

# Basal area

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## Packages and data

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

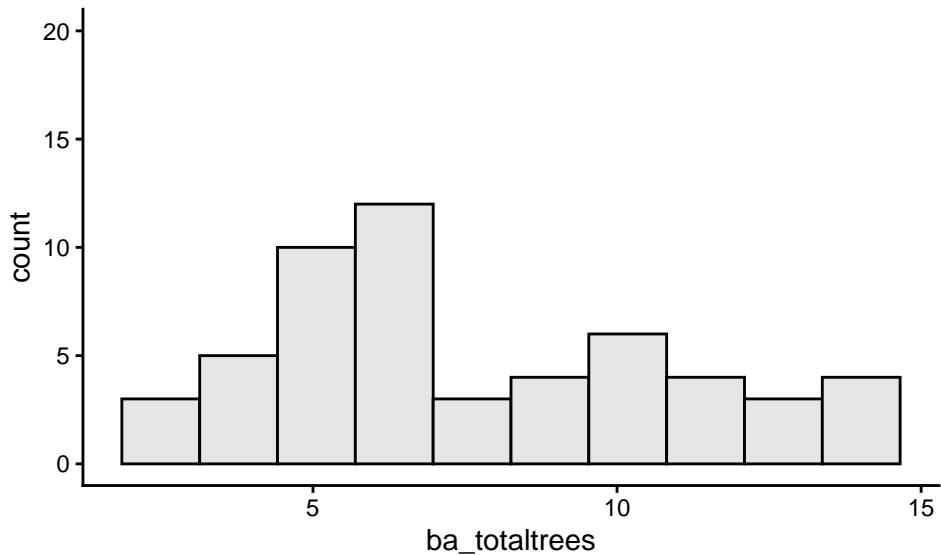
data_stems <- read_csv("data/data_stems.csv") %>%
  mutate(plot_id = as.factor(plot_id),
         size_class = as.factor(size_class),
         harvested = as.factor(harvested),
         vegetation_type = as.factor(vegetation_type),
         milpa = as.factor(milpa))
data_plots <- read_csv("data/data_plots.csv")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

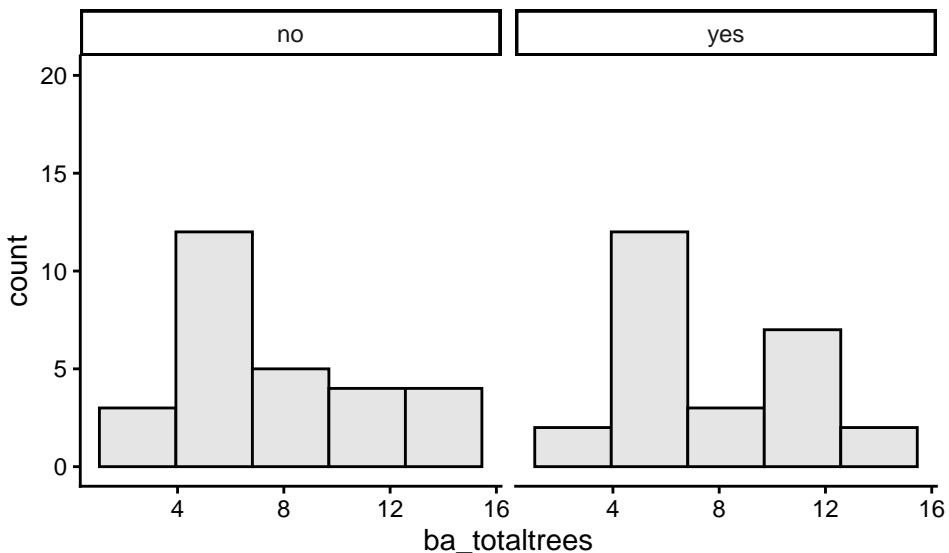
## Figures

### 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()

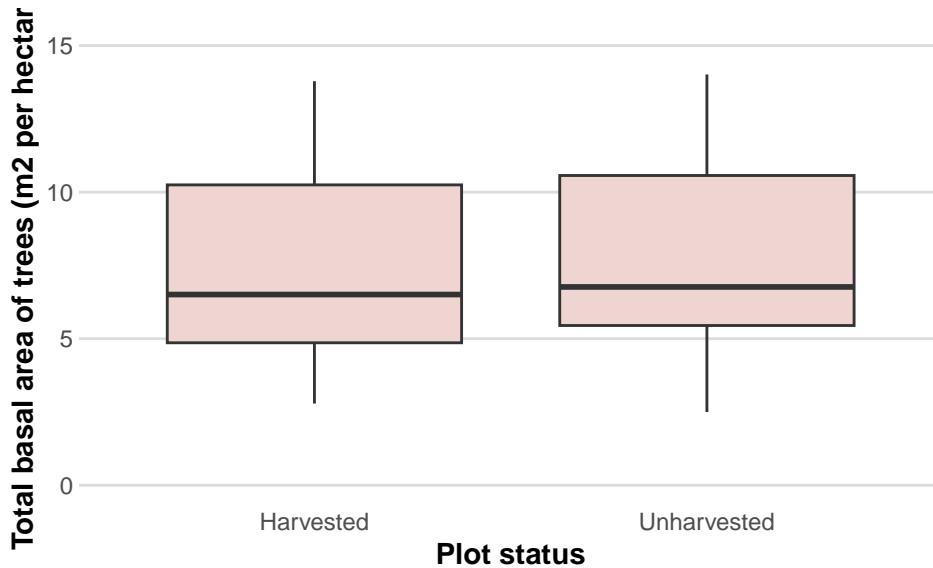
##      Min. 1st Qu. Median     Mean 3rd Qu.     Max.
##    2.788   4.860   6.506   7.550  10.248  13.785

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

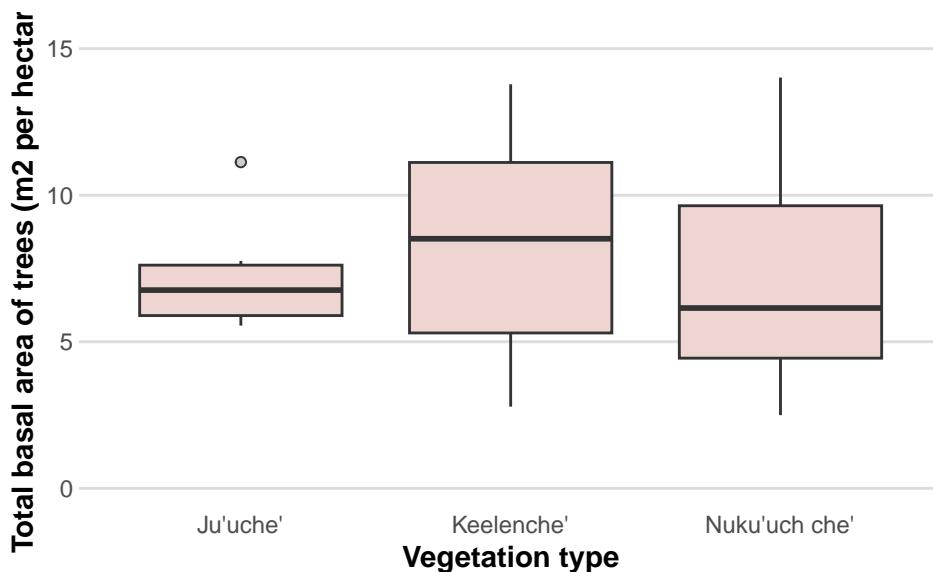
##      Min. 1st Qu. Median     Mean 3rd Qu.     Max.
##    2.498   5.450   6.765   7.763  10.568  14.015
```

## 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
```



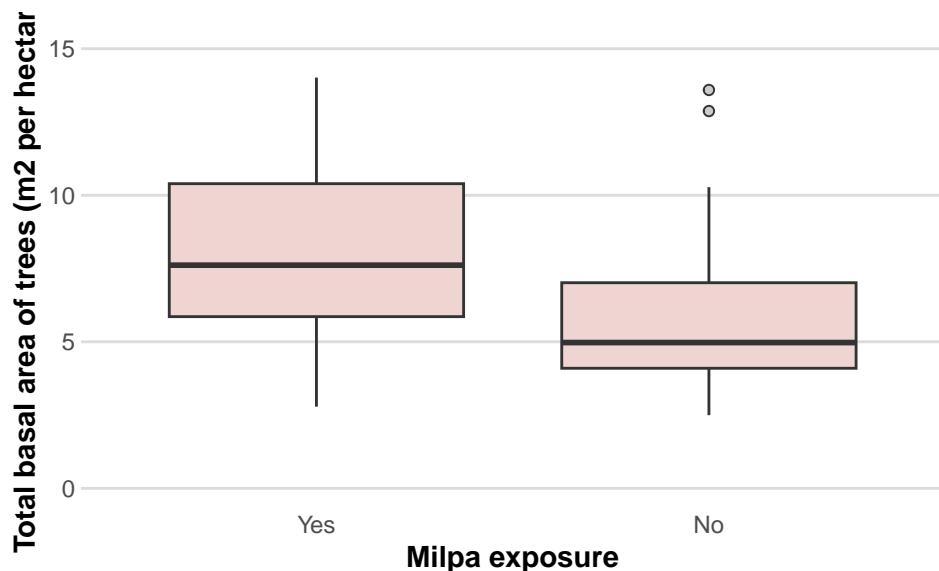
```
# By vegetation type
ba_fig2 <- data_plots %>%
  mutate(vegetation_type = fct_recode(vegetation_type,
    "Ju'uche'" = "juuche",
    "Keelenche'" = "keelenche",
    "Nuku'uch che'" = "nukuuchche")) %>%
  ggplot() +
  geom_boxplot(aes(x = vegetation_type, y = ba_totalthrees),
    fill = "mistyrose2", 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

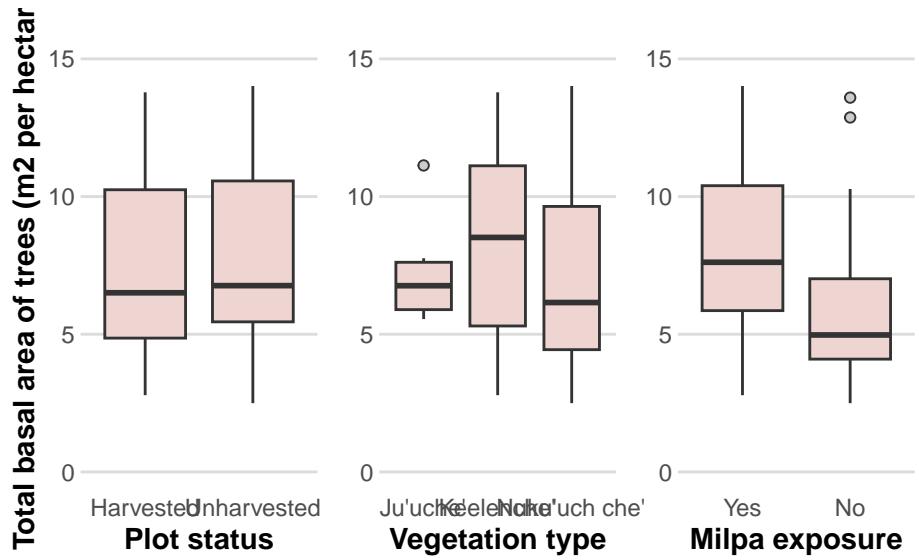
```



```

# 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

```



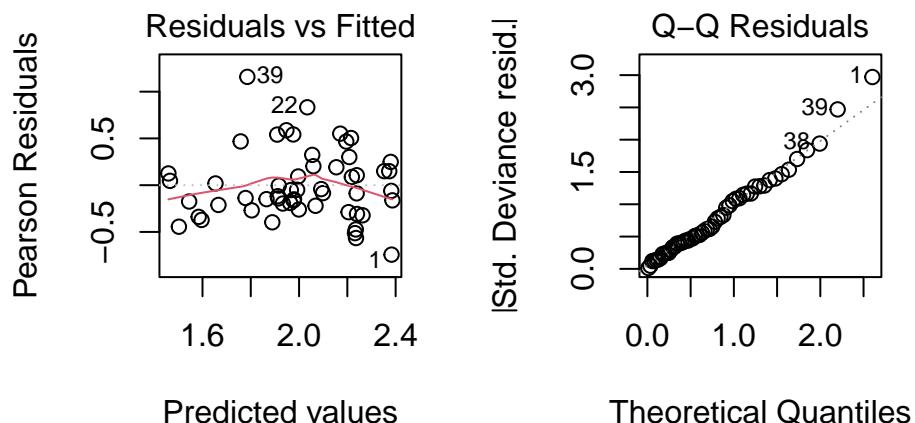
## Models

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_totalthrees
##           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

```