Forest Lab

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2022-06-16

### Basal Area

basal\_species\_summary <- basal\_area\_dat %>%  
 group\_by(Species)%>%  
 summarize(sum\_ba = sum(basal\_area))  
  
basal\_species\_by\_plot <- basal\_area\_dat %>%  
 group\_by(Plot, Species)%>%  
 summarise(sum\_ba = sum(basal\_area))

## `summarise()` has grouped output by 'Plot'. You can override using the  
## `.groups` argument.

total\_basal\_area\_p1 <- sum(filter(basal\_species\_by\_plot, Plot == 1)$sum\_ba)  
  
total\_basal\_area\_p2 <- sum(filter(basal\_species\_by\_plot, Plot == 2)$sum\_ba)  
  
basal\_species\_by\_plot <- basal\_species\_by\_plot%>%  
 mutate(total\_BA = ifelse(Plot == 1, total\_basal\_area\_p1, total\_basal\_area\_p2),  
 RBA = (sum\_ba/total\_BA)\*100)  
  
kable(basal\_species\_by\_plot, caption = "BASAL AREA", col.names = c("Plot", "Species", "Basal Area (m2/ha)", "Total Plot Basal Area (m2/ha)", "Relative Abundance (%)"), digits = 2)

BASAL AREA

| Plot | Species | Basal Area (m2/ha) | Total Plot Basal Area (m2/ha) | Relative Abundance (%) |
| --- | --- | --- | --- | --- |
| 1 | Black Cherry | 0.79 | 1658.43 | 0.05 |
| 1 | Blackgum | 2.27 | 1658.43 | 0.14 |
| 1 | Mockernut Hickory | 47.32 | 1658.43 | 2.85 |
| 1 | Pignut Hickory | 9.94 | 1658.43 | 0.60 |
| 1 | Post Oak | 2.72 | 1658.43 | 0.16 |
| 1 | Red Maple | 38.56 | 1658.43 | 2.33 |
| 1 | Red Oak | 3.46 | 1658.43 | 0.21 |
| 1 | Short Leaf Pine | 348.74 | 1658.43 | 21.03 |
| 1 | Sourwood | 48.74 | 1658.43 | 2.94 |
| 1 | White Oak | 1155.88 | 1658.43 | 69.70 |
| 2 | American Beech | 32.98 | 2350.56 | 1.40 |
| 2 | Blackgum | 9.81 | 2350.56 | 0.42 |
| 2 | Dogwood | 0.13 | 2350.56 | 0.01 |
| 2 | Mockernut Hickory | 175.78 | 2350.56 | 7.48 |
| 2 | Pignut Hickory | 14.97 | 2350.56 | 0.64 |
| 2 | Red Maple | 153.19 | 2350.56 | 6.52 |
| 2 | Red Oak | 174.21 | 2350.56 | 7.41 |
| 2 | Short Leaf Pine | 153.18 | 2350.56 | 6.52 |
| 2 | Sourwood | 37.41 | 2350.56 | 1.59 |
| 2 | Southern Sugar Maple | 11.47 | 2350.56 | 0.49 |
| 2 | White Oak | 1125.56 | 2350.56 | 47.88 |
| 2 | Yellow Poplar | 461.85 | 2350.56 | 19.65 |

rba\_plt <- basal\_species\_by\_plot %>%  
 mutate(Plot = ifelse(Plot == 1, "South/Dry", "North/Wet"))  
nb.cols <- 14  
rba\_colors <- colorRampPalette(brewer.pal(14, "Set1"))(nb.cols)

## Warning in brewer.pal(14, "Set1"): n too large, allowed maximum for palette Set1 is 9  
## Returning the palette you asked for with that many colors

ggplot(rba\_plt, aes(fill = Species, x = Plot, y = RBA))+  
 geom\_bar(position = "stack", stat = "identity") +  
 ggtitle("") +  
 theme\_ipsum() +  
 xlab("")+  
 ylab("Relative Abundance (%)")+  
 scale\_fill\_manual(values = rba\_colors)

## Warning in grid.Call(C\_stringMetric, as.graphicsAnnot(x$label)): font family not  
## found in Windows font database

## Warning in grid.Call(C\_stringMetric, as.graphicsAnnot(x$label)): font family not  
## found in Windows font database

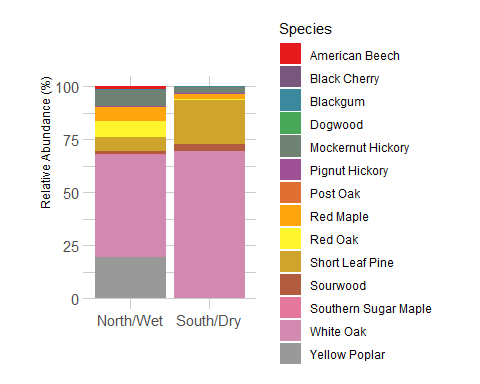
## Warning in grid.Call(C\_textBounds, as.graphicsAnnot(x$label), x$x, x$y, : font  
## family not found in Windows font database

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## Warning in grid.Call.graphics(C\_text, as.graphicsAnnot(x$label), x$x, x$y, :  
## font family not found in Windows font database

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## family not found in Windows font database



### Density

density\_table <- table(basal\_area\_dat$Plot, basal\_area\_dat$Species)  
  
 A <- 100  
   
 density\_table <- as.data.frame(density\_table)%>%  
 rename(Plot = Var1,  
 Species = Var2)%>%  
 mutate(di = Freq\*10000/A)  
  
 density\_sum\_plot1 <- sum(filter(density\_table, Plot == 1)$di)  
 density\_sum\_plot2 <- sum(filter(density\_table, Plot == 2)$di)  
   
 density\_table <- density\_table%>%  
 mutate(total\_plot\_density = ifelse(Plot == 1, density\_sum\_plot1, density\_sum\_plot2),  
 RD = (di/total\_plot\_density)\*100)  
   
kable(density\_table, caption = "DENSITY", col.names = c("Plot", "Species", "# Stems", "Species Density (stems/ha)", "Total Site Density (stems/ha)", "Relative Density (%)"), digits = 2)

DENSITY

| Plot | Species | # Stems | Species Density (stems/ha) | Total Site Density (stems/ha) | Relative Density (%) |
| --- | --- | --- | --- | --- | --- |
| 1 | American Beech | 0 | 0 | 11900 | 0.00 |
| 2 | American Beech | 9 | 900 | 11300 | 7.96 |
| 1 | Black Cherry | 1 | 100 | 11900 | 0.84 |
| 2 | Black Cherry | 0 | 0 | 11300 | 0.00 |
| 1 | Blackgum | 1 | 100 | 11900 | 0.84 |
| 2 | Blackgum | 2 | 200 | 11300 | 1.77 |
| 1 | Dogwood | 0 | 0 | 11900 | 0.00 |
| 2 | Dogwood | 1 | 100 | 11300 | 0.88 |
| 1 | Mockernut Hickory | 10 | 1000 | 11900 | 8.40 |
| 2 | Mockernut Hickory | 9 | 900 | 11300 | 7.96 |
| 1 | Pignut Hickory | 3 | 300 | 11900 | 2.52 |
| 2 | Pignut Hickory | 2 | 200 | 11300 | 1.77 |
| 1 | Post Oak | 2 | 200 | 11900 | 1.68 |
| 2 | Post Oak | 0 | 0 | 11300 | 0.00 |
| 1 | Red Maple | 10 | 1000 | 11900 | 8.40 |
| 2 | Red Maple | 12 | 1200 | 11300 | 10.62 |
| 1 | Red Oak | 1 | 100 | 11900 | 0.84 |
| 2 | Red Oak | 5 | 500 | 11300 | 4.42 |
| 1 | Short Leaf Pine | 27 | 2700 | 11900 | 22.69 |
| 2 | Short Leaf Pine | 6 | 600 | 11300 | 5.31 |
| 1 | Sourwood | 11 | 1100 | 11900 | 9.24 |
| 2 | Sourwood | 17 | 1700 | 11300 | 15.04 |
| 1 | Southern Sugar Maple | 0 | 0 | 11900 | 0.00 |
| 2 | Southern Sugar Maple | 6 | 600 | 11300 | 5.31 |
| 1 | White Oak | 53 | 5300 | 11900 | 44.54 |
| 2 | White Oak | 27 | 2700 | 11300 | 23.89 |
| 1 | Yellow Poplar | 0 | 0 | 11900 | 0.00 |
| 2 | Yellow Poplar | 17 | 1700 | 11300 | 15.04 |

master\_tbl <- merge(basal\_species\_by\_plot,  
 density\_table,  
 by.x = c("Plot", "Species"),   
 by.y = c("Plot", "Species"),  
 all = TRUE)%>%  
 mutate(IV = (RBA+RD)/2)%>%  
 filter(Freq != 0)  
  
iv\_tbl <- master\_tbl%>%  
 select(Plot, Species, RBA, RD, IV)  
kable(iv\_tbl, caption = "Importance Value (IV)", col.names = c("Plot", "Species", "Relative Abundance (%)", "Relative Density (%)", "IMPORTANCE VALUE"), digits = 2)

Importance Value (IV)

| Plot | Species | Relative Abundance (%) | Relative Density (%) | IMPORTANCE VALUE |
| --- | --- | --- | --- | --- |
| 1 | Black Cherry | 0.05 | 0.84 | 0.44 |
| 1 | Blackgum | 0.14 | 0.84 | 0.49 |
| 1 | Mockernut Hickory | 2.85 | 8.40 | 5.63 |
| 1 | Pignut Hickory | 0.60 | 2.52 | 1.56 |
| 1 | Post Oak | 0.16 | 1.68 | 0.92 |
| 1 | Red Maple | 2.33 | 8.40 | 5.36 |
| 1 | Red Oak | 0.21 | 0.84 | 0.52 |
| 1 | Short Leaf Pine | 21.03 | 22.69 | 21.86 |
| 1 | Sourwood | 2.94 | 9.24 | 6.09 |
| 1 | White Oak | 69.70 | 44.54 | 57.12 |
| 2 | American Beech | 1.40 | 7.96 | 4.68 |
| 2 | Blackgum | 0.42 | 1.77 | 1.09 |
| 2 | Dogwood | 0.01 | 0.88 | 0.45 |
| 2 | Mockernut Hickory | 7.48 | 7.96 | 7.72 |
| 2 | Pignut Hickory | 0.64 | 1.77 | 1.20 |
| 2 | Red Maple | 6.52 | 10.62 | 8.57 |
| 2 | Red Oak | 7.41 | 4.42 | 5.92 |
| 2 | Short Leaf Pine | 6.52 | 5.31 | 5.91 |
| 2 | Sourwood | 1.59 | 15.04 | 8.32 |
| 2 | Southern Sugar Maple | 0.49 | 5.31 | 2.90 |
| 2 | White Oak | 47.88 | 23.89 | 35.89 |
| 2 | Yellow Poplar | 19.65 | 15.04 | 17.35 |

S\_1 <- n\_distinct(filter(basal\_area\_dat, Plot == 1)$Species)  
  
S\_2 <- n\_distinct(filter(basal\_area\_dat, Plot == 2)$Species)  
  
total\_trees\_1 <- sum(filter(density\_table, Plot == 1)$Freq)  
total\_trees\_2 <- sum(filter(density\_table, Plot == 2)$Freq)  
  
div\_tbl <- density\_table %>%  
 select(Plot, Species, Freq)%>%  
 filter(Freq != 0)%>%  
 mutate(total\_trees\_by\_plot = ifelse(Plot == 1, total\_trees\_1, total\_trees\_2),  
 pi = Freq/total\_trees\_by\_plot,  
 pilnpi = pi\*log(pi))  
kable(div\_tbl, caption = "DIVERSITY TABLE USED TO CALCULATE SHANNON DIVERSITY INDEX & SORENSON SIMILARITY INDEX", col.names = c("Plot", "Species", "# Stems","# Stems/Plot", "pi", "piln(pi)"), digits = 2)

DIVERSITY TABLE USED TO CALCULATE SHANNON DIVERSITY INDEX & SORENSON SIMILARITY INDEX

| Plot | Species | # Stems | # Stems/Plot | pi | piln(pi) |
| --- | --- | --- | --- | --- | --- |
| 2 | American Beech | 9 | 113 | 0.08 | -0.20 |
| 1 | Black Cherry | 1 | 119 | 0.01 | -0.04 |
| 1 | Blackgum | 1 | 119 | 0.01 | -0.04 |
| 2 | Blackgum | 2 | 113 | 0.02 | -0.07 |
| 2 | Dogwood | 1 | 113 | 0.01 | -0.04 |
| 1 | Mockernut Hickory | 10 | 119 | 0.08 | -0.21 |
| 2 | Mockernut Hickory | 9 | 113 | 0.08 | -0.20 |
| 1 | Pignut Hickory | 3 | 119 | 0.03 | -0.09 |
| 2 | Pignut Hickory | 2 | 113 | 0.02 | -0.07 |
| 1 | Post Oak | 2 | 119 | 0.02 | -0.07 |
| 1 | Red Maple | 10 | 119 | 0.08 | -0.21 |
| 2 | Red Maple | 12 | 113 | 0.11 | -0.24 |
| 1 | Red Oak | 1 | 119 | 0.01 | -0.04 |
| 2 | Red Oak | 5 | 113 | 0.04 | -0.14 |
| 1 | Short Leaf Pine | 27 | 119 | 0.23 | -0.34 |
| 2 | Short Leaf Pine | 6 | 113 | 0.05 | -0.16 |
| 1 | Sourwood | 11 | 119 | 0.09 | -0.22 |
| 2 | Sourwood | 17 | 113 | 0.15 | -0.28 |
| 2 | Southern Sugar Maple | 6 | 113 | 0.05 | -0.16 |
| 1 | White Oak | 53 | 119 | 0.45 | -0.36 |
| 2 | White Oak | 27 | 113 | 0.24 | -0.34 |
| 2 | Yellow Poplar | 17 | 113 | 0.15 | -0.28 |

H1 <- -sum(filter(div\_tbl, Plot == 1)$pilnpi)  
H2 <- -sum(filter(div\_tbl, Plot == 2)$pilnpi)  
  
j\_n <- sum(duplicated(div\_tbl$Species)) # 8   
Cn <- (2\*j\_n)/(S\_1+S\_2)

idx\_tbl <- data.frame(Plot = numeric(),  
 species = numeric(),  
 shannon\_div\_idx = numeric())  
idx\_tbl <- rbind(idx\_tbl, c(1, S\_1, H1), c(2, S\_2, H2))%>%  
 rename(Plot = c.1..2.,  
 Species = c.10..12.,  
 Shannon\_Idx = c.1.61505838480761..2.18750584362665.)  
  
summary\_by\_plot <- basal\_area\_dat %>%  
 group\_by(Plot)%>%  
 summarize(mean\_basal\_area = mean(basal\_area))  
mean\_plot\_density <- master\_tbl %>%  
 group\_by(Plot) %>%  
 summarise(mean\_plot\_density = mean(di))  
idx\_tbl <- idx\_tbl %>%  
 merge(summary\_by\_plot, by = "Plot", all = TRUE) %>%  
 merge(mean\_plot\_density, by = "Plot", all = TRUE)  
kable(idx\_tbl, caption = "SUMMARY - SITE", col.names = c("Plot", "Total Species Richness", "Shannon Diversity Index","Mean Basal Area (m2/ha)", "Mean Plot Density (stems/ha)"), digits = 2)

SUMMARY - SITE

| Plot | Total Species Richness | Shannon Diversity Index | Mean Basal Area (m2/ha) | Mean Plot Density (stems/ha) |
| --- | --- | --- | --- | --- |
| 1 | 10 | 1.62 | 13.94 | 1190.00 |
| 2 | 12 | 2.19 | 20.80 | 941.67 |

species\_ba <- basal\_area\_dat %>%  
 group\_by(Species)%>%  
 summarise(mean\_sp\_ba = mean(basal\_area))  
species\_mast <- master\_tbl %>%  
 group\_by(Species)%>%  
 summarise(mean\_sp\_density = mean(di),   
 mean\_RD = mean(RD),   
 mean\_RBA = mean(RBA),   
 mean\_IV = mean(IV))  
summary\_sp <- merge(species\_ba,  
 species\_mast,   
 by = "Species",   
 all = TRUE)  
kable(summary\_sp, caption = "SUMMARY - SPECIES", col.names = c("Species", "Mean Species Basal Area (m2/ha)", "Mean Species Density", "Mean Species Relative Density", "Mean Species Relative Basal Area", "Mean Species Importance Value"), digits = 2)

SUMMARY - SPECIES

| Species | Mean Species Basal Area (m2/ha) | Mean Species Density | Mean Species Relative Density | Mean Species Relative Basal Area | Mean Species Importance Value |
| --- | --- | --- | --- | --- | --- |
| American Beech | 3.66 | 900 | 7.96 | 1.40 | 4.68 |
| Black Cherry | 0.79 | 100 | 0.84 | 0.05 | 0.44 |
| Blackgum | 4.03 | 150 | 1.31 | 0.28 | 0.79 |
| Dogwood | 0.13 | 100 | 0.88 | 0.01 | 0.45 |
| Mockernut Hickory | 11.74 | 950 | 8.18 | 5.17 | 6.67 |
| Pignut Hickory | 4.98 | 250 | 2.15 | 0.62 | 1.38 |
| Post Oak | 1.36 | 200 | 1.68 | 0.16 | 0.92 |
| Red Maple | 8.72 | 1100 | 9.51 | 4.42 | 6.97 |
| Red Oak | 29.61 | 300 | 2.63 | 3.81 | 3.22 |
| Short Leaf Pine | 15.21 | 1650 | 14.00 | 13.77 | 13.89 |
| Sourwood | 3.08 | 1400 | 12.14 | 2.27 | 7.20 |
| Southern Sugar Maple | 1.91 | 600 | 5.31 | 0.49 | 2.90 |
| White Oak | 28.52 | 4000 | 34.22 | 58.79 | 46.50 |
| Yellow Poplar | 27.17 | 1700 | 15.04 | 19.65 | 17.35 |

**SORENSEN SIMILARITY INDEX = 0.73**  
**Lower Abundance Values for Common Species in Sites 1 and 2 (Jn) = 8**  
**Total Abundance for Sites 1 and 2 = 22**

species\_ba\_ov <- basal\_area\_dat %>%  
 group\_by(Species)%>%  
 summarise(sum\_basal\_area = sum(basal\_area))  
species\_density\_ov <- master\_tbl%>%  
 select(Species,Freq)%>%  
 group\_by(Species)%>%  
 summarise(agg\_counts = sum(Freq),   
 density = agg\_counts\*100)  
  
  
summary <- data.frame(agg\_unit = c("Plot Means Across All Plots", "Species Means"),  
 mean\_ba = c(mean(total\_basal\_area\_p1, total\_basal\_area\_p2), mean(species\_ba\_ov$sum\_basal\_area)),  
 mean\_d = c(mean(density\_sum\_plot1, density\_sum\_plot2), sum(species\_density\_ov$density)/2),   
 mean\_sp = c(mean(total\_trees\_1, total\_trees\_2), sum(species\_density\_ov$agg\_counts)/2))  
kable(summary, caption = "Summary Across Plots and Species", col.names = c("","Basal Area", "Species Density", "# of Species"), digits = 2)

Summary Across Plots and Species

|  | Basal Area | Species Density | # of Species |
| --- | --- | --- | --- |
| Plot Means Across All Plots | 1658.43 | 11900 | 119 |
| Species Means | 286.36 | 11600 | 116 |