

Basal area

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Packages and data

```
library(car)
library(tidyverse)
library(patchwork)

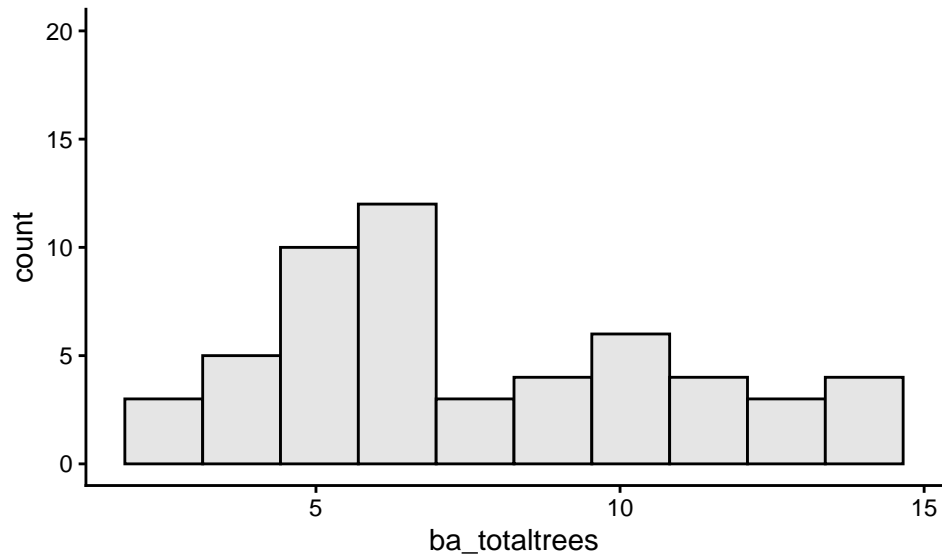
data_stems <- read_csv("data/data_stems.csv") %>%
  mutate(plot_id = as.factor(plot_id),
         size_class = as.factor(size_class),
         harvested = as.factor(harvested),
         vegetation_type = as.factor(vegetation_type),
         milpa = as.factor(milpa))
data_plots <- read_csv("data/data_plots.csv")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

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"))
```

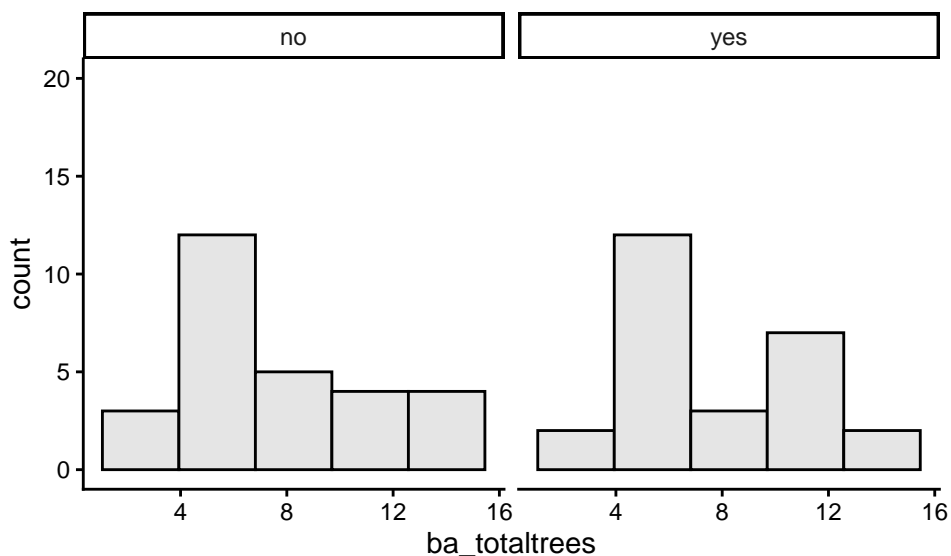
Figures

Histograms of total basal area of trees

```
# All plots
data_plots %>%
  ggplot() +
    geom_histogram(aes(x = ba_totaltrees), bins = 10, fill = "gray90", col = "black") +
    theme_classic() + ylim(c(0,20))
```



```
# Harvested vs. unharvested plots
data_plots %>%
  ggplot() +
    geom_histogram(aes(x = ba_totaltrees), bins = 5, fill = "gray90", col = "black") +
    facet_wrap(~harvested) +
    theme_classic() + ylim(c(0,20))
```



Five-number summaries of total basal area of trees

```
# All plots
```

```
summary(data_plots$ba_totaltrees)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      2.498   5.161   6.639   7.660  10.316   14.015
```

```
# Harvested vs. unharvested plots
```

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

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      2.788   4.860   6.506   7.550  10.248   13.785
```

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

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      2.498   5.450   6.765   7.763  10.568   14.015
```

Box plots of total basal area of trees

```
# By harvesting status
```

```
ba_fig1 <- data_plots %>%
```

```
  mutate(harvested = fct_recode(harvested,
                                "Harvested" = "yes", "Unharvested" = "no")) %>%
```

```
  ggplot() +
    geom_boxplot(aes(x = fct_relevel(harvested, "Harvested", "Unharvested"),
                      y = ba_totaltrees),
                 fill = "mistyrose2", outlier.shape = 21,
                 outlier.color = "gray20", outlier.fill = "gray80") +
```

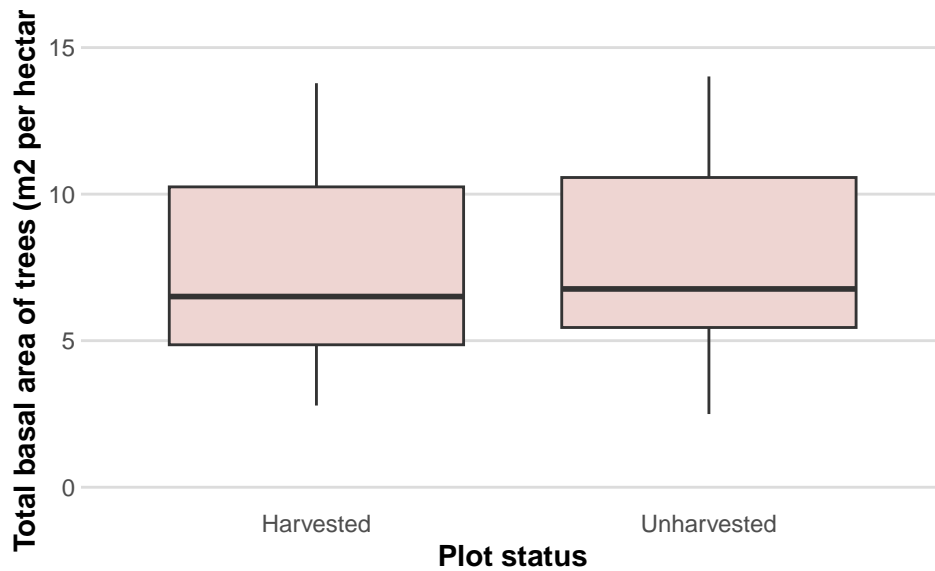
```
  plot_theme +
```

```
  coord_cartesian(ylim = c(0, 15)) +
```

```
  labs(x = "Plot status", y = "Total basal area of trees (m2 per hectare)")
```

```
ggsave("figures/not_in_manuscript/basal_area_harvest_boxplot.png", height = 4, width = 6)
```

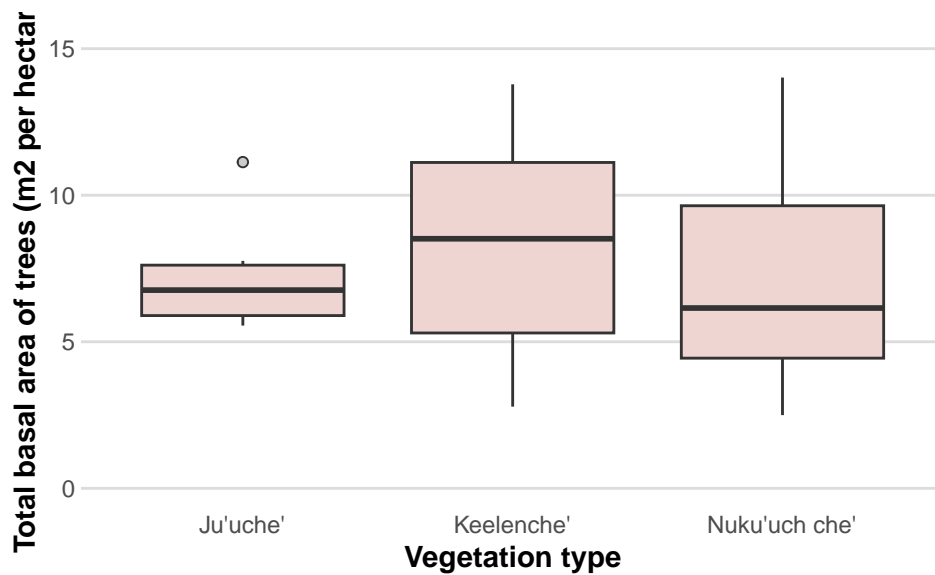
```
ba_fig1
```



```
# By vegetation type
ba_fig2 <- data_plots %>%
  mutate(vegetation_type = fct_recode(vegetation_type,
    "Ju'uche'" = "juuche",
    "Keelenche'" = "keelenche",
    "Nuku'uch che'" = "nukuuchche")) %>%

  ggplot() +
  geom_boxplot(aes(x = vegetation_type, y = ba_totaltrees),
    fill = "mistyrose2", outlier.shape = 21,
    outlier.color = "gray20", outlier.fill = "gray80") +

  plot_theme +
  coord_cartesian(ylim = c(0, 15)) +
  labs(x = "Vegetation type", y = "Total basal area of trees (m2 per hectare)")
ggsave("figures/not_in_manuscript/basal_area_vegetation_boxplot.png", height = 4, width = 6)
ba_fig2
```



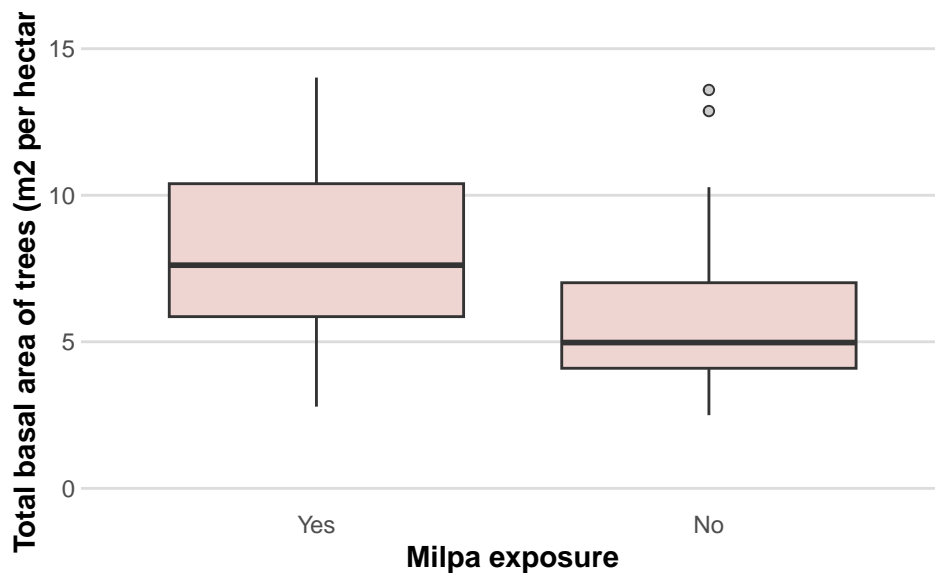
```

# By milpa
ba_fig3 <- data_plots %>%
  mutate(milpa = fct_recode(milpa,
                             "Yes" = "yes", "No" = "no")) %>%

  ggplot() +
  geom_boxplot(aes(x = fct_relevel(milpa, "Yes", "No"), y = ba_totaltrees),
               fill = "mistyrose2", outlier.shape = 21,
               outlier.color = "gray20", outlier.fill = "gray80") +

  plot_theme +
  coord_cartesian(ylim = c(0, 15)) +
  labs(x = "Milpa exposure", y = "Total basal area of trees (m2 per hectare)")
ggsave("figures/not_in_manuscript/basal_area_milpa_boxplot.png", height = 4, width = 6)
ba_fig3

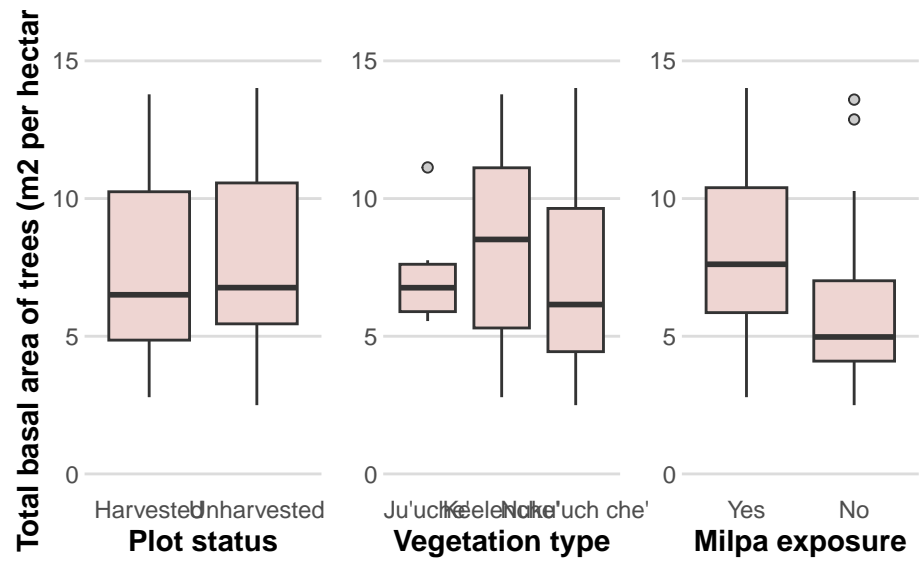
```



```

# Combined side-by-side box plots
ba_fig_combined <- ba_fig1 +
  (ba_fig2 + labs(y = NULL) + theme(axis.title.y = element_blank())) +
  (ba_fig3 + labs(y = NULL) + theme(axis.title.y = element_blank())) +
  plot_layout(ncol = 3)
ggsave("figures/basal_area_boxplots.png", ba_fig_combined, height = 4, width = 8)
ba_fig_combined

```



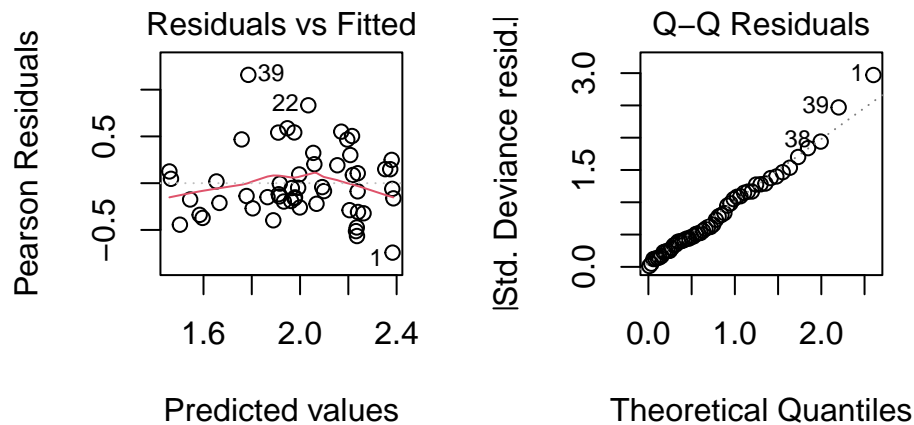
Models

We found that the residuals of a standard linear model had heteroscedastic variance. We considered a Gaussian GLM and a gamma GLM, both with log link. The residuals of the former also had heteroscedastic variance, so we decide to proceed with the latter.

Fit gamma model and check residual plots

```
mod <- glm(ba_totaltrees ~ harvested + vegetation_type + milpa + latitude + longitude,
           family = Gamma(link="log"), data = data_plots)
```

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



Summarize the model

```
summary(mod)
```

```
##
## Call:
## glm(formula = ba_totaltrees ~ harvested + vegetation_type + milpa +
##       latitude + longitude, family = Gamma(link = "log"), data = data_plots)
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.49958    0.23192   6.466 5.29e-08 ***
## harvestedyes       0.01319    0.10639   0.124  0.90184
## vegetation_typekeelenche 0.07888    0.17891   0.441  0.66133
## vegetation_typenukuuchche 0.27827    0.22012   1.264  0.21241
## milpayes          0.51144    0.15402   3.321  0.00174 **
## latitude         -0.05475    0.05890  -0.929  0.35740
## longitude        -0.21507    0.06816  -3.155  0.00280 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## (Dispersion parameter for Gamma family taken to be 0.1521501)
##
## Null deviance: 10.3415 on 53 degrees of freedom
## Residual deviance: 7.3464 on 47 degrees of freedom
## AIC: 272.3
##
## Number of Fisher Scoring iterations: 7
```

Construct analysis of deviance table

```
Anova(mod, type = 2, test.statistic = "LR")
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: ba_totaltrees
##          LR Chisq Df Pr(>Chisq)
## harvested    0.0152  1  0.9019590
## vegetation_type 2.1595  2  0.3396839
## milpa        11.1473  1  0.0008416 ***
## latitude      0.8519  1  0.3560094
## longitude     10.3153  1  0.0013193 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```