Seasonal population distribution of Connecticut Warbler

Proportion of breeding population with BBS monitoring

The goal is to use eBird status and trend results to calculate the proportion of `species` breeding season population that is within the region with BBS monitoring data (i.e., the coverage of the population by the BBS).

- It will also be worth exploring the Boreal Avian Modeling estimates of breeding season population.

- using a 1-degree lat x long grid for now, but worth re-visiting.

- method assumes a relatively stationary population during a survey-season (breeding season or non-breeding season, but not applicable to migration monitoring yet)

- If the species' range has shifted, we will need to make some strong assumptions about how to link historical breeding distributions (e.g., 1970) with the available data on current breeding ranges (e.g., areas with monitoring data 50-years ago but no modeled abundance today).

downloading eBird seasonal abundance

```
library(ebirdst)
library(tidyverse)
library(bbsBayes2)
library(terra)
library(sf)
library(patchwork)
```

Extraction for Connecticut Warbler

Download species data and load seasonal mean abundance

```
species <- "Connecticut Warbler"

ebirdst_download_status(species)
abd_seasonal_percent <- load_raster(species = species,
                                    product = "proportion-population",
                                    period = "seasonal", #metric = "mean",
                                    resolution = "3km") #3km high resolution
abd_breeding_percent <- abd_seasonal_percent$breeding

abd_seasonal_abundance <- load_raster(species = species,
                                      product = "abundance",
                                      period = "seasonal", metric = "mean",
                                      resolution = "3km") #3km high resolution
abd_breeding_abundance <- abd_seasonal_abundance$breeding
```

Calculate the mean relative abundance within each stratum. First load the degree-block stratification map, and adjust the coordinate reference system (crs) to match the crs of the eBird map.

```
latlong_orig <- bbsBayes2::load_map("latlong") # version with original crs

latlong <- bbsBayes2::load_map("latlong")%>% #loading the 1-degree cell strata
  st_transform(st_crs(abd_breeding_percent))


# extract(fun = sum()) generates sum of pixel values within latlong polygons
percent_strata <- terra::extract(abd_breeding_percent,
                          latlong,
                          fun = sum,
                          na.rm = TRUE) %>%
  mutate(strata_name = latlong$strata_name)

abundance_strata <- extract(abd_breeding_abundance,
                          latlong,
                          fun = sum,
                          na.rm = TRUE) %>%
  mutate(strata_name = latlong$strata_name)
```

```r
# abundance raster from BAM
bam_rast <- rast("data/pred-CONW-CAN-Mean.tif")
latlong_bam <- bbsBayes2::load_map("latlong")%>% #loading the 1-degree cell strata
  st_transform(st_crs(bam_rast))

density_strata_bam <- extract(bam_rast,
                              latlong_bam,
                              fun = mean,
                              na.rm = TRUE) %>%
  mutate(strata_name = latlong_bam$strata_name) %>%
  rename(density = starts_with("pred"))


map_percent_strata <- latlong_orig %>%
  inner_join(.,percent_strata,
             by = "strata_name") %>%
  filter(!is.na(breeding),
         breeding > 0) %>%
  mutate(source = "eBird")


map_abundance_strata <- latlong_orig %>%
  inner_join(.,abundance_strata,
             by = "strata_name") %>%
  filter(!is.na(breeding),
         breeding > 0)

map_percent_bam_strata <- latlong_orig %>%
  mutate(area_km = st_area(latlong_orig)/1e6) %>%
  inner_join(.,density_strata_bam,
             by = "strata_name") %>%
  filter(!is.na(density),
         density > 0.001) %>%
  mutate(abundance = as.numeric(density*area_km),
         breeding = as.numeric(abundance/(sum(abundance))),
         source = "BAM")


map_percent <- ggplot()+
  geom_sf(data = map_percent_strata,
          aes(fill = breeding))+
```

```
    guides(fill = guide_colorbar(title = "Proportion of \n population (eBird)"))+
    scale_fill_viridis_c()
#map_abundance <- ggplot()+
#  geom_sf(data = map_abundance_strata,
#          aes(fill = breeding))+
#  guides(fill = guide_colorbar(title = "Predicted \n abundance"))+
#  scale_fill_viridis_c()

map_density <- ggplot()+
    geom_sf(data = map_percent_bam_strata,
            aes(fill = breeding))+
    guides(fill = guide_colorbar(title = "Proportion of \n population (BAM)"))+
    scale_fill_viridis_c()


pdf("figures/eBird_BAM_distribution_comparison.pdf",
    width = 11,
    height = 8.5)
print(map_percent / map_density)
dev.off()
```

pdf
  2

```
#
# map_both_percent <- map_percent_strata %>%
#   bind_rows(., map_percent_bam_strata)
#
# map_percent_facet <- ggplot()+
#   geom_sf(data = map_both_percent,
#           aes(fill = breeding))+
#   guides(fill = guide_colorbar(title = "Proportion of \n population"))+
#   scale_fill_viridis_c() +
#   facet_wrap(vars(source))
#
# map_percent_facet
```

mismatches in range through time

There are some important mismatches between the eBird breeding range and the BBS breeding range (i.e., the regions with BBS observations). These may reflect changes in the species'

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breeding range through time (e.g., `species`'s range shifting North since 1966).

```r
bbs_range <- stratify(species,by = "latlong") %>%
  prepare_data(.,
               min_n_routes = 1,
               min_max_route_years = 2)
strata_w_bbs <- bbs_range$meta_strata %>%
  select(strata_name) %>%
  mutate(bbs = TRUE)

strata_w_eBird <- abundance_strata %>%
  filter(breeding > 0) %>%
  select(strata_name, breeding) %>%
  mutate(ebird = TRUE)

strata_w_either <- full_join(strata_w_bbs,
                             strata_w_eBird,
                             by = "strata_name") %>%
  mutate(ebird = ifelse(is.na(ebird),FALSE,ebird),
         bbs = ifelse(is.na(bbs),FALSE,bbs),
         survey = ifelse(ebird,"eBird only","BBS only"),
         survey = ifelse(ebird & bbs,"Both",survey),
         survey = factor(survey,
                         levels = c("BBS only",
                                    "eBird only",
                                    "Both")))

map_strata_w_either = latlong_orig %>%
  inner_join(strata_w_either,
             by = "strata_name")

overlap_map <- ggplot()+
  geom_sf(data = load_map("bbs_usgs"),
          fill = NA)+
  geom_sf(data = map_strata_w_either,
          aes(fill = survey))+
  scale_colour_viridis_d(aesthetics = "fill")+
  labs(subtitle = paste(species,"strata with BBS observations and eBird \n breeding season
  theme_bw()+
  theme(plot.subtitle = element_text(size = 8))

overlap_map
```
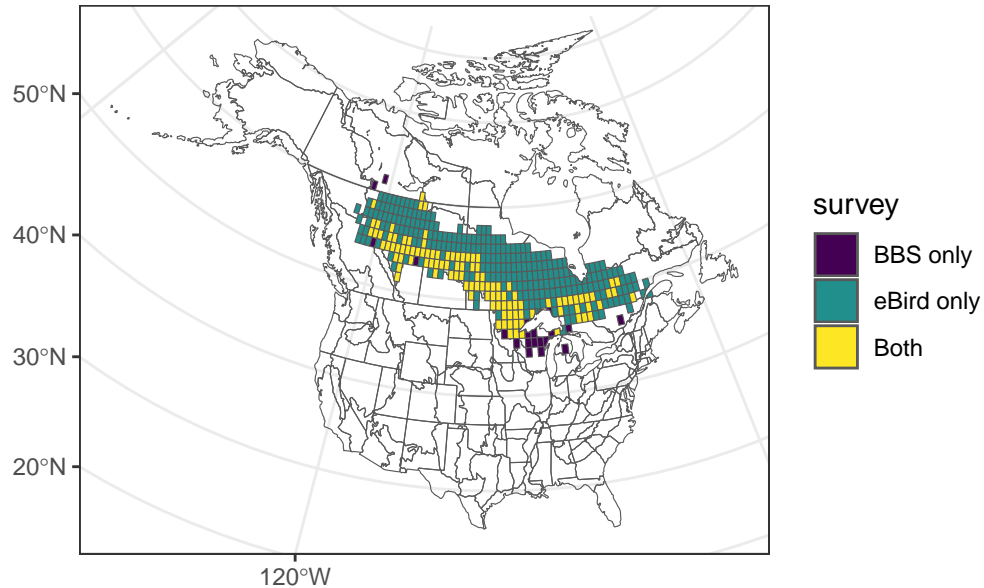
Connecticut Warbler strata with BBS observations and eBird
breeding season relative abundance estimates

These mismatches may also reflect a mismatch between the seasonal period of time that eBird considers breeding range and the survey timing of the BBS.

```
species_breeding <- ebirdst_runs %>%
  filter(common_name == species) %>%
  select(common_name,breeding_start,breeding_end)
```

For example, the eBird breeding period for Connecticut Warbler only includes a two week window of time in late June (2022-06-21 to 2022-06-28).

An alternative to using the breeding season relative abundance is to re-calculate a BBS-season relative abundance using the weekly relative abundance values. Here, I've used just the median relative abundance values and averaged them over the BBS-survey window.

```
abd_weekly_abundance <- load_raster(species = species,
                                    product = "abundance",
                                    period = "weekly", metric = "median",
                                    resolution = "3km") #3km high resolution

weeks_in_bbs <- names(abd_weekly_abundance) %>%
  lubridate::as_date()
```

```r
# approximate and excluding late May given the northern distribution
weeks_in_bbs <- as.character(weeks_in_bbs[which(weeks_in_bbs > as_date("2022-05-27") & wee

abd_bbs_season_mean <- extract(abd_weekly_abundance,latlong,
                               fun = sum,
                               na.rm = TRUE) %>%
  select(ID,all_of(weeks_in_bbs)) %>%
  group_by(ID) %>%
  mutate(breeding_bbs = rowMeans(pick(all_of(weeks_in_bbs)),na.rm = TRUE)) %>%
  arrange(ID) %>%
  ungroup() %>%
  mutate(strata_name = latlong$strata_name) %>%
  select(strata_name,breeding_bbs)
# this generates a data frame of rows for each cell and a column for the mean seasonal



strata_w_eBird2 <- abd_bbs_season_mean %>%
  filter(breeding_bbs > 0) %>%
  select(strata_name, breeding_bbs) %>%
  mutate(ebird = TRUE)

strata_w_either2 <- full_join(strata_w_bbs,
                              strata_w_eBird2,
                              by = "strata_name") %>%
  mutate(ebird = ifelse(is.na(ebird),FALSE,ebird),
         bbs = ifelse(is.na(bbs),FALSE,bbs),
         survey = ifelse(ebird,"eBird only","BBS only"),
         survey = ifelse(ebird & bbs,"Both",survey),
         survey = factor(survey,
                         levels = c("BBS only",
                                    "eBird only",
                                    "Both")))

map_strata_w_either2 = latlong_orig %>%
  inner_join(strata_w_either2,
             by = "strata_name")

overlap_map2 <- ggplot()+
  geom_sf(data = load_map("bbs_usgs"),
          fill = NA)+
```

```
  geom_sf(data = map_strata_w_either2,
          aes(fill = survey))+
  scale_colour_viridis_d(aesthetics = "fill")+
  labs(subtitle = paste0("strata with BBS observations and eBird relative \n abundance est
  theme_bw()+
  theme(plot.subtitle = element_text(size = 8))

overlap_map + overlap_map2 + plot_layout(guides = "collect")
```


Connecticut Warbler strata with BBS observations and BBS observations and eBird relative
breeding season relative abundance estimates abundance estimates during 05–31 to 07–05
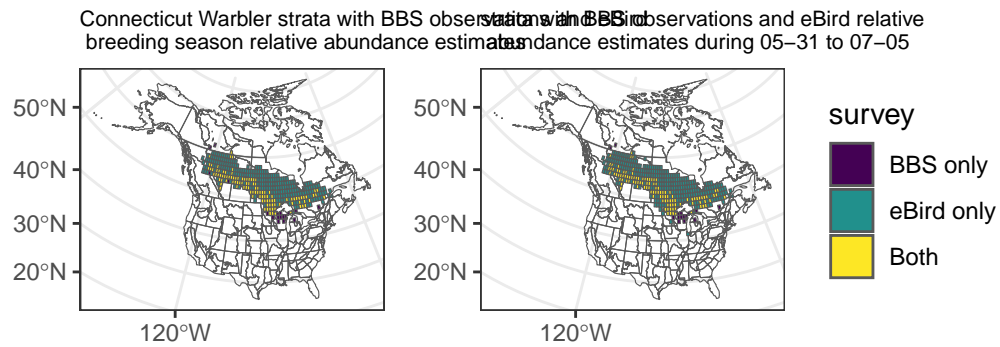
For Connecticut Warbler, expanding the breeding season beyond the weeks identified in the eBird status and trend products does not seem to improve the overlap between BBS and eBird. This suggests that the mismatch is largely a function of a shift in the species' range since the early years of the BBS surveys. Therefore, a better approach to reconciling the two sources of information may be to create a spatial join, where the strata with BBS observations are assigned the relative abundance values of their nearest neighbour strata that do have relative abundance information.

```
# strata_names with ebird breeding season relative abundance
strata_w_eBird <- abundance_strata %>%
  filter(breeding > 0) %>%
  select(strata_name, breeding) %>%
```

```
  mutate(ebird = TRUE)

# strata_names with BBS monitoring observations
strata_w_bbs <- bbs_range$meta_strata %>%
  select(strata_name) %>%
  mutate(bbs = TRUE)

# spatial polygon of strata_w_eBird
strata_map_eBird <- latlong_orig %>%
  inner_join(.,strata_w_eBird, by = "strata_name") %>%
  group_by(strata_name) %>%
  summarise(breeding = sum(breeding,na.rm = TRUE)) #summarise the breeding abundance acros


# spatial polygon of straat_w_bbs
strata_map_bbs <- latlong_orig %>%
  inner_join(.,strata_w_bbs, by = "strata_name")%>%
  group_by(strata_name) %>%
  summarise() #unions multi-polygon strata

# calculating areas of polygons so that nearest neighbour substitution can
# adjust for different areas
#calculating the area of each stratum with eBird data
area_sq_km_ebird = sf::st_area(strata_map_eBird)/1e6
strata_map_eBird <- strata_map_eBird %>%
  mutate(area_sq_km_ebird = area_sq_km_ebird)

#calculating the area of each stratum with BBS data
area_sq_km = sf::st_area(strata_map_bbs)/1e6
strata_map_bbs <- strata_map_bbs %>%
  mutate(area_sq_km = area_sq_km)

# identifying the strata with only BBS data
strata_map_fill <- strata_map_bbs %>%
  rename(strata_name_true = strata_name) %>%
  filter(!strata_name_true %in% strata_map_eBird$strata_name) %>%
  sf::st_join(.,strata_map_eBird,
              join = st_nearest_feature) %>% #nearest neighbour join to strata with eBird
  rename(strata_name_nearest = strata_name,
         strata_name = strata_name_true) %>%
  group_by(strata_name) %>%
```

```r
    mutate(breeding = as.numeric(breeding*(area_sq_km/area_sq_km_ebird))) %>% # area adjustm
    select(strata_name,breeding)

#appending the nearest neighbour substituted abundances to the ebird abundance map
final_ebird_abundance_strata <- strata_map_eBird %>%
  bind_rows(.,strata_map_fill) %>%
  select(strata_name,breeding) %>%
  mutate(percent_breeding = breeding/sum(breeding),
         with_bbs = ifelse(strata_name %in% strata_w_bbs$strata_name,
                           TRUE,FALSE))
## species aou number for concise file naming
aou <- search_species(species)[1,"aou"]


saveRDS(final_ebird_abundance_strata,paste0("output/saved_ebird_breeding_abundance_",aou,"


# percent of new breeding abundance covered by BBS
p_covered <- final_ebird_abundance_strata %>%
  filter(with_bbs) %>%
  summarise(percent_breeding = sum(percent_breeding)) %>%
  sf::st_drop_geometry()

strata_base_map <- load_map("bbs_usgs")

bbox <- sf::st_bbox(final_ebird_abundance_strata)
xlm <- bbox[c("xmin","xmax")]
ylm <- bbox[c("ymin","ymax")]

capt <- paste0("Overlap of 1-degree grid-cells with long-term BBS monitoring data (grey ou
               and the eBird estimated proportion of ",species," population during the bre
               Approximately ",100*round(p_covered$percent_breeding,2),
               "% of the species' population is within the 1-degree grid cells
               with BBS monitoring data")
# map showing the relative species distribution and BBS coverage
test_map <- ggplot()+
  geom_sf(data = final_ebird_abundance_strata,
          aes(fill = percent_breeding))+
  geom_sf(data = strata_map_bbs,
          fill = NA,
          colour = grey(0.8),
```
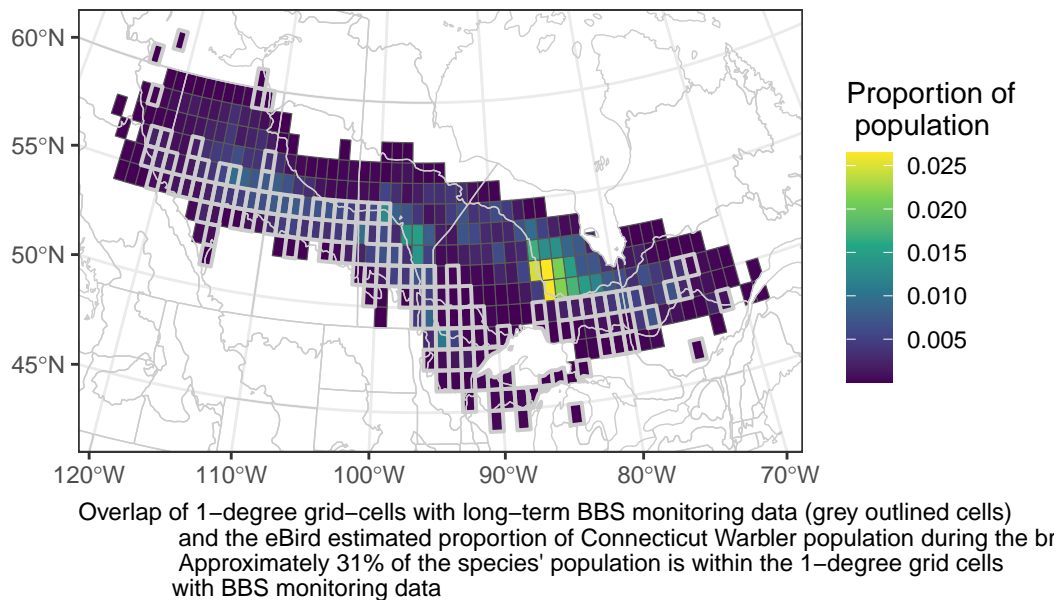
```
            linewidth = 0.7)+
     geom_sf(data = strata_base_map,
             fill = NA,
             colour = grey(0.8),
             linewidth = 0.25)+
      coord_sf(xlim = xlm,ylim = ylm)+
    theme_bw()+
    labs(caption = capt)+
    theme(plot.caption = element_text(hjust = 0))+
    guides(fill = guide_colorbar(title = "Proportion of \n population"))+
    scale_fill_viridis_c()

  test_map
```


Overlap of 1−degree grid−cells with long−term BBS monitoring data (grey outlined cells)
and the eBird estimated proportion of Connecticut Warbler population during the br
Approximately 31% of the species' population is within the 1−degree grid cells
with BBS monitoring data

```
  pdf(paste0("figures/Overlap BBS monitoring with breeding season population",species,".pdf"
     width = 7.5,
     height = 7)
  test_map
  dev.off()
```

pdf

By filling in the abundance values for each stratum where there are BBS observations outside of the modeled breeding range for the species, we can generate a complete relative abundance surface that covers all of the available BBS locations, and does so using the area-corrected nearest neighbour value.

If we consider each cell within the range of the BBS surveys "covered" by BBS monitoring, then 31% of the species' population in 2021 is covered.