

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"))

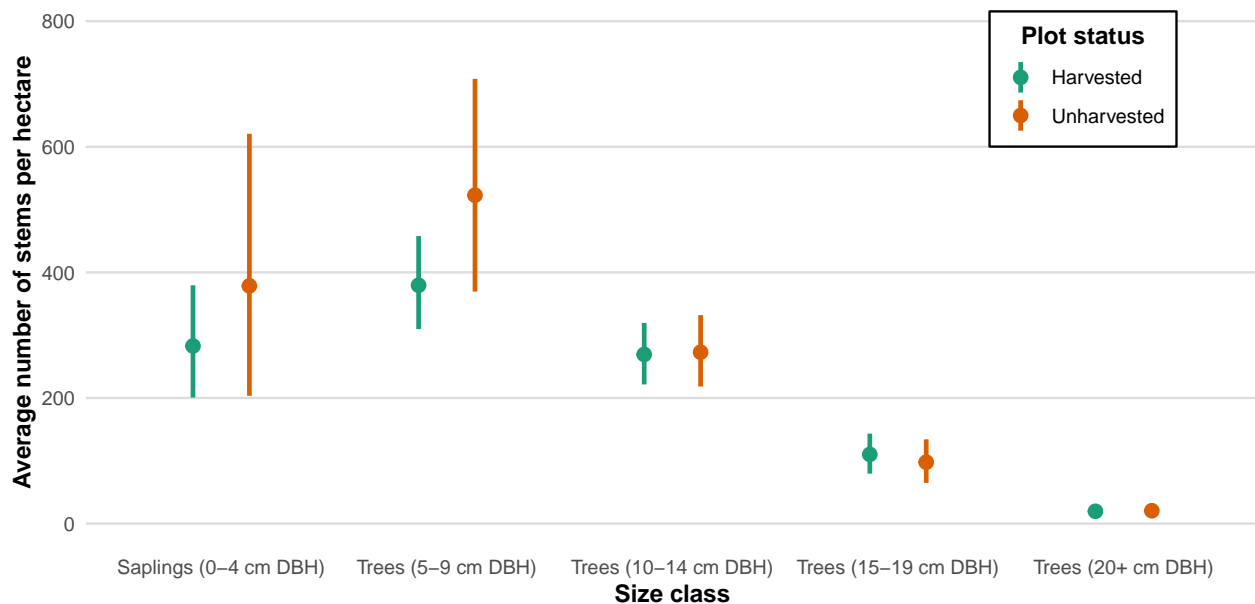
```

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

```



```

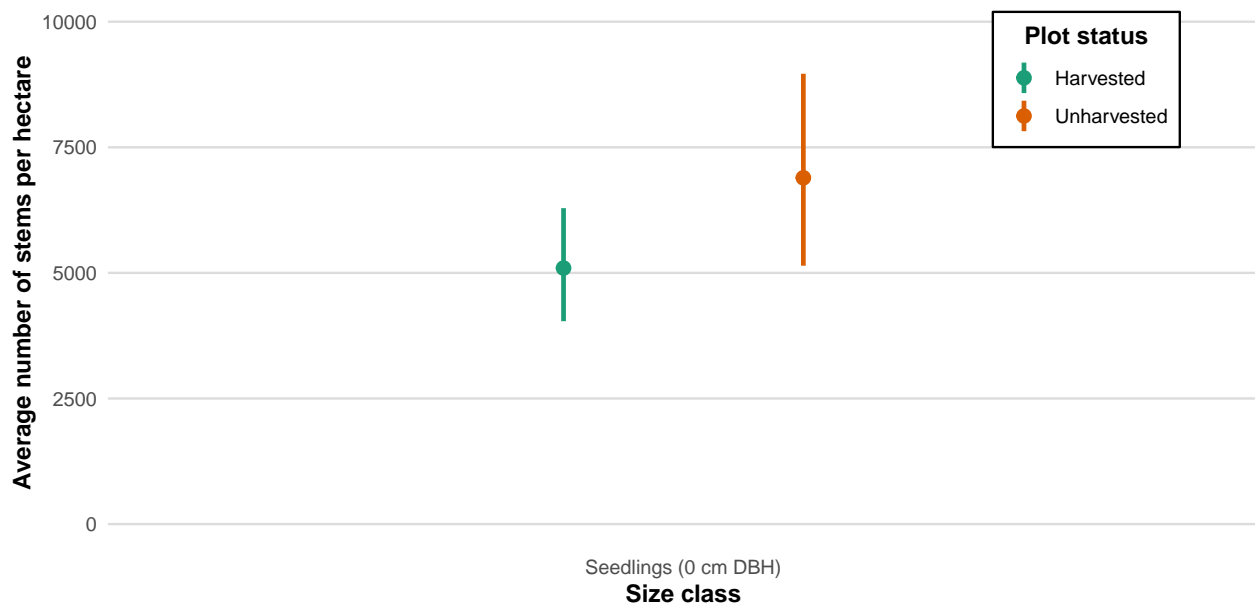
# Seedlings only
stemden_sizeclass_fig1_seedlings <- stemden_mean_data_seedlings %>%
  ggplot() +

```

```

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

```

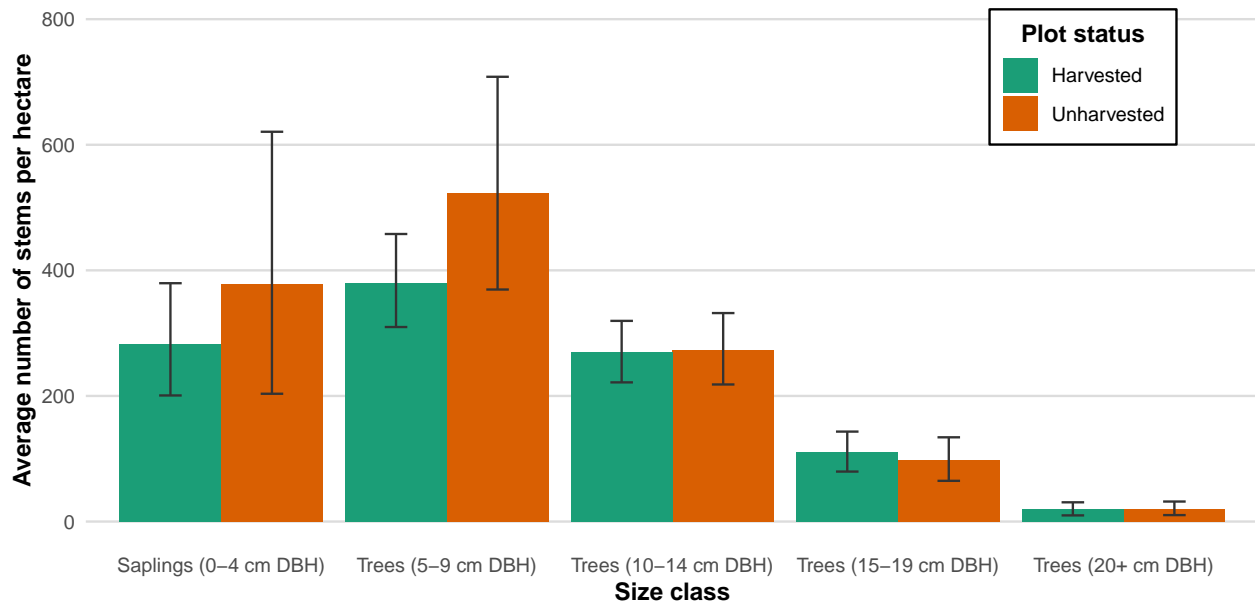


Bar plots

```

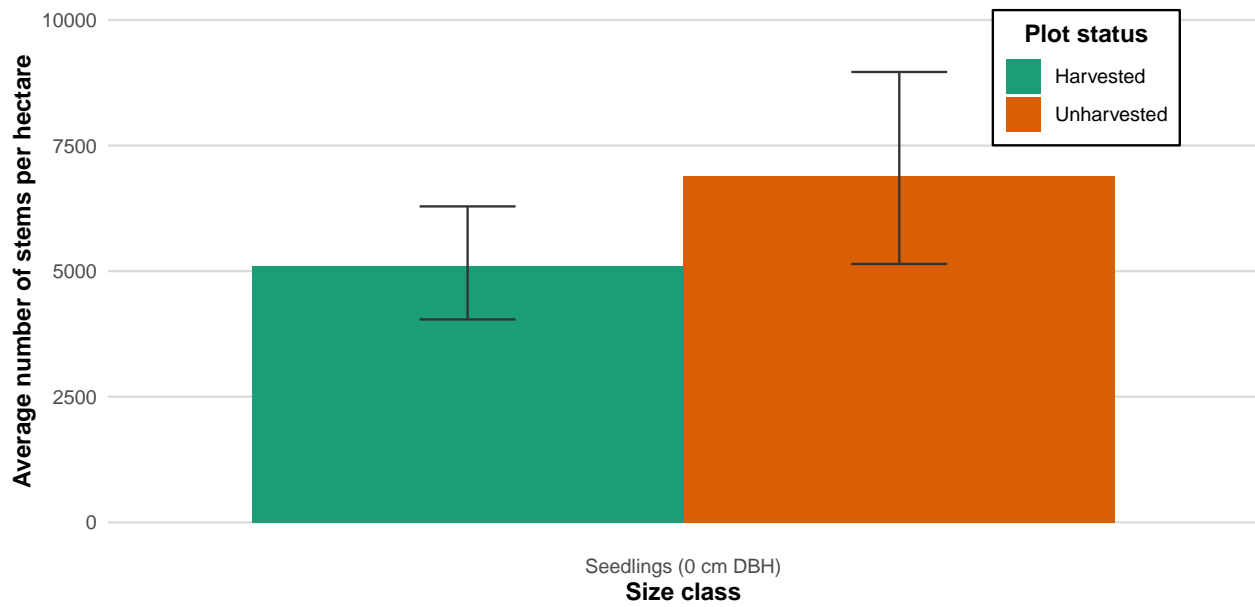
# All size classes except seedlings
stemden_sizeclass_fig2_noseedlings <- stemden_mean_data_noseedlings %>%
  ggplot(aes(x = size_class,
    fill = fct_relevel(harvested, "Harvested", "Unharvested"))) +
  geom_col(aes(y = mean),
    position = "dodge") +
  geom_errorbar(aes(x = size_class, ymin = lower, 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

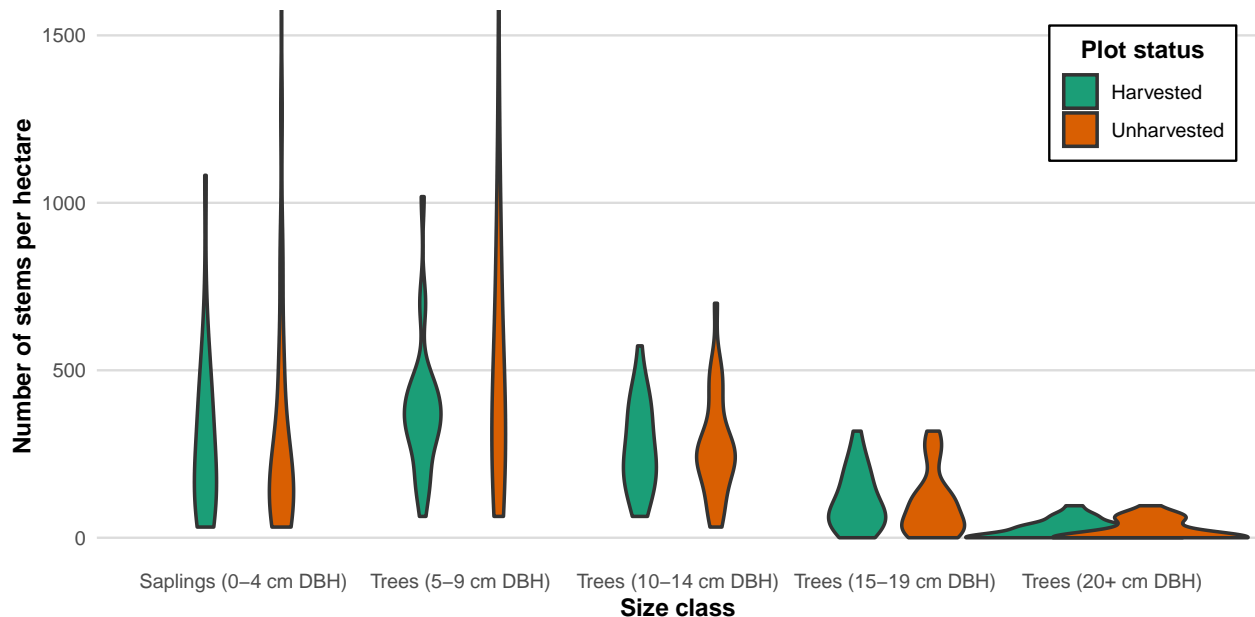
```
stemden_dist_data <- data_plots %>%
  select(harvested, stemden_seedlings,
         stemden_saplings, starts_with("stemden_trees")) %>%
  pivot_longer(cols = starts_with("stemden"),
               names_prefix = "stemden_",
               names_to = "size_class",
               values_to = "num_stems") %>%
  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"))

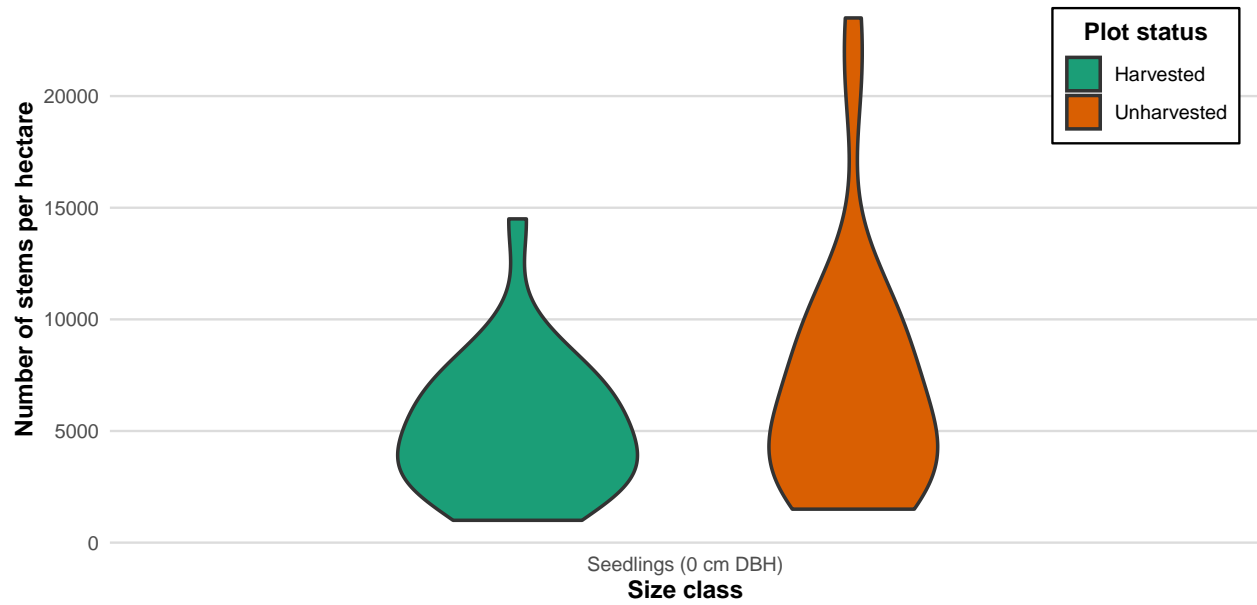
stemden_dist_data_seedlings <- stemden_dist_data %>%
  filter(size_class == "seedlings") %>%
  mutate(size_class = fct_recode(size_class,
                                "Seedlings (0 cm DBH)" = "seedlings"))
```

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"))
```

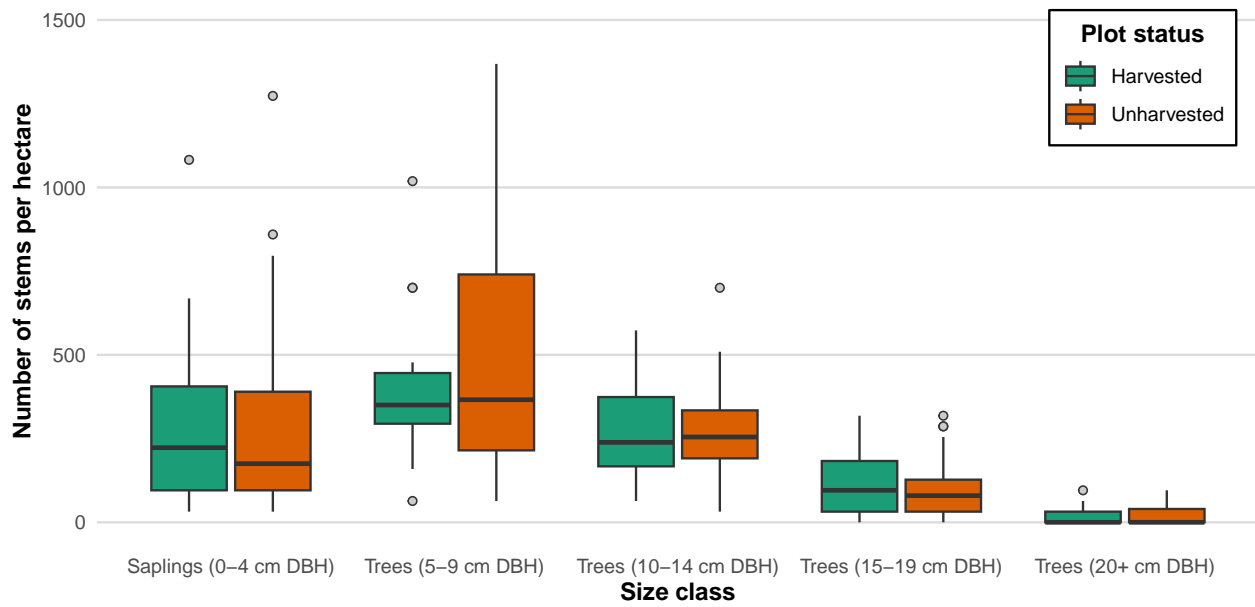


```
# Seedlings only
stemden_dist_data_seedlings %>%
  ggplot() +
    geom_violin(aes(x = size_class, y = num_stems,
                    fill = fct_relevel(harvested, "Harvested", "Unharvested")),
                scale = "area", width = 0.5, position = position_dodge(width = 0.7),
                lwd = 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"))
```

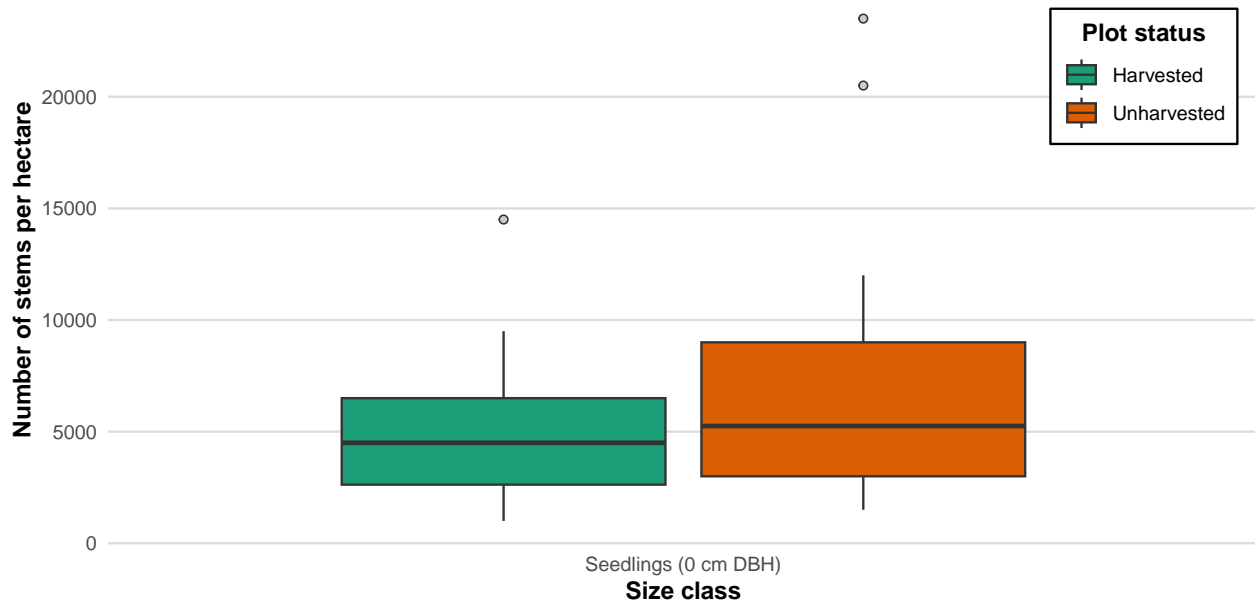


Box plots

```
# 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
```

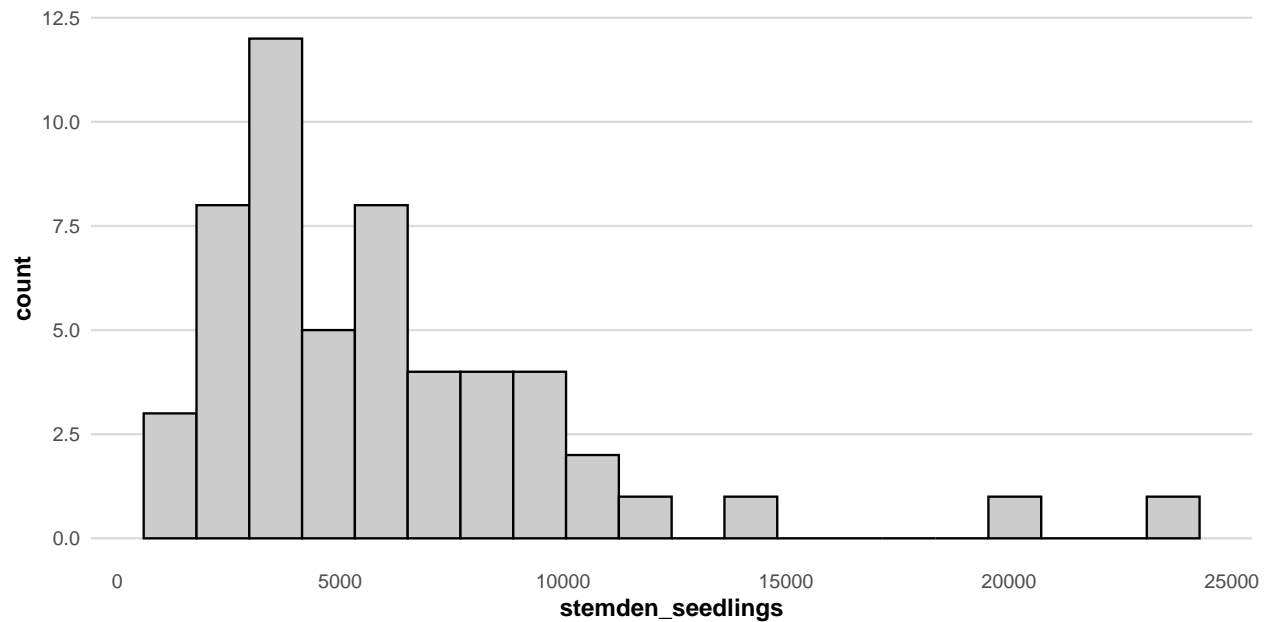
```
# Seedlings only
stemden_sizeclass_fig3_seedlings <- stemden_dist_data_seedlings %>%
  ggplot() +
  geom_boxplot(aes(x = size_class, y = num_stems,
    fill = fct_relevel(harvested, "Harvested", "Unharvested")),
    outlier.shape = 21, outlier.color = "gray20",
    outlier.fill = "gray80") +
  plot_theme +
  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
```



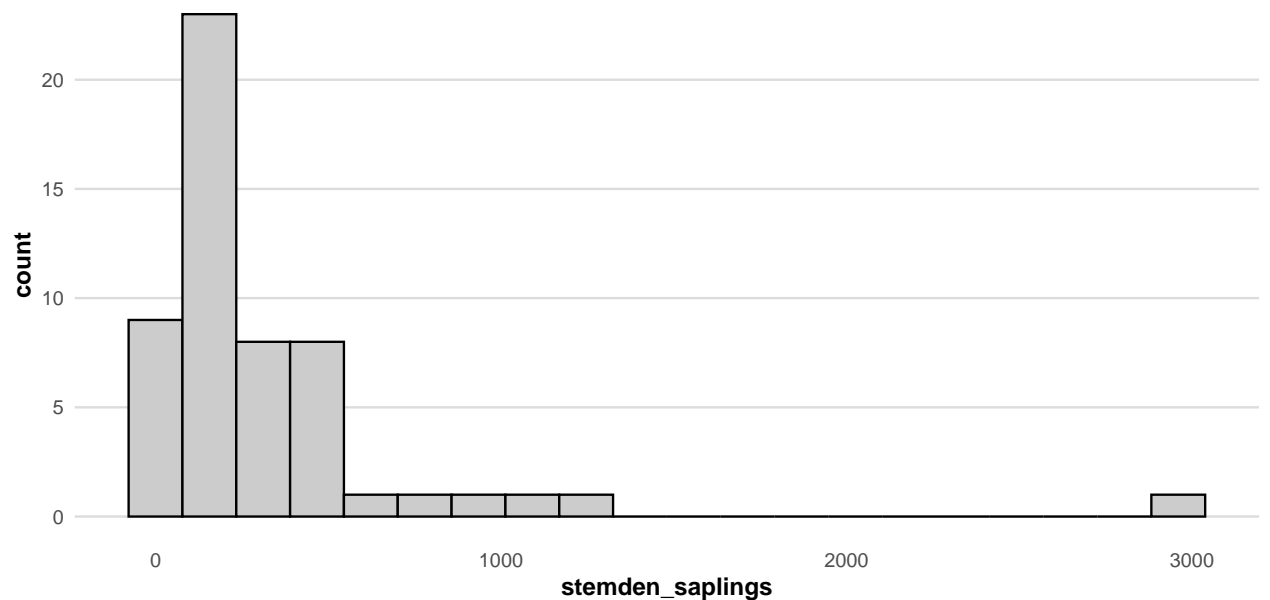
Stem density by size class for different covariates

Histograms, harvesting status

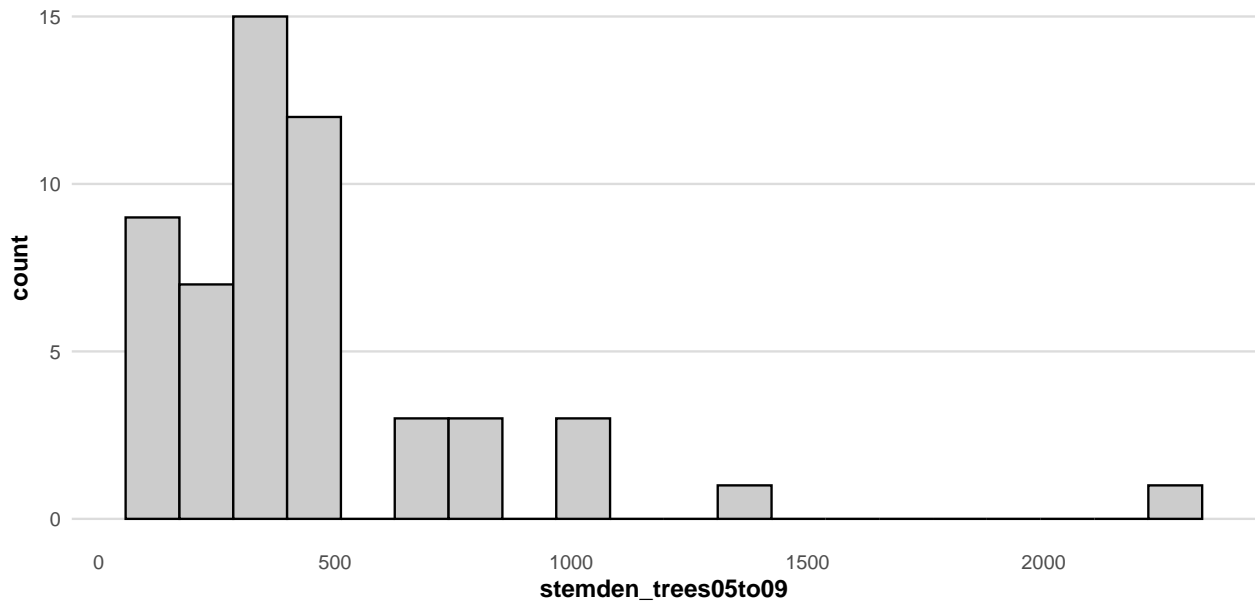
```
data_plots %>%  
  ggplot() + geom_histogram(aes(x = stemden_seedlings), bins = 20,  
                             col = "black", fill = "gray80") + plot_theme
```



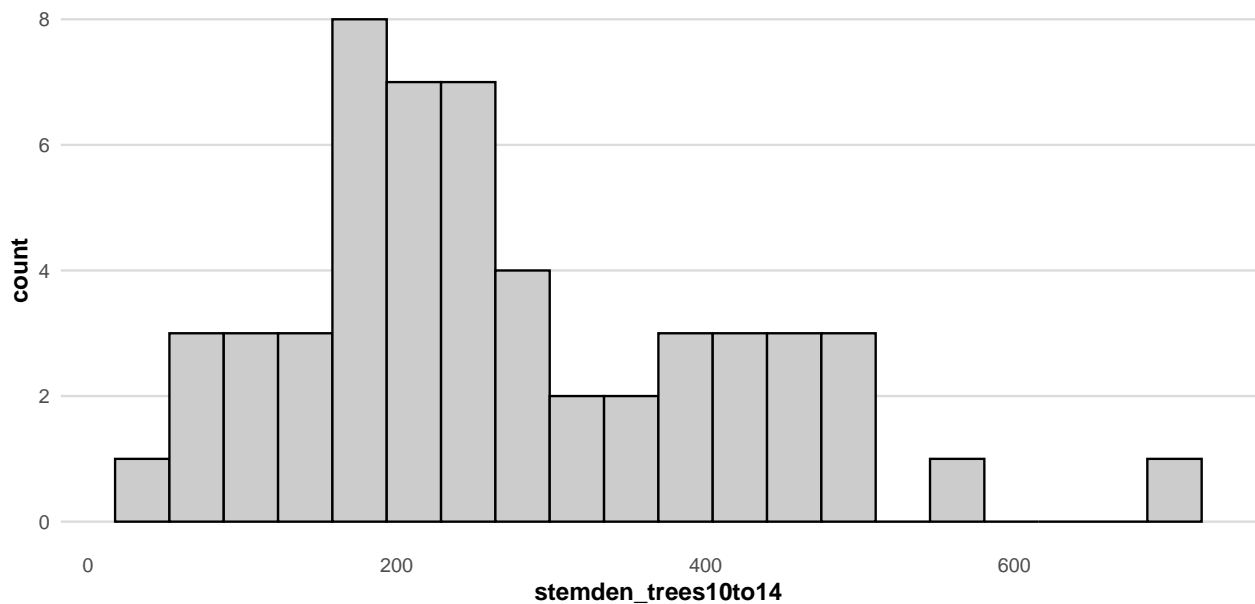
```
data_plots %>%  
  ggplot() + geom_histogram(aes(x = stemden_saplings), bins = 20,  
                             col = "black", fill = "gray80") + plot_theme
```



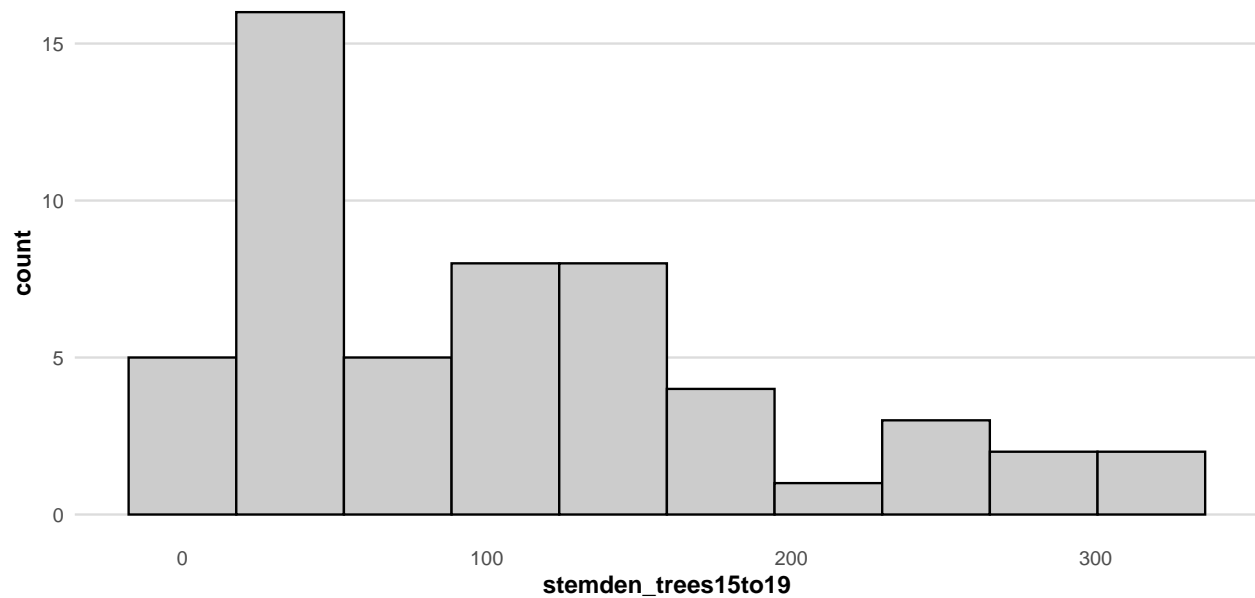
```
data_plots %>%
  ggplot() + geom_histogram(aes(x = stemden_trees05to09), bins = 20,
                             col = "black", fill = "gray80") + plot_theme
```



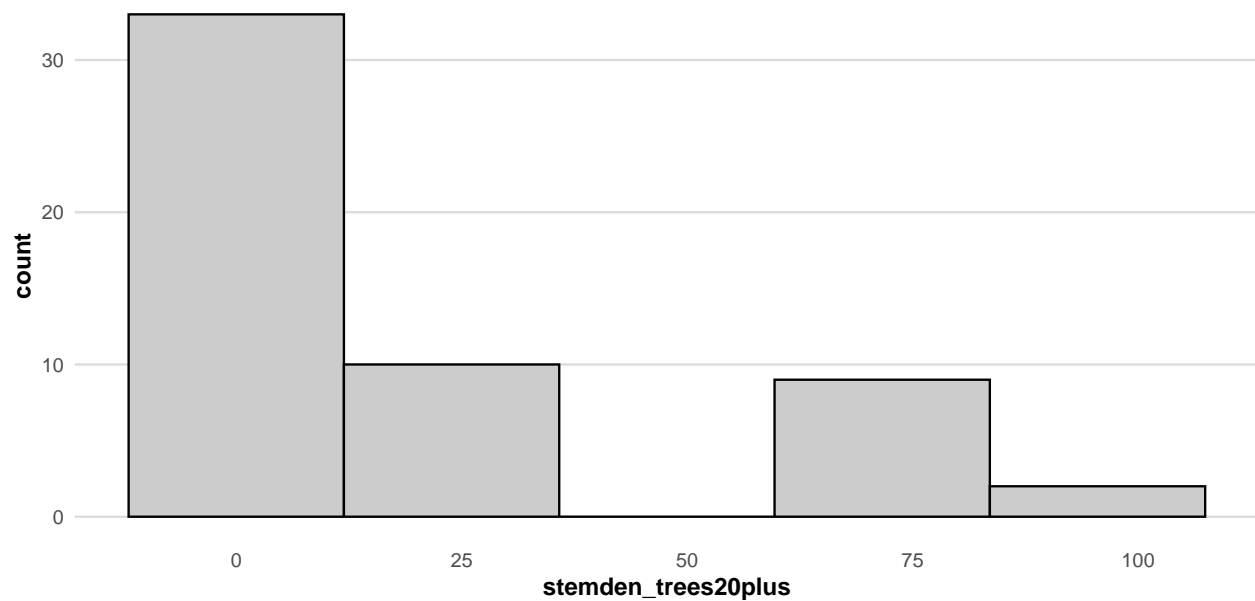
```
data_plots %>%
  ggplot() + geom_histogram(aes(x = stemden_trees10to14), bins = 20,
                             col = "black", fill = "gray80") + plot_theme
```



```
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()
```

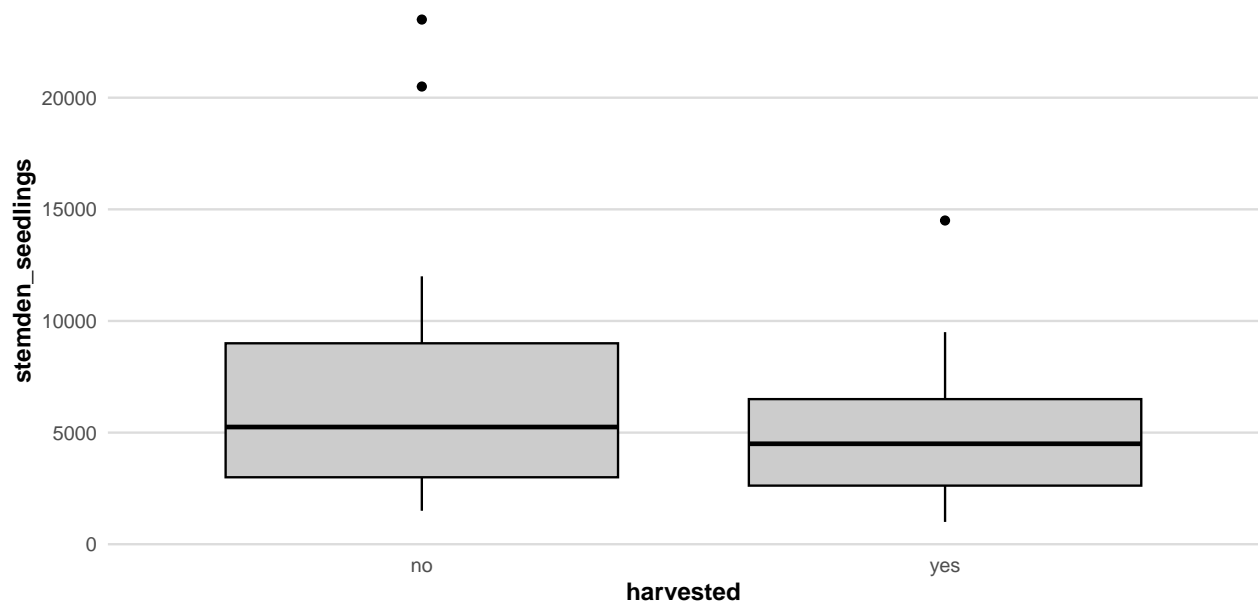
```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    0.00    0.00    0.00   19.59   31.83   95.49
```

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

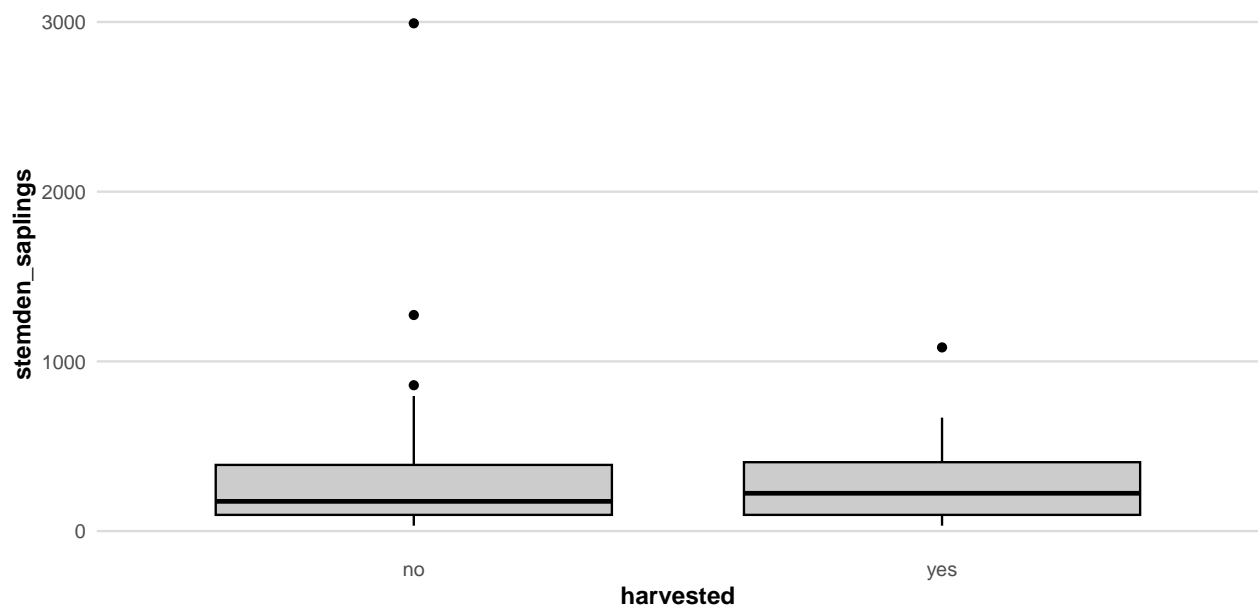
```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    0.00    0.00    0.00   20.46   39.79   95.49
```

Box plots, harvesting status

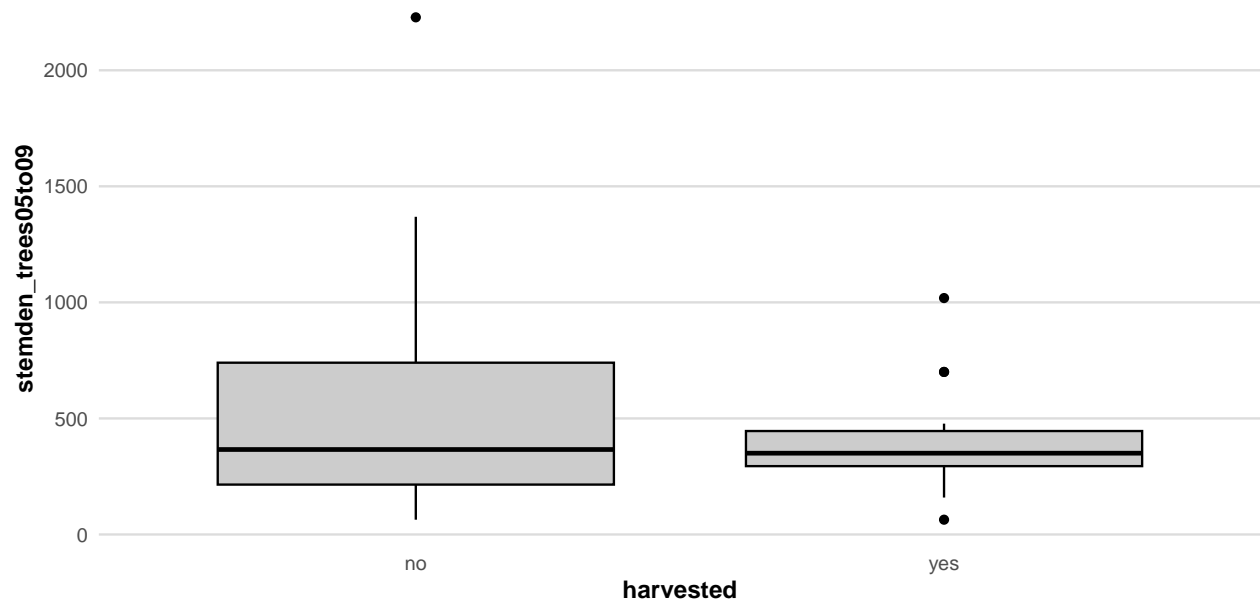
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = harvested, y = stemden_seedlings),
    col = "black", fill = "gray80") + plot_theme
```



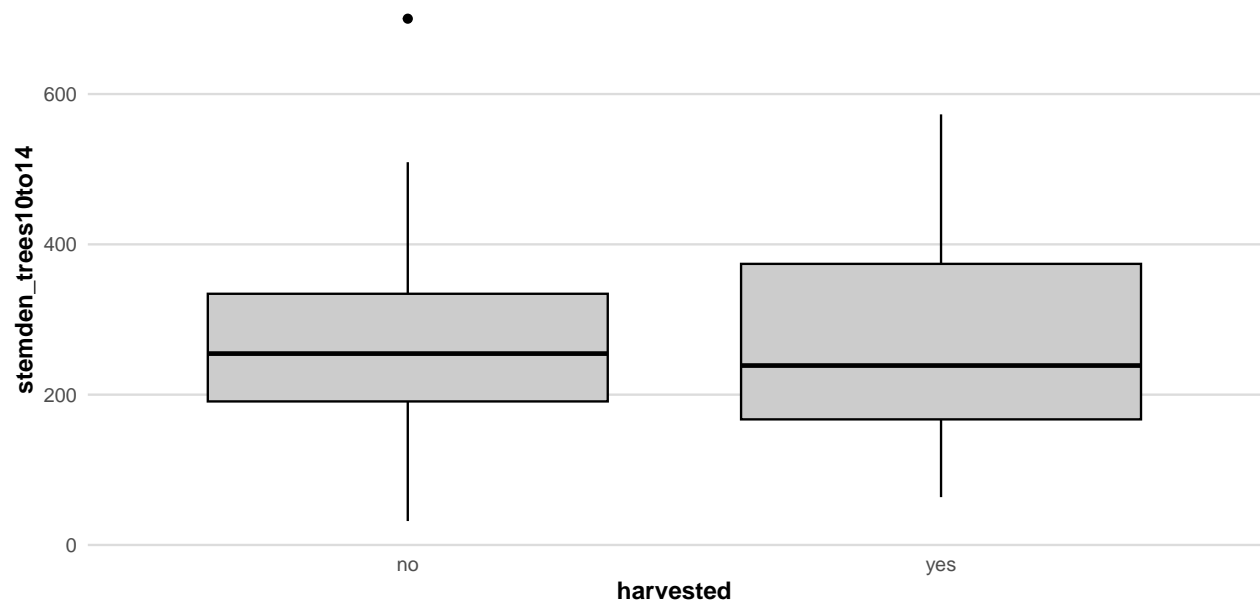
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = harvested, y = stemden_saplings),
    col = "black", fill = "gray80") + plot_theme
```



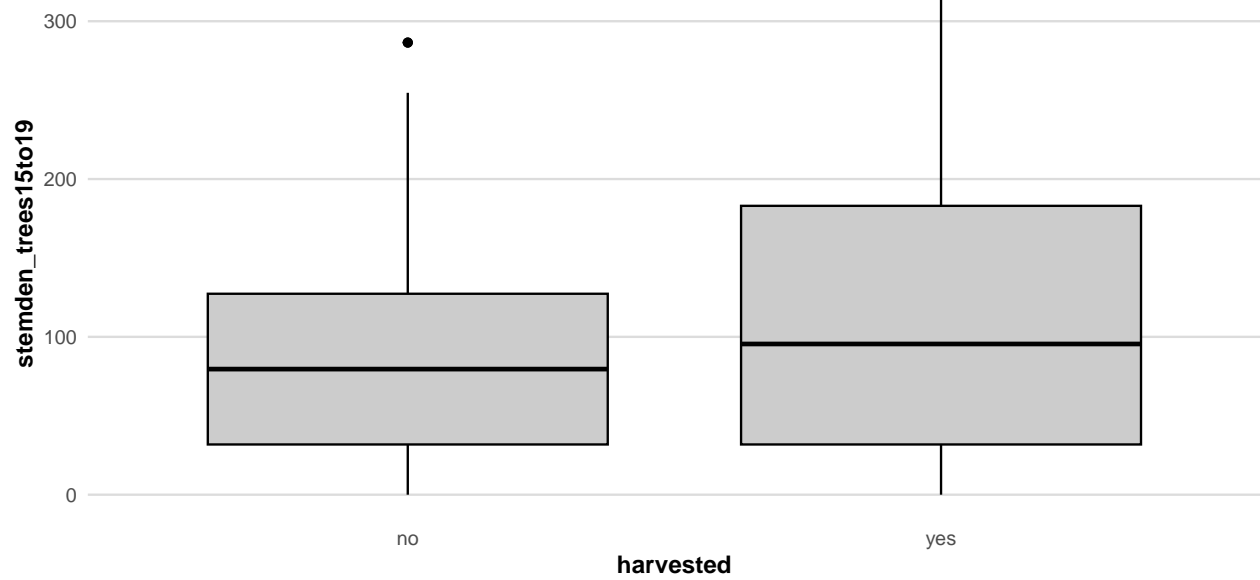
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = harvested, y = stemden_trees05to09),
    col = "black", fill = "gray80") + plot_theme
```



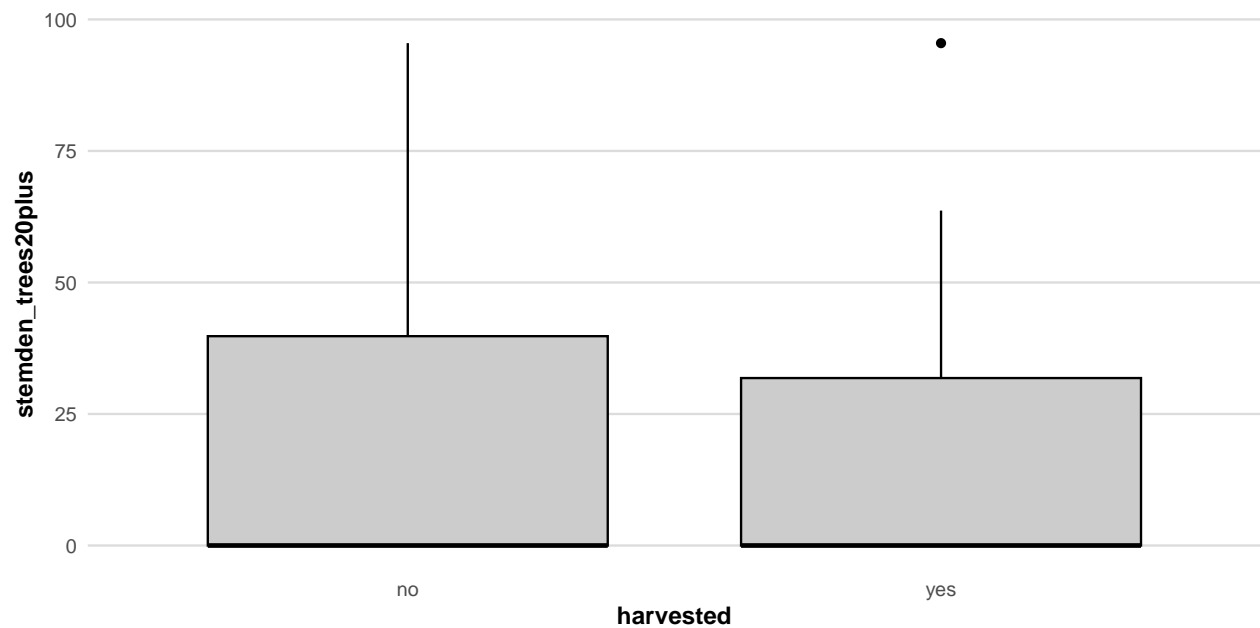
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = harvested, y = stemden_trees10to14),
    col = "black", fill = "gray80") + plot_theme
```



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

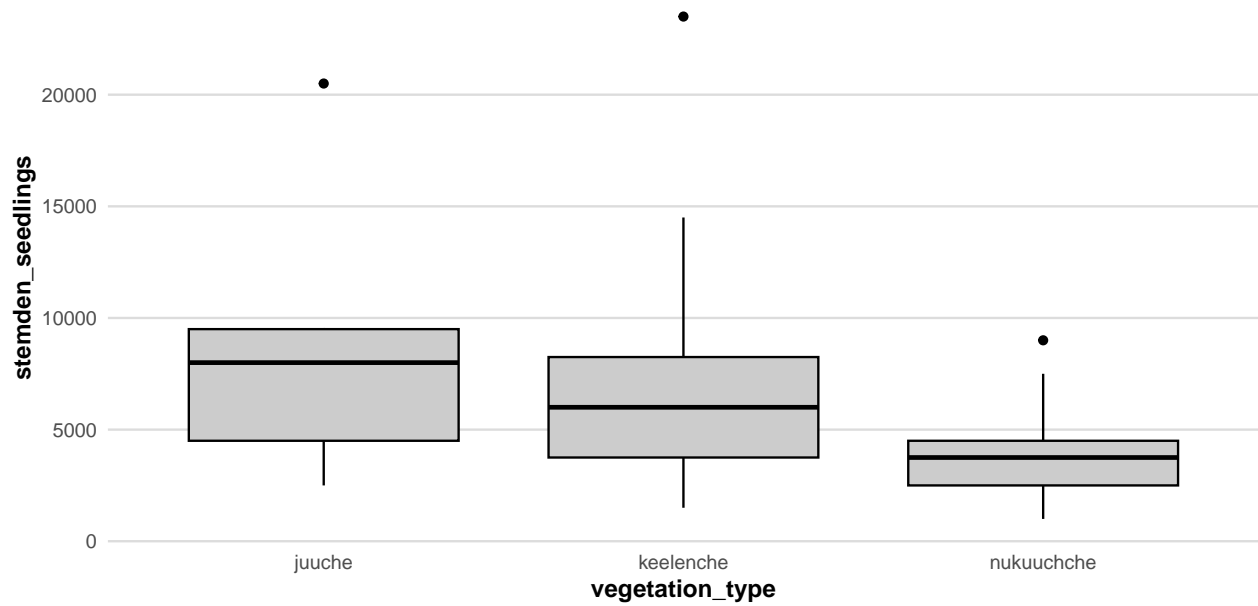



```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = harvested, y = stemden_trees20plus),
    col = "black", fill = "gray80") + plot_theme
```

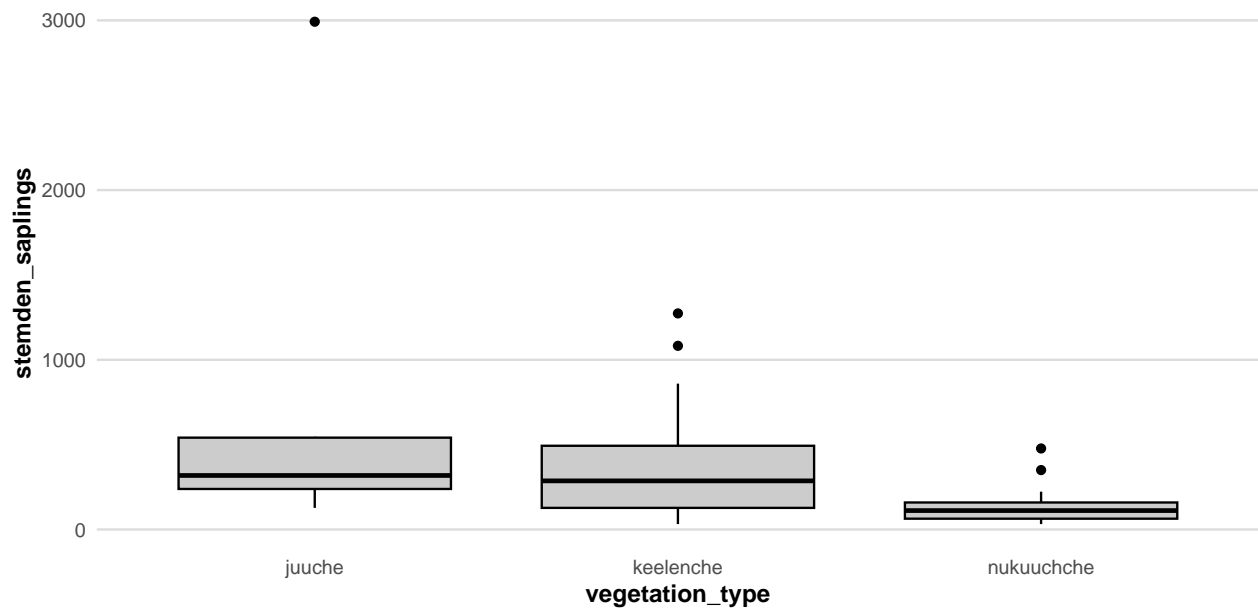


Box plots, vegetation type

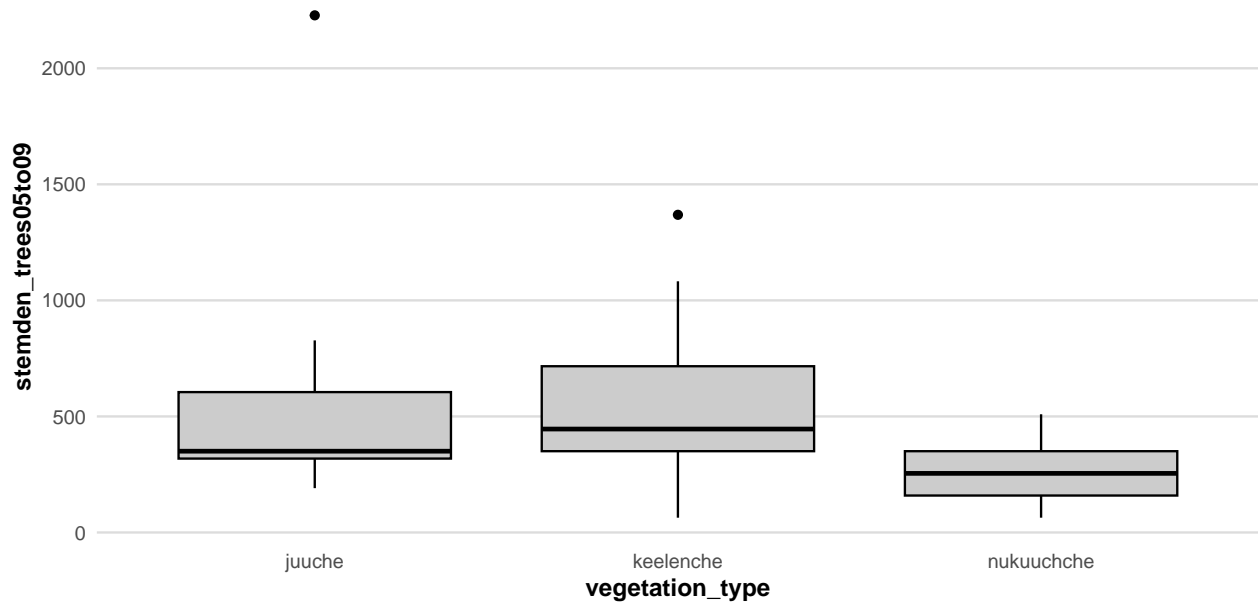
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = vegetation_type, y = stemden_seedlings),
    col = "black", fill = "gray80") + plot_theme
```



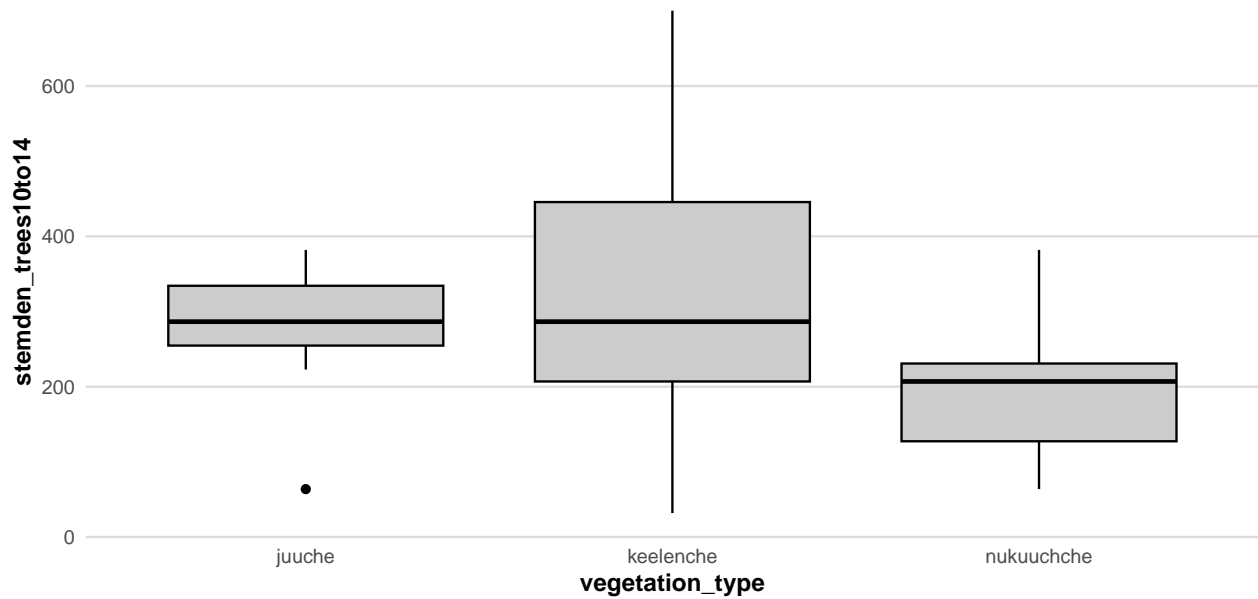
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = vegetation_type, y = stemden_saplings),
    col = "black", fill = "gray80") + plot_theme
```



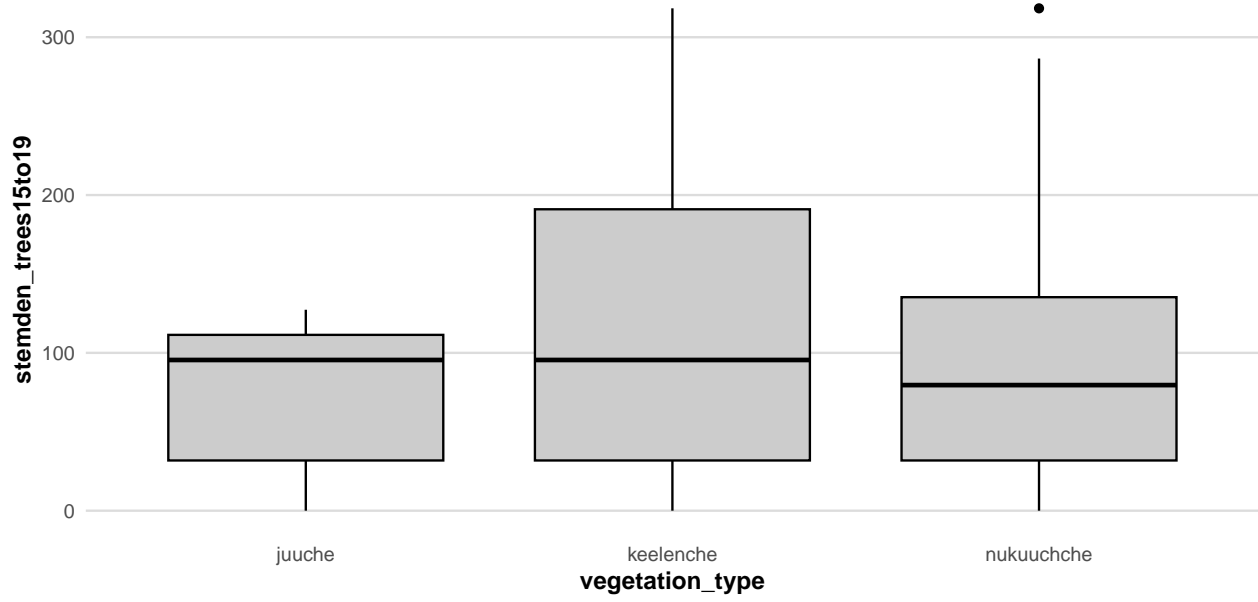
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = vegetation_type, y = stemden_trees05to09),
    col = "black", fill = "gray80") + plot_theme
```



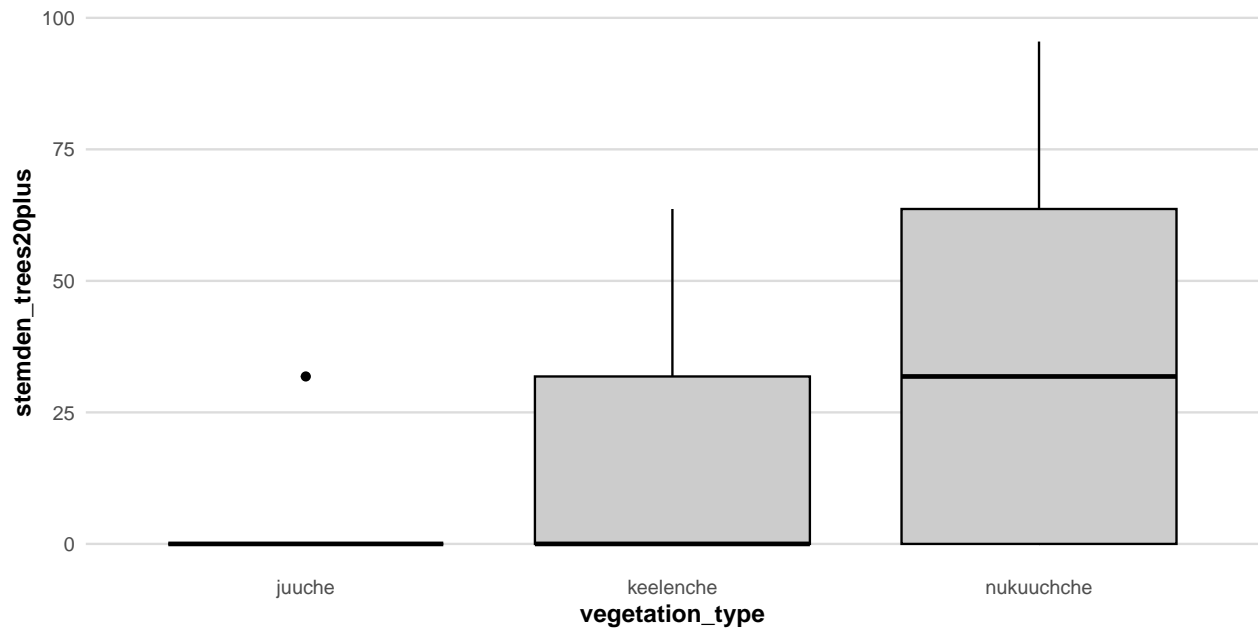
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = vegetation_type, y = stemden_trees10to14),
    col = "black", fill = "gray80") + plot_theme
```



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

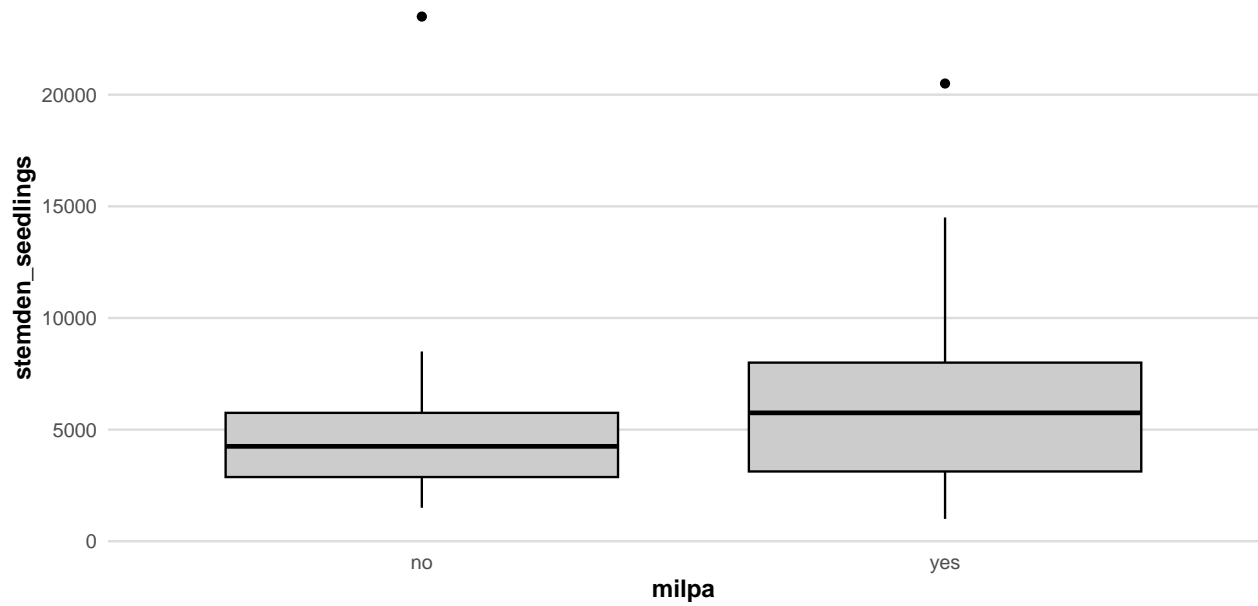


```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = vegetation_type, y = stemden_trees20plus),
    col = "black", fill = "gray80") + plot_theme
```

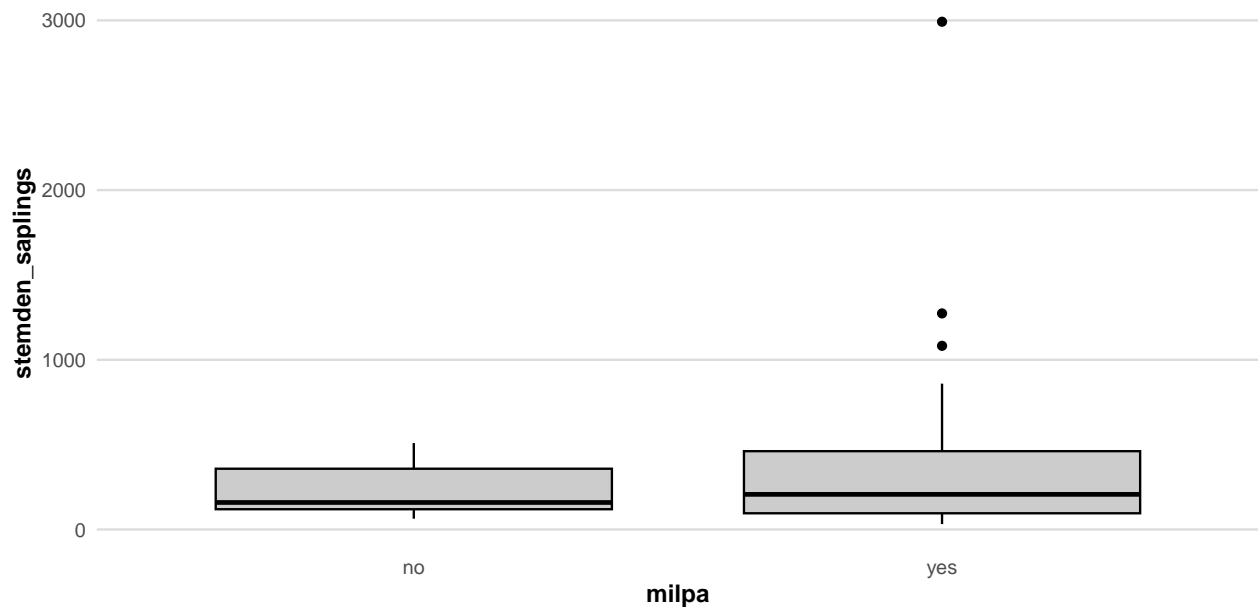


Box plots, milpa exposure

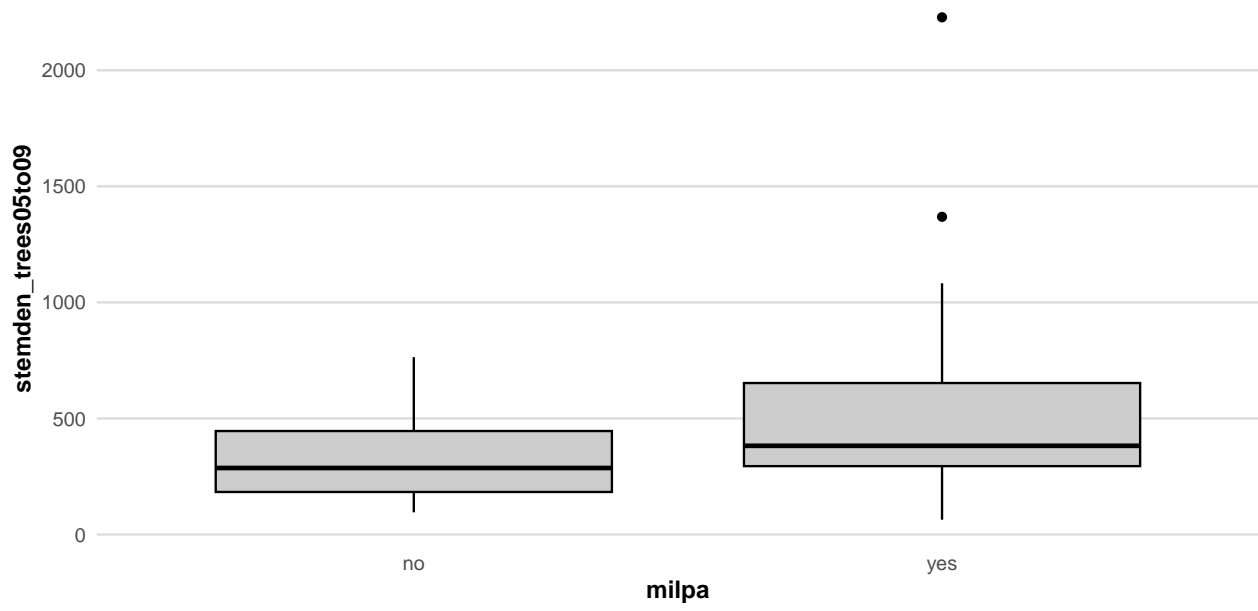
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = milpa, y = stemden_seedlings),
    col = "black", fill = "gray80") + plot_theme
```



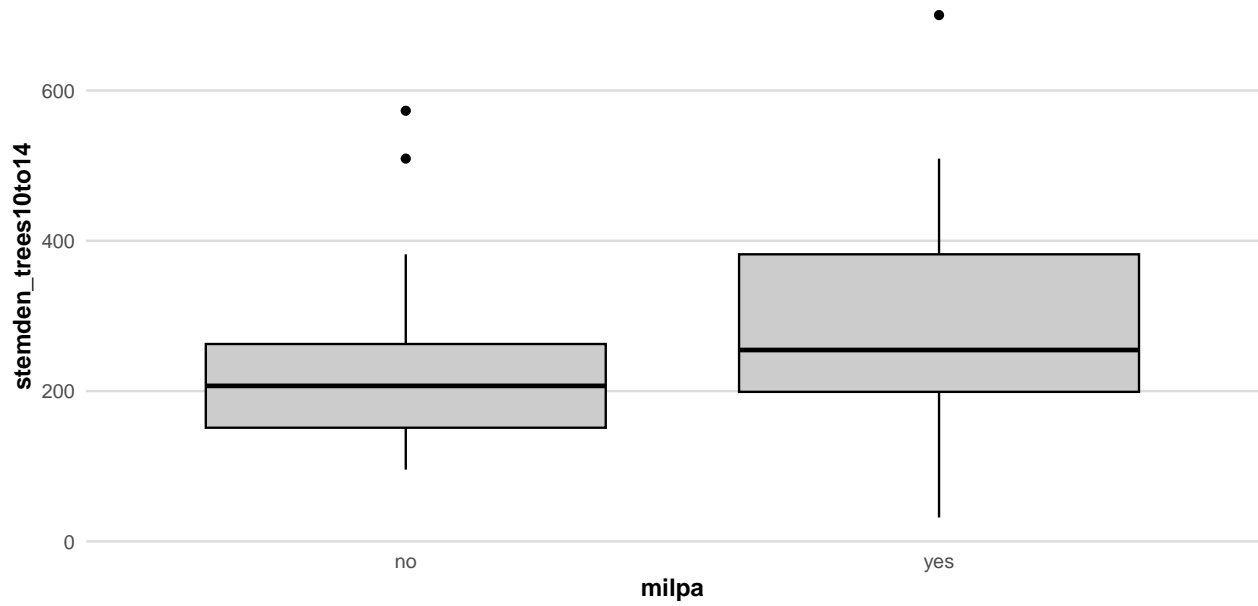
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = milpa, y = stemden_saplings),
    col = "black", fill = "gray80") + plot_theme
```



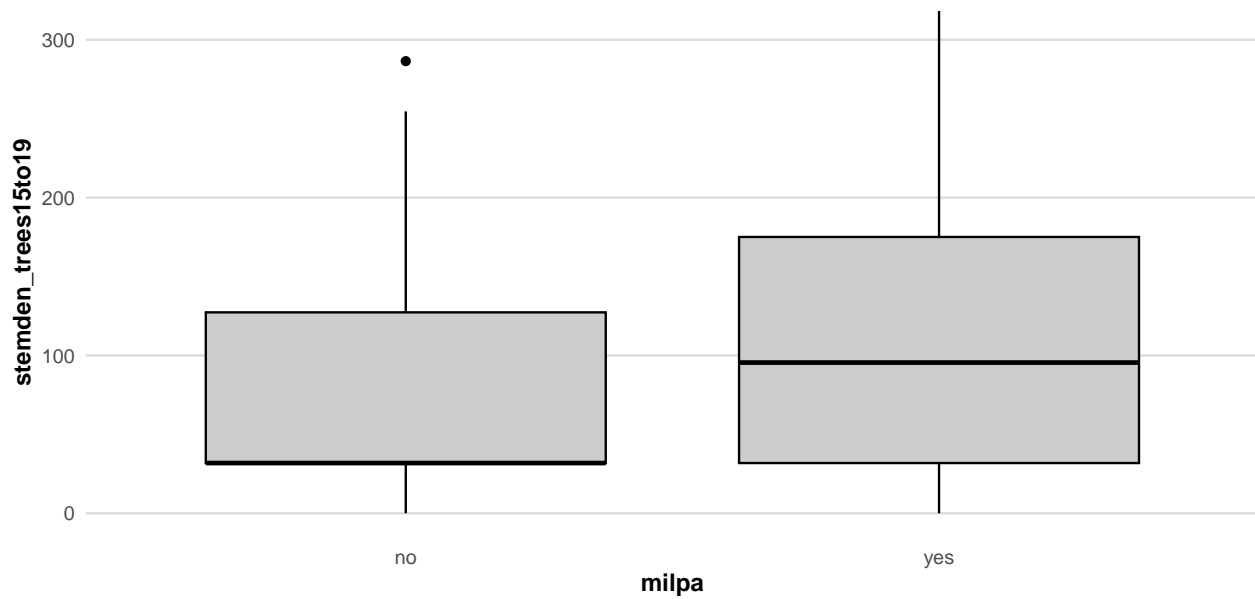
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = milpa, y = stemden_trees05to09),
    col = "black", fill = "gray80") + plot_theme
```



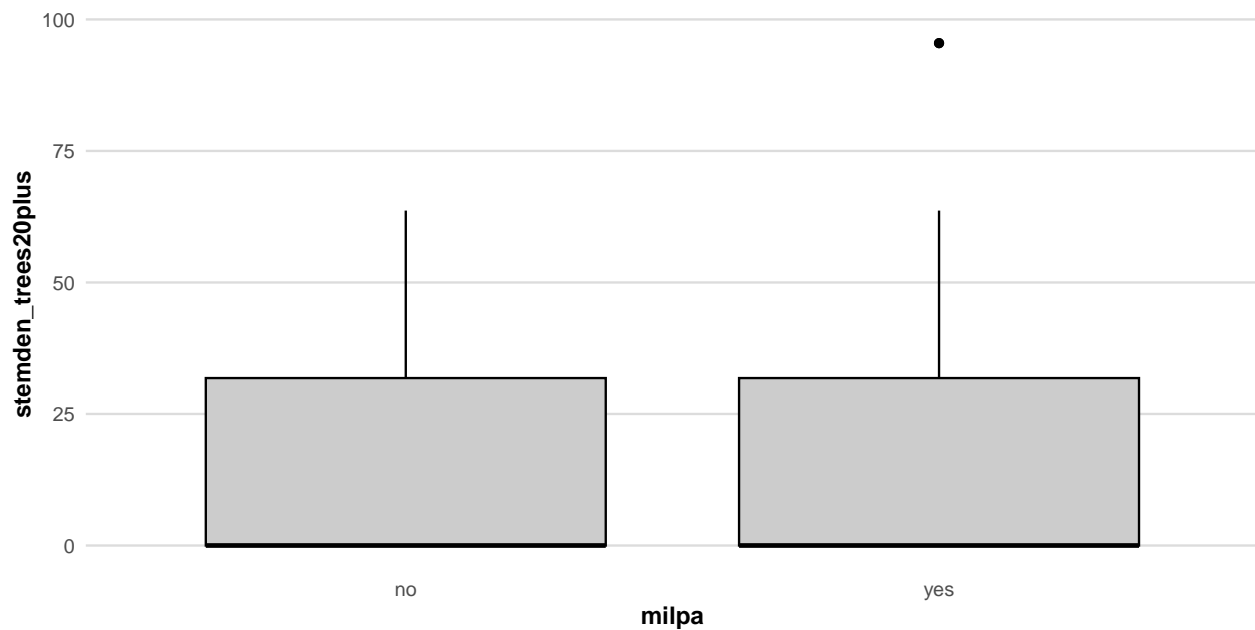
```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = milpa, y = stemden_trees10to14),
    col = "black", fill = "gray80") + plot_theme
```



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

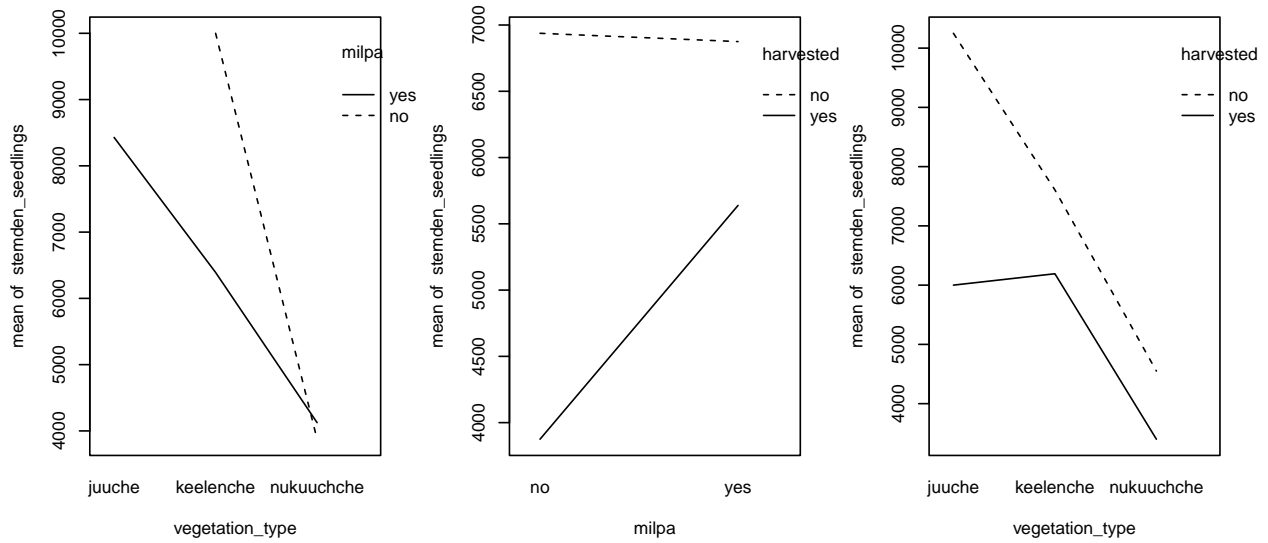


```
data_plots %>% ggplot() +
  geom_boxplot(aes(x = milpa, y = stemden_trees20plus),
    col = "black", fill = "gray80") + plot_theme
```

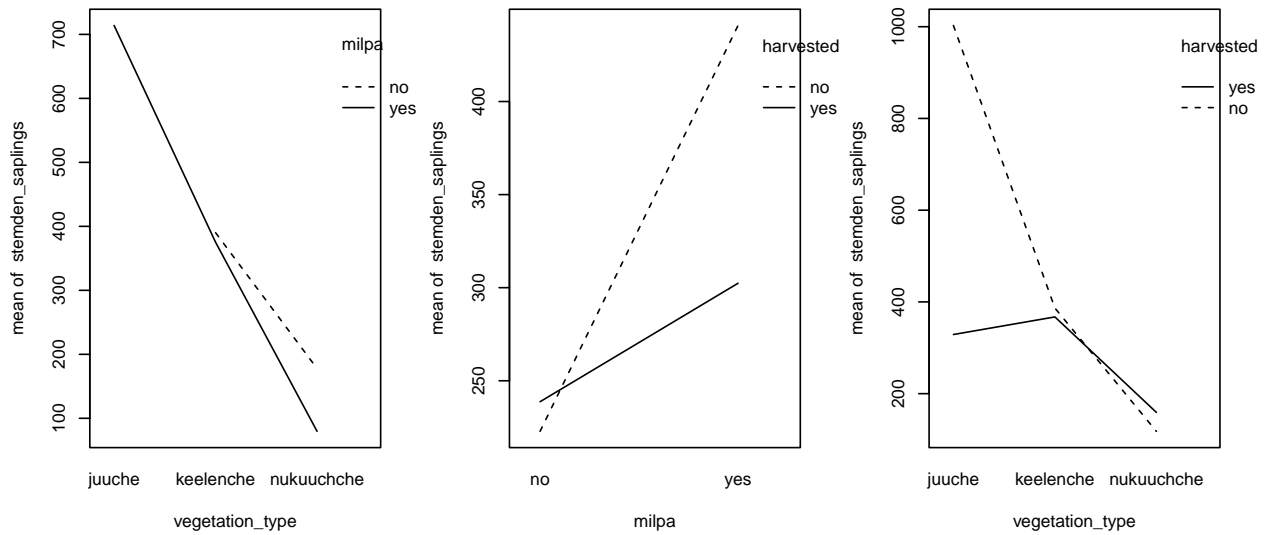


Interaction plots

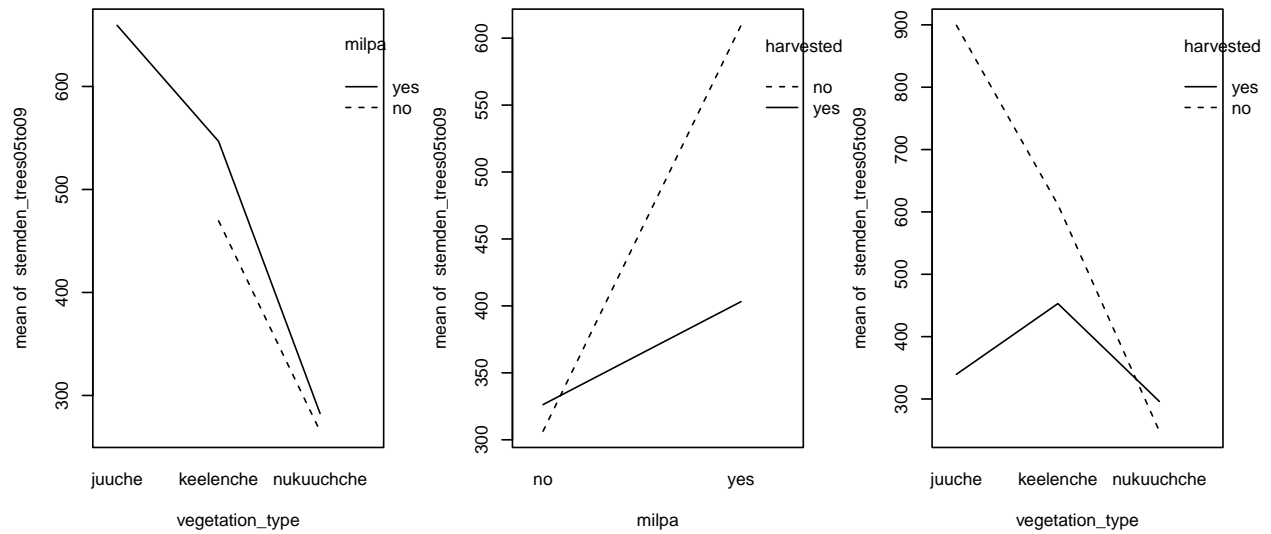
```
par(mfrow = c(1,3))
with(data_plots, {interaction.plot(vegetation_type, milpa, stemden_seedlings)
  interaction.plot(milpa, harvested, stemden_seedlings)
  interaction.plot(vegetation_type, harvested, stemden_seedlings)})
```



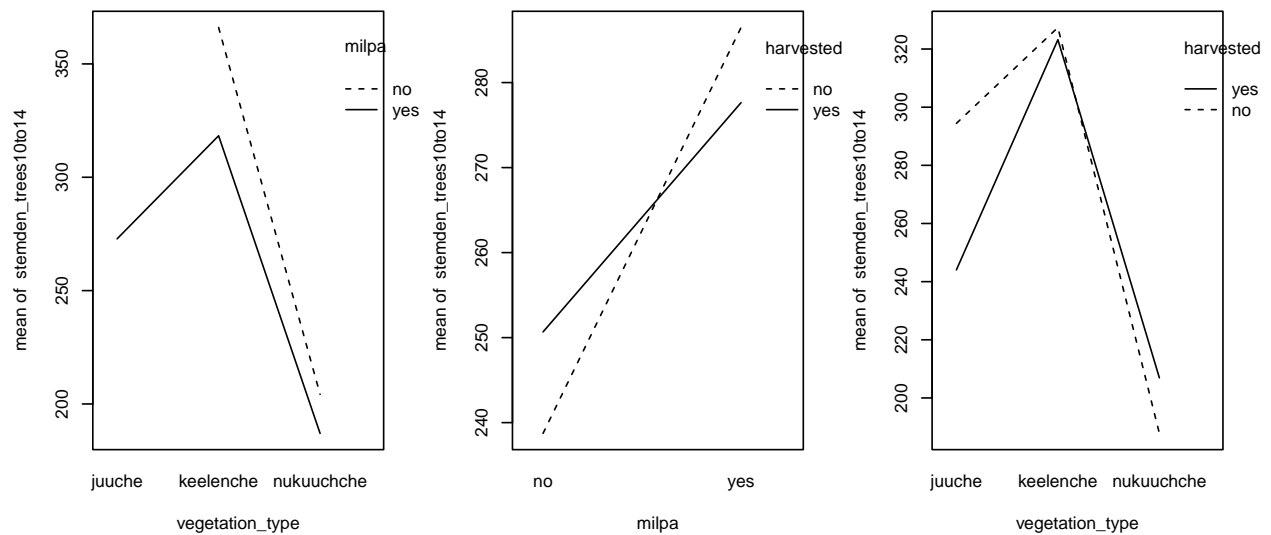
```
with(data_plots, {interaction.plot(vegetation_type, milpa, stemden_saplings)
                  interaction.plot(milpa, harvested, stemden_saplings)
                  interaction.plot(vegetation_type, harvested, stemden_saplings)})
```



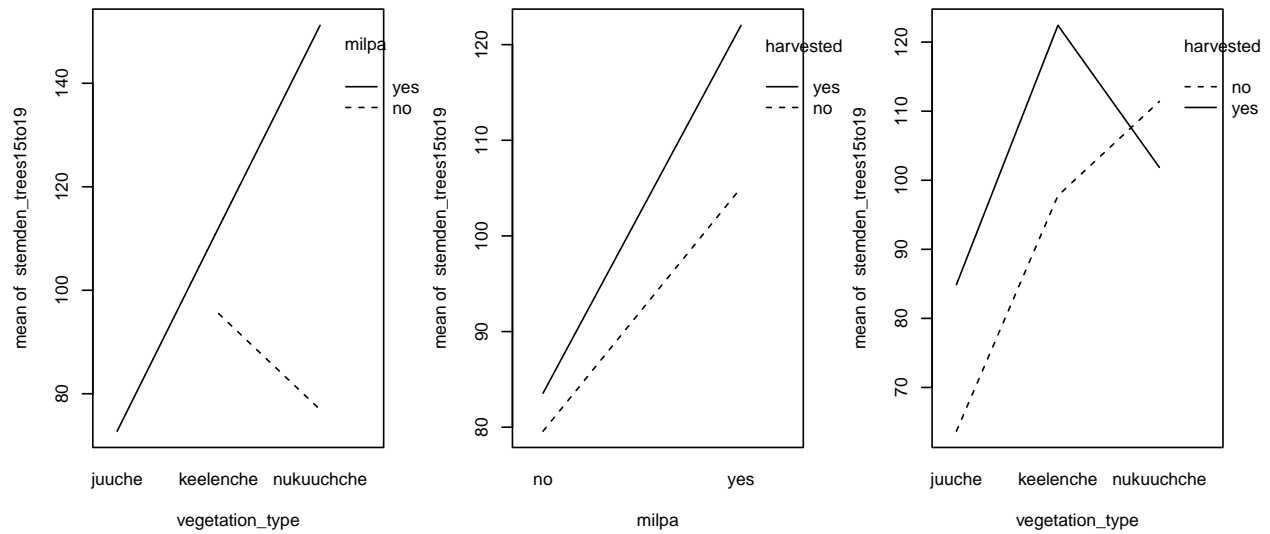
```
with(data_plots, {interaction.plot(vegetation_type, milpa, stemden_trees05to09)
                  interaction.plot(milpa, harvested, stemden_trees05to09)
                  interaction.plot(vegetation_type, harvested, stemden_trees05to09)})
```

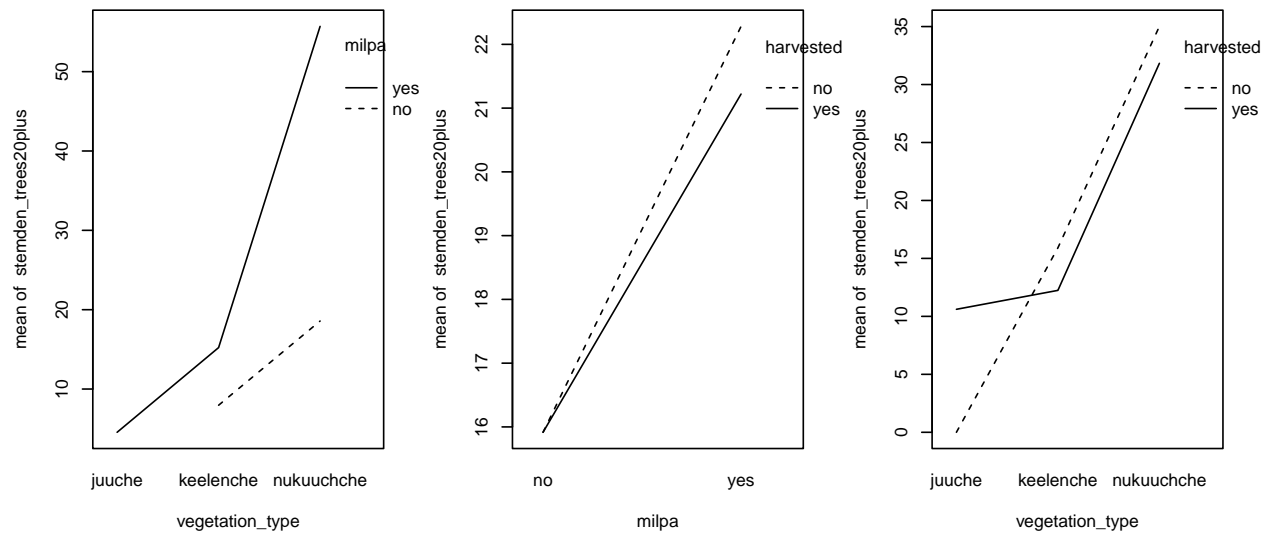
```
with(data_plots, {interaction.plot(vegetation_type, milpa, stemden_trees10to14)
               interaction.plot(milpa, harvested, stemden_trees10to14)
               interaction.plot(vegetation_type, harvested, stemden_trees10to14)})
```



```
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)})
```



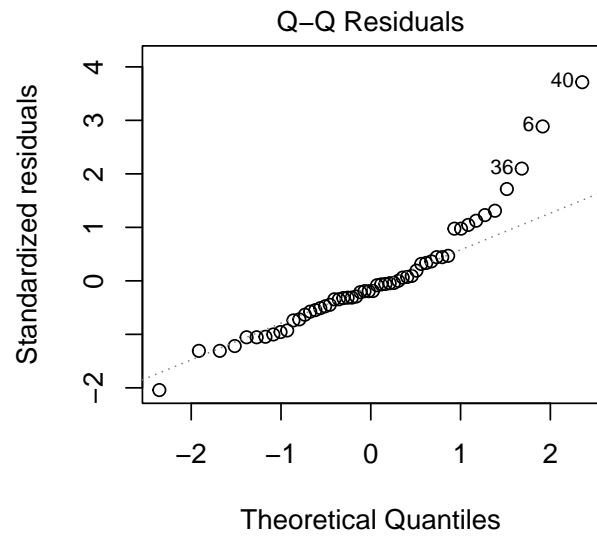
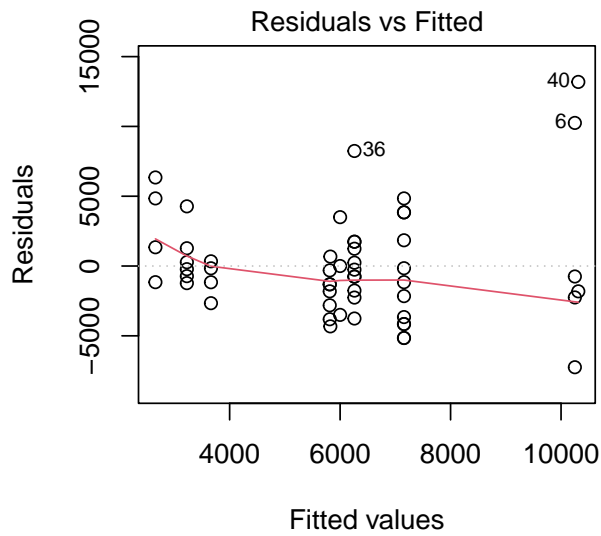
Models

Seedlings

Fit model and check assumptions

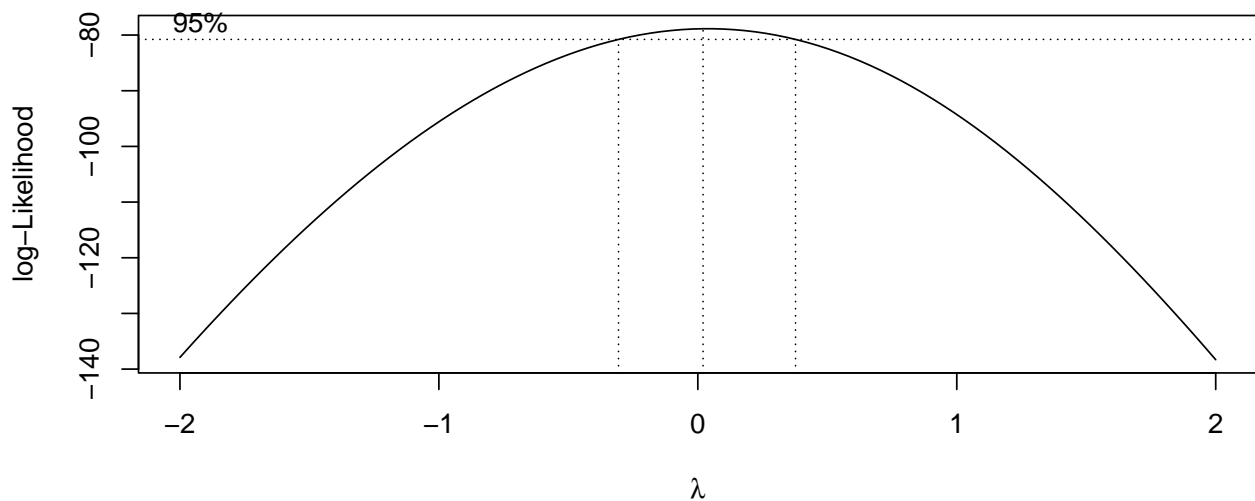
```
mod.2b.seedlings <- lm(stemden_seedlings ~ harvested + vegetation_type + milpa +
harvested:vegetation_type + harvested:milpa, data = data_plots)

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



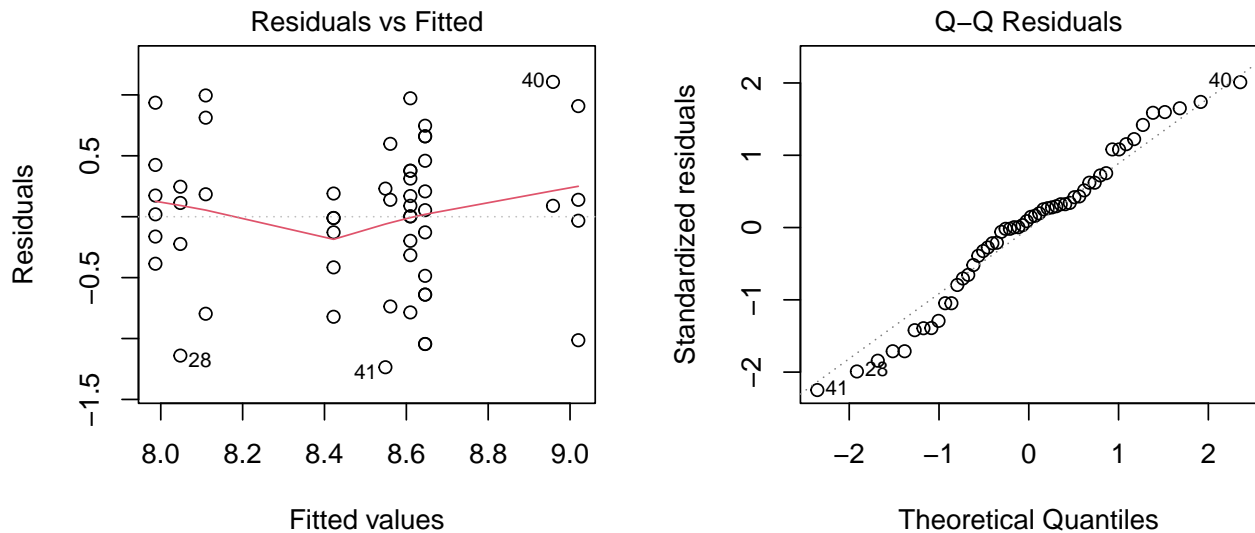
Attempt transformation of response

```
# 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:
##              Estimate Std. Error t value Pr(>|t|)
## (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_typenukuuchche 0.3974 0.6222 0.639 0.5261
## harvestedyes:milpayes 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 then 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
##
```

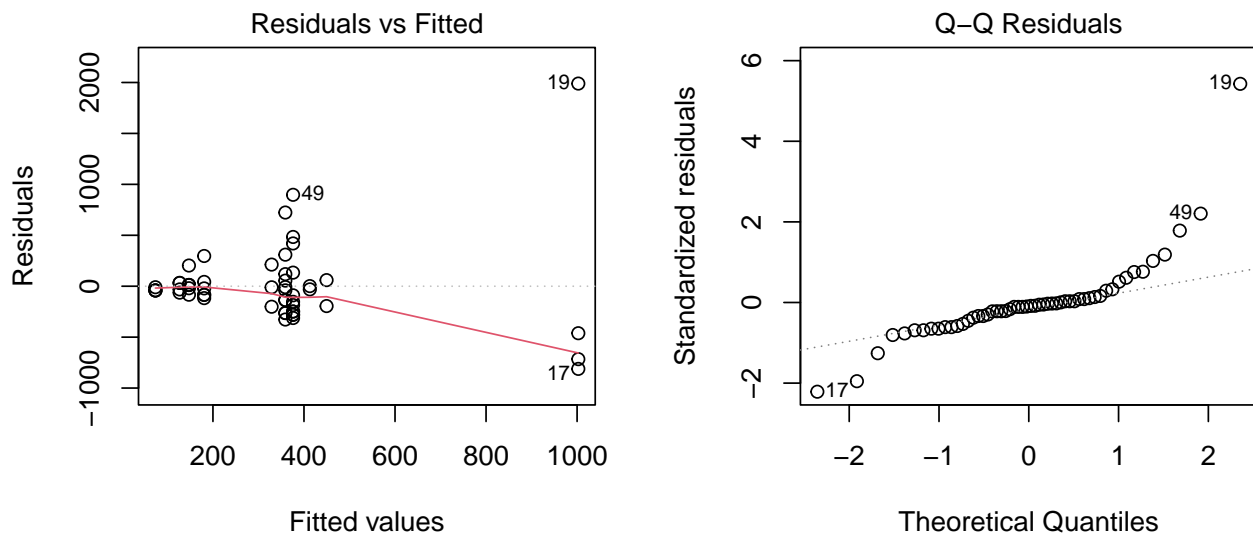
```
## Fit: aov(formula = mod.2b.seedlings.transform)
##
## $harvested
##           diff           lwr           upr           p adj
## yes-no -0.227877 -0.5762009 0.120447 0.1944098
```

Saplings (0-4 cm DBH)

Fit model and check assumptions

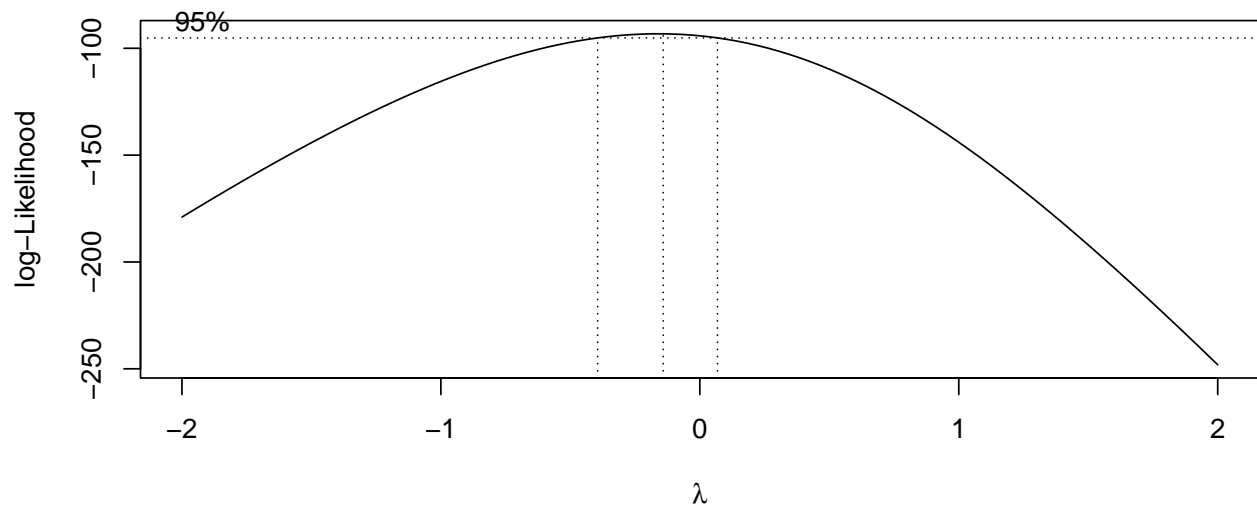
```
mod.2b.saplings <- lm(stemden_saplings ~ harvested + vegetation_type + milpa +
                      harvested:vegetation_type + harvested:milpa, data = data_plots)

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



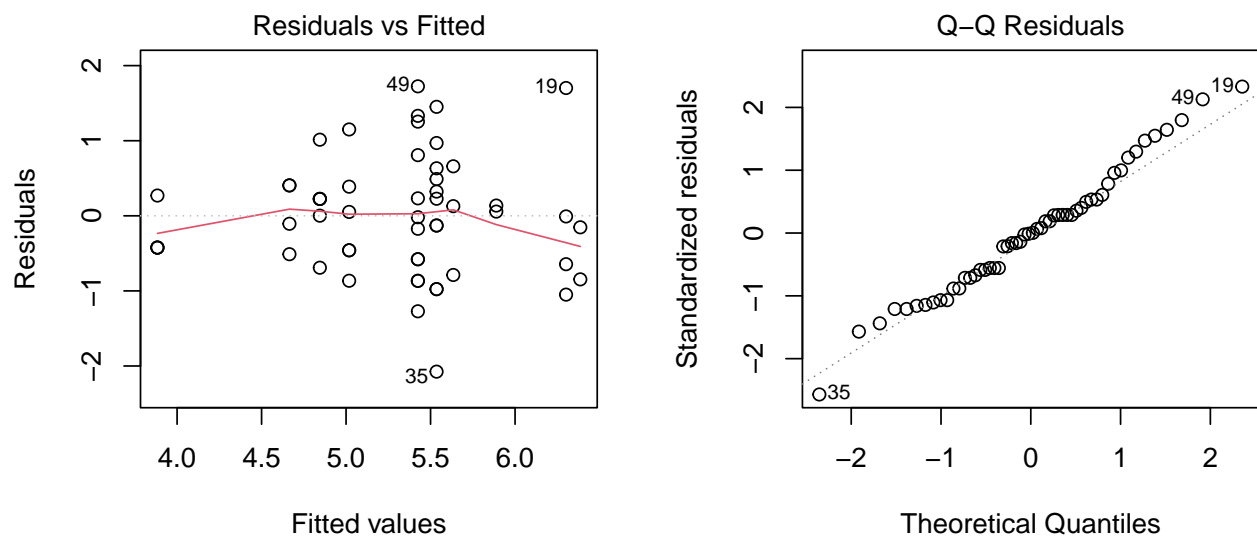
Attempt transformation of response

```
# 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)
```

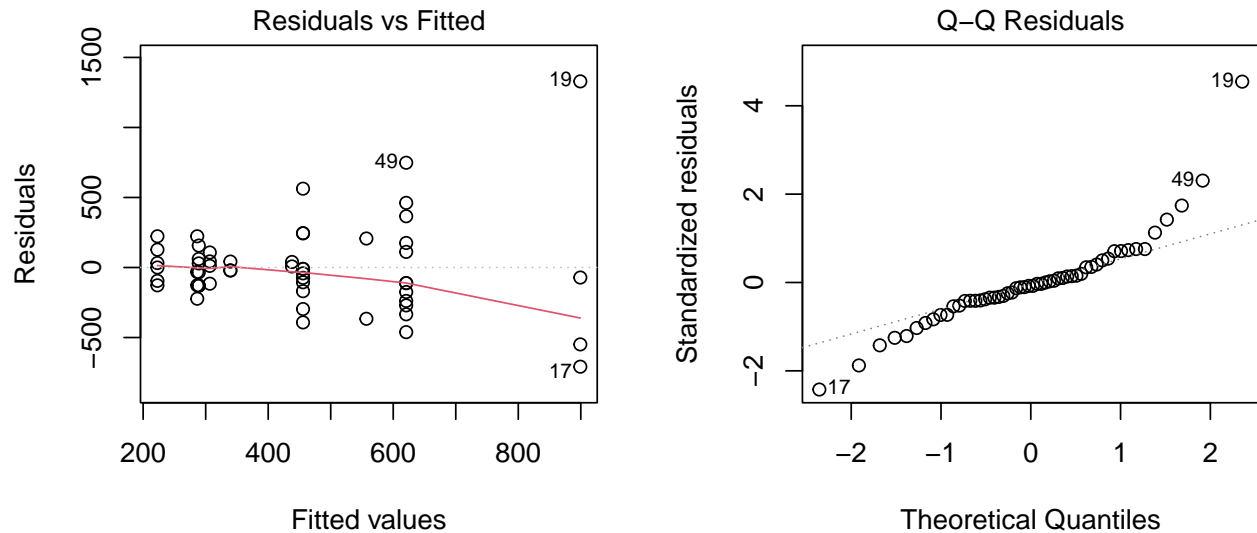
```
## Tukey multiple comparisons of means  
## 95% family-wise confidence level  
##  
## Fit: aov(formula = mod.2b.saplings.transform)  
##  
## $harvested  
## diff lwr upr p adj  
## yes-no 0.04643418 -0.4157128 0.5085812 0.8406166
```

Trees (5-9 cm DBH)

Fit model and check assumptions

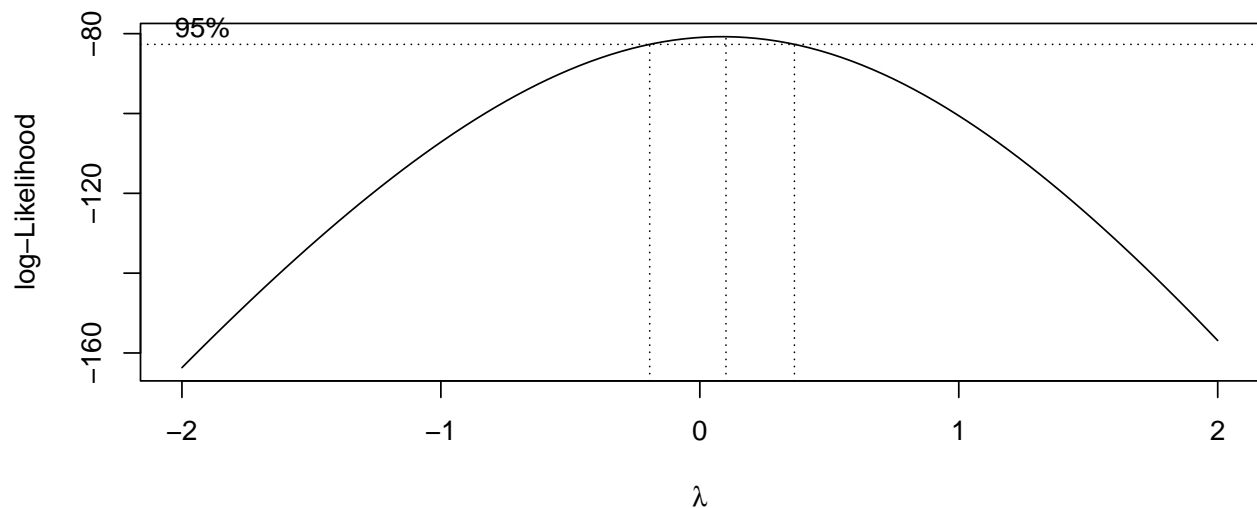
```
mod.2b.05to09 <- lm(stemden_trees05to09 ~ harvested + vegetation_type + milpa +
                    harvested:vegetation_type + harvested:milpa, data = data_plots)

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



Attempt transformation of response

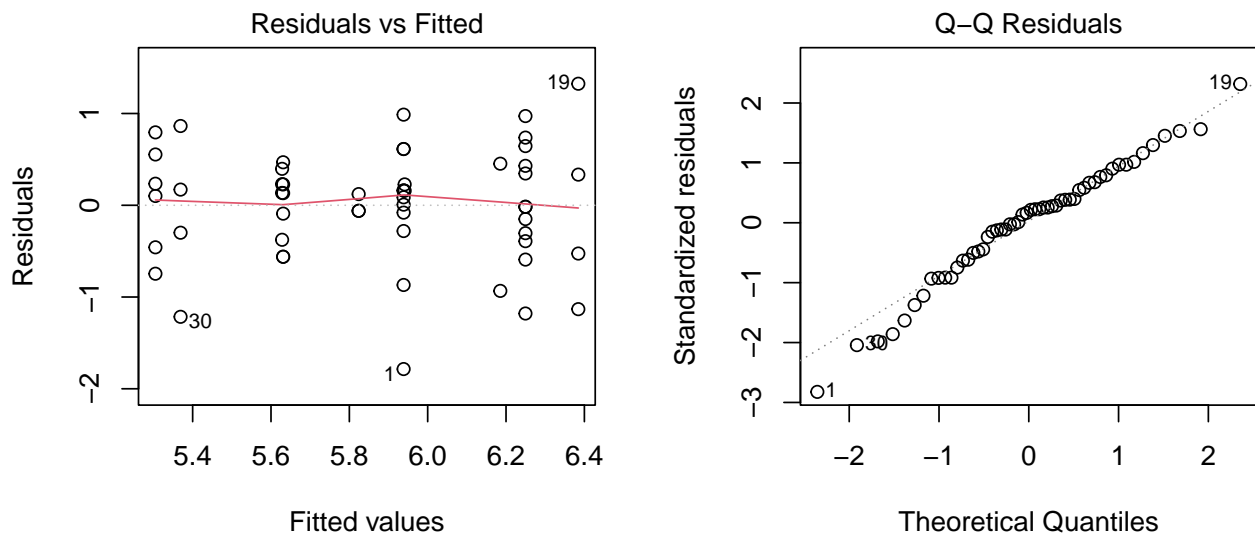
```
# Very distinct megaphone shape on the residuals vs. fitted; try Box-Cox
MASS::boxcox(mod.2b.05to09)
```



```
# 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 then 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)
```

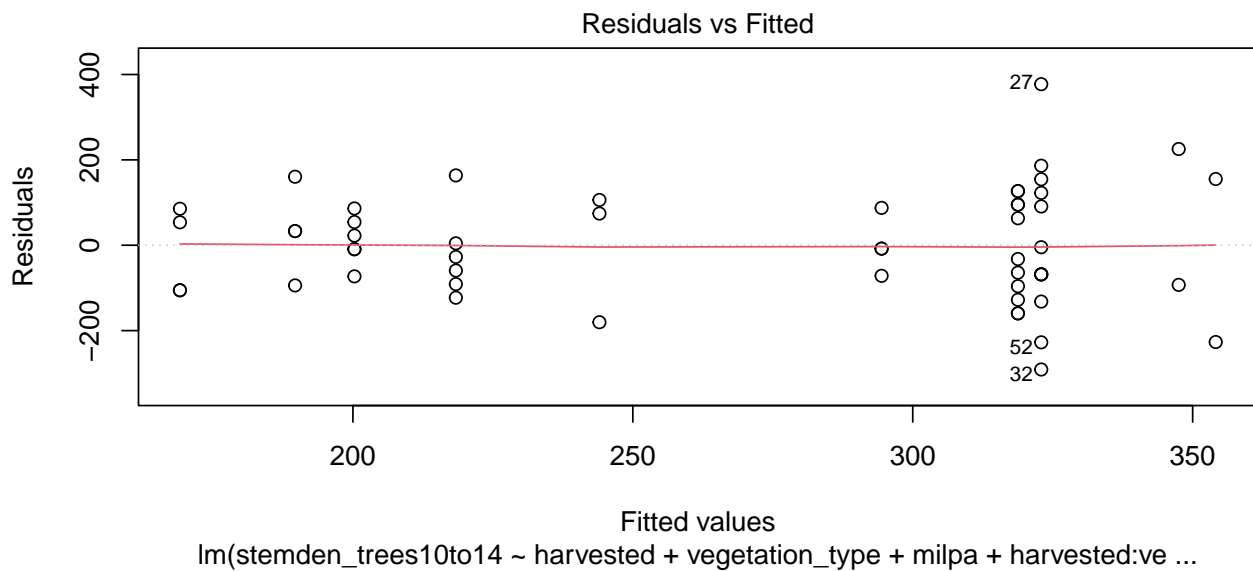
```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = mod.2b.05to09.transform)
##
## $harvested
##           diff           lwr           upr           p adj
## yes-no -0.1292511 -0.4910977 0.2325956 0.4757758
```

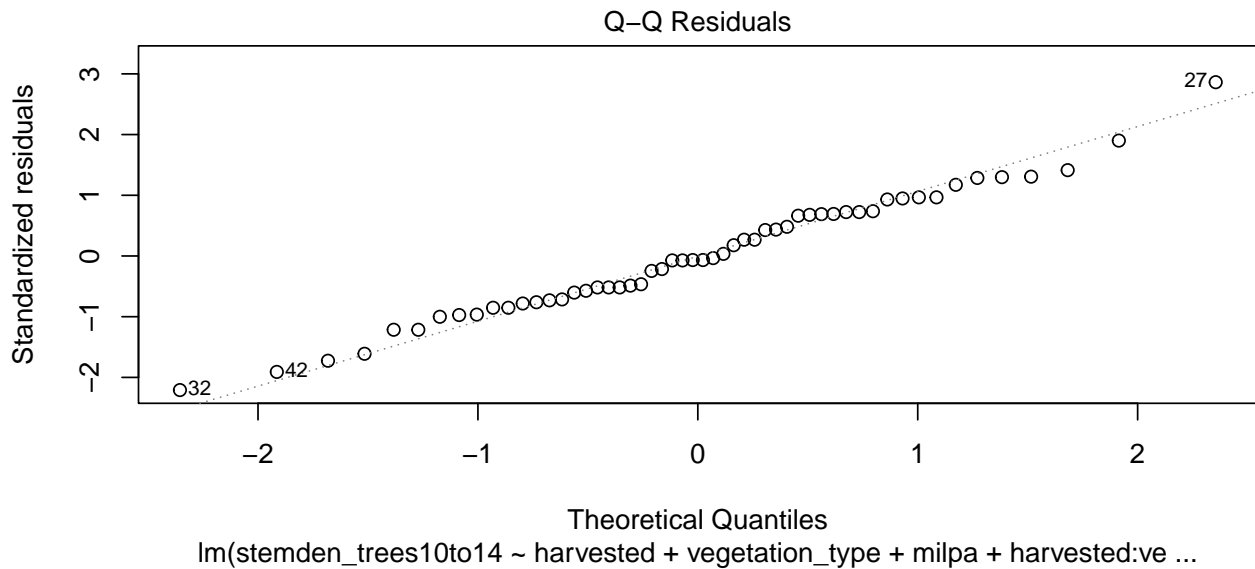
Trees (10-14 cm DBH)

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_typenukuuchche 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)
##
```

	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
##
```

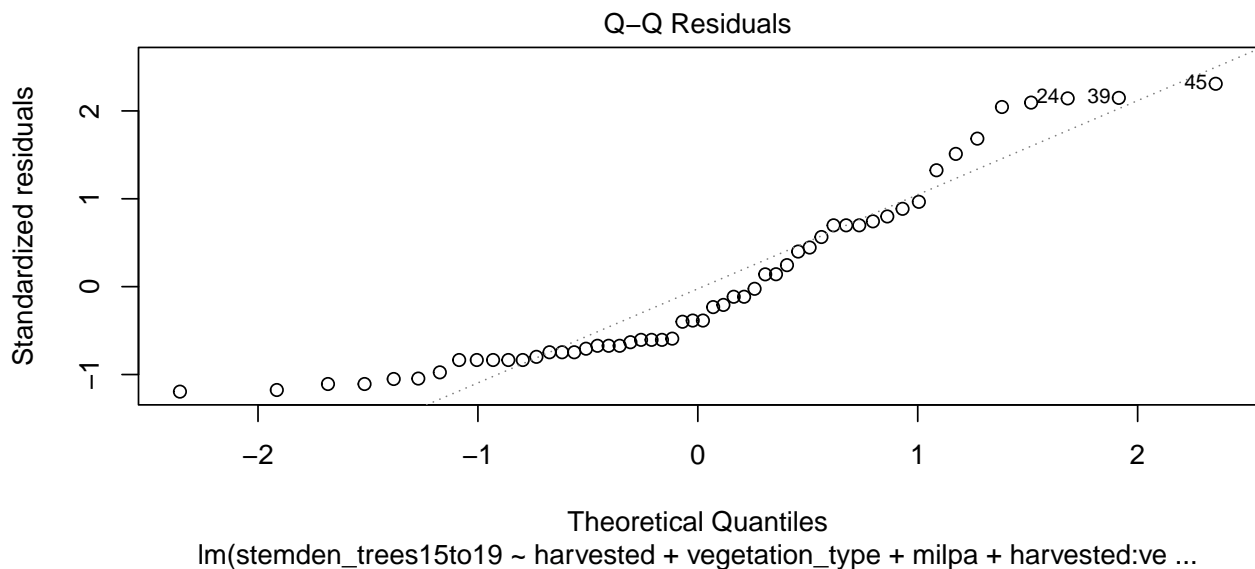
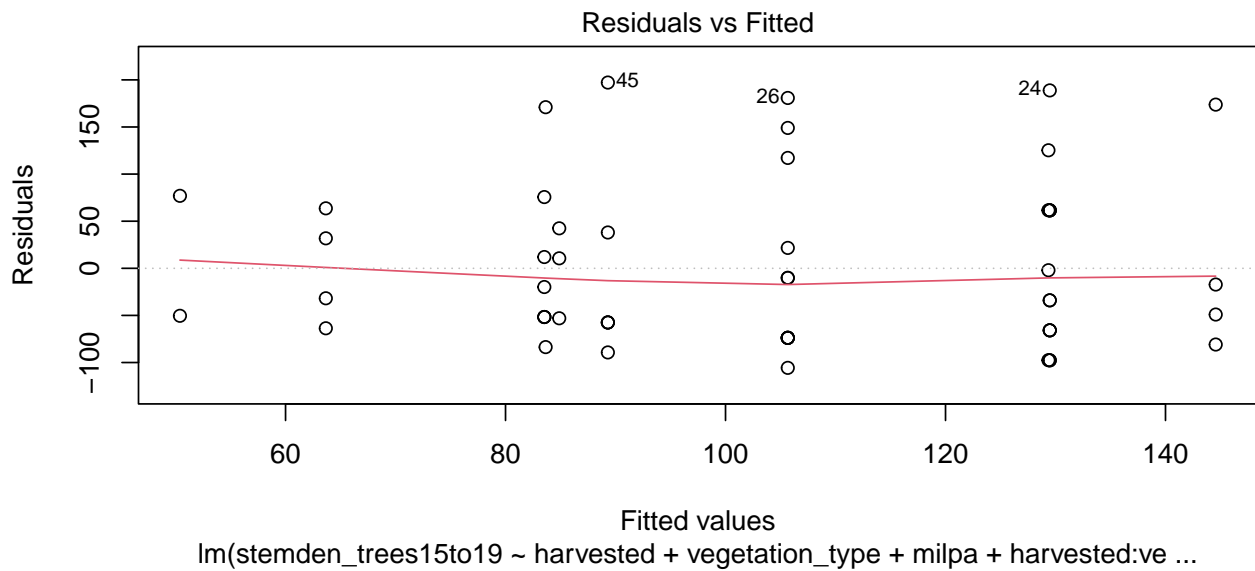
```
## Fit: aov(formula = mod.2b.10to14)
##
## $harvested
##           diff          lwr          upr      p adj
## yes-no -3.497911 -78.69058  71.69476  0.925803
```

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)
```

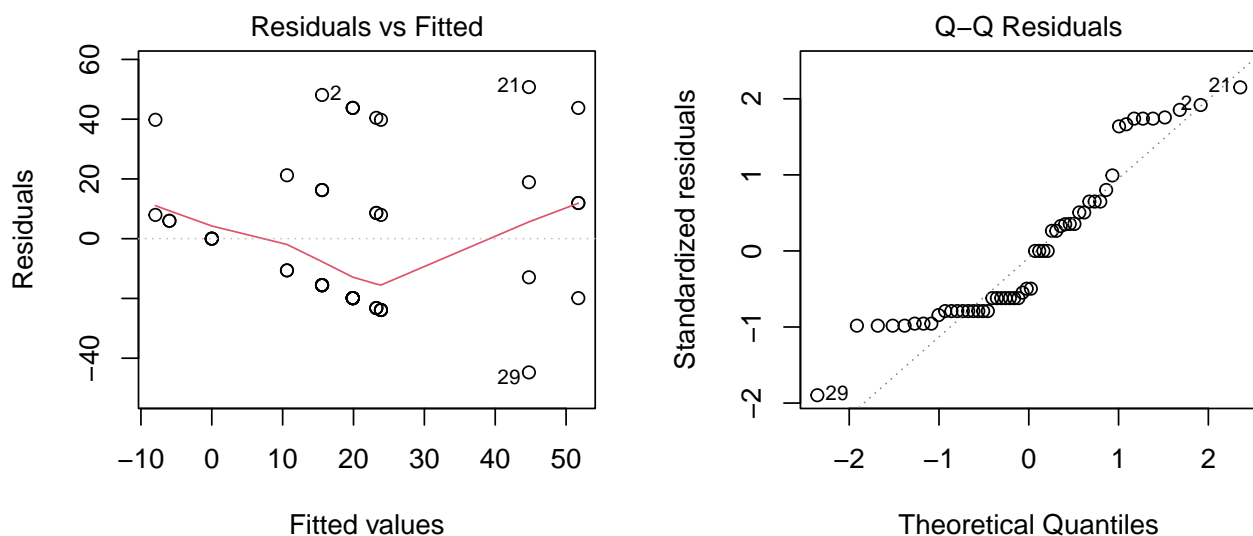
```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = mod.2b.15to19)
##
## $harvested
##          diff          lwr          upr          p adj
## yes-no 12.41758 -38.03383 62.869 0.6226531
```

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)
```

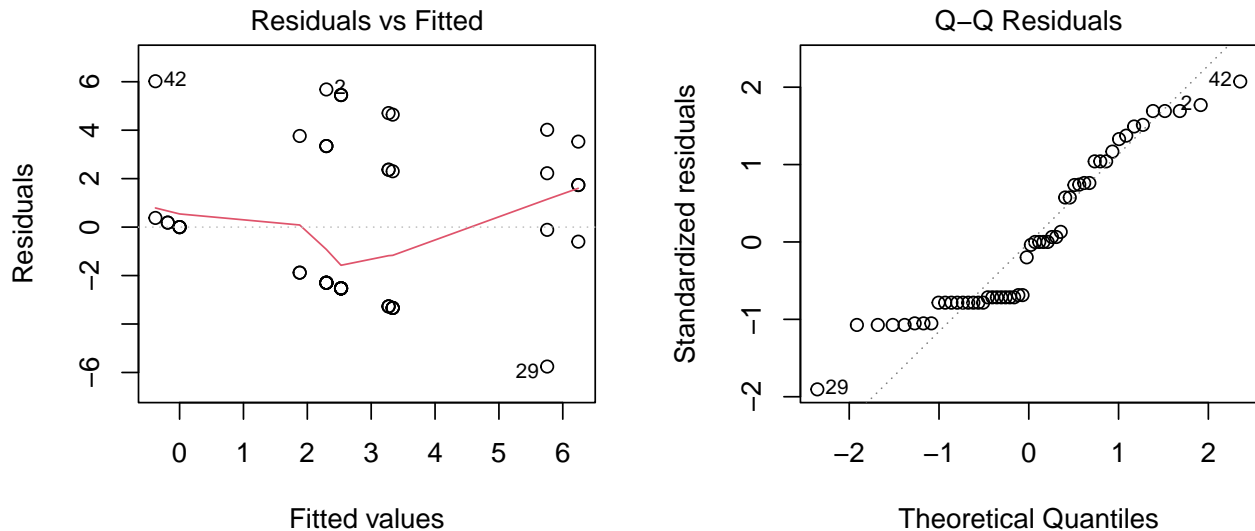


There is a little bit of a megaphone shape on the residuals vs. fitted. We can't do a log transformation since the response has zeros, so we'll try a square root transformation.

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:
##              Estimate Std. Error t value Pr(>|t|)
## (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
```