

# Basal area

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## Packages and data

```
library(car)
library(tidyverse)

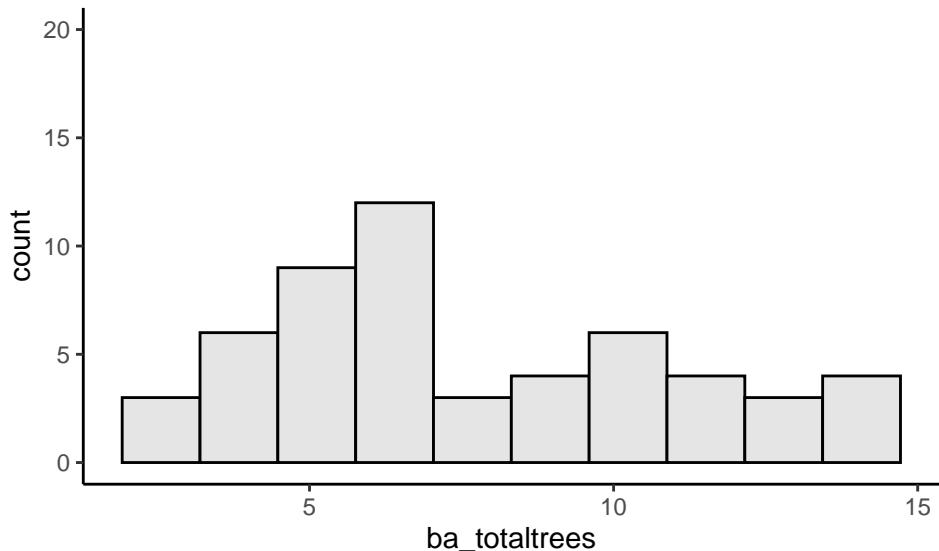
data_stems <- read_csv("data/data_stems.csv") %>%
  mutate(plot_id = as.factor(plot_id),
        size_class = as.factor(size_class),
        harvested = as.factor(harvested),
        vegetation_type = as.factor(vegetation_type),
        milpa = as.factor(milpa))
data_plots <- read_csv("data/data_plots.csv")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

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"))
```

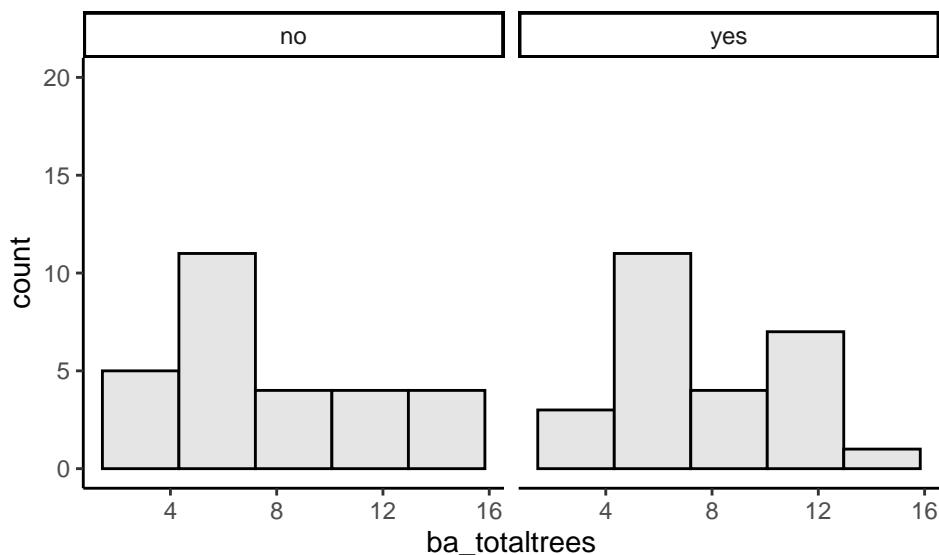
## Figures

### 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()

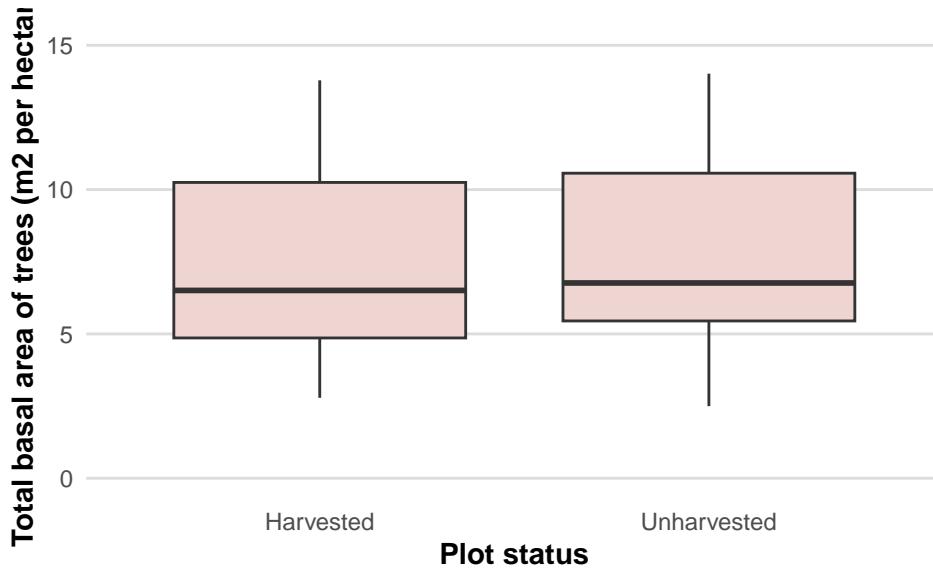
##      Min. 1st Qu. Median     Mean 3rd Qu.     Max.
##    2.788   4.860   6.506   7.550  10.248  13.785

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

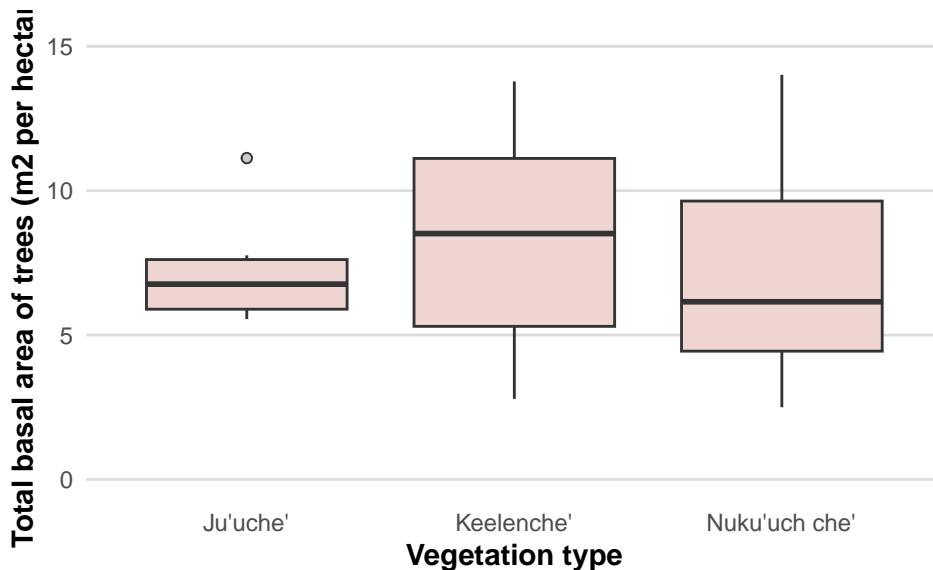
##      Min. 1st Qu. Median     Mean 3rd Qu.     Max.
##    2.498   5.450   6.765   7.763  10.568  14.015
```

## 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/ba_fig1.png", height = 4, width = 6)
ba_fig1
```



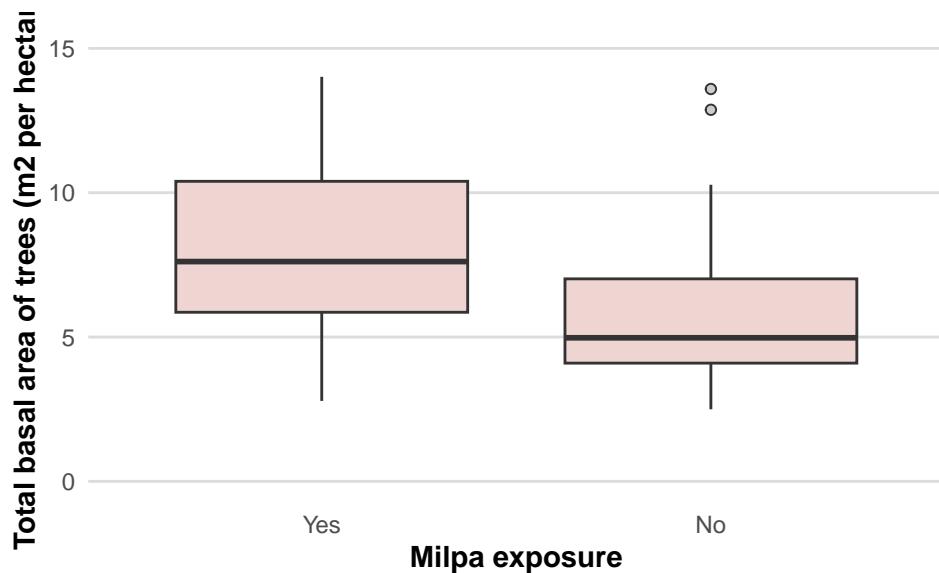
```
# By vegetation type
ba_fig2 <- data_plots %>%
  mutate(vegetation_type = fct_recode(vegetation_type,
                                      "Ju'uche'" = "juuche",
                                      "Keelenche'" = "keelenche",
                                      "Nuku'uch che'" = "nukuuchche")) %>%
  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/ba_fig2.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/ba_fig3.png", height = 4, width = 6)
ba_fig3

```



## 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.

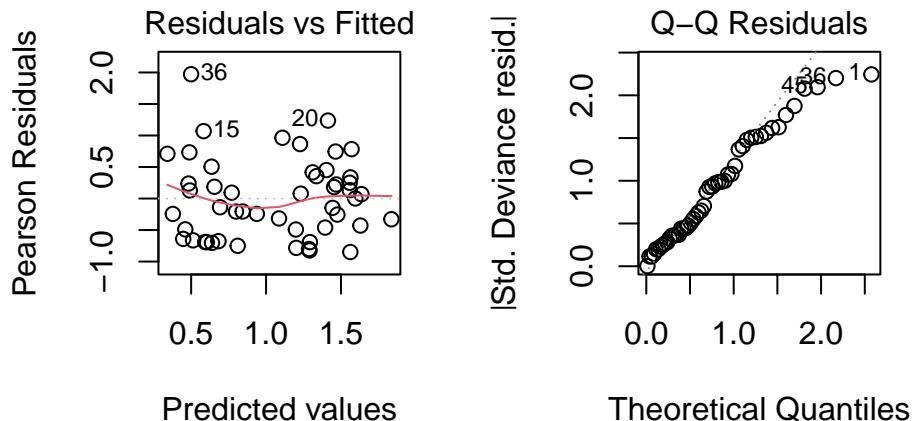
### Fit gamma model and check residual plots

```

mod <- glm(ba_trees15plus ~ harvested + vegetation_type + milpa + latitude + longitude, family = Gamma()

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

```



## Summarize the model

```
summary(mod)
```

```
##  
## Call:  
## glm(formula = ba_trees15plus ~ harvested + vegetation_type +  
##     milpa + latitude + longitude, family = Gamma(link = "log"),  
##     data = data_plots %>% filter(ba_trees15plus > 0))  
##  
## Coefficients:  
##                                     Estimate Std. Error t value Pr(>|t|)  
## (Intercept)                 -0.2001    0.4302  -0.465  0.64429  
## harvestedyes                0.1277    0.1906   0.670  0.50658  
## vegetation_typekeelenche   0.2176    0.3294   0.661  0.51240  
## vegetation_typenukuuchche  1.1181    0.3986   2.805  0.00752 **  
## milpayes                     0.9024    0.2867   3.148  0.00299 **  
## latitude                      -0.1389   0.1062  -1.308  0.19790  
## longitude                   -0.3637    0.1203  -3.023  0.00420 **  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## (Dispersion parameter for Gamma family taken to be 0.452262)  
##  
## Null deviance: 32.826  on 49  degrees of freedom  
## Residual deviance: 23.479  on 43  degrees of freedom  
## AIC: 206.41  
##  
## Number of Fisher Scoring iterations: 14
```

## Construct analysis of deviance table

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

```
## Analysis of Deviance Table (Type II tests)
```

```
##  
## Response: ba_trees15plus  
##          LR Chisq Df Pr(>Chisq)  
## harvested      0.4367  1   0.508735  
## vegetation_type 13.5138  2   0.001163 **  
## milpa          10.1466  1   0.001446 **  
## latitude        1.4942  1   0.221559  
## longitude       9.5168  1   0.002036 **  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```