

Forest Lab

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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",
```

Table 1: 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

Plot	Species	Basal Area (m2/ha)	Total Plot Basal Area (m2/ha)	Relative Abundance (%)
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

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", "Total Site Density", "Relative Density"))
```

Table 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

Plot	Species	# Stems	Species Density (stems/ha)	Total Site Density (stems/ha)	Relative Density (%)
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)%>%
  select(Plot, Species, RBA, RD, IV)
kable(master_tbl, caption = "Importance Value (IV)", col.names = c("Plot", "Species", "Relative Abundanc

```

Table 3: Importance Value (IV)

Plot	Species	Relative Abundance (%)	Relative Density (%)	IMPORTANCE VALUE
1	American Beech	NA	0.00	NA
1	Black Cherry	0.05	0.84	-0.40
1	Blackgum	0.14	0.84	-0.35
1	Dogwood	NA	0.00	NA
1	Mockernut Hickory	2.85	8.40	-2.77
1	Pignut Hickory	0.60	2.52	-0.96
1	Post Oak	0.16	1.68	-0.76
1	Red Maple	2.33	8.40	-3.04
1	Red Oak	0.21	0.84	-0.32
1	Short Leaf Pine	21.03	22.69	-0.83
1	Sourwood	2.94	9.24	-3.15
1	Southern Sugar Maple	NA	0.00	NA
1	White Oak	69.70	44.54	12.58
1	Yellow Poplar	NA	0.00	NA
2	American Beech	1.40	7.96	-3.28

Plot	Species	Relative Abundance (%)	Relative Density (%)	IMPORTANCE VALUE
2	Black Cherry	NA	0.00	NA
2	Blackgum	0.42	1.77	-0.68
2	Dogwood	0.01	0.88	-0.44
2	Mockernut Hickory	7.48	7.96	-0.24
2	Pignut Hickory	0.64	1.77	-0.57
2	Post Oak	NA	0.00	NA
2	Red Maple	6.52	10.62	-2.05
2	Red Oak	7.41	4.42	1.49
2	Short Leaf Pine	6.52	5.31	0.60
2	Sourwood	1.59	15.04	-6.73
2	Southern Sugar Maple	0.49	5.31	-2.41
2	White Oak	47.88	23.89	12.00
2	Yellow Poplar	19.65	15.04	2.30

```

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")

```

Table 4: 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

Plot	Species	# Stems	# Stems/Plot	pi	pi ln(pi)
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))
kable(idx_tbl, caption = "SUMMARY", col.names = c("Plot", "Species Richness (# species)", "Shannon Diversity Index (H')"))
```

Table 5: SUMMARY

Plot	Species Richness (# species)	Shannon Diversity Index (H')
1	10	1.62
2	12	2.19

SORENSEN SIMILARITY INDEX = 0.73

** Lower Abundance Values for Common Species in Sites 1 and 2 (J_n) = 8**

** Total Abundance for Sites 1 and 2 = 22**