = stemden_trees10to14),
               col = "black", fill = "gray80") + plot_theme
```



```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = vegetation_type, y = stemden_trees15to19),
               col = "black", fill = "gray80") + plot_theme
```

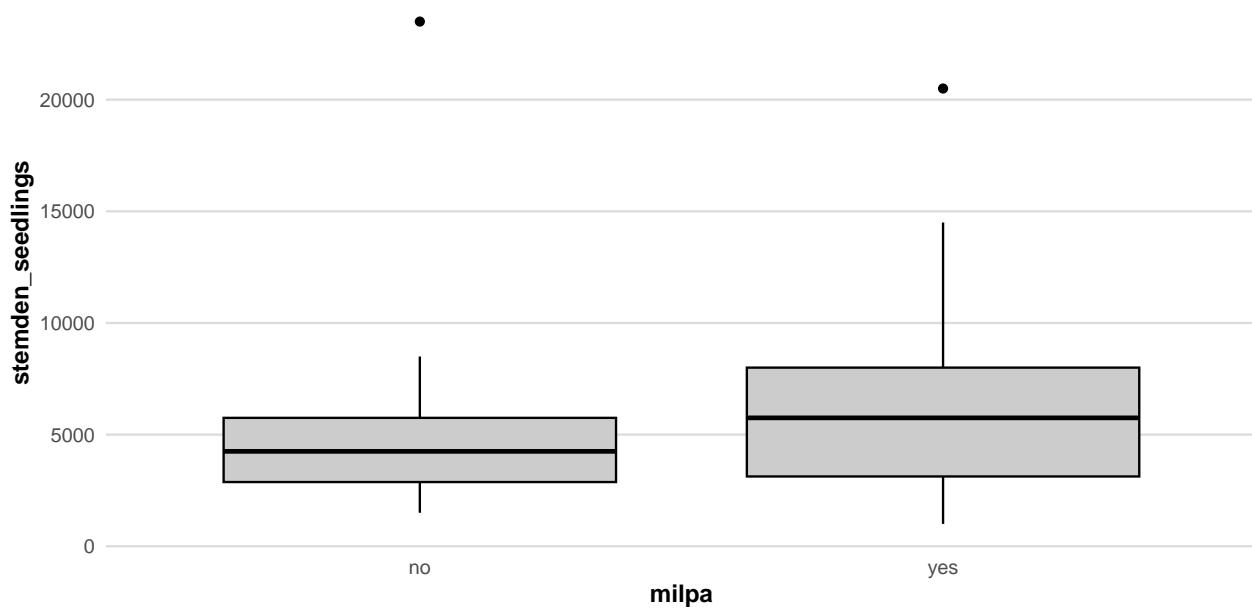


```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = vegetation_type, y = stemden_trees20plus),
               col = "black", fill = "gray80") + plot_theme
```

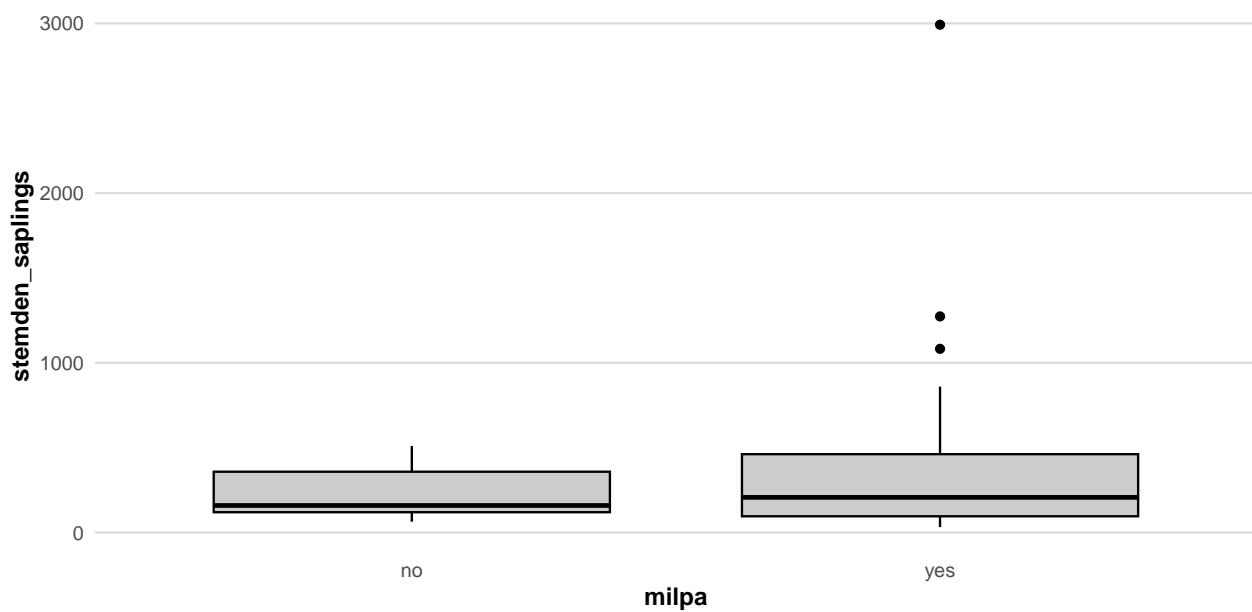


Box plots, milpa exposure

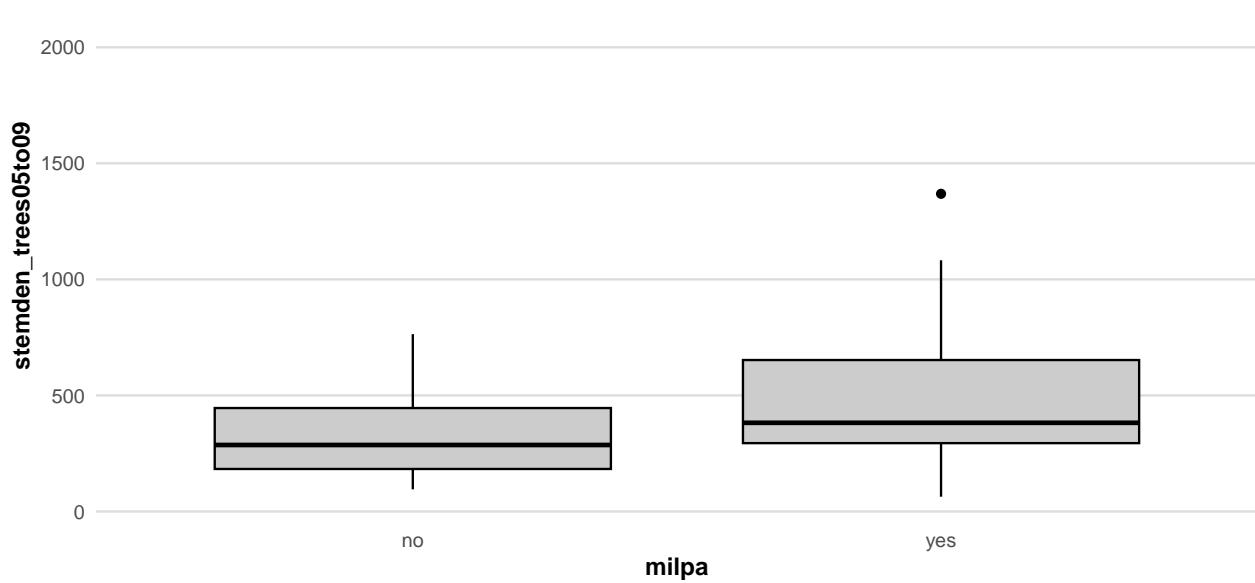
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = milpa, y = stemden_seedlings),
               col = "black", fill = "gray80") + plot_theme
```



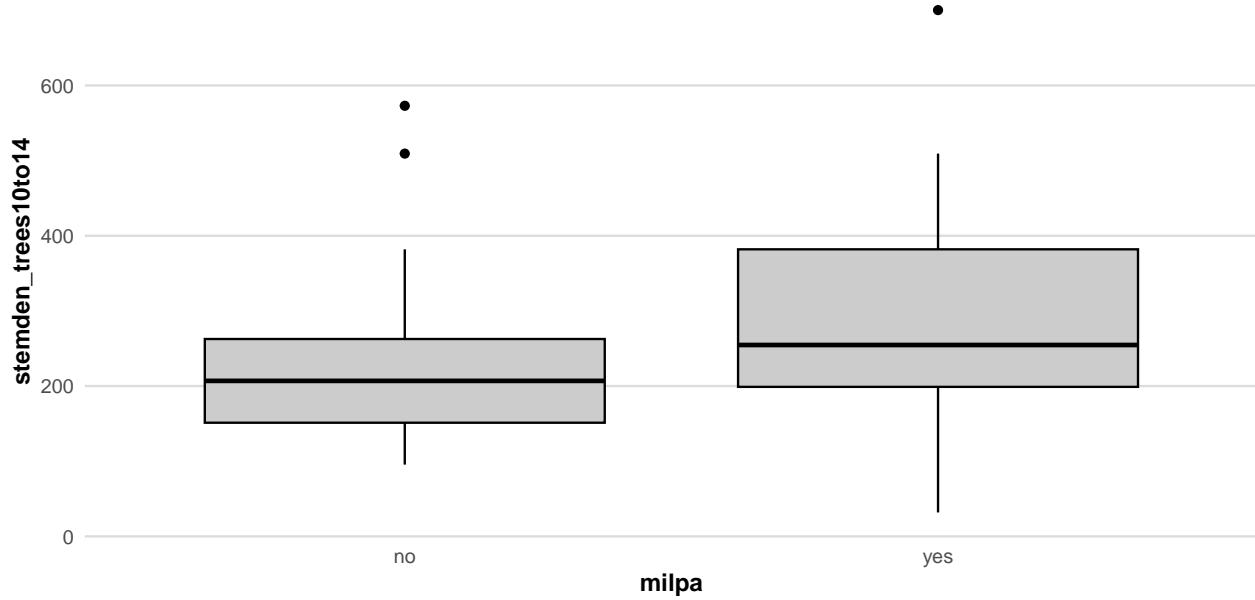
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = milpa, y = stemden_saplings),
               col = "black", fill = "gray80") + plot_theme
```



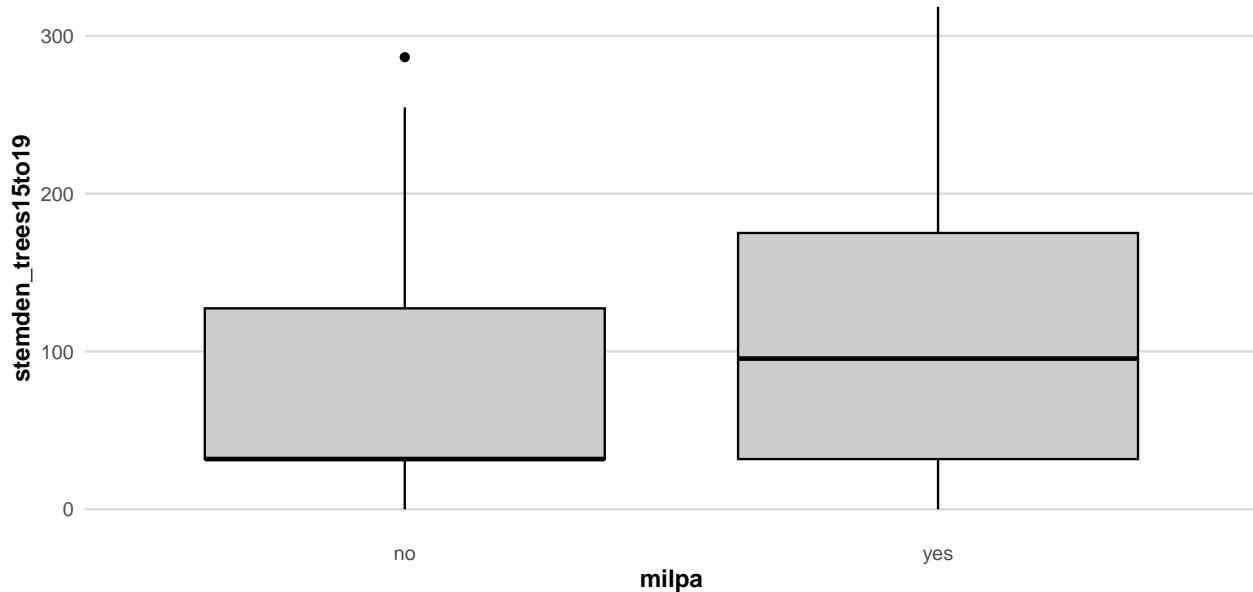
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = milpa, y = stemden_trees05to09),
               col = "black", fill = "gray80") + plot_theme
```



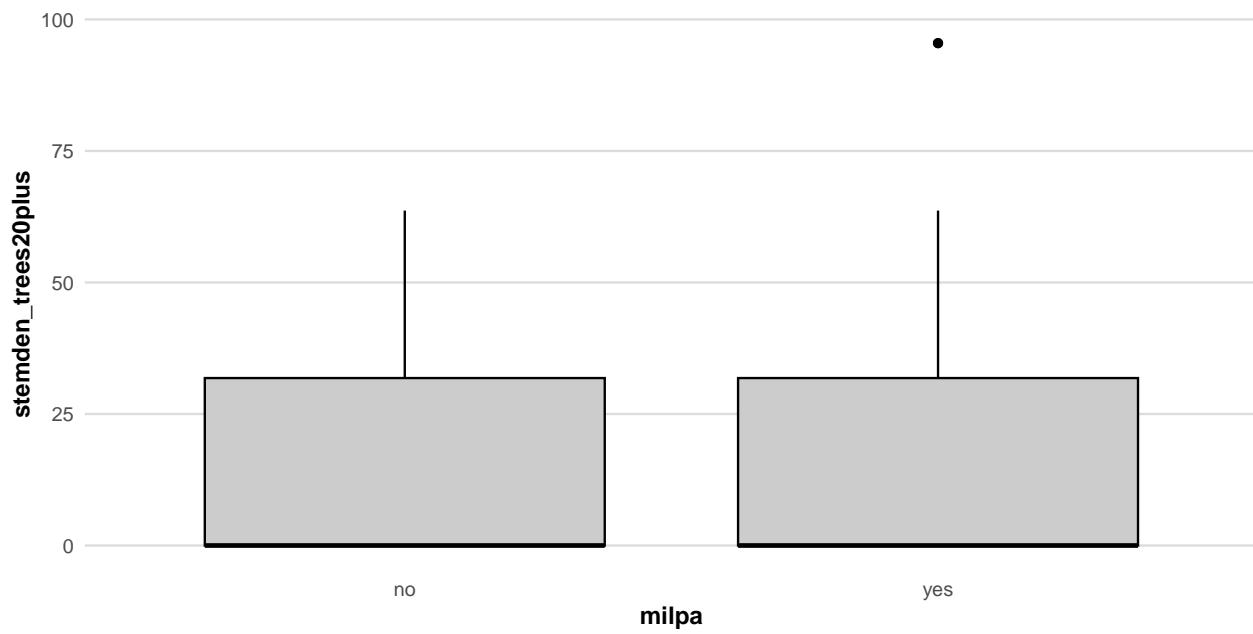
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = milpa, y = stemden_trees05to09),
               col = "black", fill = "gray80") + plot_theme
```



```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = milpa, y = stemden_trees10to14),
               col = "black", fill = "gray80") + plot_theme
```

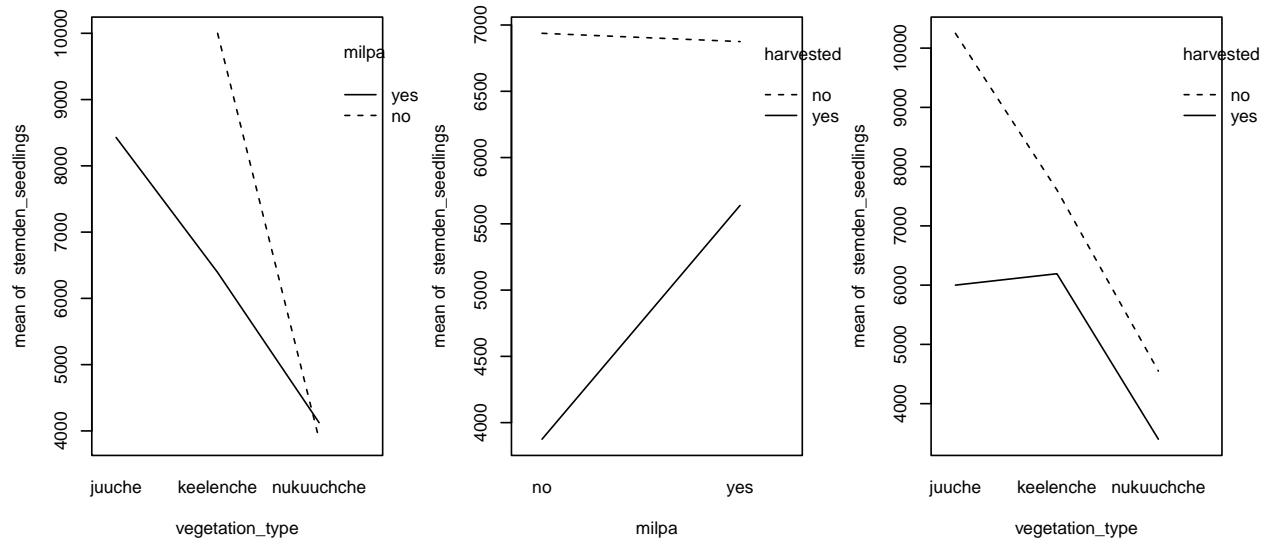


```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = milpa, y = stemden_trees20plus),
               col = "black", fill = "gray80") + plot_theme
```

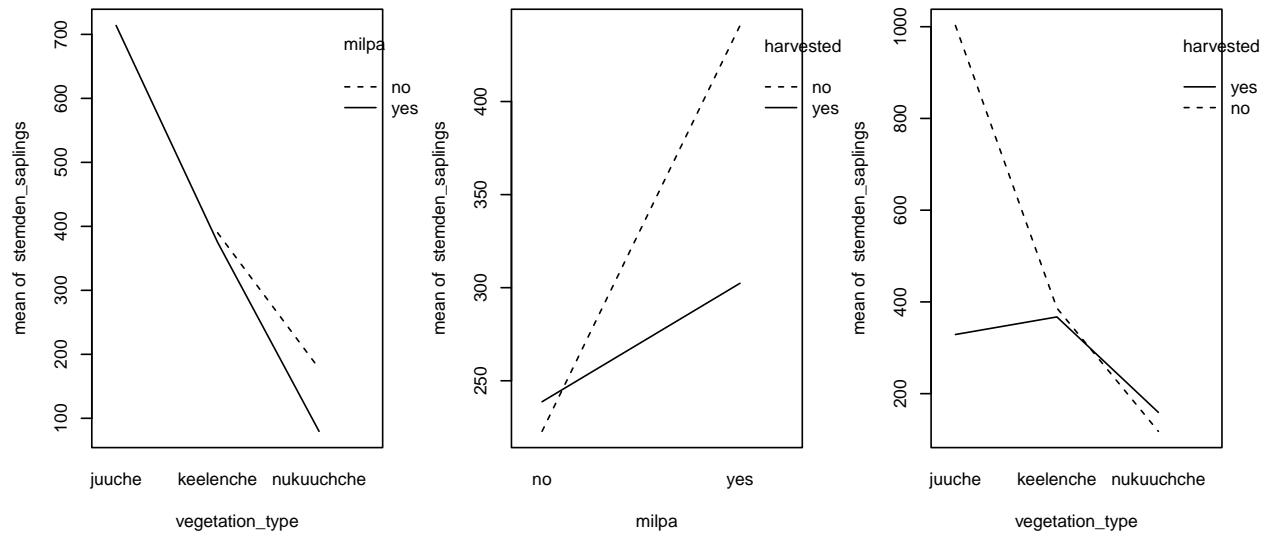


Interaction plots

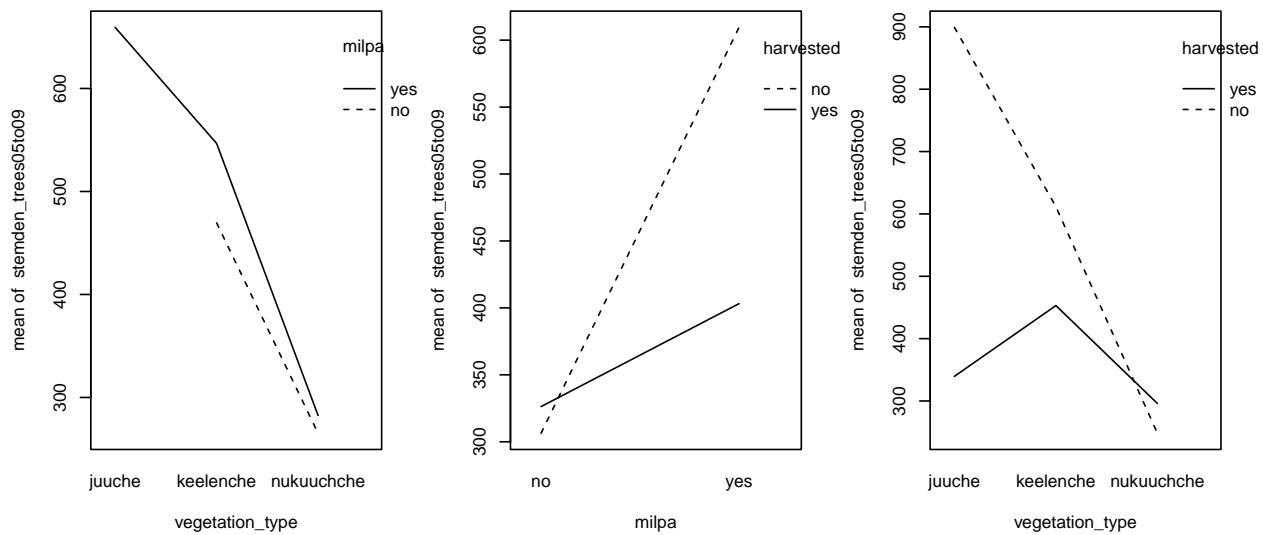
```
par(mfrow = c(1,3))
with(data_plots, {interaction.plot(vegetation_type, milpa, stemden_seedlings)
                 interaction.plot(milpa, harvested, stemden_seedlings)
                 interaction.plot(vegetation_type, harvested, stemden_seedlings)})
```



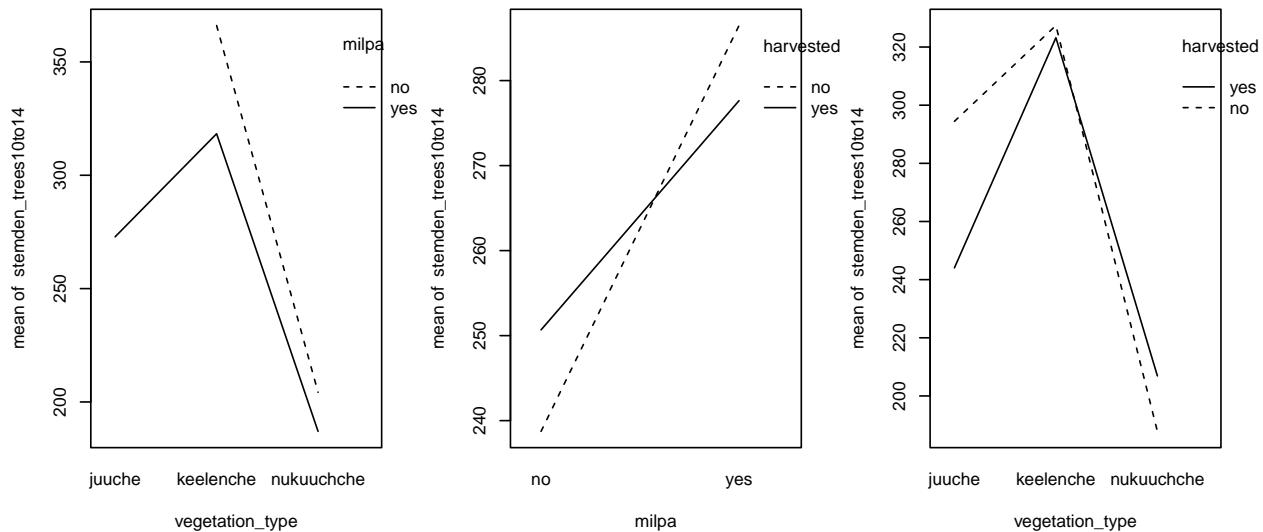
```
with(data_plots, {interaction.plot(vegetation_type, milpa, stemden_saplings)
                  interaction.plot(milpa, harvested, stemden_saplings)
                  interaction.plot(vegetation_type, harvested, stemden_saplings)})
```



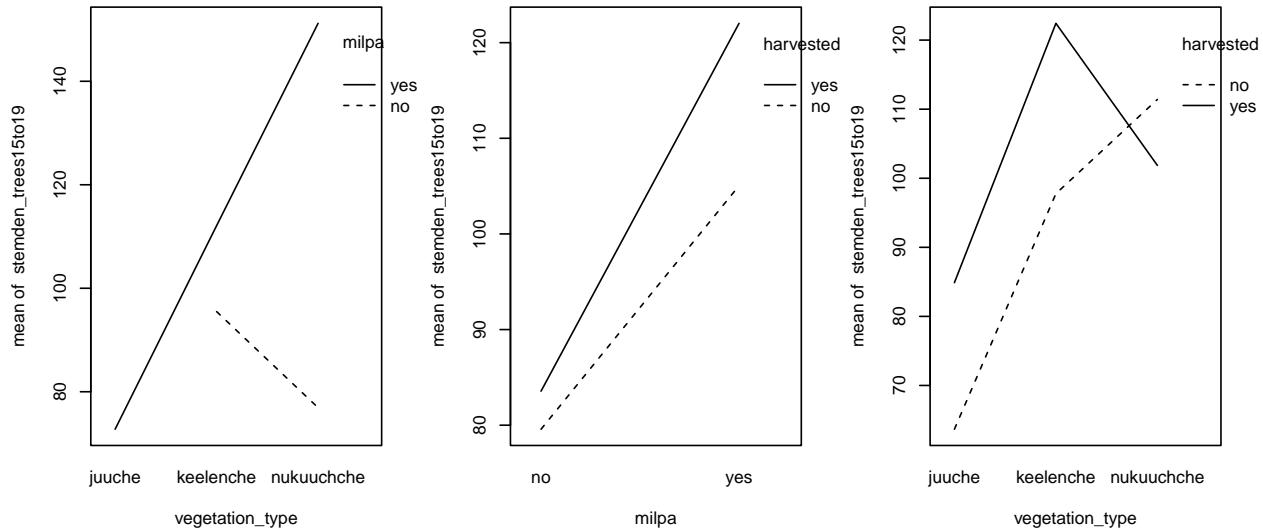
```
with(data_plots, {interaction.plot(vegetation_type, milpa, stemden_trees05to09)
                  interaction.plot(milpa, harvested, stemden_trees05to09)
                  interaction.plot(vegetation_type, harvested, stemden_trees05to09)})
```



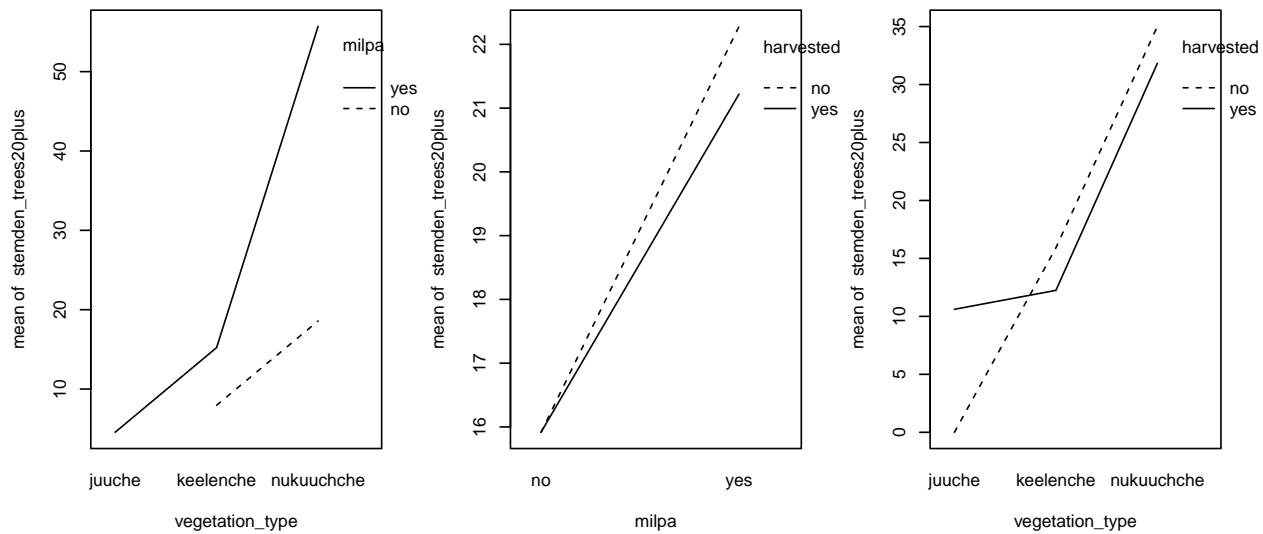
```
with(data_plots, {interaction.plot(vegetation_type, milpa, stemden_trees10to14)
                  interaction.plot(milpa, harvested, stemden_trees10to14)
                  interaction.plot(vegetation_type, harvested, stemden_trees10to14)})
```



```
with(data_plots, {interaction.plot(vegetation_type, milpa, stemden_trees15to19)
                  interaction.plot(milpa, harvested, stemden_trees15to19)
                  interaction.plot(vegetation_type, harvested, stemden_trees15to19)})
```



```
with(data_plots, {interaction.plot(vegetation_type, milpa, stemden_trees20plus)
                  interaction.plot(milpa, harvested, stemden_trees20plus)
                  interaction.plot(vegetation_type, harvested, stemden_trees20plus)})
```



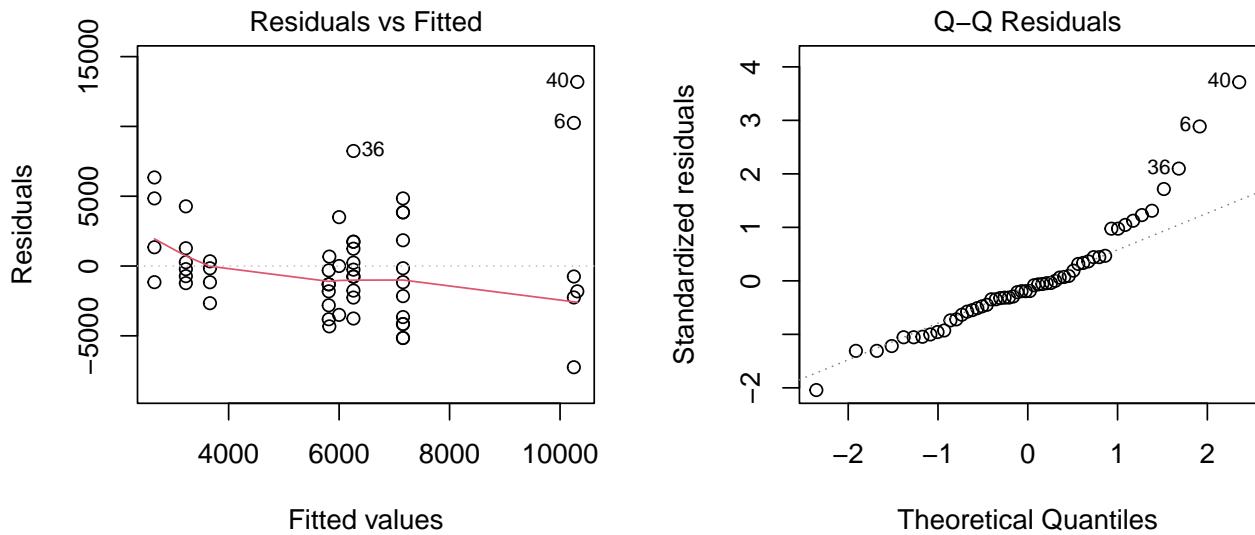
Models

Seedlings

Fit model and check assumptions

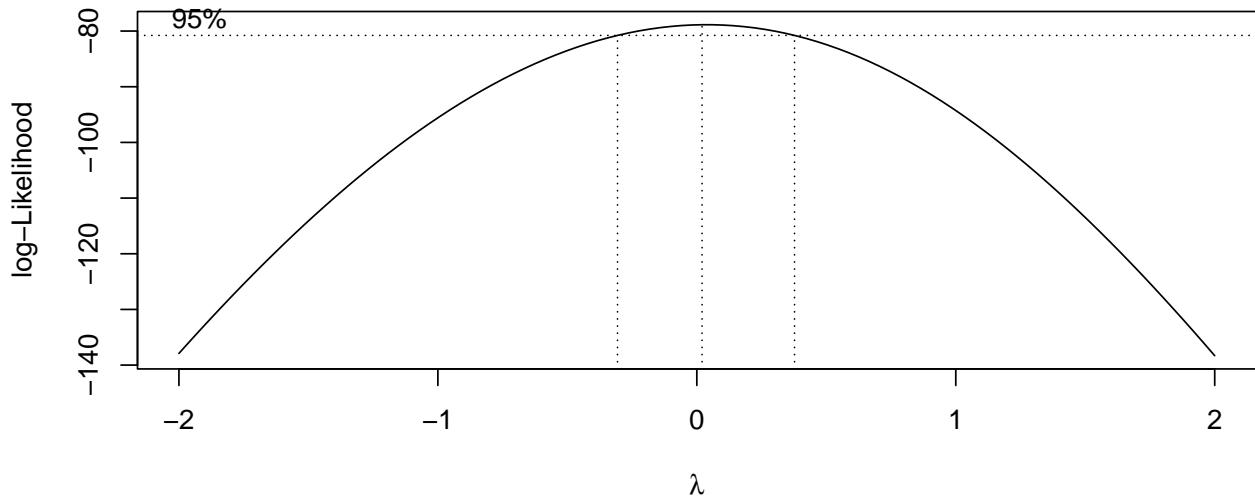
```
mod.2b.seedlings <- lm(stemden_seedlings ~ harvested + vegetation_type + milpa +
                         harvested:vegetation_type + harvested:milpa, data = data_plots)

par(mfrow = c(1,2))
plot(mod.2b.seedlings, which = 1:2)
```



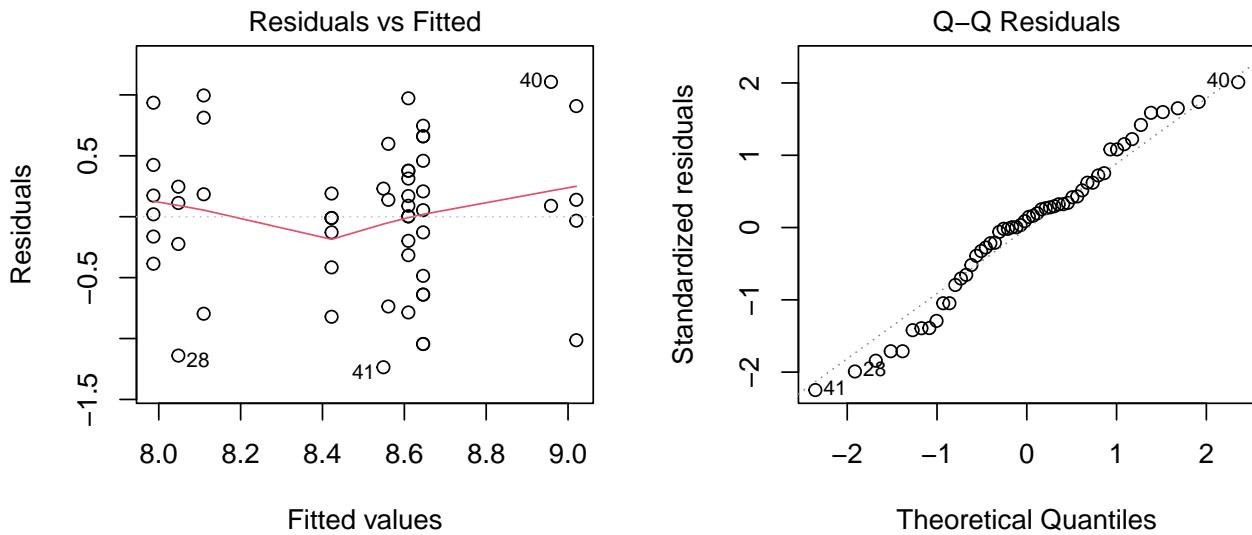
Attempt transformation of response

```
# There is a megaphone shape on the residuals vs. fitted; try Box-Cox
MASS:::boxcox(mod.2b.seedlings)
```



```
# Box-Cox suggests log transformation; re-fit with logged response
mod.2b.seedlings.transform <- lm(log(stemden_seedlings) ~ harvested + vegetation_type + milpa +
harvested:vegetation_type + harvested:milpa, data = data_plots)

# Check constant variance assumption again
par(mfrow = c(1,2))
plot(mod.2b.seedlings.transform, which = 1:2)
```



Constant variance and normality assumptions appear to be satisfied now. We proceed with the transformed model.

Summarize selected model and run ANOVA

```
# Check for outliers
outlierTest(mod.2b.seedlings.transform)

## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 41 -2.357157          0.022826       NA

# No significant outliers; look at model summary
summary(mod.2b.seedlings.transform)

##
## Call:
## lm(formula = log(stemden_seedlings) ~ harvested + vegetation_type +
##     milpa + harvested:vegetation_type + harvested:milpa, data = data_plots)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -1.23565 -0.36843  0.07157  0.36124  1.10642 
##
## Coefficients:
## (Intercept)             9.3327   0.4461  20.918   <2e-16 ***
## harvestedyes            -0.8328   0.6575  -1.267   0.2117    
## vegetation_typekeelenche -0.3743   0.3630  -1.031   0.3078    
## vegetation_typenukuuchche -0.9104   0.4203  -2.166   0.0355 *  
## milpayes                -0.3125   0.3132  -0.998   0.3237    
## harvestedyes:vegetation_typekeelenche  0.4233   0.5475  0.773   0.4434
```

```

## harvestedyes:vegetation_type nukuchche    0.3974      0.6222      0.639      0.5261
## harvestedyes:milpa yes            0.3734      0.4436      0.842      0.4042
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6354 on 46 degrees of freedom
## Multiple R-squared:  0.2101, Adjusted R-squared:  0.08995
## F-statistic: 1.748 on 7 and 46 DF,  p-value: 0.1213

# Construct ANOVA table (use type 2 SS since data are unbalanced)
Anova(mod.2b.seedlings.transform, type = 2)

```

```

## Anova Table (Type II tests)
##
## Response: log(stemden_seedlings)
##                         Sum Sq Df F value Pr(>F)
## harvested                  0.5968  1 1.4783 0.23025
## vegetation_type             3.3009  2 4.0883 0.02322 *
## milpa                      0.1308  1 0.3241 0.57192
## harvested:vegetation_type  0.2451  2 0.3035 0.73967
## harvested:milpa              0.2861  1 0.7087 0.40424
## Residuals                   18.5703 46
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

We find that vegetation_type is significant, but harvested, milpa, and the interaction terms are not.

Pairwise comparisons

```

# Pairwise comparison for vegetation_type using Tukey HSD
# Keelenche' has a significantly higher seedling density than Nuku'uch che'
TukeyHSD(aov(mod.2b.seedlings.transform), "vegetation_type", conf.level = 0.95)

```

```

## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = mod.2b.seedlings.transform)
##
## $vegetation_type
##                diff      lwr      upr     p adj
## keelenche-juuche -0.1641490 -0.8168028 0.48850476 0.8158813
## nukuuchche-juuche -0.6528113 -1.3285708 0.02294822 0.0602667
## nukuuchche-keelenche -0.4886623 -0.9426314 -0.03469310 0.0322919

```

```

# Confirm lack of significance of harvested using Tukey HSD
TukeyHSD(aov(mod.2b.seedlings.transform), "harvested", conf.level = 0.95)

```

```

## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
```

```

## Fit: aov(formula = mod.2b.seedlings.transform)
##
## $harvested
##      diff      lwr      upr   p adj
## yes-no -0.227877 -0.5762009 0.120447 0.1944098

```

Saplings (0-4 cm DBH)

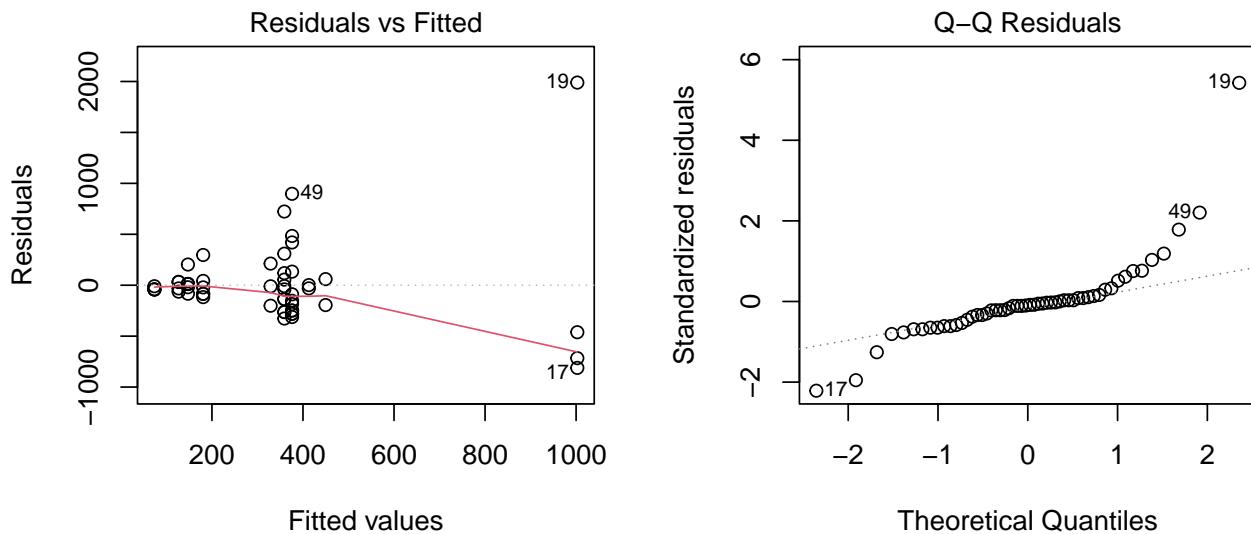
Fit model and check assumptions

```

mod.2b.saplings <- lm(stemden_saplings ~ harvested + vegetation_type + milpa +
                         harvested:vegetation_type + harvested:milpa, data = data_plots)

par(mfrow = c(1,2))
plot(mod.2b.saplings, which = 1:2)

```

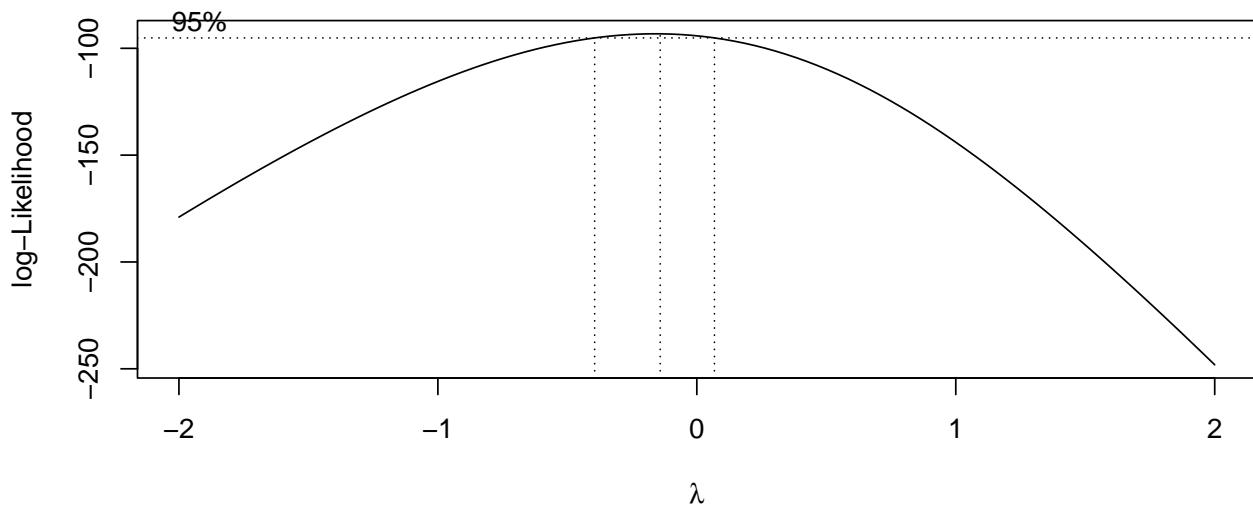


Attempt transformation of response

```

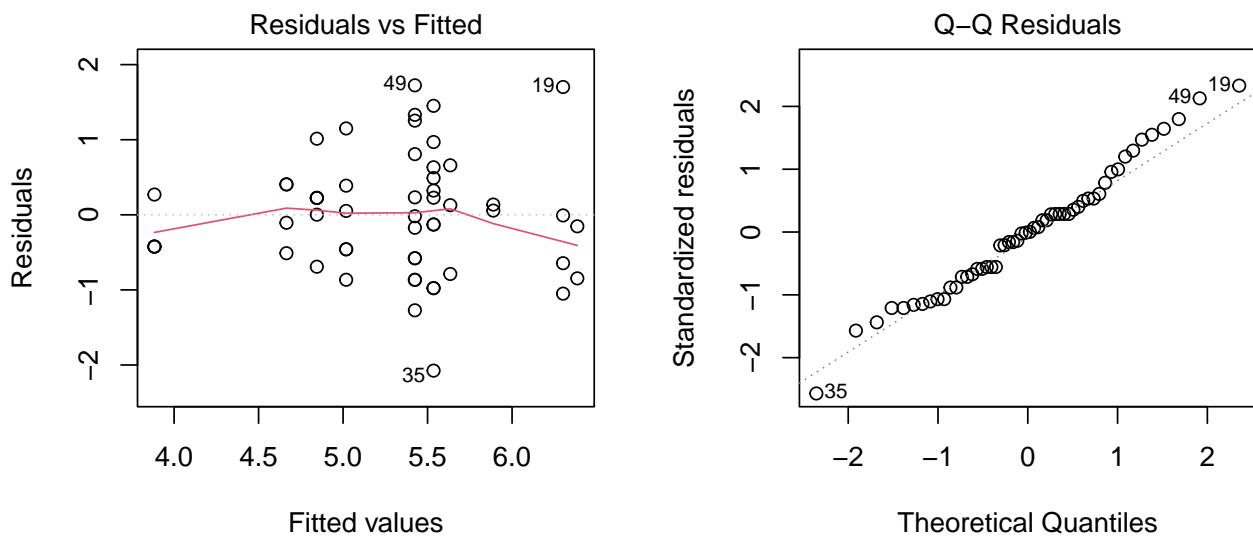
# Very distinct megaphone shape on the residuals vs. fitted; try Box-Cox
MASS::boxcox(mod.2b.saplings)

```



```
# Box-Cox strongly suggests log transformation
mod.2b.saplings.transform <- lm(log(stemden_saplings) ~ harvested + vegetation_type + milpa +
harvested:vegetation_type + harvested:milpa, data = data_plots)

# Check constant variance assumption again
par(mfrow = c(1,2))
plot(mod.2b.saplings.transform, which = 1:2)
```



Assumptions look significantly better, so we will proceed with the transformed model.

Summarize selected model and run ANOVA

```
# Check for outliers
outlierTest(mod.2b.saplings.transform)
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
```

```

##      rstudent unadjusted p-value Bonferroni p
## 35 -2.746954          0.00862      0.46548

# No significant outliers; look at model summary
summary(mod.2b.saplings.transform)

## 
## Call:
## lm(formula = log(stemden_saplings) ~ harvested + vegetation_type +
##     milpa + harvested:vegetation_type + harvested:milpa, data = data_plots)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -2.07512 -0.56151 -0.00311  0.40079  1.72433 
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 7.2630    0.5919 12.270 4.14e-16 ***
## harvestedyes -1.2752    0.8723 -1.462  0.1506    
## vegetation_typekeelenche -0.8768    0.4816 -1.821  0.0752 .  
## vegetation_typenukuuchche -2.4182    0.5576 -4.337 7.81e-05 ***
## milpayes      -0.9612    0.4156 -2.313  0.0253 *  
## harvestedyes:vegetation_typekeelenche  0.7779    0.7264  1.071  0.2898    
## harvestedyes:vegetation_typenukuuchche  1.4486    0.8255  1.755  0.0859 .  
## harvestedyes:milpayes                  0.6079    0.5885  1.033  0.3071 
## ---                                 
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## 
## Residual standard error: 0.843 on 46 degrees of freedom
## Multiple R-squared:  0.3743, Adjusted R-squared:  0.2791 
## F-statistic: 3.932 on 7 and 46 DF,  p-value: 0.001938

```

```

# Construct ANOVA table (use type 2 SS since data are unbalanced)
Anova(mod.2b.saplings.transform, type = 2)

```

```

## Anova Table (Type II tests)
## 
## Response: log(stemden_saplings)
##              Sum Sq Df F value    Pr(>F)    
## harvested        0.086  1 0.1211    0.72939
## vegetation_type 17.150  2 12.0663 6.127e-05 ***
## milpa           3.554  1  5.0013   0.03022 *  
## harvested:vegetation_type 2.274  2  1.6003   0.21287
## harvested:milpa    0.758  1  1.0667   0.30709
## Residuals        32.690 46
## ---                                 
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

We find that vegetation_type and milpa are significant, but harvested and the interaction terms are not.

Pairwise comparisons

```
# Pairwise comparison for vegetation_type using Tukey HSD
# Nuku'uch che' has significantly lower sapling density than Ju'uche' and Keelenche'
TukeyHSD(aov(mod.2b.saplings.transform), "vegetation_type", conf.level = 0.95)
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = mod.2b.saplings.transform)
##
## $vegetation_type
##              diff      lwr      upr      p adj
## keelenche-juuche -0.4426658 -1.308590  0.4232580 0.4372257
## nukuuchche-juuche -1.3505259 -2.247106 -0.4539460 0.0019092
## nukuuchche-keelenche -0.9078601 -1.510174 -0.3055458 0.0018959
```

```
# Pairwise comparison for milpa using Tukey HSD
# Plots that have been milpa have higher sapling density
# (note that the sign flips because of the log transformation)
TukeyHSD(aov(mod.2b.saplings.transform), "milpa", conf.level = 0.95)
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = mod.2b.saplings.transform)
##
## $milpa
##              diff      lwr      upr      p adj
## yes-no -0.4792989 -0.9850001  0.0264024 0.0626704
```

```
# Confirm lack of significance of harvested using Tukey HSD
TukeyHSD(aov(mod.2b.saplings.transform), "harvested", conf.level = 0.95)
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = mod.2b.saplings.transform)
##
## $harvested
##              diff      lwr      upr      p adj
## yes-no 0.04643418 -0.4157128  0.5085812 0.8406166
```

Trees (5-9 cm DBH)

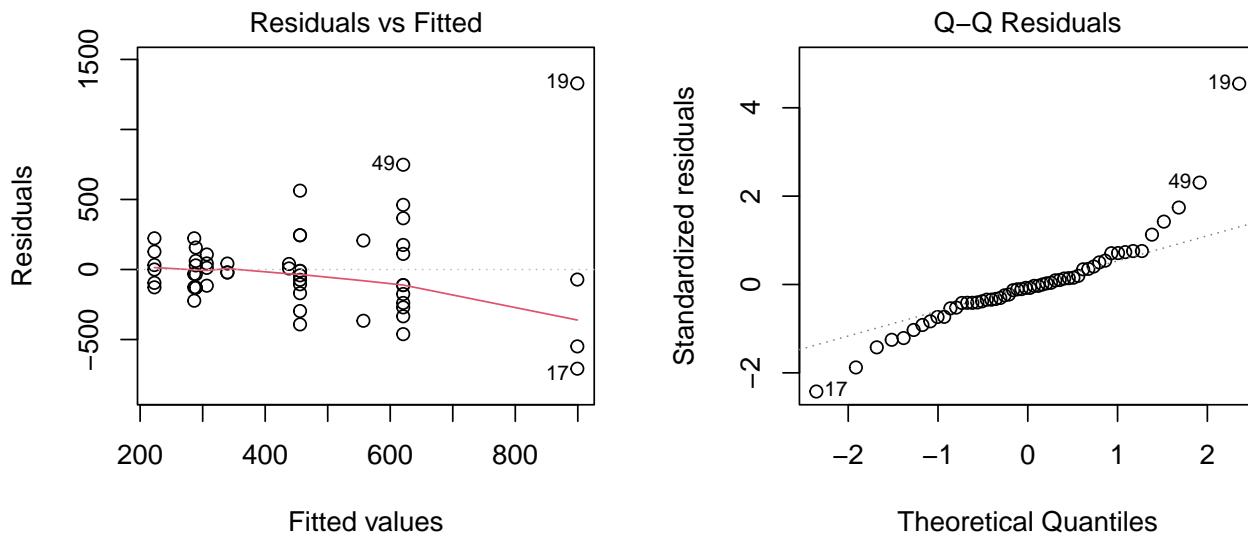
Fit model and check assumptions

```

mod.2b.05to09 <- lm(stemden_trees05to09 ~ harvested + vegetation_type + milpa +
                      harvested:vegetation_type + harvested:milpa, data = data_plots)

par(mfrow = c(1,2))
plot(mod.2b.05to09, which = 1:2)

```

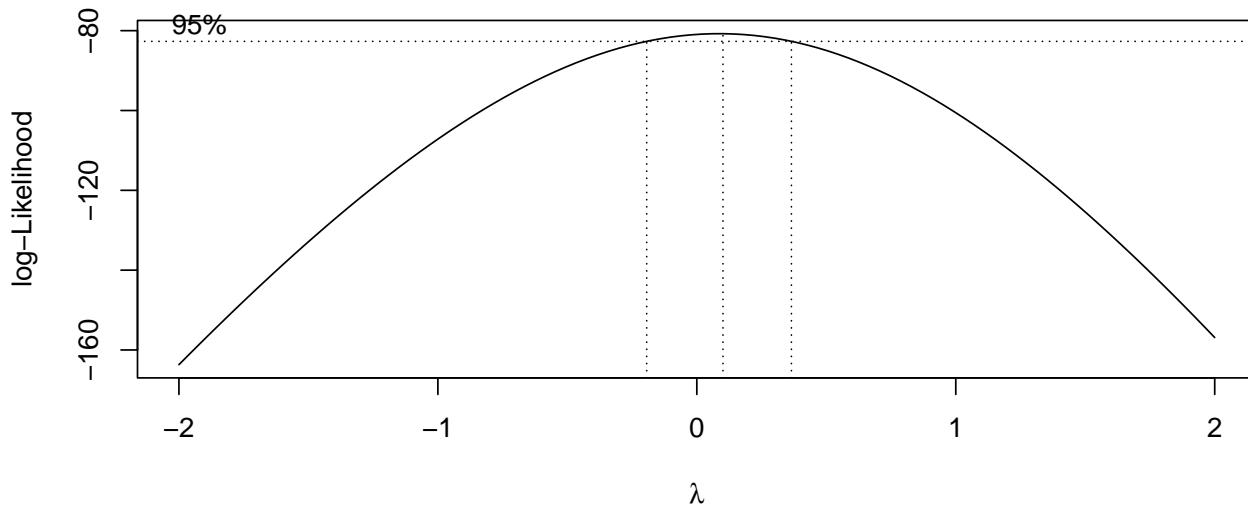


Attempt transformation of response

```

# Very distinct megaphone shape on the residuals vs. fitted; try Box-Cox
MASS::boxcox(mod.2b.05to09)

```



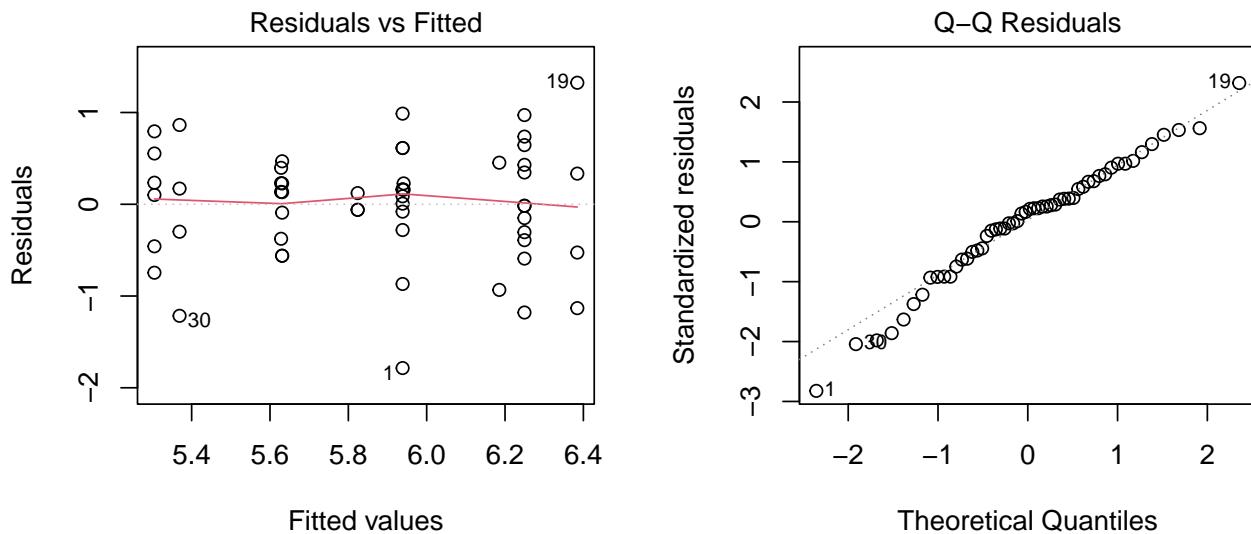
```

# Box-Cox suggests log transformation; re-fit model with logged response
mod.2b.05to09.transform <- lm(log(stemden_trees05to09) ~ harvested + vegetation_type + milpa +
                                harvested:vegetation_type + harvested:milpa, data = data_plots)

# Check constant variance assumption again

```

```
par(mfrow = c(1,2))
plot(mod.2b.05to09.transform, which = 1:2)
```



Assumptions look significantly better, so we will proceed with the transformed model.

Summarize selected model and run ANOVA

```
# Check for outliers
outlierTest(mod.2b.05to09.transform)

## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 1 -3.071552          0.0036067     0.19476

# No significant outliers; look at model summary
summary(mod.2b.05to09.transform)

##
## Call:
## lm(formula = log(stemden_trees05to09) ~ harvested + vegetation_type +
##     milpa + harvested:vegetation_type + harvested:milpa, data = data_plots)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -1.7850 -0.3582  0.1115  0.3844  1.3244 
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 6.32034   0.46347 13.637 <2e-16 ***
## harvestedyes -0.49387   0.68299 -0.723  0.4733  
## vegetation_typekeelenche -0.13494   0.37709 -0.358  0.7221
```

```

## vegetation_typenukuuchche          -1.01538   0.43658  -2.326   0.0245 *
## milpayes                           0.06416   0.32541   0.197   0.8446
## harvestedyes:vegetation_typekeelenche 0.24967   0.56872   0.439   0.6627
## harvestedyes:vegetation_typenukuuchche 0.81992   0.64630   1.269   0.2110
## harvestedyes:milpayes            -0.06683   0.46081  -0.145   0.8853
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.66 on 46 degrees of freedom
## Multiple R-squared:  0.2463, Adjusted R-squared:  0.1316
## F-statistic: 2.148 on 7 and 46 DF,  p-value: 0.05703

```

```

# Construct ANOVA table (use type 2 SS since data are unbalanced)
Anova(mod.2b.05to09.transform, type = 2)

```

```

## Anova Table (Type II tests)
##
## Response: log(stemden_trees05to09)
##                                         Sum Sq Df F value Pr(>F)
## harvested                           0.1659  1  0.3809 0.54019
## vegetation_type                     3.3734  2  3.8716 0.02792 *
## milpa                               0.0078  1  0.0179 0.89411
## harvested:vegetation_type        0.9474  2  1.0874 0.34561
## harvested:milpa                  0.0092  1  0.0210 0.88532
## Residuals                          20.0402 46
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

We find that vegetation_type is significant, but harvested, milpa, and the interaction terms are not

Pairwise comparisons

```

# Pairwise comparison for vegetation_type using Tukey HSD
# Keelenche' has a significantly higher 5-9 cm tree density than Nuku'uch che'
TukeyHSD(aov(mod.2b.05to09.transform), "vegetation_type", conf.level = 0.95)

```

```

## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = mod.2b.05to09.transform)
##
## $vegetation_type
##               diff      lwr      upr     p adj
## keelenche-juuche -0.04210571 -0.720097 0.63588555 0.9876095
## nukuuchche-juuche -0.65468473 -1.356679 0.04730927 0.0720911
## nukuuchche-keelenche -0.61257902 -1.084172 -0.14098576 0.0080139

```

```

# Confirm lack of significance of Harvested using Tukey HSD
TukeyHSD(aov(mod.2b.05to09.transform), "harvested", conf.level = 0.95)

```

```

## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = mod.2b.05to09.transform)
##
## $harvested
##      diff      lwr      upr     p adj
## yes-no -0.1292511 -0.4910977 0.2325956 0.4757758

```

Trees (10-14 cm DBH)

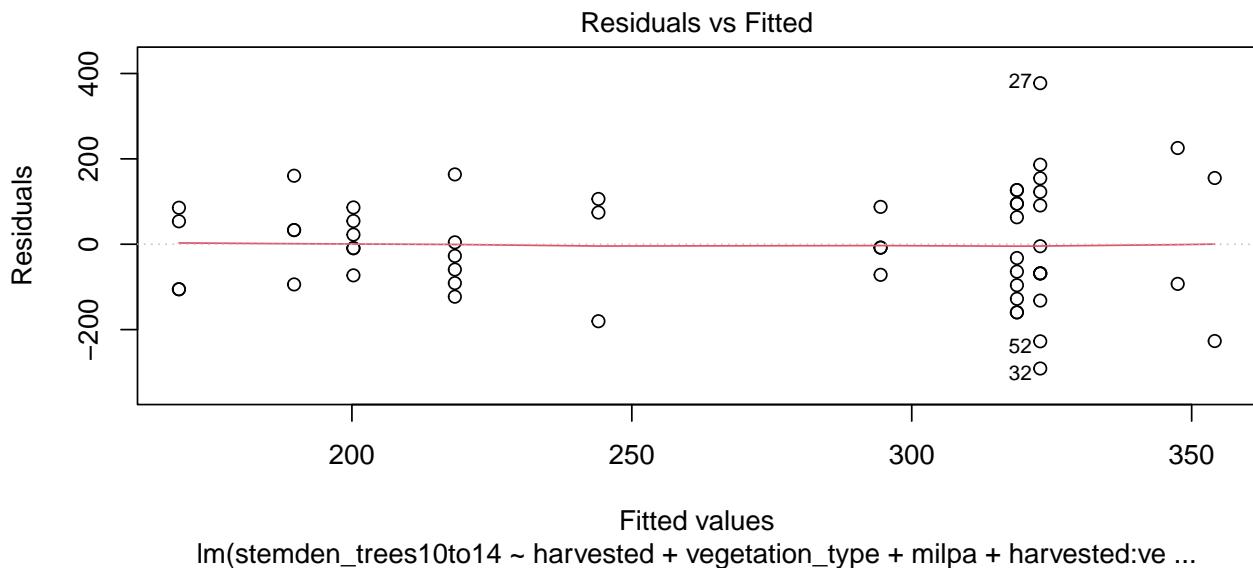
Fit model and check assumptions

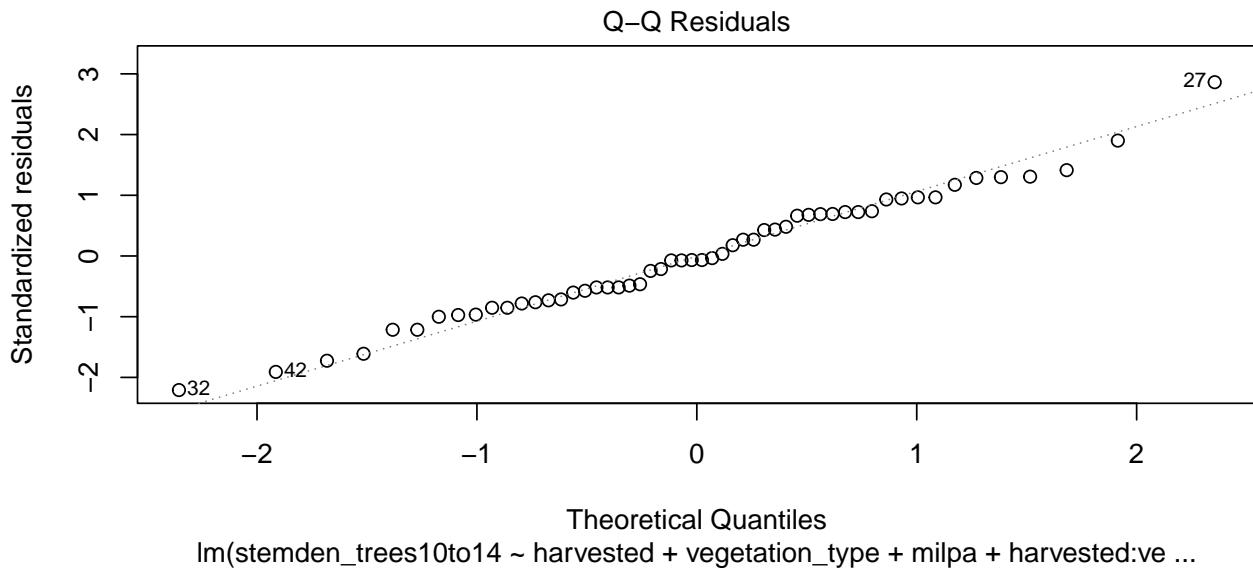
```

mod.2b.10to14 <- lm(stemden_trees10to14 ~ harvested + vegetation_type + milpa +
                      harvested:vegetation_type + harvested:milpa, data = data_plots)

plot(mod.2b.10to14, which = 1:2)

```





Assumptions appear to be satisfied.

Summarize selected model and run ANOVA

```
# Check for outliers
outlierTest(mod.2b.10to14)

## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##   rstudent unadjusted p-value Bonferroni p
## 27 3.123062      0.0031265     0.16883

# No significant outliers; look at model summary
summary(mod.2b.10to14)

##
## Call:
## lm(formula = stemden_trees10to14 ~ harvested + vegetation_type +
##     milpa + harvested:vegetation_type + harvested:milpa, data = data_plots)
##
## Residuals:
##    Min     1Q Median     3Q    Max 
## -291.12 -92.41  -7.96  90.02 377.33 
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 325.604    96.310   3.381  0.00148 ** 
## harvestedyes -52.847   141.928  -0.372  0.71134    
## vegetation_typekeelenche 28.515    78.359   0.364  0.71760    
## vegetation_typenukuuchche -125.335   90.722  -1.382  0.17379    
## milpayes      -31.168   67.620  -0.461  0.64702    
## harvestedyes:vegetation_typekeelenche 46.236   118.182   0.391  0.69744
```

```

## harvestedyes:vegetation_type nukuchche    70.967     134.304   0.528  0.59976
## harvestedyes:milpayes          2.448      95.758   0.026  0.97971
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 137.2 on 46 degrees of freedom
## Multiple R-squared:  0.1893, Adjusted R-squared:  0.0659
## F-statistic: 1.534 on 7 and 46 DF,  p-value: 0.1797

# Construct ANOVA table (use type 2 SS since data are unbalanced)
Anova(mod.2b.10to14, type = 2)

```

```

## Anova Table (Type II tests)
##
## Response: stemden_trees10to14
##           Sum Sq Df F value Pr(>F)
## harvested            34   1  0.0018 0.96623
## vegetation_type     179553  2  4.7722 0.01308 *
## milpa                7360  1  0.3912 0.53475
## harvested:vegetation_type 5253  2  0.1396 0.87007
## harvested:milpa       12   1  0.0007 0.97971
## Residuals            865374 46
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

We find that vegetation_type is significant, but harvested, milpa, and the interaction terms are not.

Pairwise comparisons

```

# Pairwise comparison for vegetation_type using Tukey HSD
# Keelenche' has a significantly higher 10-14 cm tree density than Nuku'uch che'
TukeyHSD(aov(mod.2b.10to14), "vegetation_type", conf.level = 0.95)

```

```

## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = mod.2b.10to14)
##
## $vegetation_type
##             diff      lwr      upr      p adj
## keelenche-juuche  52.73147 -88.15686 193.61979 0.6390295
## nukuuchche-juuche -75.23507 -221.11122  70.64109 0.4309542
## nukuuchche-keelenche -127.96653 -225.96482 -29.96824 0.0076578

```

```

# Confirm lack of significance of harvested using Tukey HSD
TukeyHSD(aov(mod.2b.10to14), "harvested", conf.level = 0.95)

```

```

## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
```

```

## Fit: aov(formula = mod.2b.10to14)
##
## $harvested
##      diff      lwr      upr   p adj
## yes-no -3.497911 -78.69058 71.69476 0.925803

```

Trees (15-19 cm DBH)

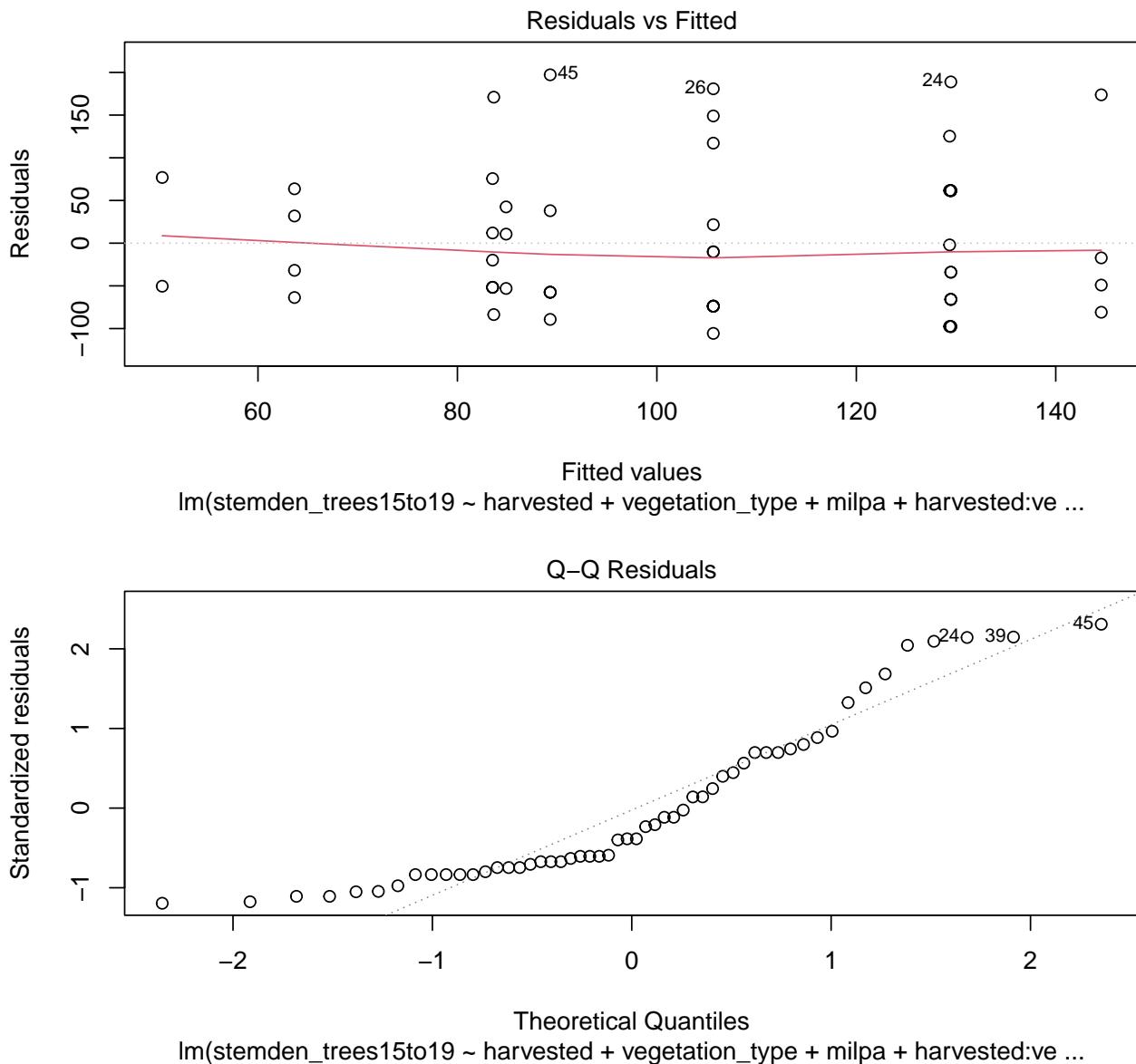
Fit model and check assumptions

```

mod.2b.15to19 <- lm(stemden_trees15to19 ~ harvested + vegetation_type + milpa +
                      harvested:vegetation_type + harvested:milpa, data = data_plots)

plot(mod.2b.15to19, which = 1:2)

```



Constant variance and normality assumptions appear to be satisfied.

Summarize selected model and run ANOVA

```
# Look at model summary
summary(mod.2b.15to19)

## 
## Call:
## lm(formula = stemden_trees15to19 ~ harvested + vegetation_type +
##     milpa + harvested:vegetation_type + harvested:milpa, data = data_plots)
##
## Residuals:
##      Min    1Q Median    3Q   Max 
## -105.66 -65.82 -32.91  61.51 197.18 
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)                 8.400     64.620   0.130   0.897    
## harvestedyes                30.651     95.228   0.322   0.749    
## vegetation_typekeelenche   41.999     52.576   0.799   0.428    
## vegetation_typenukuuchche  80.904     60.871   1.329   0.190    
## milpayes                   55.262     45.371   1.218   0.229    
## harvestedyes:vegetation_typekeelenche  2.596     79.295   0.033   0.974    
## harvestedyes:vegetation_typenukuuchche -36.428     90.113  -0.404   0.688    
## harvestedyes:milpayes        -9.430     64.250  -0.147   0.884    
## 
## Residual standard error: 92.03 on 46 degrees of freedom
## Multiple R-squared:  0.08095,   Adjusted R-squared:  -0.0589 
## F-statistic: 0.5788 on 7 and 46 DF,  p-value: 0.7694
```

```
# Construct ANOVA table (use type 2 SS since data are unbalanced)
Anova(mod.2b.15to19, type = 2)
```

```
## Anova Table (Type II tests)
## 
## Response: stemden_trees15to19
##                         Sum Sq Df F value Pr(>F)    
## harvested                  1869  1  0.2207 0.6407    
## vegetation_type             16858  2  0.9952 0.3775    
## milpa                      20978  1  2.4770 0.1224    
## harvested:vegetation_type   3480  2  0.2054 0.8150    
## harvested:milpa              182  1  0.0215 0.8840    
## Residuals                  389583 46
```

We find that no predictors are significant.

Pairwise comparisons

```
# Confirm lack of significance of harvested using Tukey HSD
TukeyHSD(aov(mod.2b.15to19), "harvested", conf.level = 0.95)
```

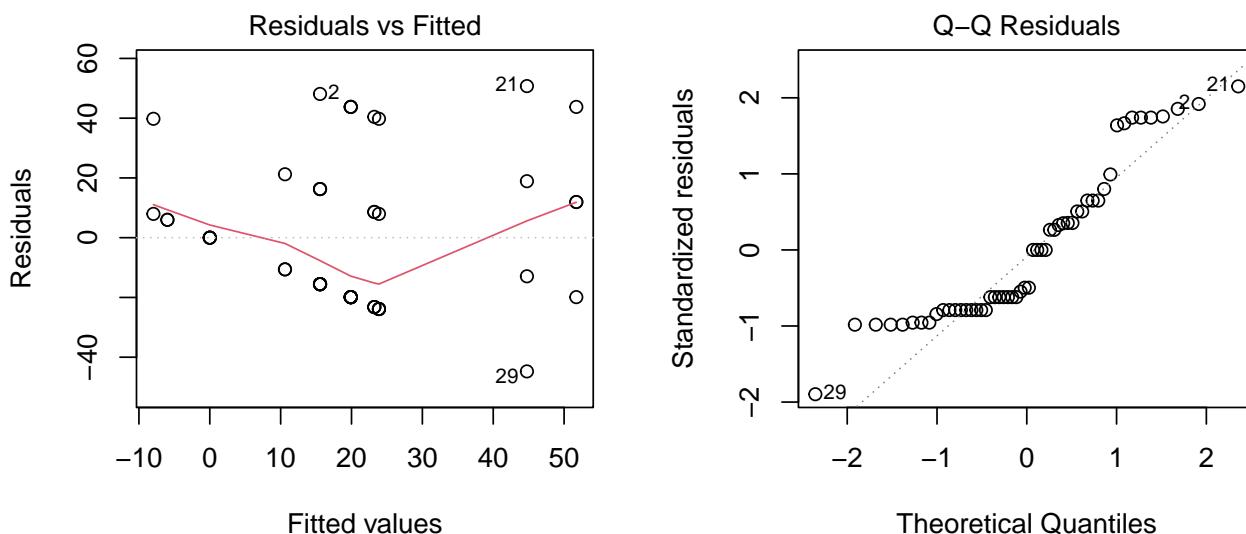
```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = mod.2b.15to19)
##
## $harvested
##          diff      lwr      upr     p adj
## yes-no 12.41758 -38.03383 62.869 0.6226531
```

Trees (20+ cm DBH)

Fit model and check assumptions

```
mod.2b.20plus <- lm(stemden_trees20plus ~ harvested + vegetation_type + milpa +
                     harvested:vegetation_type + harvested:milpa, data = data_plots)

par(mfrow = c(1,2))
plot(mod.2b.20plus, which = 1:2)
```

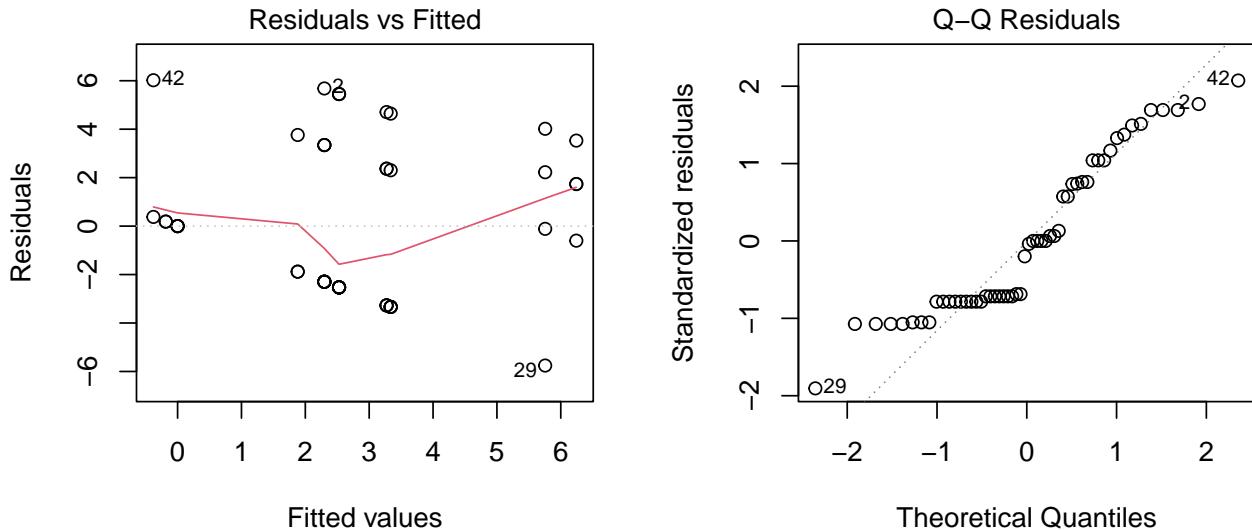


There is a little bit of a megaphone shape on the residuals vs. fitted. We can't do a log transformation since the response has zeros, so we'll try a square root transformation.

Attempt transformation of response

```
mod.2b.20plus.transform <- lm(sqrt(stemden_trees20plus) ~ harvested + vegetation_type + milpa +
                           harvested:vegetation_type + harvested:milpa, data = data_plots)
```

```
# Check constant variance assumption again
par(mfrow = c(1,2))
plot(mod.2b.20plus.transform, which = 1:2)
```



No substantial improvement in assumptions, so we will proceed with the untransformed model.

Summarize selected model and run ANOVA

```
# Look at model summary
summary(mod.2b.20plus)
```

```
##
## Call:
## lm(formula = stemden_trees20plus ~ harvested + vegetation_type +
##     milpa + harvested:vegetation_type + harvested:milpa, data = data_plots)
##
## Residuals:
##    Min      1Q  Median      3Q     Max 
## -44.76 -19.89 -10.61  15.19  50.74 
##
## Coefficients:
## (Intercept)          27.852   18.384  -1.515  0.13661  
## harvestedyes         16.923   27.091   0.625  0.53529  
## vegetation_typekeelenche 19.894   14.957   1.330  0.19005  
## vegetation_typenukuuchche 51.725   17.317   2.987  0.00451 ** 
## milpayes             27.852   12.907   2.158  0.03620 *  
## harvestedyes:vegetation_typekeelenche -14.948   22.559  -0.663  0.51087  
## harvestedyes:vegetation_typenukuuchche -17.581   25.636  -0.686  0.49629  
## harvestedyes:milpayes                 -6.312   18.278  -0.345  0.73141  
## ---                                 
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

## Residual standard error: 26.18 on 46 degrees of freedom
## Multiple R-squared:  0.2694, Adjusted R-squared:  0.1582
## F-statistic: 2.423 on 7 and 46 DF,  p-value: 0.03366

# Construct ANOVA table (use type 2 SS since data are unbalanced)
Anova(mod.2b.20plus, type = 2)

```

```

## Anova Table (Type II tests)
##
## Response: stemden_trees20plus
##                               Sum Sq Df F value    Pr(>F)
## harvested                  31.7   1  0.0462 0.830682
## vegetation_type            10868.4  2  7.9279 0.001101 **
## milpa                      5008.5  1  7.3069 0.009592 **
## harvested:vegetation_type  358.3   2  0.2613 0.771157
## harvested:milpa             81.7   1  0.1193 0.731410
## Residuals                  31530.8 46
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

We find that vegetation type and milpa are significant, but Harvested and the interaction terms are not

Pairwise comparisons

```

# Pairwise comparison for vegetation type using Tukey HSD
# Nuku'uch che' has significantly HIGHER 20+ cm tree density than ju'uche' and keelenche';
# no significant difference between the latter two
TukeyHSD(aov(mod.2b.20plus), "vegetation_type", conf.level = 0.95)

```

```

## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = mod.2b.20plus)
##
## $vegetation_type
##                diff      lwr      upr     p adj
## keelenche-juuche  9.646091 -17.2469987 36.53918 0.6625591
## nukuuchche-juuche 28.937717  1.0925384 56.78289 0.0400616
## nukuuchche-keelenche 19.291626  0.5854857 37.99777 0.0419191

```

```

# Pairwise comparison for milpa using Tukey HSD
# Plots that have been milpa have a significantly higher 20+ cm tree density than
# plots that have not been milpa
TukeyHSD(aov(mod.2b.20plus), "milpa", conf.level = 0.95)

```

```

## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = mod.2b.20plus)
##
```

```
## $milpa
##      diff     lwr      upr      p adj
## yes-no 18.01959 2.313967 33.72521 0.0254595

# Confirm lack of significance of harvested using Tukey HSD
TukeyHSD(aov(mod.2b.20plus), "harvested", conf.level = 0.95)
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = mod.2b.20plus)
##
## $harvested
##      diff     lwr      upr      p adj
## yes-no -0.8744777 -15.22743 13.47847 0.9029272
```