demo\_species\_stats

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# Purpose

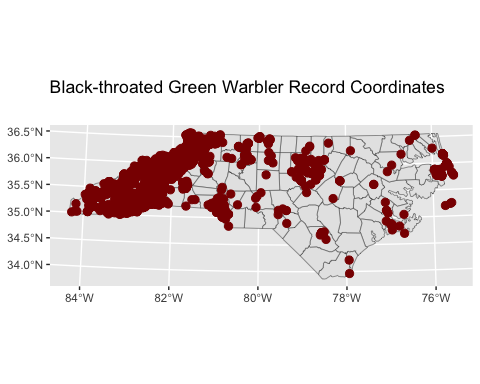
This document demonstrates species-level data summaries that are available from the NCBA code repository.

Identify a species and get the observations.

species <- "Black-throated Green Warbler"  
  
observations <- get\_observations(species = species, project = "EBIRD\_ATL\_NC",   
 EBD\_fields\_only = FALSE) %>%  
 to\_EBD\_format() %>%  
 auk\_unique()

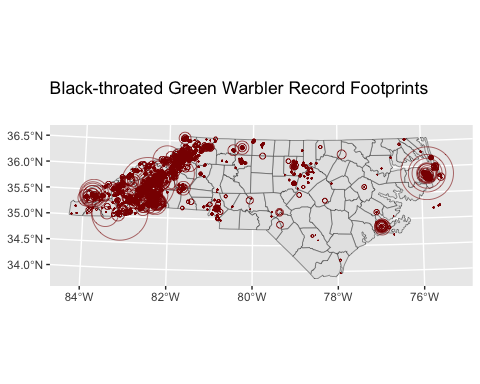
Plot the coordinates.

# Get spatial data frame of observations  
obs.spatial <- records\_as\_sf(records\_df = observations,   
 kind = "observations", method = "points")  
  
# Make a simple map  
ggplot(data = counties\_NC()) +  
 geom\_sf() +  
 geom\_sf(data = obs.spatial, size = 4, shape = 20,   
 crs = st\_crs(6542), colour = "darkred", fill = NA) +   
 ggtitle(paste(species, "Record Coordinates"), subtitle = "")



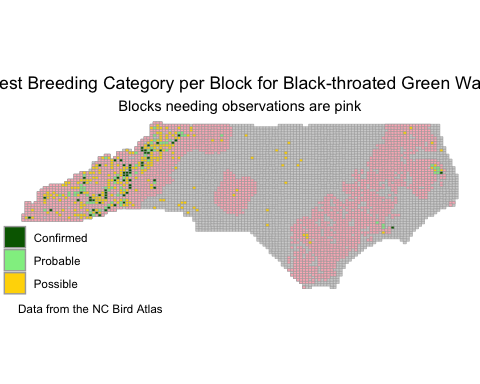
Plot the footprints.

# Get spatial data frame of observations  
obs.spatial <- records\_as\_sf(records\_df = observations,   
 kind = "observations", method = "point-radius")  
  
# Make a simple map  
ggplot(data = counties\_NC()) +  
 geom\_sf() +  
 geom\_sf(data = obs.spatial, size = 4, shape = 20,   
 crs = st\_crs(6542), colour = "darkred", fill = NA) +   
 ggtitle(paste(species, "Record Footprints"), subtitle = "")



Map the highest reported breeding code by block with needed blocks identified.

show(map\_needed\_highest(species = "Black-throated Green Warbler"))



Get a boxplot of breeding phenology

breeding\_boxplot(species = species, data = observations, type = "ecoregional",   
 drop = FALSE, lump = breeding\_codes())

