

Forest Lab

Cindy J. Pang

2022-06-15

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
```

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)%>%
  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 (IV)"))

```

Table 3: 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

Plot	Species	Relative Abundance (%)	Relative Density (%)	IMPORTANCE VALUE
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")

```

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
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

Plot	Species	# Stems	# Stems/Plot	pi	pi ln(pi)
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 Divi
```

Table 5: 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/
```

Table 6: 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	11.74	950	8.18	5.17	6.67
Hickory					
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)),
  mean_sp = c(mean(total_trees_1, total_trees_2), sum(species_density_ov$agg_counts))
kable(summary, caption = "Summary Across Plots and Species", col.names = c("", "Basal Area", "Species Density"))

```

Table 7: 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