Exploration of Data for an Individual Species

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

Print the number of observations.

print(nrow(observations))

## [1] 1528

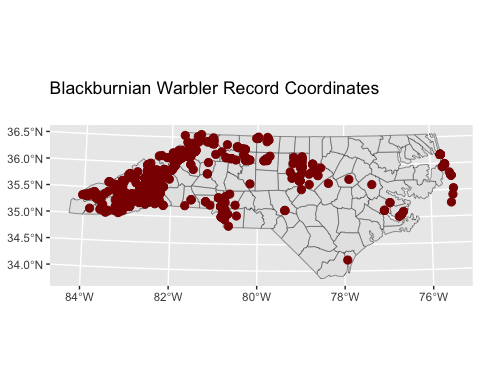
Print the total number of individuals reported.

print(sum(as.integer(observations$observation\_count)))

## [1] 2870

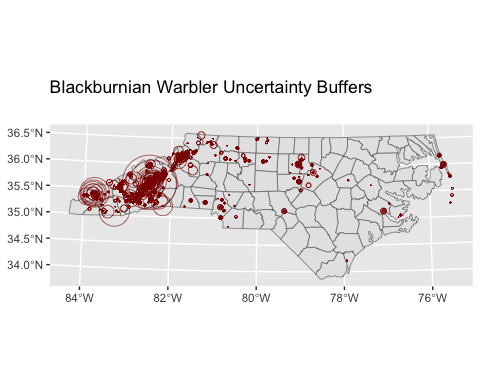
Plot the coordinates.

# 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 = "")



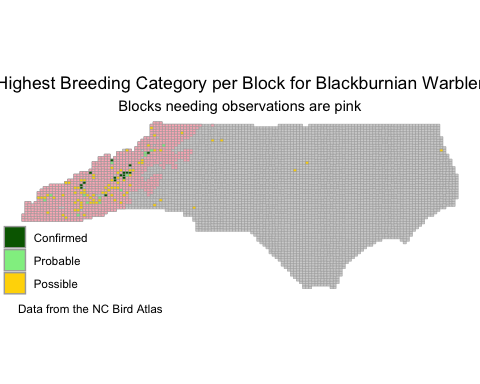
Plot the footprints.

# 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, "Uncertainty Buffers"), subtitle = "")



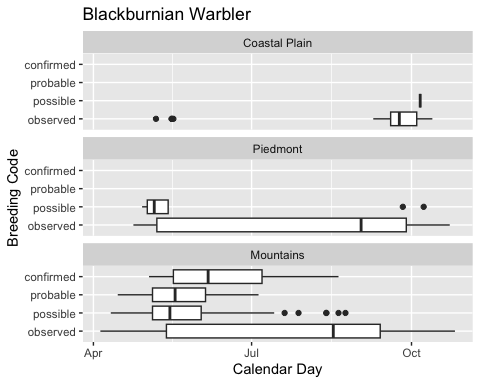
Map the highest reported breeding code by block with needed blocks identified.

show(map\_needed\_highest(species = species))



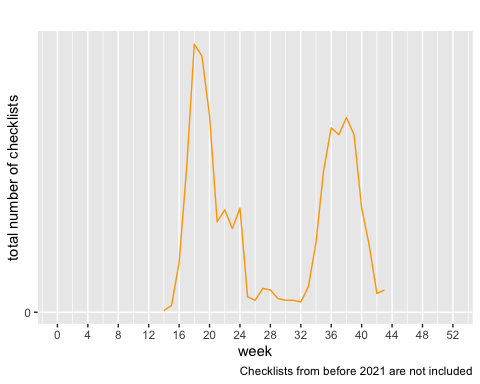
Get a boxplot of breeding phenology

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



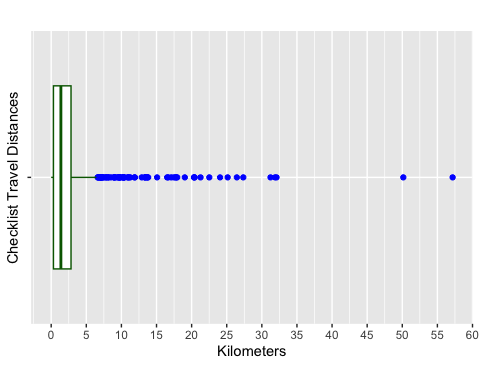
Plot observations by week.

lists\_by\_week(observations)



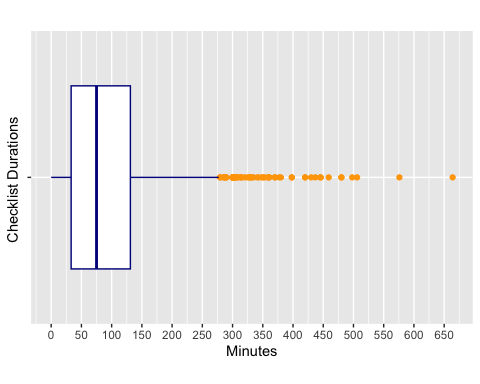
Summarize checklist distance.

show(effort\_distance\_boxplot(observations))



Summarize duration

show(duration\_minutes\_boxplot(observations))

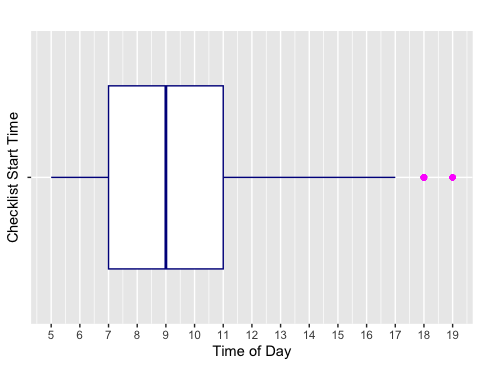


duration\_distance\_table(observations)

## min median max mean sd count  
## duration (hours) 0 1.2500 11.06667 1.596760 1.408301 1528  
## distance (km) 0 1.3815 57.17000 2.211505 3.692735 1528

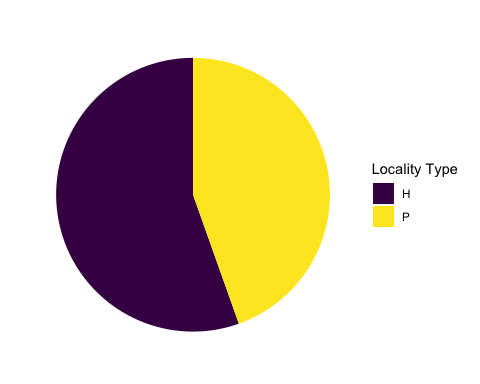
Summarize start times.

show(start\_time\_boxplot(observations))



Summarize locality type.

show(locality\_type\_pie(observations))



Summarize protocol in a table.

protocol\_table(observations)

## # A tibble: 3 × 4  
## protocol\_type number percentage duration\_hours  
## <chr> <int> <dbl> <dbl>  
## 1 Incidental 30 1.96 0   
## 2 Stationary 269 17.6 256.  
## 3 Traveling 1229 80.4 2184.

Summarize protocol in a figure.

protocol\_table(observations)

## # A tibble: 3 × 4  
## protocol\_type number percentage duration\_hours  
## <chr> <int> <dbl> <dbl>  
## 1 Incidental 30 1.96 0   
## 2 Stationary 269 17.6 256.  
## 3 Traveling 1229 80.4 2184.

Summarize checklist completeness.

complete\_checklist\_table(observations)

## # A tibble: 2 × 4  
## all\_species\_reported number percentage duration\_hours  
## <lgl> <int> <dbl> <dbl>  
## 1 FALSE 50 3.27 19.6  
## 2 TRUE 1478 96.7 2420.

Summarize observations per year.

show(year\_bar(observations))

