

# DensityAnalysisCapstone

```
pkg <- c("lme4", "lmerTest", "emmeans", "rstatix", "dplyr", "ggplot2", "readxl",  
"boot", "car", "MASS", "ggpubr", "patchwork", "gridExtra", "performance", "tidyverse", "forcats")  
  
new_pkg <- pkg[!(pkg %in% installed.packages()[, "Package"])]  
if (length(new_pkg)) install.packages(new_pkg)  
lapply(pkg, library, character.only = TRUE)
```

Warning: package 'lme4' was built under R version 4.5.1

Loading required package: Matrix

Warning: package 'lmerTest' was built under R version 4.5.1

Attaching package: 'lmerTest'

The following object is masked from 'package:lme4':

lmer

The following object is masked from 'package:stats':

step

Warning: package 'emmeans' was built under R version 4.5.1

Welcome to emmeans.

Caution: You lose important information if you filter this package's results.

See '? untidy'

Warning: package 'rstatix' was built under R version 4.5.1

Attaching package: 'rstatix'

The following object is masked from 'package:stats':

filter

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

Warning: package 'ggplot2' was built under R version 4.5.1

Warning: package 'readxl' was built under R version 4.5.1

Warning: package 'car' was built under R version 4.5.1

Loading required package: carData

Attaching package: 'car'

The following object is masked from 'package:boot':

logit

The following object is masked from 'package:dplyr':

recode

Attaching package: 'MASS'

The following object is masked from 'package:dplyr':

select

The following object is masked from 'package:rstatix':

select

Warning: package 'ggpubr' was built under R version 4.5.1

Warning: package 'patchwork' was built under R version 4.5.1

Attaching package: 'patchwork'

The following object is masked from 'package:MASS':

area

Warning: package 'gridExtra' was built under R version 4.5.1

Attaching package: 'gridExtra'

The following object is masked from 'package:dplyr':

combine

Warning: package 'performance' was built under R version 4.5.1

— Attaching core tidyverse packages — tidyverse 2.0.0 —

```
✓ forcats 1.0.0    ✓ stringr 1.5.1
✓ lubridate 1.9.4  ✓ tibble 3.2.1
✓ purrr 1.0.4     ✓ tidyr 1.3.1
✓ readr 2.1.5
```

— Conflicts — tidyverse\_conflicts() —

```
✗ gridExtra::combine() masks dplyr::combine()
✗ tidyr::expand()       masks Matrix::expand()
✗ dplyr::filter()       masks rstatix::filter(), stats::filter()
✗ dplyr::lag()          masks stats::lag()
✗ tidyr::pack()         masks Matrix::pack()
✗ car::recode()         masks dplyr::recode()
✗ MASS::select()       masks dplyr::select(), rstatix::select()
✗ purrr::some()        masks car::some()
✗ tidyr::unpack()      masks Matrix::unpack()
```

! Use the conflicted package (<<http://conflicted.r-lib.org/>>) to force all conflicts to become errors

[[1]]

```
[1] "lme4"      "Matrix"    "stats"     "graphics"  "grDevices" "utils"
[7] "datasets" "methods"   "base"
```

[[2]]

```
[1] "lmerTest" "lme4"      "Matrix"    "stats"     "graphics"  "grDevices"
[7] "utils"    "datasets"  "methods"   "base"
```

[[3]]

```
[1] "emmeans"  "lmerTest"  "lme4"      "Matrix"    "stats"     "graphics"
[7] "grDevices" "utils"     "datasets"  "methods"   "base"
```

[[4]]

```
[1] "rstatix"  "emmeans"  "lmerTest"  "lme4"      "Matrix"    "stats"
[7] "graphics" "grDevices" "utils"     "datasets"  "methods"   "base"
```

[[5]]

```
[1] "dplyr"    "rstatix"  "emmeans"  "lmerTest"  "lme4"      "Matrix"
[7] "stats"    "graphics" "grDevices" "utils"     "datasets"  "methods"
[13] "base"
```

[[6]]

```
[1] "ggplot2"  "dplyr"    "rstatix"  "emmeans"  "lmerTest"  "lme4"
[7] "Matrix"   "stats"    "graphics" "grDevices" "utils"     "datasets"
[13] "methods"  "base"
```

[[7]]

[1]	"readxl"	"ggplot2"	"dplyr"	"rstatix"	"emmeans"	"lmerTest"
[7]	"lme4"	"Matrix"	"stats"	"graphics"	"grDevices"	"utils"
[13]	"datasets"	"methods"	"base"			

[[8]]

[1]	"boot"	"readxl"	"ggplot2"	"dplyr"	"rstatix"	"emmeans"
[7]	"lmerTest"	"lme4"	"Matrix"	"stats"	"graphics"	"grDevices"
[13]	"utils"	"datasets"	"methods"	"base"		

[[9]]

[1]	"car"	"carData"	"boot"	"readxl"	"ggplot2"	"dplyr"
[7]	"rstatix"	"emmeans"	"lmerTest"	"lme4"	"Matrix"	"stats"
[13]	"graphics"	"grDevices"	"utils"	"datasets"	"methods"	"base"

[[10]]

[1]	"MASS"	"car"	"carData"	"boot"	"readxl"	"ggplot2"
[7]	"dplyr"	"rstatix"	"emmeans"	"lmerTest"	"lme4"	"Matrix"
[13]	"stats"	"graphics"	"grDevices"	"utils"	"datasets"	"methods"
[19]	"base"					

[[11]]

[1]	"ggpubr"	"MASS"	"car"	"carData"	"boot"	"readxl"
[7]	"ggplot2"	"dplyr"	"rstatix"	"emmeans"	"lmerTest"	"lme4"
[13]	"Matrix"	"stats"	"graphics"	"grDevices"	"utils"	"datasets"
[19]	"methods"	"base"				

[[12]]

[1]	"patchwork"	"ggpubr"	"MASS"	"car"	"carData"	"boot"
[7]	"readxl"	"ggplot2"	"dplyr"	"rstatix"	"emmeans"	"lmerTest"
[13]	"lme4"	"Matrix"	"stats"	"graphics"	"grDevices"	"utils"
[19]	"datasets"	"methods"	"base"			

[[13]]

[1]	"gridExtra"	"patchwork"	"ggpubr"	"MASS"	"car"	"carData"
[7]	"boot"	"readxl"	"ggplot2"	"dplyr"	"rstatix"	"emmeans"
[13]	"lmerTest"	"lme4"	"Matrix"	"stats"	"graphics"	"grDevices"
[19]	"utils"	"datasets"	"methods"	"base"		

[[14]]

[1]	"performance"	"gridExtra"	"patchwork"	"ggpubr"	"MASS"	
[6]	"car"	"carData"	"boot"	"readxl"	"ggplot2"	
[11]	"dplyr"	"rstatix"	"emmeans"	"lmerTest"	"lme4"	
[16]	"Matrix"	"stats"	"graphics"	"grDevices"	"utils"	
[21]	"datasets"	"methods"	"base"			

[[15]]

[1]	"lubridate"	"forcats"	"stringr"	"purrr"	"readr"	
[6]	"tidyr"	"tibble"	"tidyverse"	"performance"	"gridExtra"	
[11]	"patchwork"	"ggpubr"	"MASS"	"car"	"carData"	
[16]	"boot"	"readxl"	"ggplot2"	"dplyr"	"rstatix"	

```
[21] "emmeans"      "lmerTest"      "lme4"          "Matrix"        "stats"
[26] "graphics"     "grDevices"     "utils"         "datasets"      "methods"
[31] "base"
```

```
[[16]]
```

```
[1] "lubridate"    "forcats"       "stringr"       "purrr"         "readr"
[6] "tidyr"        "tibble"        "tidyverse"     "performance"   "gridExtra"
[11] "patchwork"    "ggpubr"        "MASS"          "car"           "carData"
[16] "boot"         "readxl"        "ggplot2"       "dplyr"         "rstatix"
[21] "emmeans"     "lmerTest"      "lme4"          "Matrix"        "stats"
[26] "graphics"     "grDevices"     "utils"         "datasets"      "methods"
[31] "base"
```

$\text{lmer}(\log(\text{Density}) \sim \text{Plot} + (1 \mid \text{Location}), \text{data} = \text{capstone})$

$$\log(\text{Density}_{ijk}) = \beta_0 + \beta_{1j} + u_k + \epsilon_{ijk}$$

$\log(\text{Density}_{ijk})$  = log-transformed tree density (dependent variable)

$\beta_0$  = fixed intercept (mean log-density for the reference Plot category, Edge)

$\beta_{1j}$  = fixed effect of Plot  $j$  (difference in mean log-density for Transition and Interior compared to Edge)

$u_k \sim N(0, \sigma_{\text{Location}}^2)$  = random intercept for Location, capturing variability among locations

$\epsilon_{ijk} \sim N(0, \sigma^2)$  = residual error for individual plots

$$u_k \sim N(0, \sigma_{\text{Location}}^2), \quad \epsilon_{ijk} \sim N(0, \sigma^2)$$

Where:

$\sigma_{\text{Location}}^2$  is the variance component due to Location (between-site variability), and

$\sigma^2$  is the residual variance component (within-site, unexplained variability).

```
file_path <- "C:/Users/Nicho/OneDrive/Desktop/Density.xlsx"
capstone <- read_excel(file_path, sheet = "Sheet1")

capstone <- capstone %>%
  mutate(

    Plot = as.character(Plot),
    Plot = case_when(
      Plot %in% c("1", "Edge") ~ "Edge",
      Plot %in% c("2", "Transition") ~ "Transition",
      Plot %in% c("3", "Interior") ~ "Interior",
      TRUE ~ NA_character_
    ),
    Plot = factor(Plot, levels = c("Edge", "Transition", "Interior")),

    Location = as.factor(Location),

    density_ha = density * 2.47105,

    log_density = log(density_ha)
```

```
)
```

```
summary(capstone$log_density)
```

```

  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 2.696  3.207   3.470   3.555  3.900   4.370

```

```
unique(capstone$Plot)
```

```
[1] Edge      Transition Interior
```

```
Levels: Edge Transition Interior
```

```

location_order <- c(
  "Gardiner County Park",
  "Shinnecock",
  "Haven Point",
  "Ludlow Creek",
  "Pine Neck",
  "Wertheim",
  "Seatuck"
)

capstone$Location <- factor(capstone$Location, levels = location_order)

plot_box <- ggplot(capstone, aes(x = Location, y = log_density)) +
  stat_boxplot(geom = "errorbar", width = 0.5, linewidth = 0.3) +
  geom_boxplot(
    fill = "#82B1B1",
    color = "black",
    linewidth = 0.5,
    outlier.size = 1.5,
    outlier.shape = 1
  ) +
  labs(
    x = "Location",
    y = expression("Log Tree Density" ~ (log(stems/ha)))
  ) +
  coord_flip() +
  theme_bw() +
  theme(
    text = element_text(family = "sans", size = 12),
    panel.grid.major.y = element_blank(),
    panel.grid.minor = element_blank(),
    axis.line = element_line(color = "black", linewidth = 0.5),
    axis.text.x = element_text(
      angle = 30,
      hjust = 1,
      vjust = 1,
      color = "black"
    )
  )

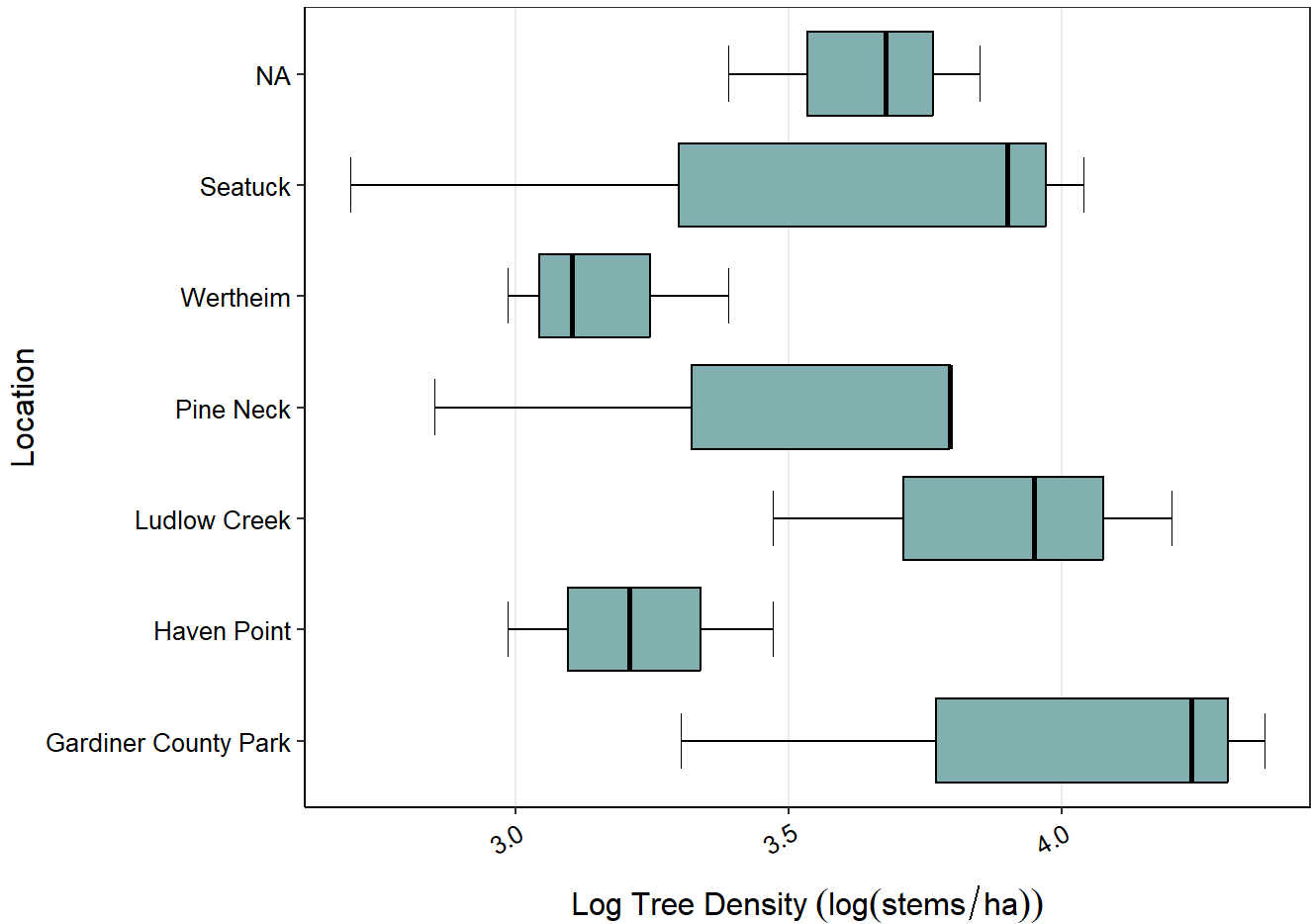
```

```

),
axis.text.y = element_text(color = "black"),
axis.title.x = element_text(margin = margin(t = 10))
)

print(plot_box)

```



```

density_model <- lmer(
  log_density ~ Plot + (1 | Location),
  data = capstone
)

summary(density_model)

```

Linear mixed model fit by REML. t-tests use Satterthwaite's method [

lmerModLmerTest]

Formula: log\_density ~ Plot + (1 | Location)

Data: capstone

REML criterion at convergence: 27.7

Scaled residuals:

Min	1Q	Median	3Q	Max

-1.35957 -0.55502 -0.08999 0.67010 1.57343

Random effects:

Groups	Name	Variance	Std.Dev.
	Location (Intercept)	0.03285	0.1812
	Residual	0.22973	0.4793

Number of obs: 18, groups: Location, 6

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t )
(Intercept)	3.5074	0.2092	14.5447	16.766	6.46e-11 ***
PlotTransition	0.2622	0.2767	10.0000	0.948	0.366
PlotInterior	-0.1607	0.2767	10.0000	-0.581	0.574

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

	(Intr)	PltTrn
PlotTranstn	-0.661	
PlotInterior	-0.661	0.500

```
anova(density_model)
```

Type III Analysis of Variance Table with Satterthwaite's method

	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
Plot	0.54691	0.27345	2	10	1.1903	0.3438

```
density_tukey <- emmeans(density_model, pairwise ~ Plot, adjust = "tukey")
summary(density_tukey)
```

\$emmeans

Plot	emmean	SE	df	lower.CL	upper.CL
Edge	3.51	0.209	14.5	3.06	3.95
Transition	3.77	0.209	14.5	3.32	4.22
Interior	3.35	0.209	14.5	2.90	3.79

Degrees-of-freedom method: kenward-roger

Confidence level used: 0.95

\$contrasts

contrast	estimate	SE	df	t.ratio	p.value
Edge - Transition	-0.262	0.277	10	-0.948	0.6243
Edge - Interior	0.161	0.277	10	0.581	0.8333
Transition - Interior	0.423	0.277	10	1.528	0.3194

Degrees-of-freedom method: kenward-roger

P value adjustment: tukey method for comparing a family of 3 estimates



```
back_means <- emmeans(density_model, ~ Plot)
bt_summary <- summary(back_means) %>%
  mutate(
    emmean_bt = exp(emmean),
    lower_bt = exp(lower.CL),
    upper_bt = exp(upper.CL)
  )

print(bt_summary)
```

	Plot	emmean	SE	df	lower.CL	upper.CL	emmean_bt	lower_bt	upper_bt
1	Edge	3.507430	0.2091948	14.54473	3.060323	3.954537	33.36240	21.33444	
2	Transition	3.769657	0.2091948	14.54473	3.322550	4.216764	43.36520	27.73098	
3	Interior	3.346731	0.2091948	14.54473	2.899624	3.793838	28.40972	18.16732	
1							52.17151		
2							67.81370		
3							44.42660		

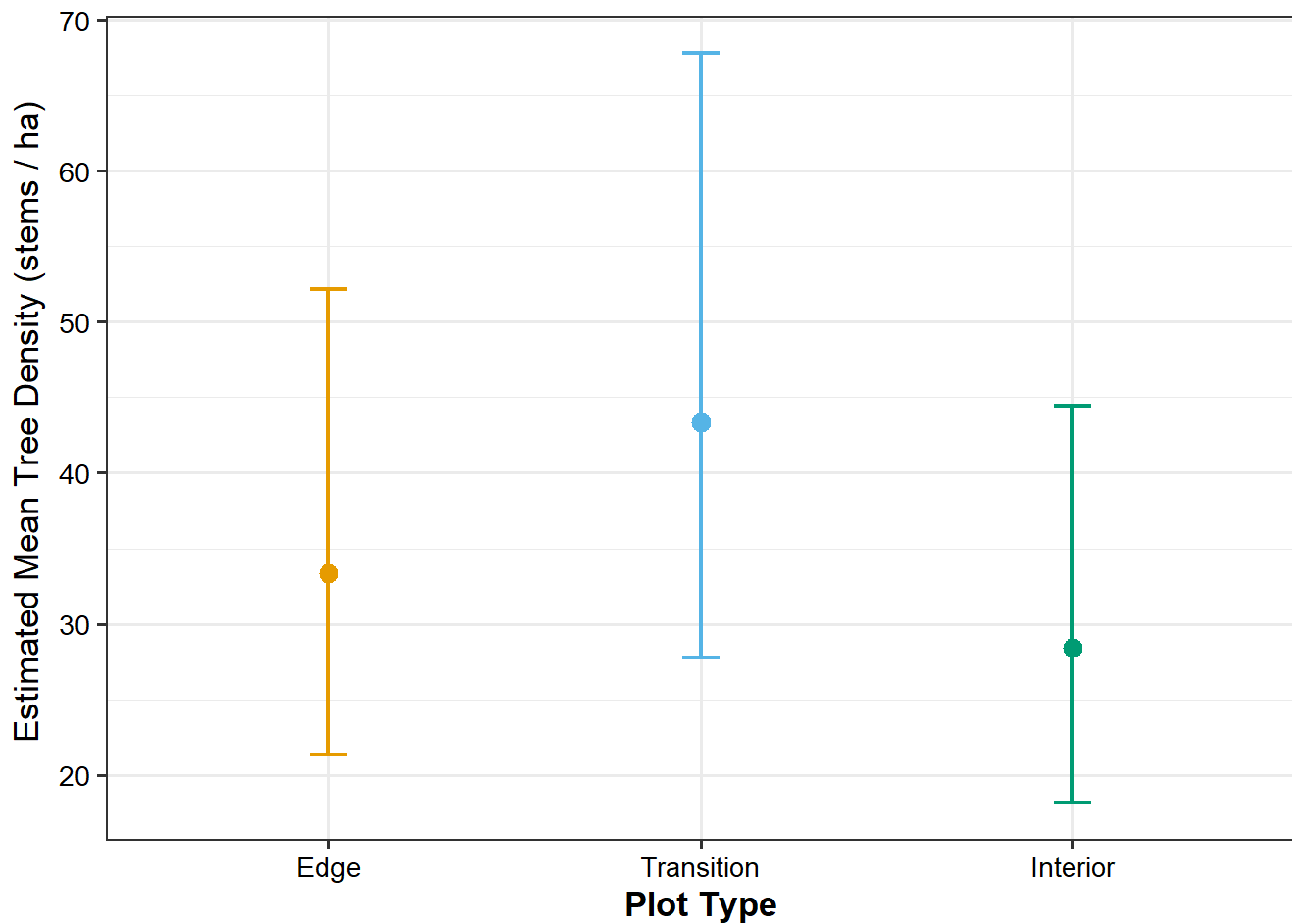
```
bt_contrasts <- pairs(back_means, adjust = "tukey") %>%
  summary() %>%
  mutate(ratio = exp(estimate))

print(bt_contrasts)
```

	contrast	estimate	SE	df	t.ratio	p.value	ratio
1	Edge - Transition	-0.2622277	0.2767226	10	-0.9476193	0.6242783	0.7693358
2	Edge - Interior	0.1606982	0.2767226	10	0.5807194	0.8332622	1.1743305
3	Transition - Interior	0.4229259	0.2767226	10	1.5283387	0.3194366	1.5264211

```
custom_colors <- c("Edge" = "#E69F00",
                  "Transition" = "#56B4E9",
                  "Interior" = "#009E73")

ggplot(bt_summary, aes(x = Plot, y = emmean_bt, color = Plot)) +
  geom_point(size = 3) +
  geom_errorbar(aes(ymin = lower_bt, ymax = upper_bt),
               width = 0.1, linewidth = 0.8) +
  scale_color_manual(values = custom_colors) +
  labs(
    x = "Plot Type",
    y = expression("Estimated Mean Tree Density (stems / ha)")
  ) +
  theme_bw(base_size = 13) +
  theme(
    legend.position = "none",
    axis.text = element_text(color = "black"),
    axis.title = element_text(color = "black", face = "bold")
  )
```



```
capstone <- capstone %>%
  mutate(

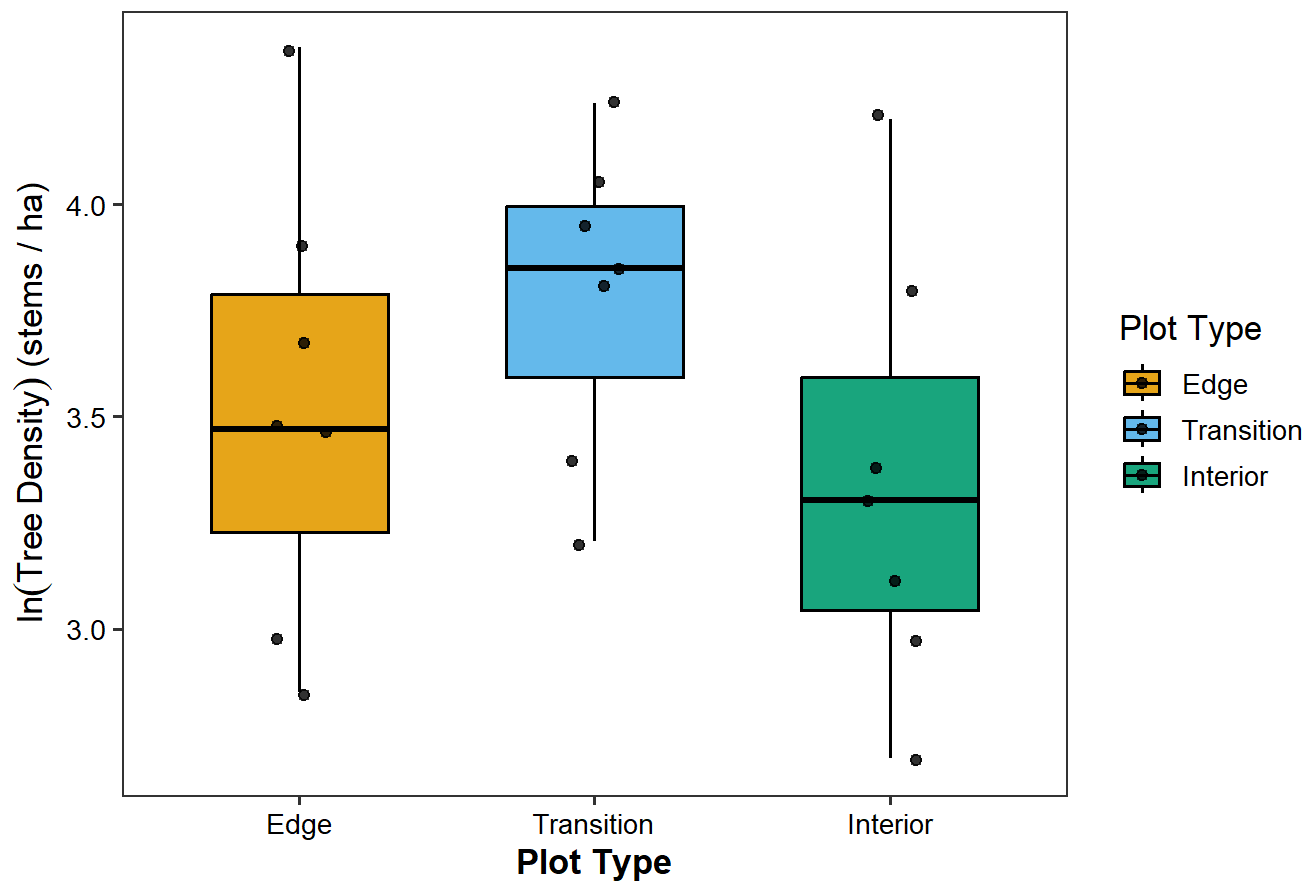
    Plot = as.character(Plot),
    Plot = case_when(
      Plot %in% c("1", "Edge") ~ "Edge",
      Plot %in% c("2", "Transition") ~ "Transition",
      Plot %in% c("3", "Interior") ~ "Interior",
      TRUE ~ NA_character_
    ),
    Plot = factor(Plot, levels = c("Edge", "Transition", "Interior")),

    density_ha = density * 2.47105,

    log_density = log(density_ha)
  )

custom_colors <- c(
  "Edge" = "#E69F00",
  "Transition" = "#56B4E9",
  "Interior" = "#009E73"
)
```

```
Figure_S7 <- ggplot(capstone, aes(x = Plot, y = log_density, fill = Plot)) +  
  geom_boxplot(  
    color = "black",  
    width = 0.6,  
    outlier.shape = NA,  
    alpha = 0.9  
  ) +  
  geom_jitter(  
    width = 0.1,  
    size = 1.8,  
    alpha = 0.8  
  ) +  
  scale_fill_manual(values = custom_colors, name = "Plot Type") +  
  labs(  
    x = "Plot Type",  
    y = expression(ln(Tree~Density)~"(stems / ha)"),  
    title = ""  
  ) +  
  theme_bw(base_size = 13) +  
  theme(  
    legend.position = "right",  
    plot.title = element_text(hjust = 0.5, face = "bold"),  
    axis.text = element_text(color = "black"),  
    axis.title = element_text(color = "black", face = "bold"),  
    panel.grid.major = element_blank(),  
    panel.grid.minor = element_blank()  
  )  
  
print(Figure_S7)
```



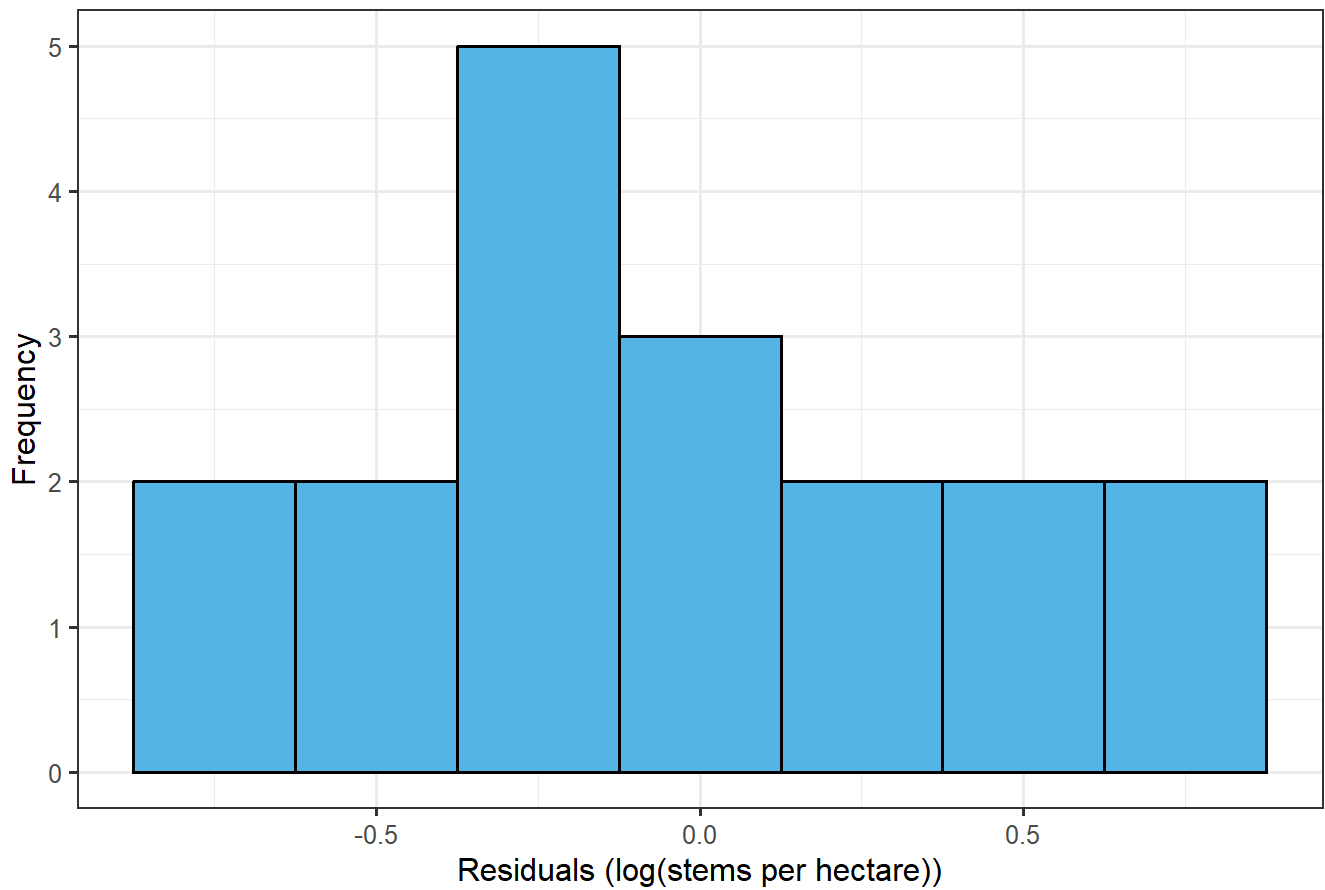
```
lmm_log_density <- lmer(log_density ~ Plot + (1 | Location), data = capstone)

diag_color <- "#56B4E9"
diag_point_color <- "darkblue"

hist2 <- ggplot(data.frame(res = residuals(lmm_log_density)), aes(x = res)) +
  geom_histogram(binwidth = 0.25, fill = diag_color, color = "black") +
  labs(
    title = "A) Log-Transformed Density Per Hectare LMM Residuals (Histogram)",
    x = "Residuals (log(stems per hectare))",
    y = "Frequency"
  ) +
  theme_bw(base_size = 12)

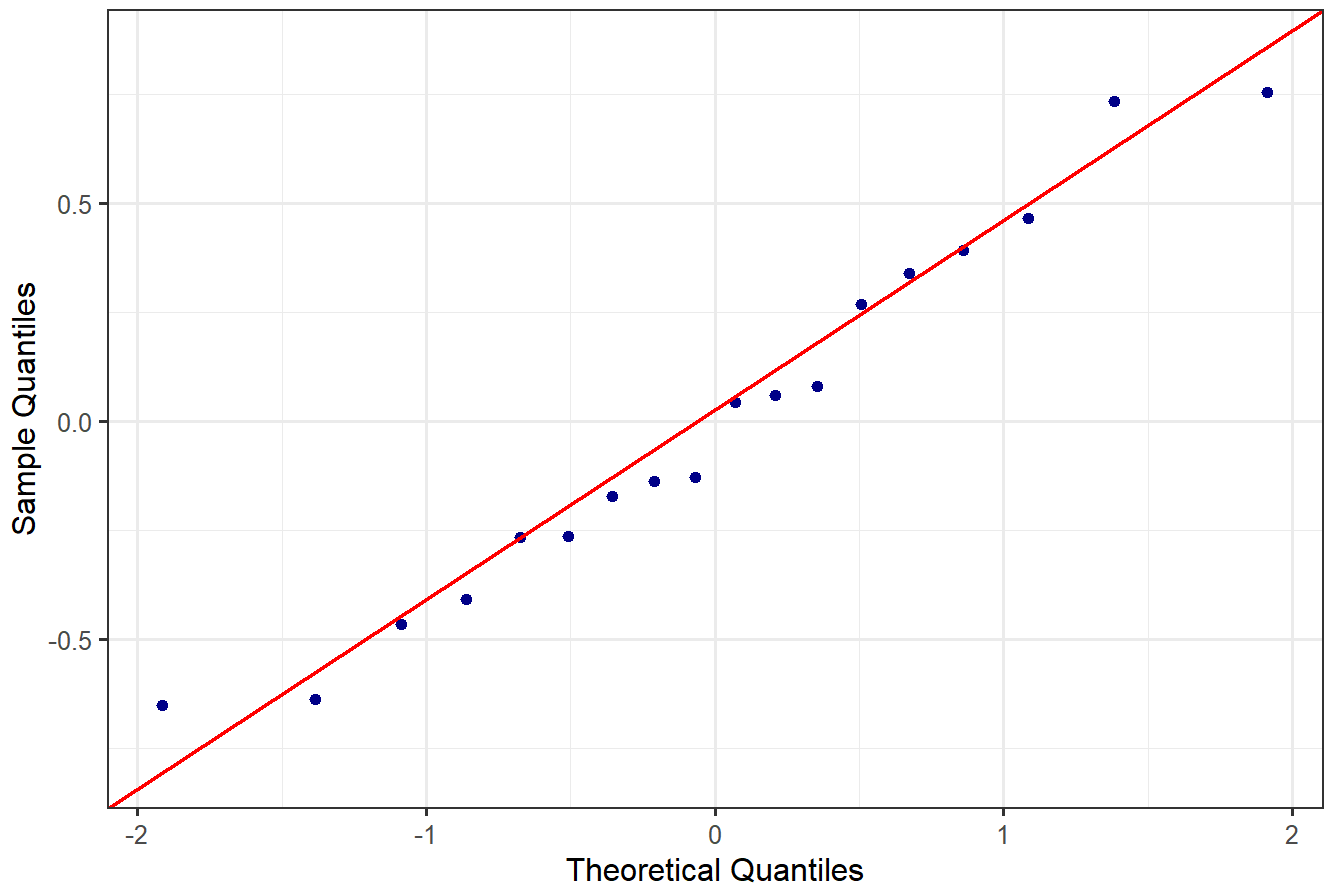
print(hist2)
```

## A) Log-Transformed Density Per Hectare LMM Residuals (Histogram)



```
qq2 <- ggplot(data.frame(res = residuals(lmm_log_density)), aes(sample = res)) +  
  stat_qq(color = diag_point_color) +  
  stat_qq_line(color = "red", linewidth = 0.8) +  
  labs(  
    title = "B) Log-Transformed Density Per Hectare LMM Residuals (Q-Q)",  
    x = "Theoretical Quantiles",  
    y = "Sample Quantiles"  
  ) +  
  theme_bw(base_size = 12)  
  
print(qq2)
```

## B) Log-Transformed Density Per Hectare LMM Residuals (Q-Q)

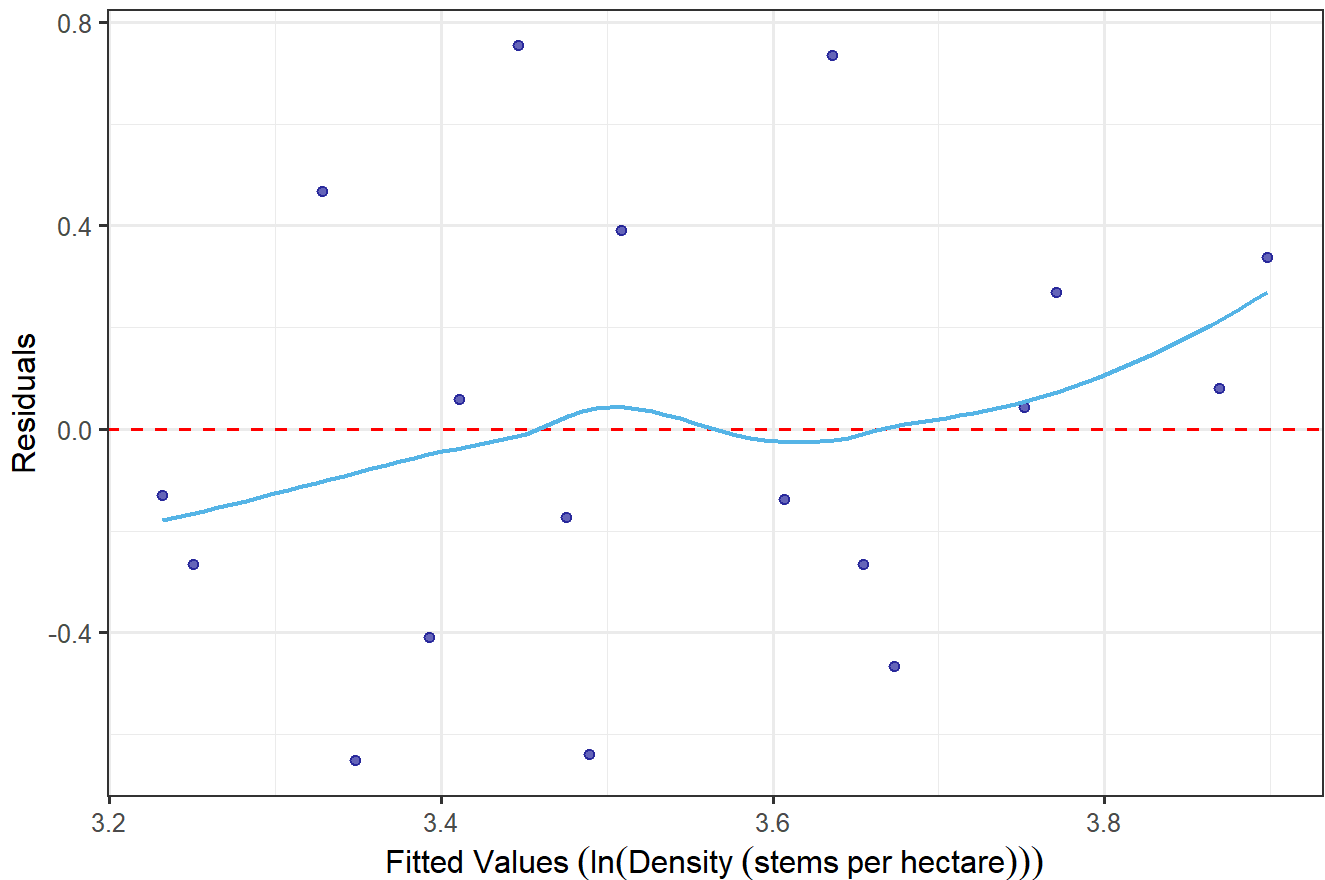


```
res_fit2 <- ggplot(data.frame(
  Fitted = fitted(lmm_log_density),
  Residuals = residuals(lmm_log_density)
), aes(x = Fitted, y = Residuals)) +
  geom_point(alpha = 0.6, color = diag_point_color) +
  geom_hline(yintercept = 0, linetype = "dashed", color = "red") +
  geom_smooth(method = "loess", se = FALSE, color = diag_color, linewidth = 0.8) +
  labs(
    title = "C) Log-Transformed Density Per Hectare LMM Residuals vs. Fitted Values",
    x = expression("Fitted Values"~(ln(Density~(stems~per~hectare)))),
    y = "Residuals"
  ) +
  theme_bw(base_size = 12)

print(res_fit2)
```

`geom\_smooth()` using formula = 'y ~ x'

## C) Log-Transformed Density Per Hectare LMM Residuals vs. Fitted Value



```
lmm_raw_density <- lmer(density * 2.47105 ~ Plot + (1 | Location), data = capstone)

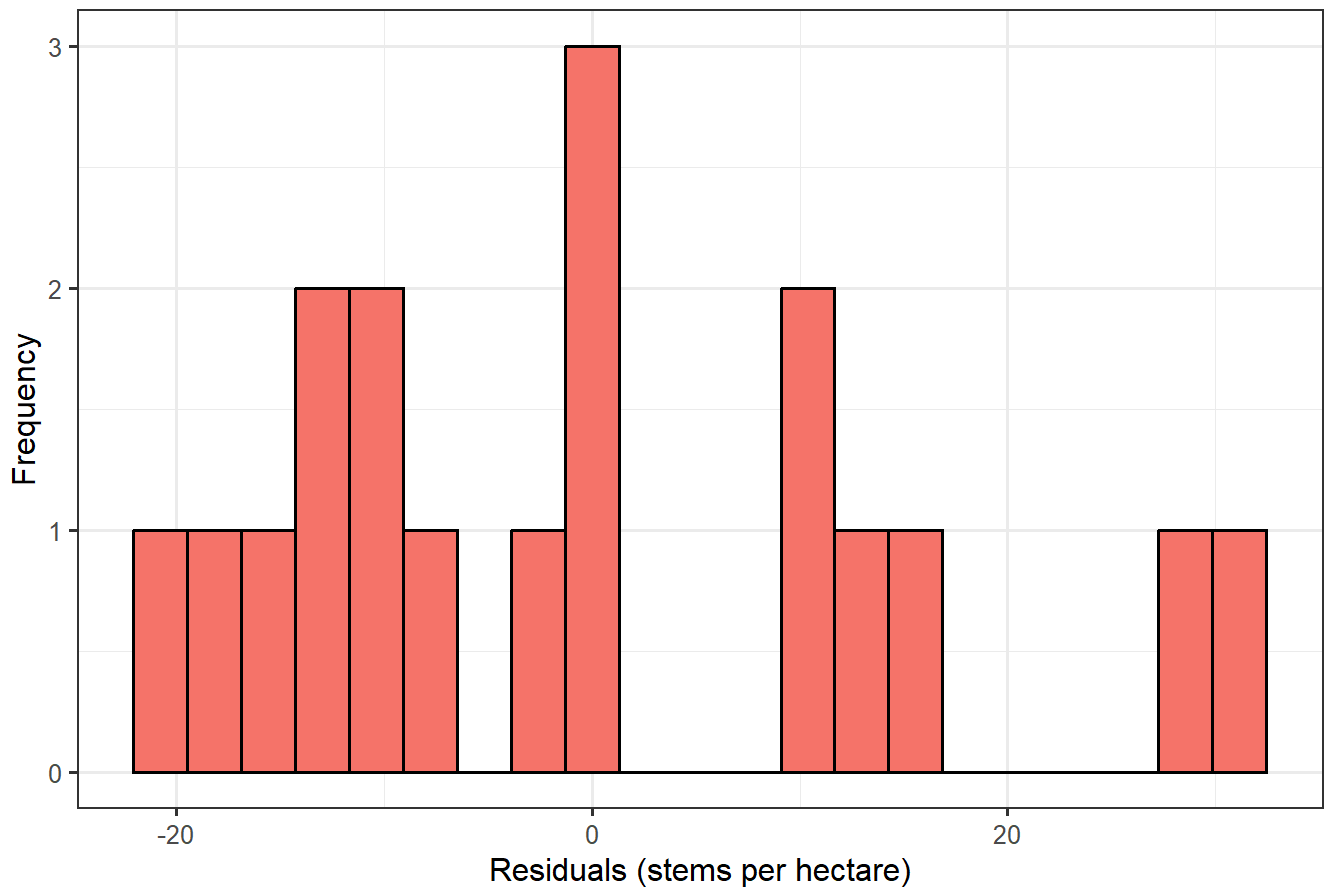
diag_color <- "#F8766D"
diag_point_color <- "#F8766D"

res_raw <- residuals(lmm_raw_density)
fit_raw <- fitted(lmm_raw_density)

hist1_raw <- ggplot(data.frame(res = res_raw), aes(x = res)) +
  geom_histogram(
    binwidth = diff(range(res_raw)) / 20,
    fill = diag_color, color = "black"
  ) +
  labs(
    title = "A) Untransformed Density Per Hectare LMM Residuals (Histogram)",
    x = "Residuals (stems per hectare)",
    y = "Frequency"
  ) +
  theme_bw(base_size = 12)

print(hist1_raw)
```

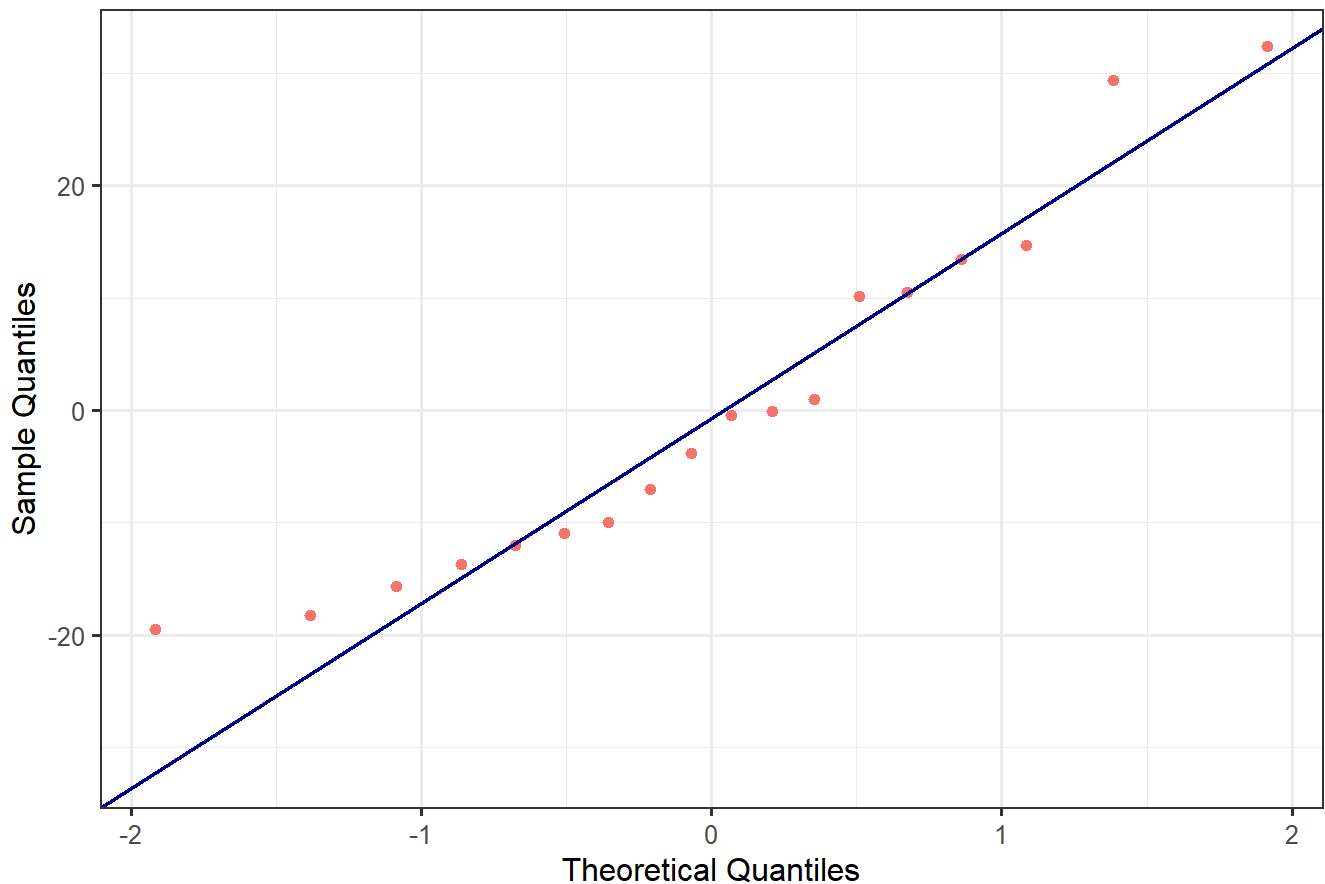
## A) Untransformed Density Per Hectare LMM Residuals (Histogram)



```
qq1_raw <- ggplot(data.frame(res = res_raw), aes(sample = res)) +  
  stat_qq(color = diag_point_color) +  
  stat_qq_line(color = "darkblue", linewidth = 0.8) +  
  labs(  
    title = "B) Untransformed Density Per Hectare LMM Residuals (Q-Q)",  
    x = "Theoretical Quantiles",  
    y = "Sample Quantiles"  
  ) +  
  theme_bw(base_size = 12)  
  
print(qq1_raw)
```



## B) Untransformed Density Per Hectare LMM Residuals (Q-Q)

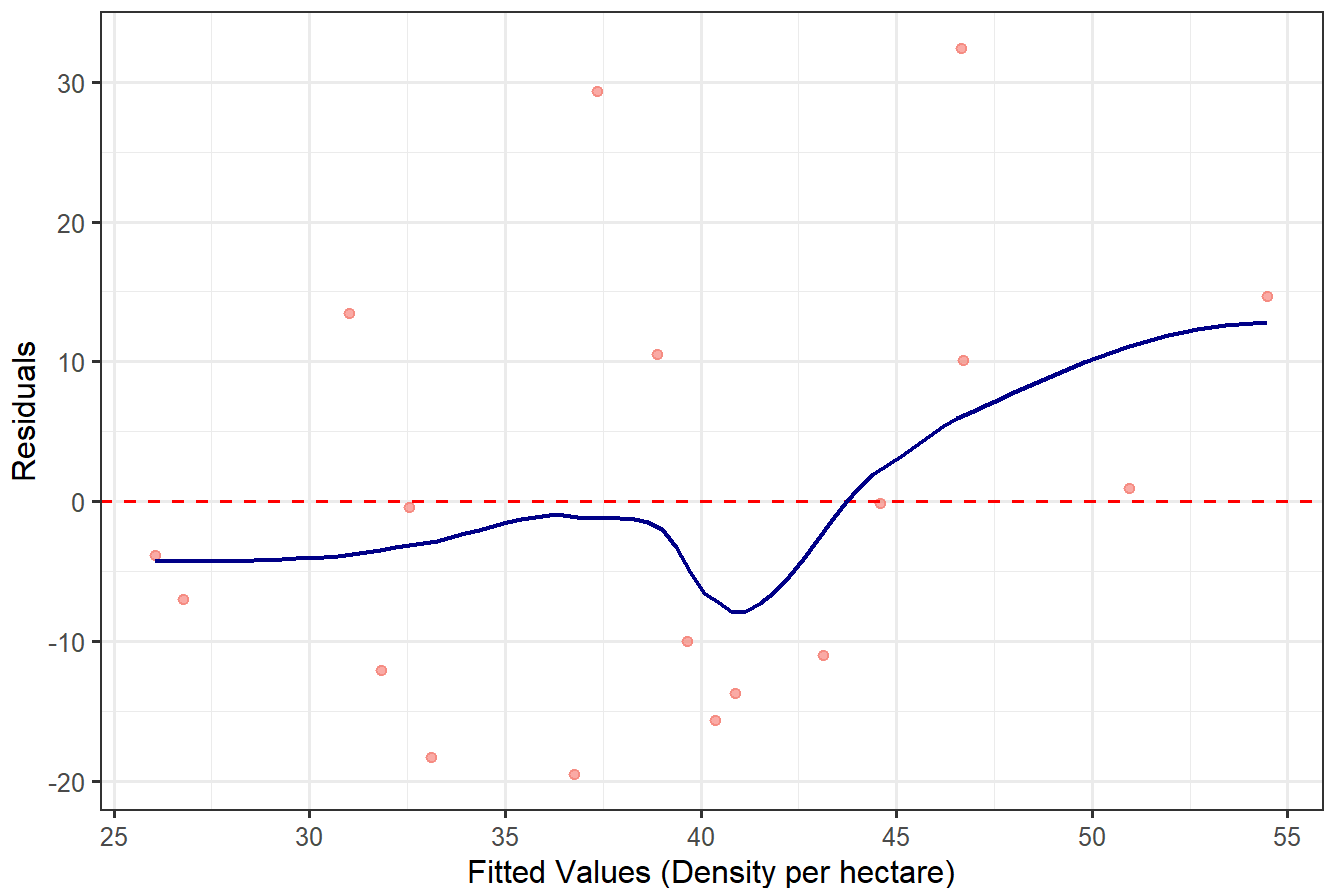


```
res_fit1_raw <- ggplot(data.frame(Fitted = fit_raw, Residuals = res_raw),
                        aes(x = Fitted, y = Residuals)) +
  geom_point(alpha = 0.6, color = diag_point_color) +
  geom_hline(yintercept = 0, linetype = "dashed", color = "red") +
  geom_smooth(method = "loess", se = FALSE, color = "darkblue", linewidth = 0.8) +
  labs(
    title = "C) Untransformed Density Per Hectare LMM Residuals vs Fitted Values",
    x = "Fitted Values (Density per hectare)",
    y = "Residuals"
  ) +
  theme_bw(base_size = 12)

print(res_fit1_raw)
```

`geom\_smooth()` using formula = 'y ~ x'

## C) Untransformed Density Per Hectare LMM Residuals vs Fitted Values



```
file_path <- "C:/Users/Nicho/OneDrive/Desktop/Density.xlsx"
capstone <- read_excel(file_path, sheet = "Sheet1")

capstone <- capstone %>%
  mutate(
    Location = as.factor(Location),
    Plot = as.factor(Plot),
    density_per_hectare = density * 2.47105,
    log_density = log(density_per_hectare)
  )

location_order <- c(
  "Gardiner County Park", "Shinnecock", "Haven Point",
  "Ludlow Creek", "Pine Neck", "Wertheim", "Seatuck"
)
capstone$Location <- fct_relevel(capstone$Location, location_order)
```

Warning: 1 unknown level in `f`: Shinnecock

```
capstone <- capstone %>%
  mutate(Plot_Label = dplyr::recode(as.character(Plot),
    "1" = "Edge",
    "2" = "Transition",
```

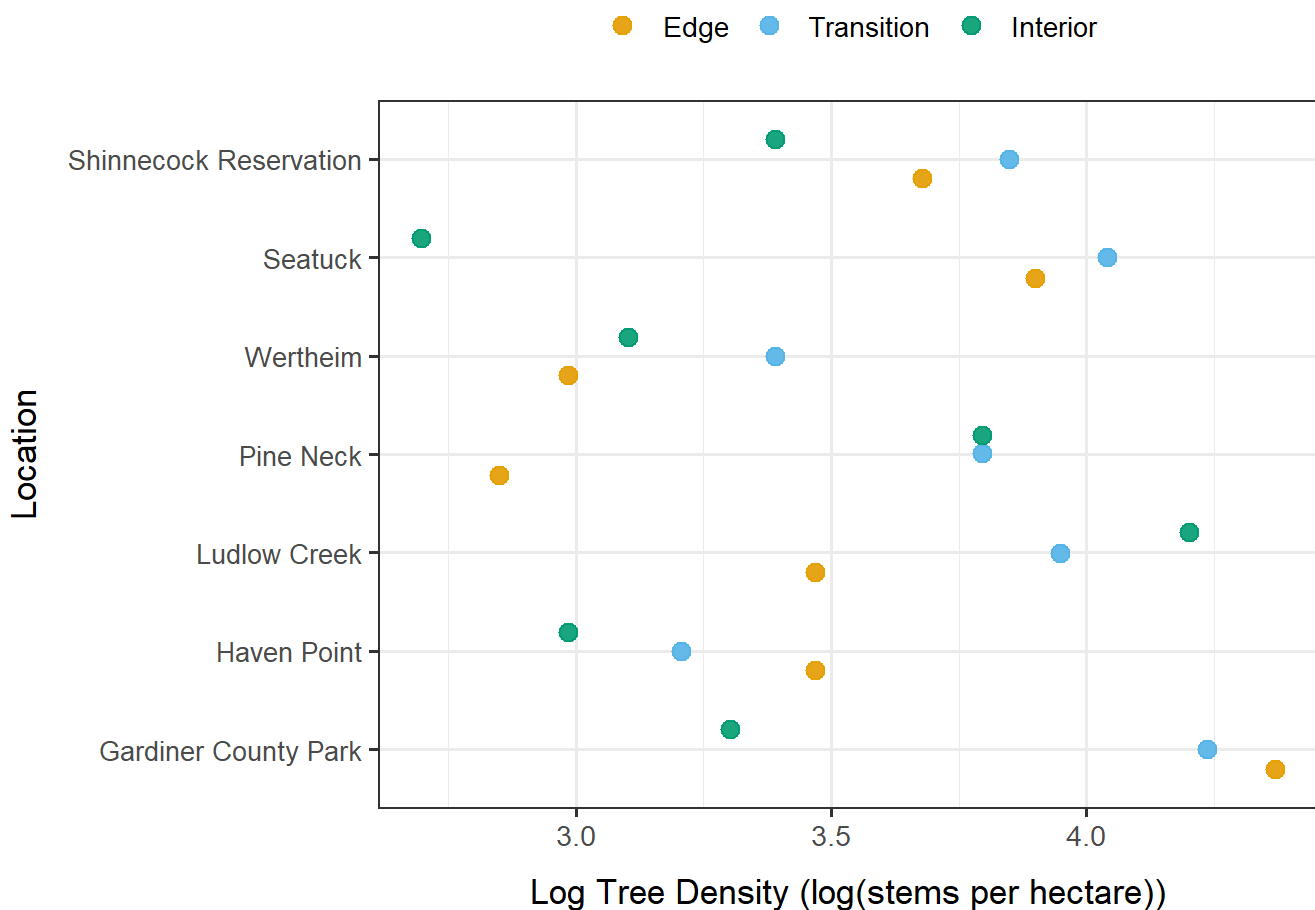
```

      "3" = "Interior")) %>%
mutate(Plot_Label = factor(Plot_Label,
      levels = c("Edge", "Transition", "Interior")))

pal_plot <- c("Edge" = "#E69F00", "Transition" = "#56B4E9", "Interior" = "#009E73")

plot_points <- ggplot(capstone, aes(x = log_density, y = Location, color = Plot_Label)) +
  geom_point(position = position_jitterdodge(jitter.width = 0.05, dodge.width = 0.6),
    size = 3, alpha = 0.9) +
  scale_color_manual(values = pal_plot, name = "Plot Type") +
  labs(
    x = "Log Tree Density (log(stems per hectare))",
    y = "Location"
  ) +
  theme_bw(base_size = 13) +
  theme(
    legend.position = "top",
    legend.title = element_blank(),
    axis.text.y = element_text(size = 10),
    axis.title.x = element_text(margin = margin(t = 10)),
    axis.title.y = element_text(margin = margin(r = 10))
  )
print(plot_points)

```



```
density_model <- lmer(log_density ~ Plot + (1 | Location), data = capstone)

density_tukey <- emmeans(density_model, pairwise ~ Plot, adjust = "tukey")
print(summary(density_tukey))
```

\$emmeans

Plot	emmean	SE	df	lower.CL	upper.CL
1	3.53	0.178	17.4	3.16	3.91
2	3.78	0.178	17.4	3.41	4.15
3	3.35	0.178	17.4	2.98	3.73

Degrees-of-freedom method: kenward-roger

Confidence level used: 0.95

\$contrasts

contrast	estimate	SE	df	t.ratio	p.value
Plot1 - Plot2	-0.249	0.234	12	-1.064	0.5528
Plot1 - Plot3	0.179	0.234	12	0.763	0.7315
Plot2 - Plot3	0.428	0.234	12	1.828	0.2023

Degrees-of-freedom method: kenward-roger

P value adjustment: tukey method for comparing a family of 3 estimates

```
back_transformed_means <- emmeans(density_model, ~ Plot, type = "response")
bt_summary <- summary(back_transformed_means)
print(bt_summary)
```

Plot	emmean	SE	df	lower.CL	upper.CL
1	3.53	0.178	17.4	3.16	3.91
2	3.78	0.178	17.4	3.41	4.15
3	3.35	0.178	17.4	2.98	3.73

Degrees-of-freedom method: kenward-roger

Confidence level used: 0.95

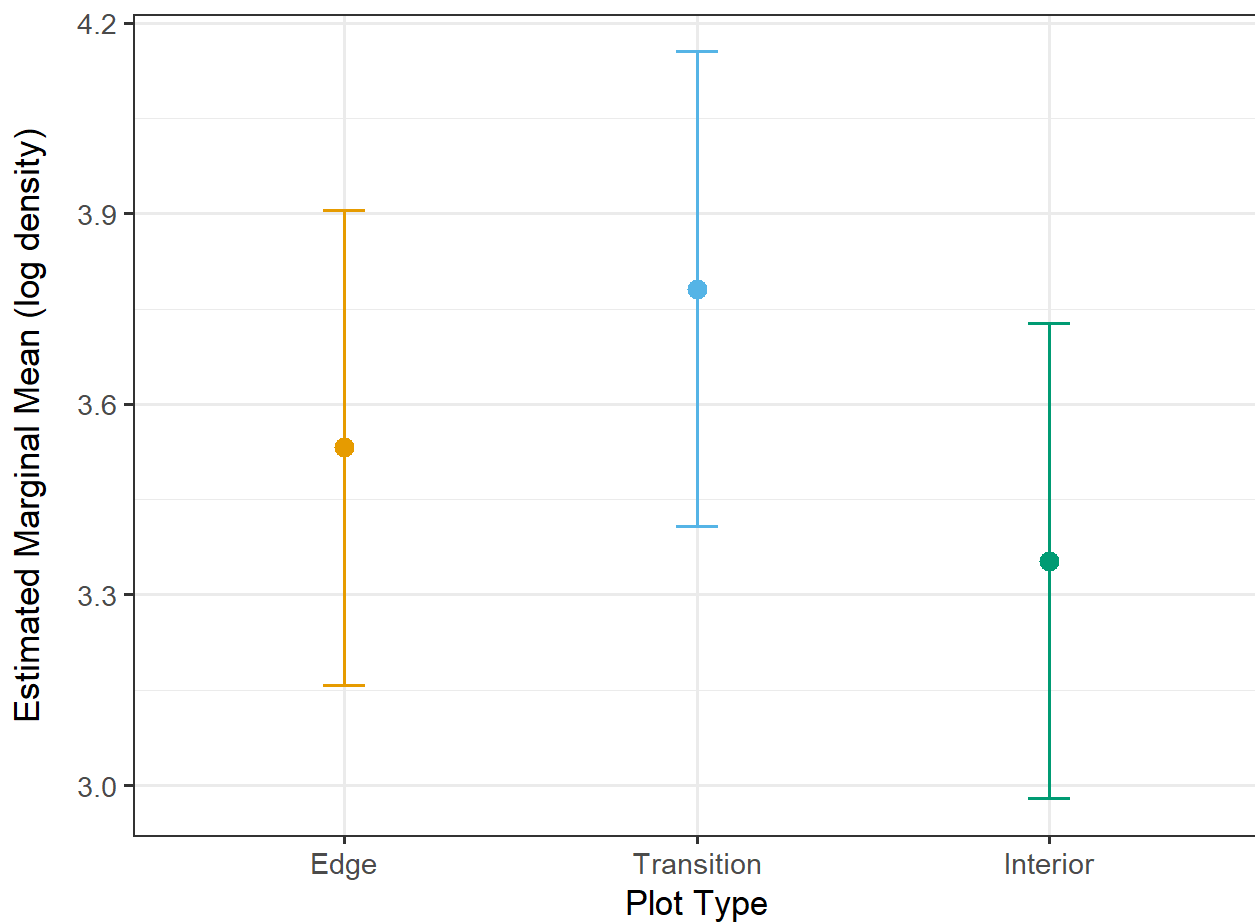
```
em_df <- as.data.frame(bt_summary)
em_df$Plot_Label <- factor(dplyr::recode(as.character(em_df$Plot), "1" = "Edge", "2" = "Transition"))
em_df_bt <- em_df %>%
  mutate(
    emmean_bt = exp(emmean),
    lower_bt = exp(lower.CL),
    upper_bt = exp(upper.CL)
  )

p_log <- ggplot(em_df_bt, aes(x = Plot_Label, y = emmean, color = Plot_Label)) +
  geom_point(size = 3) +
  geom_errorbar(aes(ymin = lower.CL, ymax = upper.CL), width = 0.12, linewidth = 0.6) +
  scale_color_manual(values = pal_plot) +
  labs(
```

```

x = "Plot Type",
y = "Estimated Marginal Mean (log density)"
) +
theme_bw(base_size = 13) +
theme(
  legend.position = "none",
  axis.text.x = element_text(size = 11),
  axis.title.y = element_text(margin = margin(r = 12)),
  plot.margin = margin(t = 10, r = 18, b = 10, l = 18)
)
print(p_log)

```



```

p_bt <- ggplot(em_df_bt, aes(x = Plot_Label, y = emmean_bt, color = Plot_Label)) +
  geom_point(size = 3) +
  geom_errorbar(aes(ymin = lower_bt, ymax = upper_bt), width = 0.12, linewidth = 0.6) +
  scale_color_manual(values = pal_plot) +
  labs(
    x = "Plot Type",
    y = "Estimated Marginal Mean Density (trees per hectare)"
  ) +
  theme_bw(base_size = 13) +
  theme(

```

```
legend.position = "none",  
axis.text.x = element_text(size = 11),  
axis.title.y = element_text(margin = margin(r = 12)),  
plot.margin = margin(t = 10, r = 18, b = 10, l = 18)  
)  
print(p_bt)
```

