

Sangres Tree Stats and Graphs

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2024-10-08

load packages, read in the data, and do some stuff

```
library(ggplot2)
library(reshape2)
library(readxl)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union
```

```
library(gridExtra)
```

```
##
## Attaching package: 'gridExtra'

## The following object is masked from 'package:dplyr':
##
##   combine
```

```
SFS4 <- read_excel("sfs4 bible 2024.xlsx")
BTN4 <- read_excel("btn4 revisit 2024.xlsx")
```

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## Warning: Expecting logical in J1201 / R1201C10: got 'BTN4-45'

## Warning: Expecting logical in J1202 / R1202C10: got 'BTN4-47'

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## Warning: Expecting logical in J1493 / R1493C10: got 'BTN4-890'
## Warning: Expecting logical in J1494 / R1494C10: got 'BTN4-891'
## Warning: Expecting logical in J1495 / R1495C10: got 'BTN4-892'
## Warning: Expecting logical in J1496 / R1496C10: got 'BTN4-893'
## Warning: Expecting logical in J1497 / R1497C10: got 'BTN4-895'
## Warning: Expecting logical in J1498 / R1498C10: got 'BTN4-896'
## Warning: Expecting logical in J1499 / R1499C10: got 'BTN4-897'
## Warning: Expecting logical in J1500 / R1500C10: got 'BTN4-898'
## Warning: Expecting logical in J1501 / R1501C10: got 'BTN4-899'
## Warning: Expecting logical in J1502 / R1502C10: got 'BTN4-900'
## Warning: Expecting logical in J1503 / R1503C10: got 'BTN4-997'
## Warning: Expecting logical in J1504 / R1504C10: got 'BTN4-998'

## New names:
## * ' ' -> '...10'
```

```
BTN4dbh <- read_excel("btn4 access for C.xlsx")
SFF1 <- read_excel("sff1 establishment 2024.xlsx")
SFF2 <- read_excel("sff2 establishment 2024.xlsx")
SFF3 <- read_excel("sff3 establishment 2024.xlsx")
SFF4 <- read_excel("sff4 establishment 2024.xlsx")
SFF5 <- read_excel("sff5 establishment 2024.xlsx")
SFF6 <- read_excel("sff6 establishment 2024.xlsx")
SFF7 <- read_excel("sff7 establishment 2024.xlsx")
SFF8 <- read_excel("sff8 establishment 2024.xlsx")
SFF9 <- read_excel("sff9 establishment 2024.xlsx")
SFF10 <- read_excel("sff10 establishment 2024.xlsx")
```

```
## New names:
## * ' ' -> '...11'
```

```
#Add plot numbers to treeIDs
```

```
SFS4$Tree_num = paste0('SFS4-', SFS4$Tree_num)
BTN4$Tree_num = paste0('BTN4-', BTN4$Tree_num)
```

```
## Warning: Unknown or uninitialised column: 'Tree_num'.
```

```

SFF1$Tree_num = paste0('SFF1-', SFF1$Tree_num)
SFF2$Tree_num = paste0('SFF2-', SFF2$Tree_num)
SFF3$Tree_num = paste0('SFF3-', SFF3$Tree_num)
SFF4$Tree_num = paste0('SFF4-', SFF4$Tree_num)
SFF5$Tree_num = paste0('SFF5-', SFF5$Tree_num)
SFF6$Tree_num = paste0('SFF6-', SFF6$Tree_num)
SFF7$Tree_num = paste0('SFF7-', SFF7$Tree_num)
SFF8$Tree_num = paste0('SFF8-', SFF8$Tree_num)
SFF9$Tree_num = paste0('SFF9-', SFF9$Tree_num)
SFF10$Tree_num = paste0('SFF10-', SFF10$Tree_num)

```

join of BTN4 DBH & Species files

```

BTN4dbh$Tree_num <- BTN4dbh$TreeID
BTN4 <- left_join(BTN4, BTN4dbh, by = "Tree_num")
BTN4$Species <- BTN4$SpeciesID
BTN4$Notes<-BTN4$Notes.x

```

#Add plot number to data

```

SFS4$PlotName <- "SFS4"
BTN4$PlotName <- "BTN4"
SFF1$PlotName <- "SFF1"
SFF2$PlotName <- "SFF2"
SFF3$PlotName <- "SFF3"
SFF4$PlotName <- "SFF4"
SFF5$PlotName <- "SFF5"
SFF6$PlotName <- "SFF6"
SFF7$PlotName <- "SFF7"
SFF8$PlotName <- "SFF8"
SFF9$PlotName <- "SFF9"
SFF10$PlotName <- "SFF10"

```

#Add treatment status

```

SFS4$TreatmentStatus <- "Treated"
BTN4$TreatmentStatus <- "Untreated"
SFF1$TreatmentStatus <- "Treated"
SFF2$TreatmentStatus <- "Untreated"
SFF3$TreatmentStatus <- "Untreated"
SFF4$TreatmentStatus <- "Untreated"
SFF5$TreatmentStatus <- "Treated"
SFF6$TreatmentStatus <- "Untreated"
SFF7$TreatmentStatus <- "Treated"
SFF8$TreatmentStatus <- "Treated"
SFF9$TreatmentStatus <- "Untreated"
SFF10$TreatmentStatus <- "Treated"

```

Add plot size

```

SFS4$PlotSize <- 1
BTN4$PlotSize <- 1
SFF1$PlotSize <- 0.25
SFF2$PlotSize <- 1
SFF3$PlotSize <- 0.25

```

```

SFF4$PlotSize <- 0.25
SFF5$PlotSize <- 0.25
SFF6$PlotSize <- 0.25
SFF7$PlotSize <- 0.25
SFF8$PlotSize <- 1
SFF9$PlotSize <- 0.25
SFF10$PlotSize <- 0.25

#Select columns of interest (make loop at some point)

SFS4 <- SFS4 %>%
  select(PlotName, PlotSize, TreatmentStatus, Tree_num, Species, Condition, DBH, OG, Notes)
BTN4 <- BTN4 %>%
  select(PlotName, PlotSize, TreatmentStatus, Tree_num, Species, Condition, DBH, OG, Notes)
SFF1 <- SFF1 %>%
  select(PlotName, PlotSize, TreatmentStatus, Tree_num, Species, Condition, DBH, OG, Notes)
SFF2 <- SFF2 %>%
  select(PlotName, PlotSize, TreatmentStatus, Tree_num, Species, Condition, DBH, OG, Notes)
SFF3 <- SFF3 %>%
  select(PlotName, PlotSize, TreatmentStatus, Tree_num, Species, Condition, DBH, OG, Notes)
SFF4 <- SFF4 %>%
  select(PlotName, PlotSize, TreatmentStatus, Tree_num, Species, Condition, DBH, OG, Notes)
SFF5 <- SFF5 %>%
  select(PlotName, PlotSize, TreatmentStatus, Tree_num, Species, Condition, DBH, OG, Notes)
SFF6 <- SFF6 %>%
  select(PlotName, PlotSize, TreatmentStatus, Tree_num, Species, Condition, DBH, OG, Notes)
SFF7 <- SFF7 %>%
  select(PlotName, PlotSize, TreatmentStatus, Tree_num, Species, Condition, DBH, OG, Notes)
SFF8 <- SFF8 %>%
  select(PlotName, PlotSize, TreatmentStatus, Tree_num, Species, Condition, DBH, OG, Notes)
SFF9 <- SFF9 %>%
  select(PlotName, PlotSize, TreatmentStatus, Tree_num, Species, Condition, DBH, OG, Notes)
SFF10 <- SFF10 %>%
  select(PlotName, PlotSize, TreatmentStatus, Tree_num, Species, Condition, DBH, OG, Notes)

# merge all the plots into one dataframe
SFS4$Condition <- as.numeric(SFS4$Condition)
merged_plots <- bind_rows(SFS4, BTN4, SFF1, SFF2, SFF3, SFF4, SFF5, SFF6, SFF7, SFF8, SFF9, SFF10)

# add a column to define MOG as Y or NA
merged_plots <- merged_plots %>%
  mutate(MOG = case_when(OG == "Y" | DBH > 30 ~ "Y"))

# calculate tree counts
merged_summary <- merged_plots %>%
  group_by(PlotName, PlotSize, TreatmentStatus) %>%
  summarize(Tree_count = n(), meanDBH = mean(DBH, na.rm = TRUE))

## 'summarise()' has grouped output by 'PlotName', 'PlotSize'. You can override
## using the '.groups' argument.

```



```
# calculate MOG stats
merged_MOG <- merged_plots %>%
  filter(MOG == "Y") %>%
  group_by(PlotName, PlotSize, TreatmentStatus) %>%
  summarize(MOG_count = n())
```

'summarise()' has grouped output by 'PlotName', 'PlotSize'. You can override
using the '.groups' argument.

```
#calculate live MOG stats
merged_MOG_live <- merged_plots %>%
  filter(MOG == "Y" & Condition != 5 & Condition != 2) %>%
  group_by(PlotName, PlotSize, TreatmentStatus) %>%
  summarize(MOG_live_count = n())
```

'summarise()' has grouped output by 'PlotName', 'PlotSize'. You can override
using the '.groups' argument.

```
#calculate OG stats
merged_OG <- merged_plots %>%
  filter(OG == "Y") %>%
  group_by(PlotName, PlotSize, TreatmentStatus) %>%
  summarize(OG_count = n())
```

'summarise()' has grouped output by 'PlotName', 'PlotSize'. You can override
using the '.groups' argument.

```
# merge them all together
merged_summary$MOG_count <- merged_MOG$MOG_count
merged_summary$MOG_live_count <- merged_MOG_live$MOG_live_count
merged_summary$OG_count <- merged_OG$OG_count

# calculate TPH
merged_summary$TPH <- merged_summary$Tree_count/merged_summary$PlotSize
est_data<-merged_summary

# Add tree colors

add_tree_colors <- function(df){
  df <- df %>%
    mutate(colors=
      case_when(Species == "ABCO" ~ "#4EDFC7",
                 Species == "ACGL" ~ "#C21E56",
                 Species == "JUMO" ~ "#FFC0CB",
                 Species == "JUSC" ~ "#95658B",
                 Species == "PIED" ~ "#FFD700",
                 Species == "PIPO" ~ "#2E8B57",
                 Species == "PIST" ~ "#89CFF0",
                 Species == "PRVI" ~ "#9F2B68",
                 Species == "PSME" ~ "#808080",
                 Species == "QUGA" ~ "#5D3FD3",
                 Species == "QUUN" ~ "#CC5500",
```

```

        Species == "SASC" ~ "#E3963E",
        Species == "unknown" ~ "#AFE1AF",
        Species == "NA" ~ "#808080"

    ))

}

merged_plots <- add_tree_colors(merged_plots)

# some treatment level stats

treatment_summary <- merged_summary %>%
  group_by(TreatmentStatus)%>%
  summarize(Tree_count = sum(Tree_count), MOG_count = sum(MOG_count), MOG_live_count = sum(MOG_live_coun

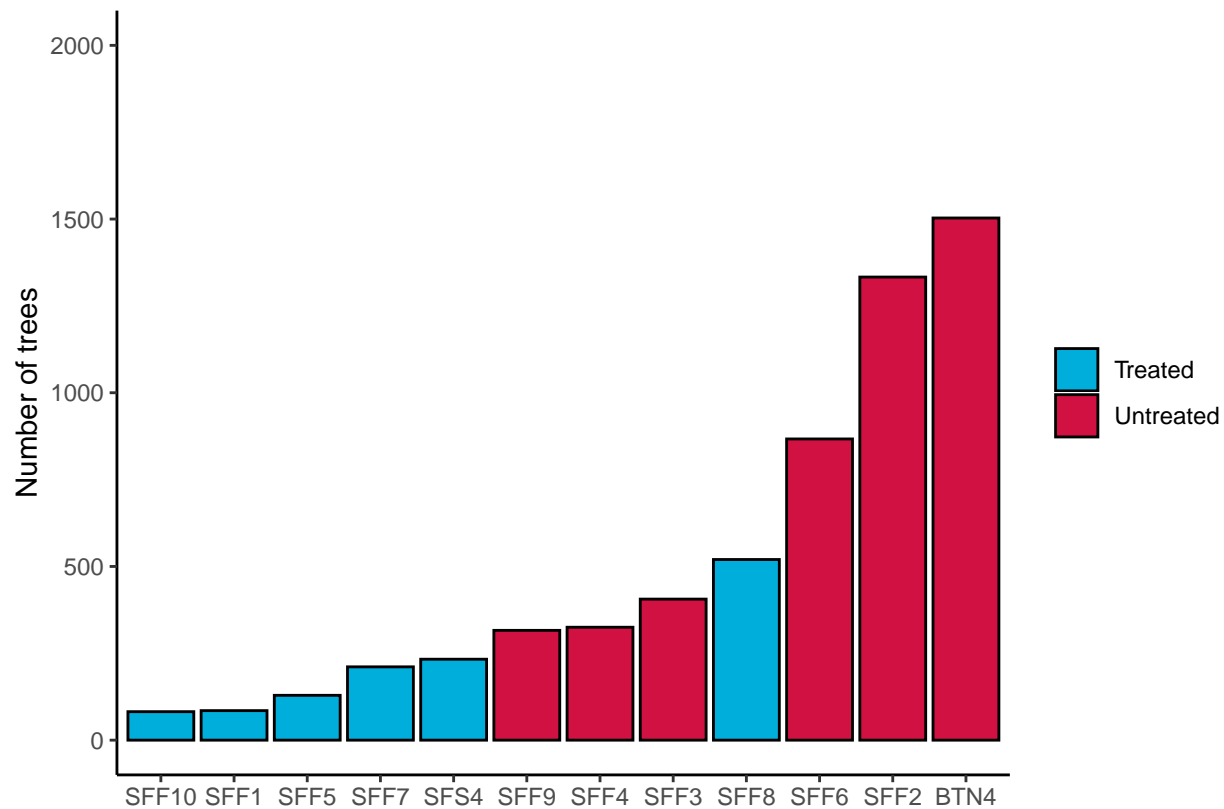
```

Makes a graph of the number of trees sampled per plot

```

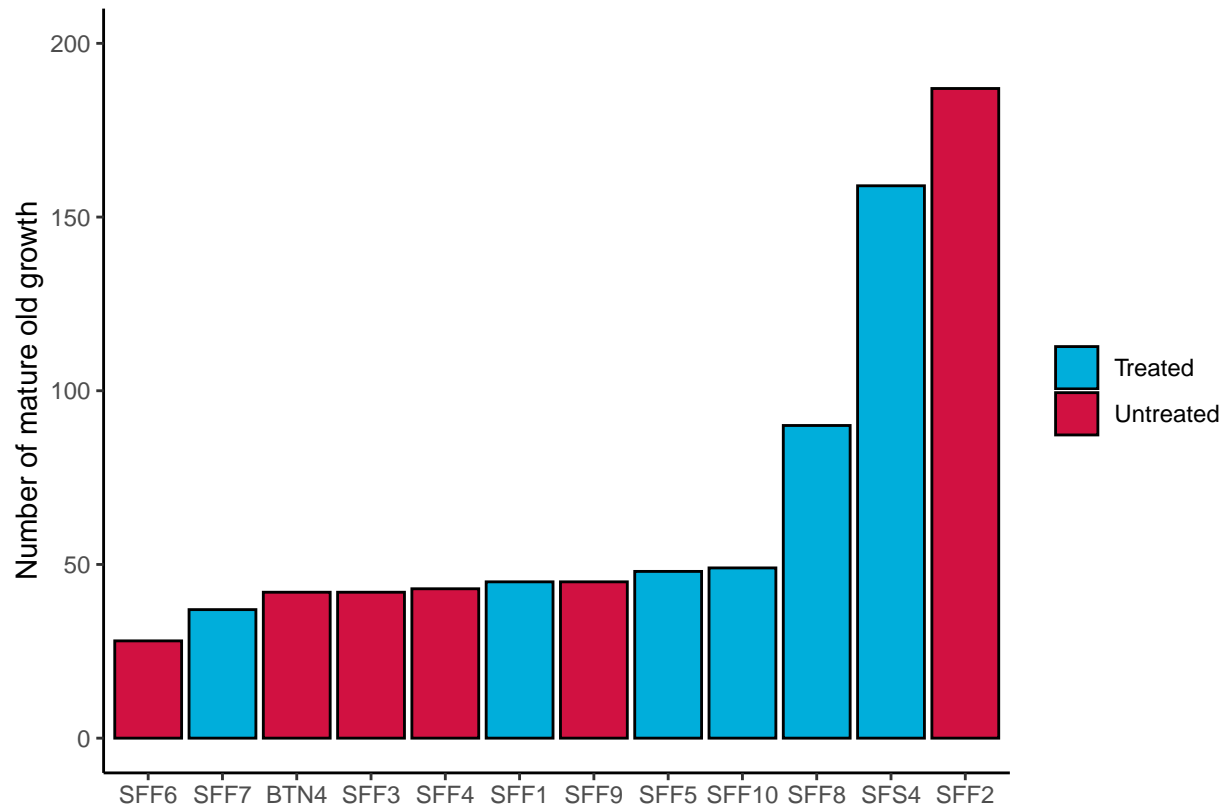
ggplot(est_data, aes(x= reorder(PlotName, Tree_count), y= Tree_count)) +
  geom_bar(stat="identity", color = 'black', aes(fill = TreatmentStatus)) +
  xlab("") +
  ylab("Number of trees") +
  ylim(0, 2000) +
  scale_fill_manual(values=c("#00aedb", "#d11141")) +
  theme_classic() +
  theme(legend.title = element_blank())

```



Makes a graph showing the number of MOG (mature old growth) sampled per plot

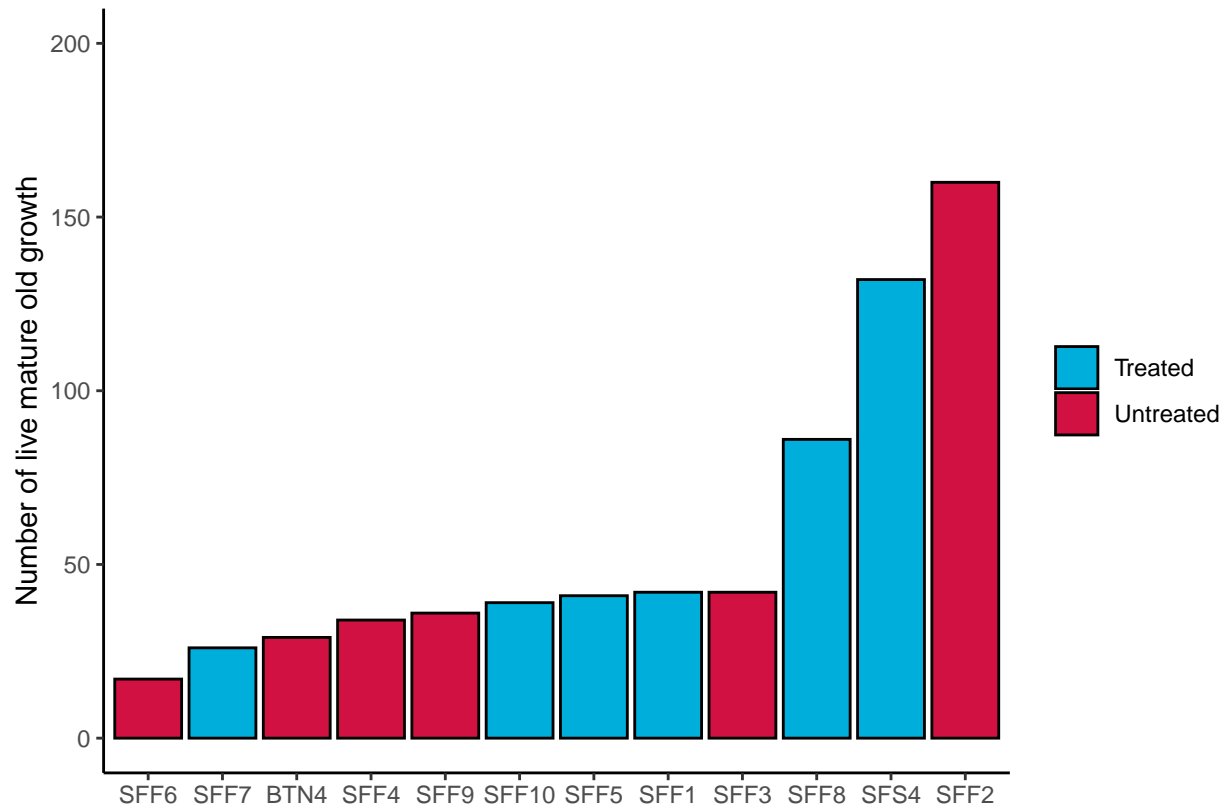
```
ggplot(est_data, aes(x= reorder(PlotName, MOG_count), y= MOG_count)) +
  geom_bar(stat="identity", color = 'black', aes(fill = TreatmentStatus)) +
  xlab("") +
  ylab("Number of mature old growth") +
  ylim(0,200) +
  scale_fill_manual(values=c("#00aedb", "#d11141")) +
  theme_classic() +
  theme(legend.title = element_blank())
```



Makes a graph showing the number of live MOG (mature old growth) sampled per

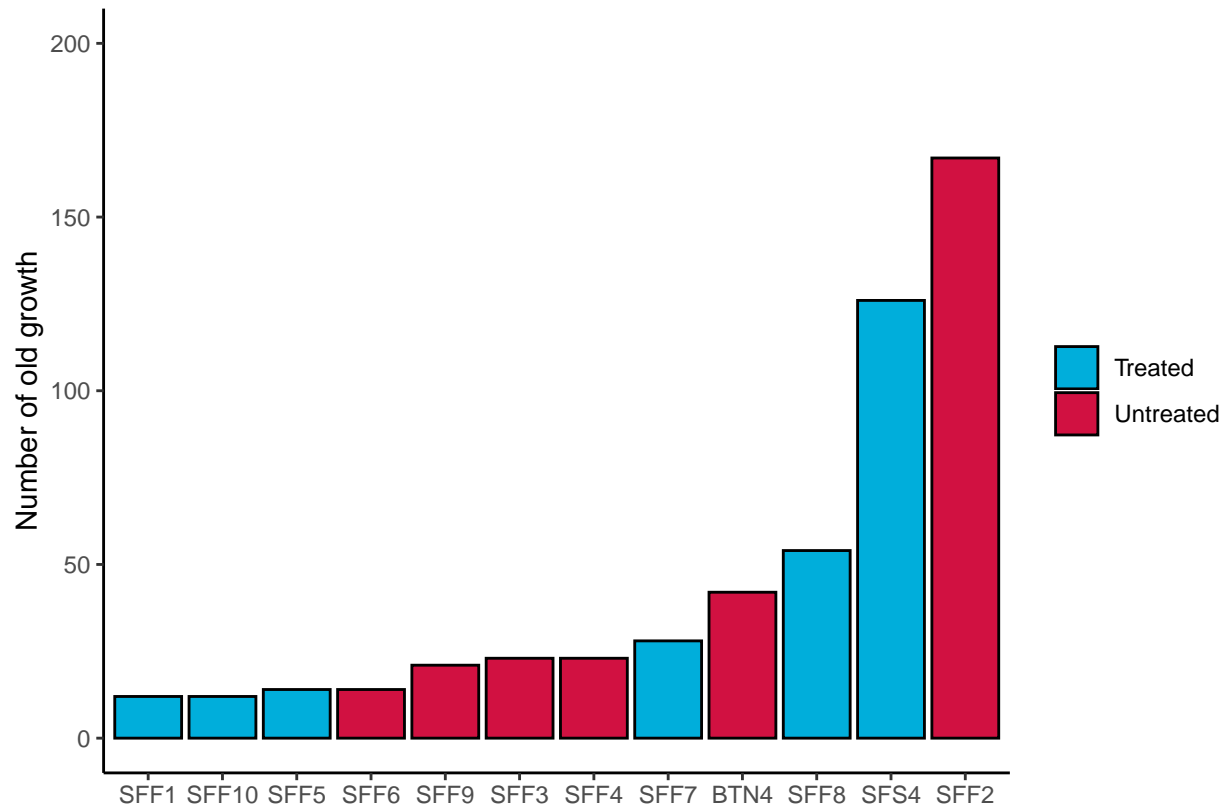
plot

```
ggplot(est_data, aes(x= reorder(PlotName, MOG_live_count), y= MOG_live_count)) +
  geom_bar(stat="identity", color = 'black', aes(fill = TreatmentStatus)) +
  xlab("") +
  ylab("Number of live mature old growth") +
  ylim(0, 200) +
  scale_fill_manual(values=c("#00aedb", "#d11141")) +
  theme_classic() +
  theme(legend.title = element_blank())
```



Makes a graph showing the number of OG sampled per plot

```
ggplot(est_data, aes(x= reorder(PlotName, OG_count), y= OG_count)) +
  geom_bar(stat="identity", color = 'black', aes(fill = TreatmentStatus)) +
  xlab("") +
  ylab("Number of old growth") +
  scale_fill_manual(values=c("#00aedb", "#d11141")) +
  ylim(0,200) +
  theme_classic() +
  theme(legend.title = element_blank())
```

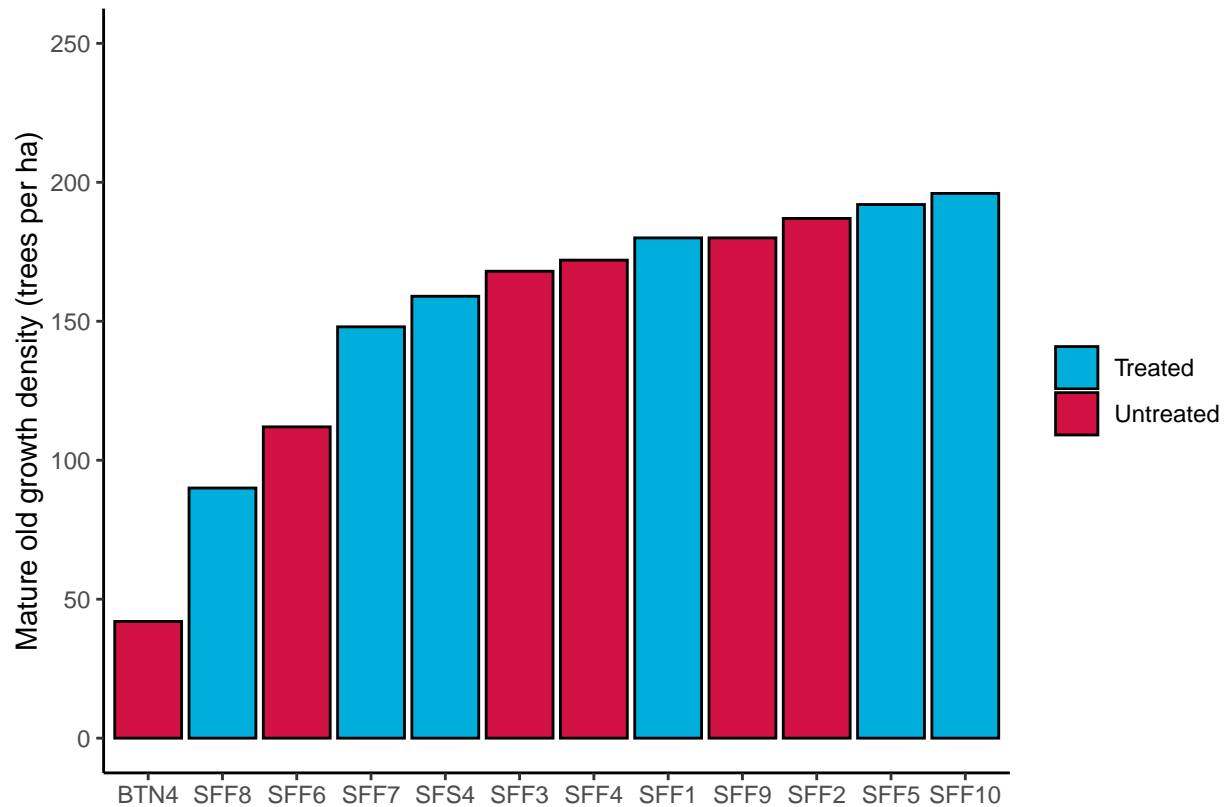


Makes a graph showing the number of MOG per ha per plot

```
MOGperHectare <- est_data$MOG_count / est_data$PlotSize

est_data$MOGperha <- MOGperHectare

ggplot(est_data, aes(x= reorder(PlotName, MOGperha), y= MOGperha)) +
  geom_bar(stat="identity", color = 'black', aes(fill = TreatmentStatus)) +
  xlab("") +
  ylab("Mature old growth density (trees per ha)") +
  scale_fill_manual(values=c("#00aedb", "#d11141")) +
  ylim(0,250) +
  theme_classic() +
  theme(legend.title = element_blank())
```



DATA BY TREATMENT

Number of trees by treatment

```
Treatment <- c("Treated", "Untreated")

TreatedNumTrees <- sum(subset(est_data, TreatmentStatus == 'Treated')$Tree_count)

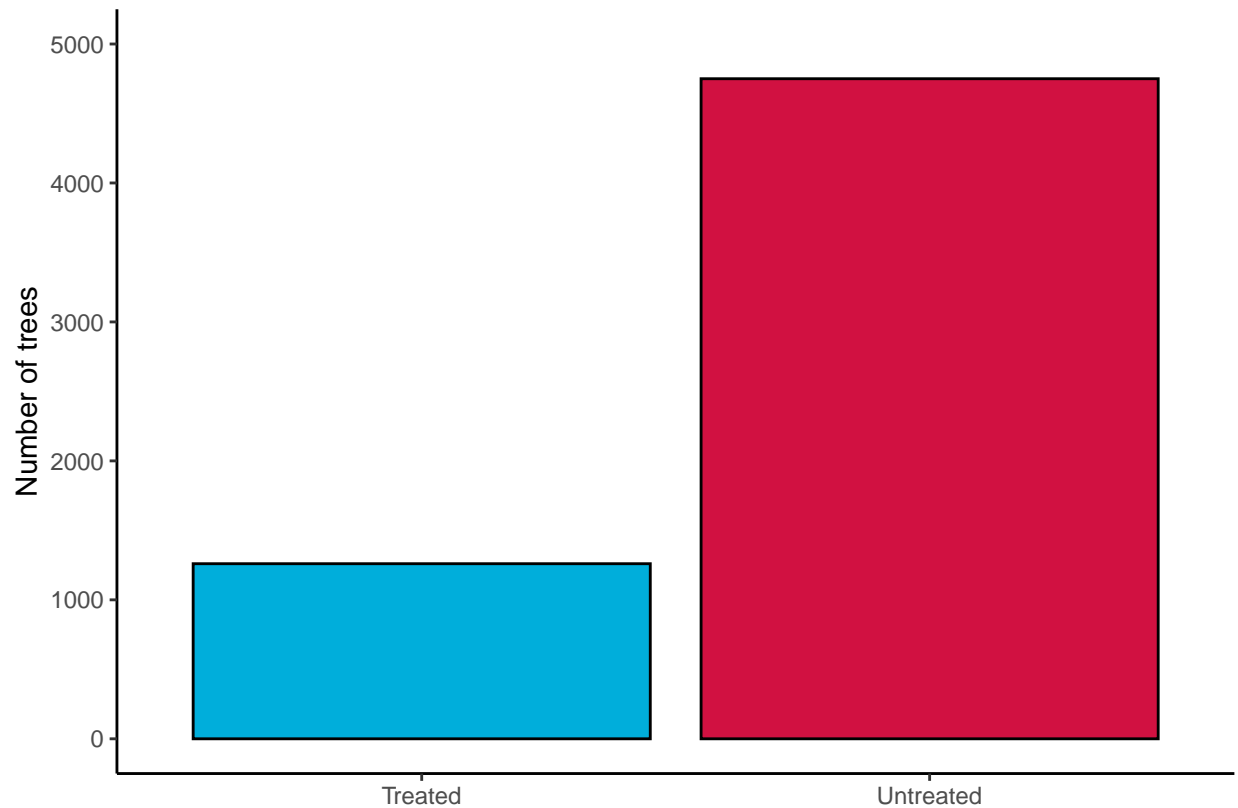
UntreatedNumTrees <- sum(subset(est_data, TreatmentStatus == 'Untreated')$Tree_count)

NumTrees <- c(TreatedNumTrees, UntreatedNumTrees)

NumTreesByTreatment <- data.frame(Treatment, NumTrees)

ggplot(NumTreesByTreatment, aes(x = Treatment, y = NumTrees)) +
  geom_bar(stat = "identity", color = 'black', aes(fill = Treatment)) +
  xlab("") +
  ylab("Number of trees") +
  ylim(0, 5000) +
  scale_fill_manual(values=c("#00aedb", "#d11141")) +
```

```
theme_classic() +
theme(legend.position = "none")
```



Number of MOG per treatment

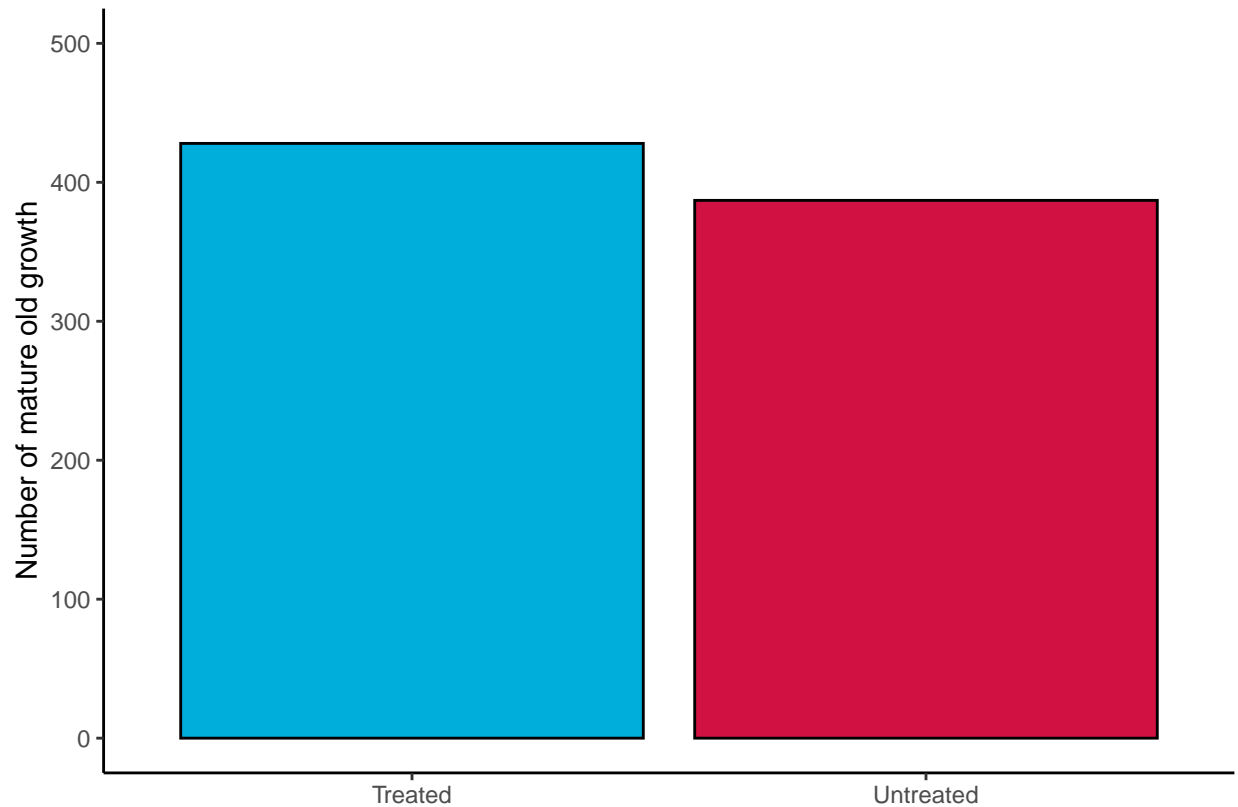
```
TreatedMOG <- sum(subset(est_data, TreatmentStatus == 'Treated')$MOG_count)

UntreatedMOG <- sum(subset(est_data, TreatmentStatus == 'Untreated')$MOG_count)

NumMOG <- c(TreatedMOG, UntreatedMOG)

NumMOGByTreatment <- data.frame(Treatment, NumMOG)

ggplot(NumMOGByTreatment, aes(x = Treatment, y = NumMOG)) +
  geom_bar(stat = "identity", color = 'black', aes(fill = Treatment)) +
  xlab("") +
  ylab("Number of mature old growth") +
  ylim(0, 500) +
  scale_fill_manual(values=c("#00aedb", "#d11141")) +
  theme_classic() +
  theme(legend.position = "none")
```

Number of live MOG per treatment

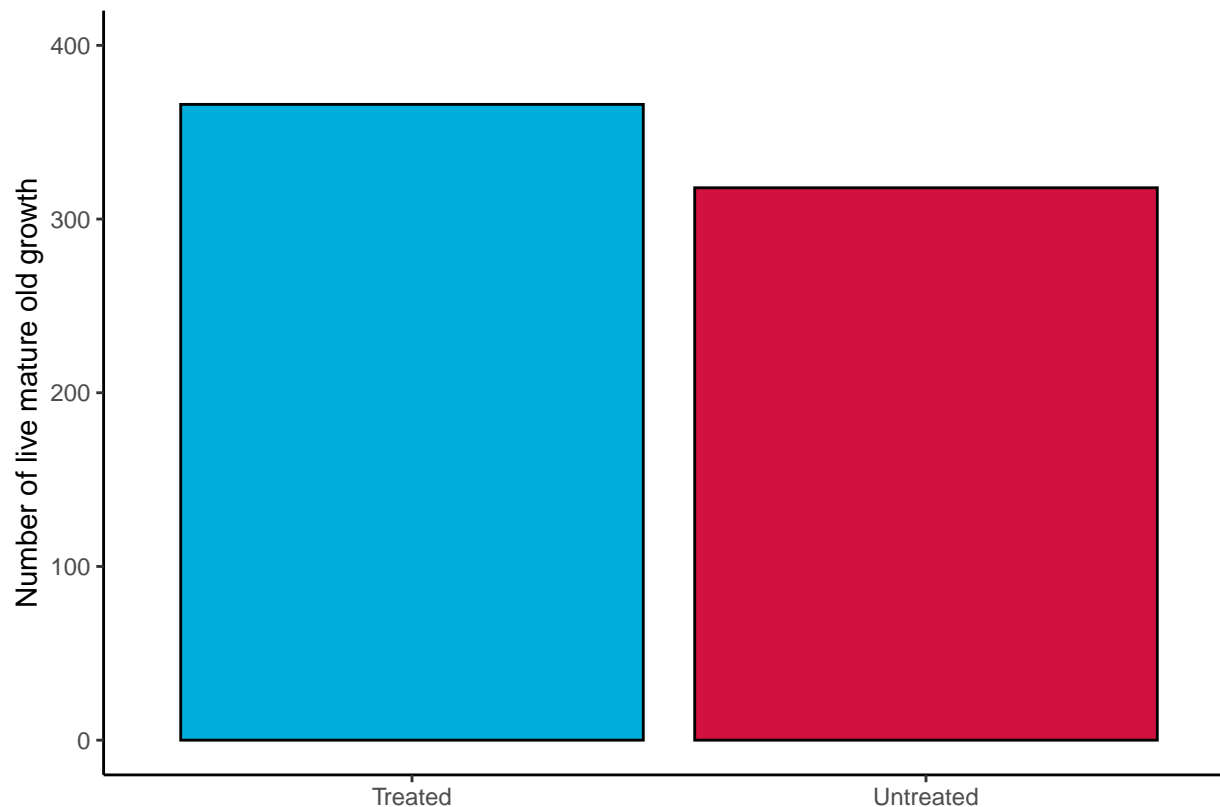
```
TreatedLiveMOG <- sum(subset(est_data, TreatmentStatus == 'Treated')$MOG_live_count)

UntreatedLiveMOG <- sum(subset(est_data, TreatmentStatus == 'Untreated')$MOG_live_count)

NumLiveMOG <- c(TreatedLiveMOG, UntreatedLiveMOG)

NumLiveMOGbyTreatment <- data.frame(Treatment, NumLiveMOG)

ggplot(NumLiveMOGbyTreatment, aes(x = Treatment, y = NumLiveMOG)) +
  geom_bar(stat = "identity", color = 'black', aes(fill = Treatment)) +
  xlab("") +
  ylab("Number of live mature old growth") +
  ylim(0, 400) +
  scale_fill_manual(values=c("#00aedb", "#d11141")) +
  theme_classic() +
  theme(legend.position = "none")
```



Number of OG's per treatment

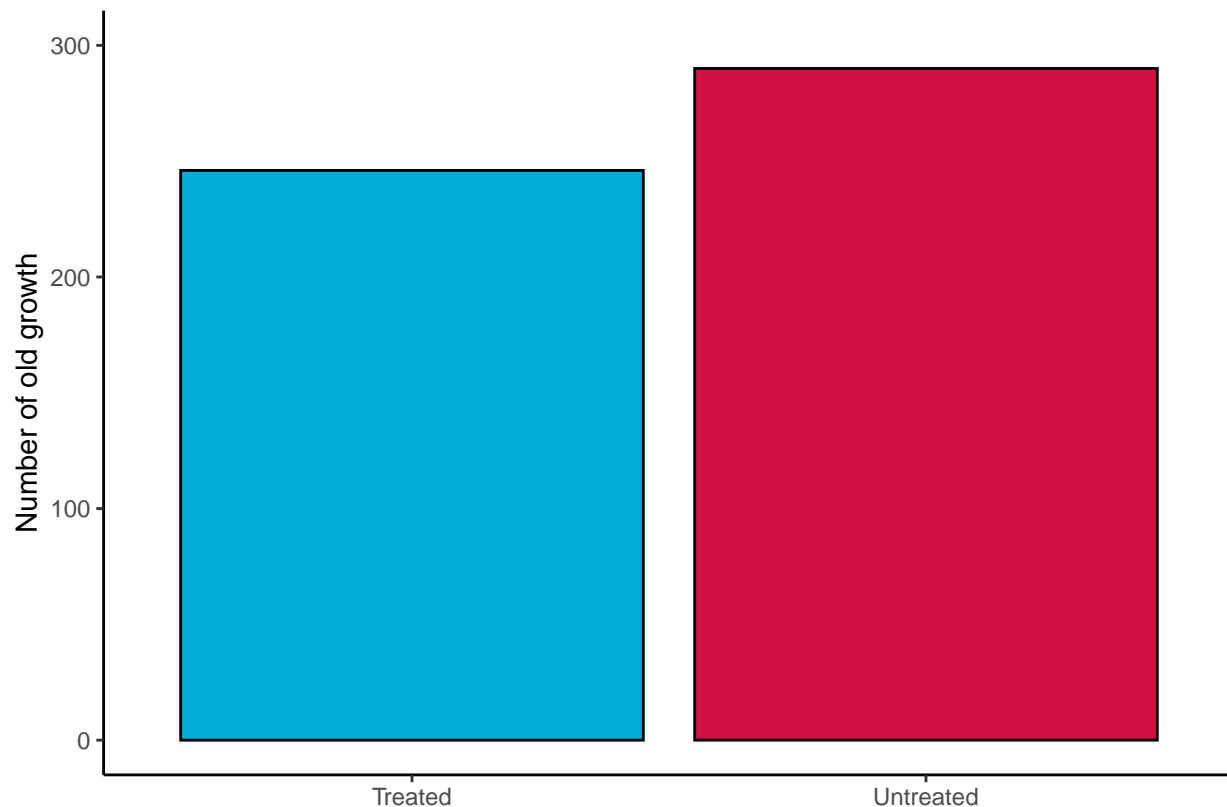
```
TreatedOG <- sum(subset(est_data, TreatmentStatus == 'Treated')$OG_count)

UntreatedOG <- sum(subset(est_data, TreatmentStatus == 'Untreated')$OG_count)

NumOG <- c(TreatedOG, UntreatedOG)

NumOGbyTreatment <- data.frame(Treatment, NumOG)

ggplot(NumOGbyTreatment, aes(x = Treatment, y = NumOG)) +
  geom_bar(stat = "identity", color = 'black', aes(fill = Treatment)) +
  xlab("") +
  ylab("Number of old growth") +
  ylim(0, 300) +
  scale_fill_manual(values=c("#00aedb", "#d11141")) +
  theme_classic() +
  theme(legend.position = "none")
```



Number of MOG per ha per plot

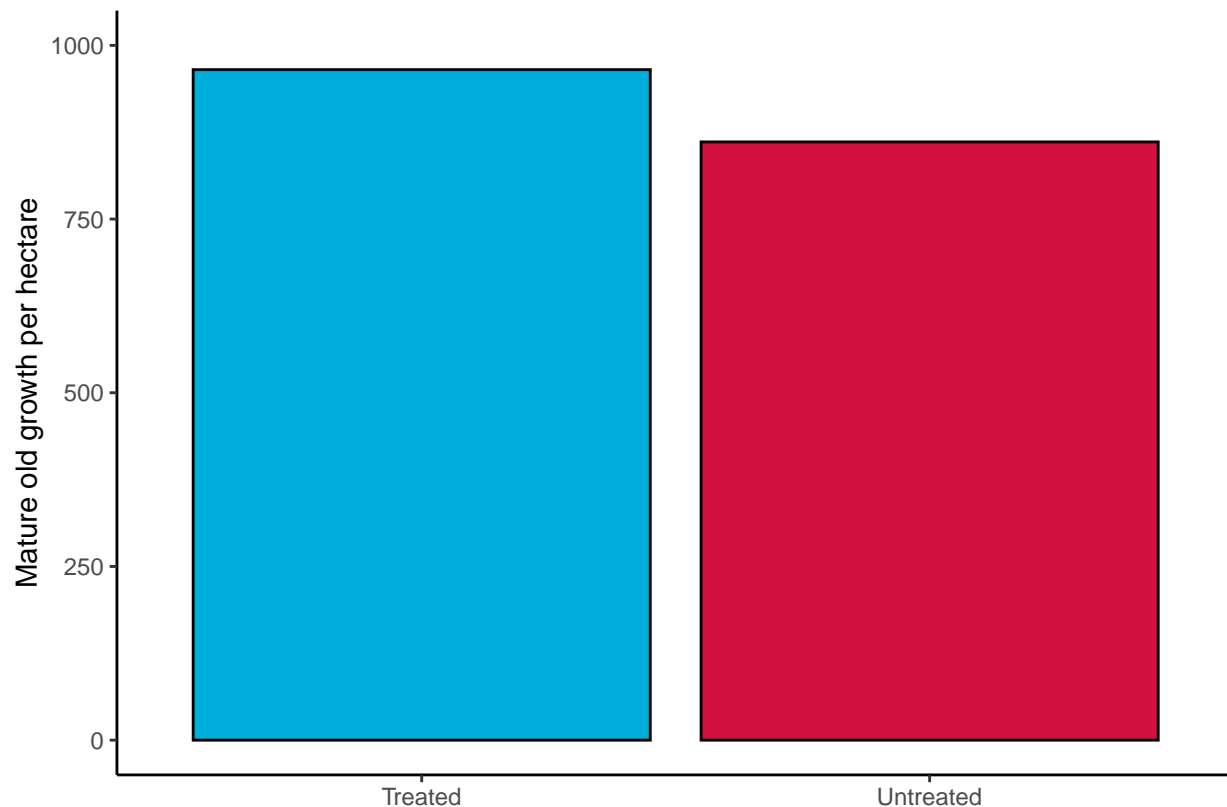
```
TreatedMOGperha <- sum(subset(est_data, TreatmentStatus == 'Treated')$MOGperha)

UntreatedMOGperha <- sum(subset(est_data, TreatmentStatus == 'Untreated')$MOGperha)

NumMOGperha <- c(TreatedMOGperha, UntreatedMOGperha)

NumMOGperhaByTreatment <- data.frame(Treatment, NumMOGperha)

ggplot(NumMOGperhaByTreatment, aes(x = Treatment, y = NumMOGperha)) +
  geom_bar(stat = "identity", color = 'black', aes(fill = Treatment)) +
  xlab("") +
  ylab("Mature old growth per hectare") +
  ylim(0, 1000) +
  scale_fill_manual(values=c("#00aedb", "#d11141")) +
  theme_classic() +
  theme(legend.position = "none")
```



OTHER COOL GRAPHS

Old growth vs. mature old growth in treated and untreated plots

```
TreatedPlotName <- subset(est_data, TreatmentStatus == "Treated")$PlotName
TreatedMOG <- subset(est_data, TreatmentStatus == "Treated")$MOG_count
TreatedOG <- subset(est_data, TreatmentStatus == "Treated")$OG_count
Treated_MOG_OG <- data.frame(TreatedPlotName, TreatedMOG, TreatedOG)

T_MOG_OG <- melt(Treated_MOG_OG[,c('TreatedPlotName', 'TreatedOG', 'TreatedMOG')], id.vars = 1)

T_MOG_OG_Plot <- ggplot(T_MOG_OG, aes(x = TreatedPlotName, y = value)) +
  geom_bar(aes(fill = variable), stat = "identity", color = 'black', position = "dodge") +
  ggtitle("Treated") +
  xlab("") +
  ylab("Number of trees") +
  ylim(0, 200) +
  scale_fill_manual(values=c("#4d7358", "#9ed670"), labels = c('Old Growth', 'Mature Old Growth')) +
  theme_classic() +
  theme(legend.title = element_blank())
```

```

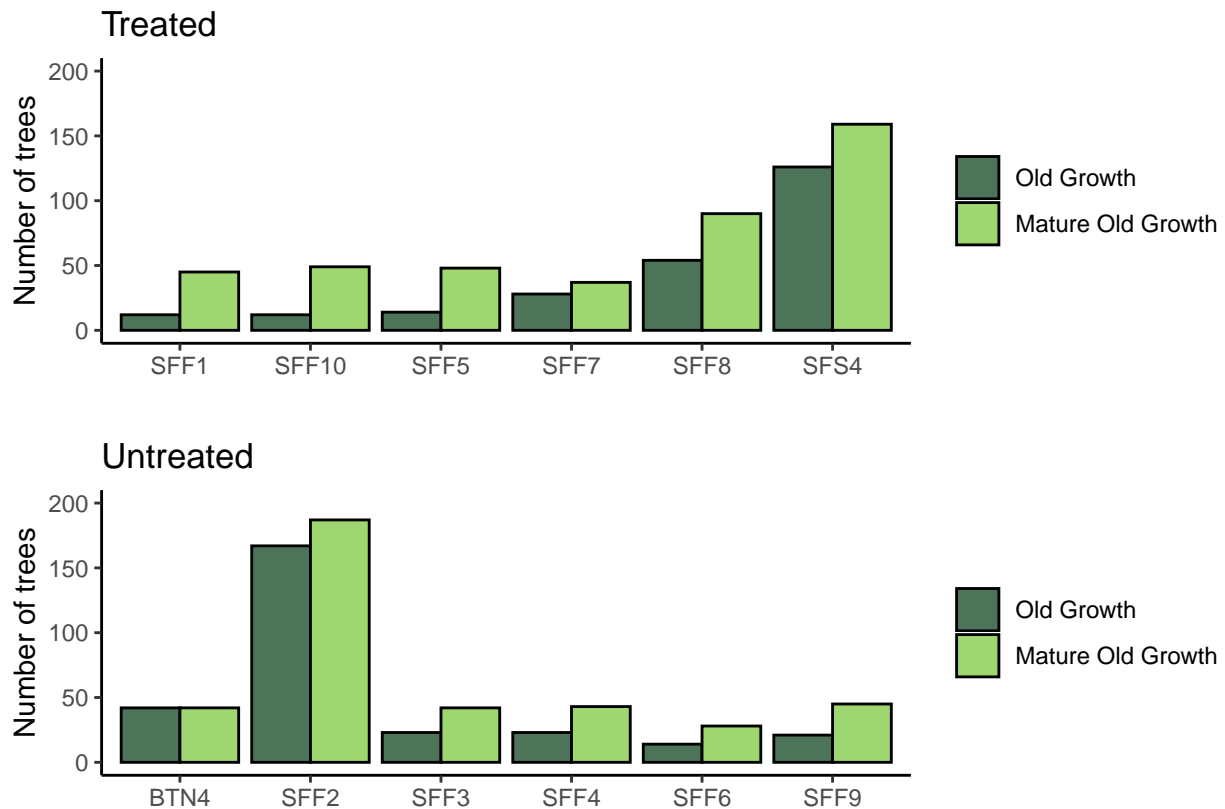
UntreatedPlotName <- subset(est_data, TreatmentStatus == "Untreated")$PlotName
UntreatedMOG <- subset(est_data, TreatmentStatus == "Untreated")$MOG_count
UntreatedOG <- subset(est_data, TreatmentStatus == "Untreated")$OG_count
Untreated_MOG_OG <- data.frame(UntreatedPlotName, UntreatedMOG, UntreatedOG)

UnT_MOG_OG <- melt(Untreated_MOG_OG[,c('UntreatedPlotName', 'UntreatedOG', 'UntreatedMOG')], id.vars = 1)

UnT_MOG_OG_Plot <- ggplot(UnT_MOG_OG, aes(x = UntreatedPlotName, y = value)) +
  geom_bar(aes(fill = variable), stat = "identity", color = 'black', position = "dodge") +
  ggtitle("Untreated") +
  xlab("") +
  ylab("Number of trees") +
  ylim(0, 200) +
  scale_fill_manual(values=c("#4d7358", "#9ed670"), labels = c('Old Growth', 'Mature Old Growth')) +
  theme_classic() +
  theme(legend.title = element_blank())

grid.arrange(T_MOG_OG_Plot, UnT_MOG_OG_Plot, ncol=1)

```



MOG and TPH stacked bar graph

```

MOGperHectare <- est_data$MOG_count / est_data$PlotSize

```

```

est_data$MOGperha <- MOGperHectare

est_data$NotMOGperha <- est_data$TPH - est_data$MOGperha

MOGPHvsTPH<- melt(est_data[,c('PlotName','MOGperha','NotMOGperha')],id.vars = 1)

MOGPHvsTPH$variable <- factor(MOGPHvsTPH$variable, levels=c("NotMOGperha", "MOGperha"))

MOGPHvsTPH$TreatmentStatus <- est_data$TreatmentStatus

ggplot(MOGPHvsTPH, aes(x = PlotName, y = value, fill = variable)) +
  geom_bar(position = "fill", stat = "identity", color = "black") +
  xlab("") +
  ylab("Trees per ha (%)") +
  scale_fill_manual(values=c("#005b96", "#6497b1"), labels=c("All other trees", "MOG")) +
  theme_classic() +
  theme(legend.title = element_blank())

```

