

Bonnie Turek

Eco 634 – Lab 3

9/22/21

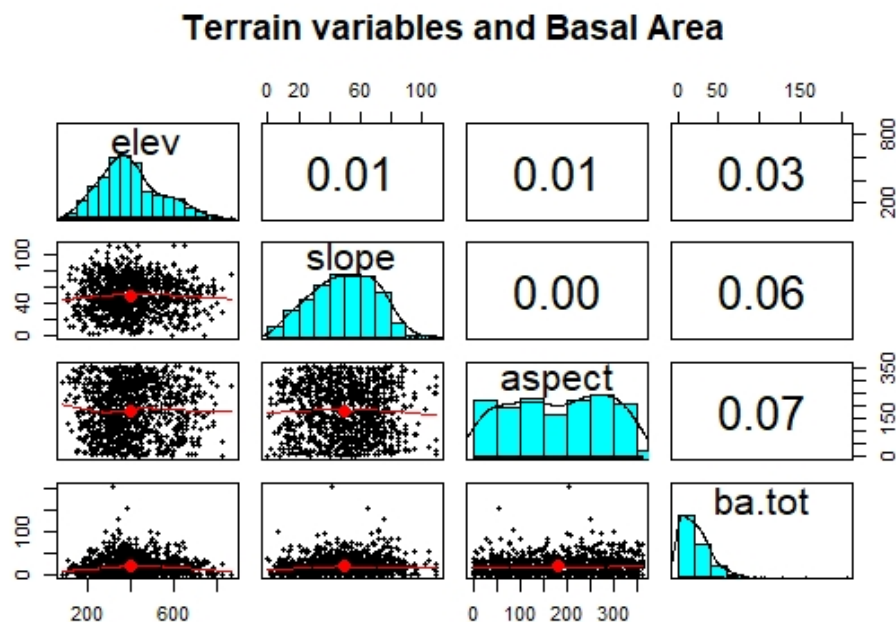
**Q1. What is Basal Area and how is it measured?**

According to the metadata file and basic online searches, basal area is the cross-sectional area of all stems of a species or all stems in a stand measured at breast height and expressed as per unit of land area. It is a common measure in forestry and land management used to describe the timber stand density, as well as timber stand volume and growth. In mathematical terms,

$$\text{Basal area (square feet)} = (\pi / (4 * 144)) * \text{DBH}^2 = 0.005454 * \text{DBH}^2$$

Where  $\pi = 3.14$ , and DBH = diameter breast height. DBH is measured on each tree with a ruler or measuring tape, at a point on the tree trunk 4 1/2 feet from the ground. This height is considered “breast height.” At this height, the DBH is the measure taken around the tree trunk to get its circumference. The number 0.005454 in the basal area calculation is the forester’s constant, which converts the measured inches into square feet. For the habitat dataset we are using, ba.tot is total basal area of all trees, including live and dead trees and regardless of conifer or hardwood. It uses the units ( $\text{m}^2/\text{ha}$ ) and is on an integer scale ranging from 0-207.

Reference: Alabama A&M and Auburn Universities. <https://www.aces.edu/blog/topics/forestry/basal-area-a-measure-made-for-management/>

**Q2. Terrain and Basal Area Pair Plots:**

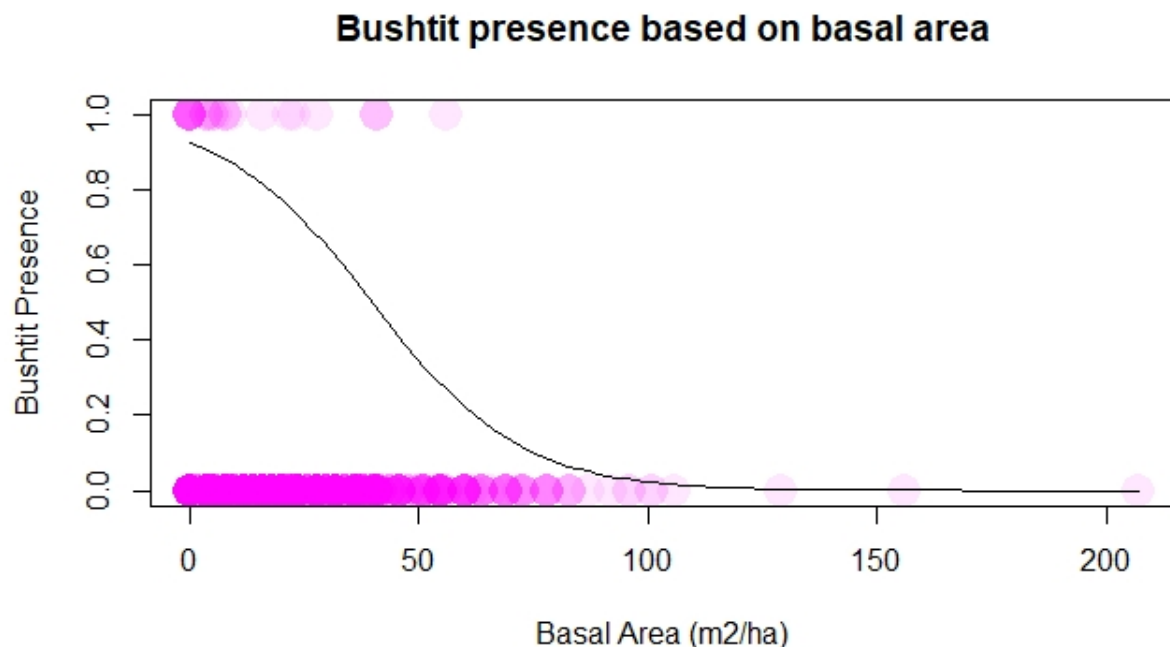
Code for above terrain and basal area pair plot figure:

\*after installing psych package and require(here) and require(psych)\*

```
dat_habitat = read.csv(
  here("data", "hab.sta.csv")
)
head(dat_habitat)

terrain = dat_habitat[, c(6,7,8,17)]
head(terrain)
pairs.panels(terrain, main = "Terrain variables and Basal Area")
```

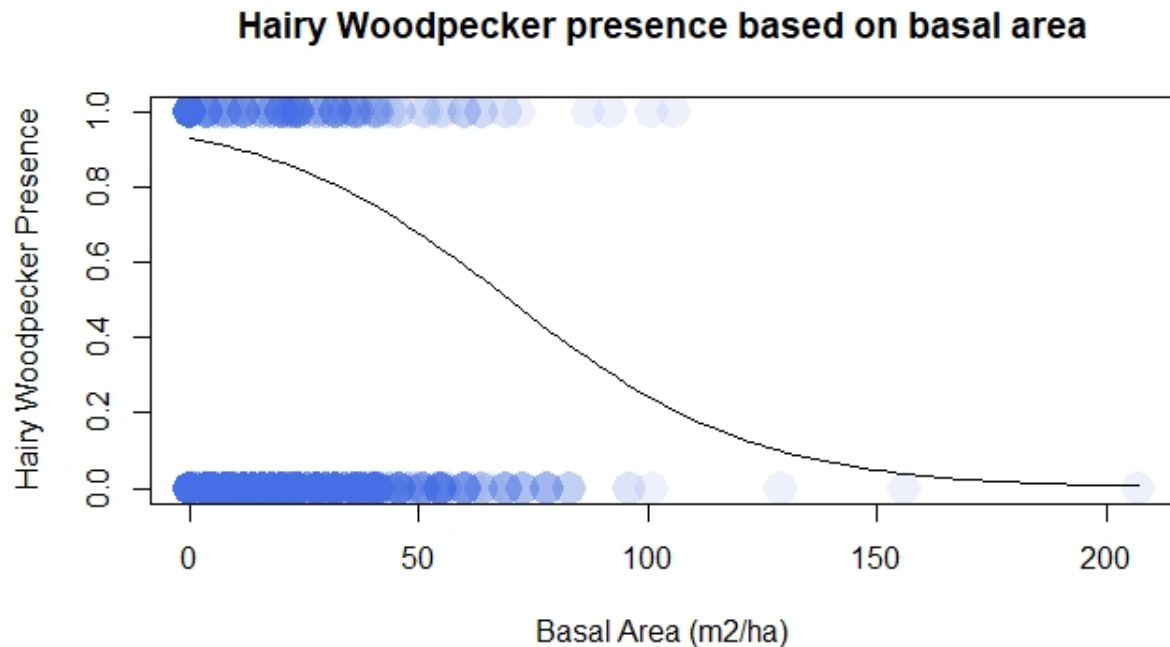
**Q3.** Bushtit bird species: Logistic Function Presence/Absence plot:



**Q4.**

Visual interpretation of the above plot tells us that there are very few observations of Bushtit birds found present in all sites with varying basal area. There are more observations of absence of the bushtit than presence of the bushtit given all sampling sites. The few occasions when bushtits were found present occurred at sites with a generally lower basal area. This tells us that the bushtit species may prefer areas with lower tree cover. The logistic model curve attempts to fit both to present (1) and absent (0) data at the top and bottom of the plot. This is quite hard, but I think the curve plotted above is just about the best fit you could make using a logistic function only. Most of the data points lie at 0, for absence, so the line falls more towards the bottom, but still accounts for the present (1) data points at the lower basal area values. Perhaps as we learn more about logistic functions and other model types, I will understand that this curve is in fact NOT the best fit for presence/absence data in general.

**Q5.** Hairy Woodpecker bird species: Logistic Function Presence/Absence plot:



**Q6.**

The hairy woodpecker was observed as present at many more sampling sites than the bushtit example above. There is more of an even split of present (1) versus absent (0) for the hairy woodpecker as seen in the plot above. The observations of its presence generally occur at slightly lower basal areas – middle basal areas. This tells us again that the hairy woodpecker may have a weak preferences for less tree cover and density. Since the data points for presence and absence are more evenly distributed at the top and bottom of the graph, that makes it visually much harder to fit a logistic curve to the data. At any given point in observed basal area measurements, you are not much more likely to observe presence or absence of the hairy woodpecker. It's rather a toss up until you get to basal areas over 110 m<sup>2</sup>/ha. The logistic curve plotted above does my best job at fitting both present and absent data points with a shallow slope and midpoint around 70. Visually, this logistic curve may not mean too much or be the best graphical representation of this data to your audience.

**Q7.** How many total number of Gray Jays were observed at all of the sites?

181

**Q8.** Code to find Gray Jay abundance:

```
sum(dat_all$GRJA)
```

**Q9.** Calculate the total number of sampling sites in which Gray Jays were observed:

110

**Q10.** R code you used to perform the presence/absence calculation:

```
#calculate the total number of sites Gray Jays present at
```

```
my_vec_GJ = dat_all$GRJA > 0
```

```
grja_present_absent = as.numeric(my_vec_GJ)
```

```
sum(my_vec_GJ)
```

```
sum(grja_present_absent)
```

```
#can either use sum function on BOOLEAN True/False vector or 0/1 numeric
```