Bird Diversity Analysis

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Summary

This project studies landscape and bird diversity change in a mountainous area (the Willmore Wilderness Park in Alberta, Canada) over the last century.

We have data on past and current land cover composition (historic and repeat photos & their land cover classifications). The 10 land cover categories are: Coniferous forest, Broadleaf forest, Mixedwood forest, Wetland, Shrub, Herbaceous, Rock, Water, Regenerating area, Snow/Ice.

We have species distribution models (made from auditory survey data and Landsat-based land cover map). The 15 bird species are: American pipit, American robin, Chipping sparrow, Dark-eyed junco, Golden-crowned kinglet, Golden-crowned sparrow, Gray jay, Hermit thrush, Pine siskin, Ruby-crowned kinglet, Savannah sparrow, Swainson's thrush, Varied thrush, Wilson's warbler, Yellow-rumped warbler.

```r
# Load packages
library(here)
library(readxl)
library(tidyverse)
library(vegan)
```

Load data

- Raw data consists of Mountain Legacy Project (MLP) photos (Photographs.zip)
- Pre-processed data consists of image classifications (LandCoverClassifications.zip)
- Processed data is in ImageAnalysis.xlsx
    - Each tab is an MLP station (i.e. photograph pair)
    - Classified photos were uploaded to the MLP's Image Analysis Toolkit
    - Land cover % outputs from IAT were copied back into ImageAnalysis.xlsx
    - Model backtransformations are done to get probability of occurrence in both historical and repeat photos for each station
    - Then there is a tab for land cover summary across all photograph pairs
    - And a tab aggregating outputs for all historical images
    - And a tab aggregating outputs for all repeat images

```r
historicdata <- read_xlsx(here("SupplementaryData","ImageAnalysis.xlsx"), sheet="Historic") %>%
  mutate(TIME = "Historic")
repeatdata <- read_xlsx(here("SupplementaryData","ImageAnalysis.xlsx"), sheet="Repeat") %>%
  mutate(TIME = "Repeat")
data <- rbind(historicdata, repeatdata) %>%
  pivot_longer(cols=CF:SN, names_to="LANDCOVER", values_to="LANDCOVER_PERCENT") %>%
  pivot_longer(cols=GRAJ:VATH, names_to="SPECIES", values_to="SPECIES_OCCURRENCE") %>%
  mutate(across(c(STATION, TIME, LANDCOVER, SPECIES), as.factor))

landcovertypes <- read.csv(here("SupplementaryData", "LandcoverLookup.csv"))
```

```r
species <- read.csv(here("SupplementaryData", "SpeciesLookup.csv")) %>%
  mutate(NAMESEP = gsub(" ", " \n ", NAME)) # for plotting later
```

Calculate diversity

Calculate diversity indices for both land cover and species.

```r
data <- data %>%
  group_by(STATION, TIME, SPECIES) %>%
  mutate(LANDCOVER_DIV = diversity(LANDCOVER_PERCENT, index="shannon")) %>%
  ungroup() %>%
  group_by(STATION, TIME, LANDCOVER) %>%
  mutate(SPECIES_DIV = diversity(SPECIES_OCCURRENCE, index="shannon")) %>%
  ungroup()
```

Examine land cover change

Run paired t-tests for each land cover type and for land cover diversity. We chose paired t-tests because the
samples (photographs) are not independent - it's the same landscape at two different times.

T-tests are relatively robust to deviations from assumptions, but assumptions are:

- Continuous data
- Random samples
- Homogeneity of variance
- Distribution approximately normal

```r
# Prep data
landcoverdata  <- data %>%
  select(STATION, TIME, LANDCOVER, LANDCOVER_PERCENT) %>%
  unique()

# Print t-test results for each land cover type
for (lc in landcovertypes$CODE) {
  print(landcovertypes$NAME[which(landcovertypes$CODE==lc)])
  print(t.test(landcoverdata %>% filter(LANDCOVER==lc, TIME=="Historic") %>% pull(LANDCOVER_PERCENT),
        landcoverdata %>% filter(LANDCOVER==lc, TIME=="Repeat") %>% pull(LANDCOVER_PERCENT),
        paired=T))
}
```

```
## [1] "Coniferous Forest"
##
##  Paired t-test
##
## data:  landcoverdata %>% filter(LANDCOVER == lc, TIME == "Historic") %>% pull(LANDCOVER_PERCENT) and
## t = -4.5633, df = 45, p-value = 3.876e-05
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -17.913748  -6.942774
## sample estimates:
## mean difference
##       -12.42826
##
## [1] "Broadleaf Forest"
##
##  Paired t-test
```

2

```
##
## data:  landcoverdata %>% filter(LANDCOVER == lc, TIME == "Historic") %>% pull(LANDCOVER_PERCENT) and
## t = 0.47923, df = 45, p-value = 0.6341
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.05570012  0.09048273
## sample estimates:
## mean difference
##       0.0173913
##
## [1] "Mixedwood Forest"
##
##  Paired t-test
##
## data:  landcoverdata %>% filter(LANDCOVER == lc, TIME == "Historic") %>% pull(LANDCOVER_PERCENT) and
## t = -0.8365, df = 45, p-value = 0.4073
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -2.896609  1.196609
## sample estimates:
## mean difference
##           -0.85
##
## [1] "Wetlands"
##
##  Paired t-test
##
## data:  landcoverdata %>% filter(LANDCOVER == lc, TIME == "Historic") %>% pull(LANDCOVER_PERCENT) and
## t = 2.8607, df = 45, p-value = 0.006389
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.1955858 1.1261533
## sample estimates:
## mean difference
##       0.6608696
##
## [1] "Shrub Cover"
##
##  Paired t-test
##
## data:  landcoverdata %>% filter(LANDCOVER == lc, TIME == "Historic") %>% pull(LANDCOVER_PERCENT) and
## t = 1.706, df = 45, p-value = 0.0949
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.2716922  3.2803879
## sample estimates:
## mean difference
##        1.504348
##
## [1] "Herbaceous Cover"
##
##  Paired t-test
##
## data:  landcoverdata %>% filter(LANDCOVER == lc, TIME == "Historic") %>% pull(LANDCOVER_PERCENT) and
```

```
## t = 6.083, df = 45, p-value = 2.351e-07
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##   4.337647 8.631918
## sample estimates:
## mean difference
##         6.484783
##
## [1] "Rock"
##
##   Paired t-test
##
## data:  landcoverdata %>% filter(LANDCOVER == lc, TIME == "Historic") %>% pull(LANDCOVER_PERCENT) and
## t = 1.8056, df = 45, p-value = 0.07767
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##   -0.08457856  1.54979595
## sample estimates:
## mean difference
##        0.7326087
##
## [1] "Water"
##
##   Paired t-test
##
## data:  landcoverdata %>% filter(LANDCOVER == lc, TIME == "Historic") %>% pull(LANDCOVER_PERCENT) and
## t = 3.6465, df = 45, p-value = 0.000687
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##   0.04379322 0.15185896
## sample estimates:
## mean difference
##       0.09782609
##
## [1] "Regenerating Area"
##
##   Paired t-test
##
## data:  landcoverdata %>% filter(LANDCOVER == lc, TIME == "Historic") %>% pull(LANDCOVER_PERCENT) and
## t = 1.2113, df = 45, p-value = 0.2321
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##   -1.994084  8.011475
## sample estimates:
## mean difference
##         3.008696
##
## [1] "Snow/Ice"
##
##   Paired t-test
##
## data:  landcoverdata %>% filter(LANDCOVER == lc, TIME == "Historic") %>% pull(LANDCOVER_PERCENT) and
## t = 1.996, df = 45, p-value = 0.052
## alternative hypothesis: true mean difference is not equal to 0
```

```
## 95 percent confidence interval:
##  -0.006732943  1.493689464
## sample estimates:
## mean difference
##        0.7434783
```

```r
# Overall landscape diversity
print(t.test(data %>% select(STATION, TIME, LANDCOVER_DIV) %>% unique() %>% filter(TIME=="Historic") %>%
             data %>% select(STATION, TIME, LANDCOVER_DIV) %>% unique() %>% filter(TIME=="Repeat") %>%
             paired=T))
```

```
##
##  Paired t-test
##
## data:  data %>% select(STATION, TIME, LANDCOVER_DIV) %>% unique() %>% filter(TIME == "Historic") %>%
## t = 5.1271, df = 45, p-value = 6.018e-06
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##   0.1228375 0.2817877
## sample estimates:
## mean difference
##        0.2023126
```

```r
# Historical landscape diversity
data %>% select(STATION, TIME, LANDCOVER_DIV) %>% unique() %>% filter(TIME=="Historic") %>% pull(LANDCO
```

```
## [1] 1.199805
```

```r
data %>% select(STATION, TIME, LANDCOVER_DIV) %>% unique() %>% filter(TIME=="Historic") %>% pull(LANDCO
```

```
## [1] 0.03935819
```

```r
# Repeat landscape diversity
data %>% select(STATION, TIME, LANDCOVER_DIV) %>% unique() %>% filter(TIME=="Repeat") %>% pull(LANDCOVE
```

```
## [1] 0.9974924
```

```r
data %>% select(STATION, TIME, LANDCOVER_DIV) %>% unique() %>% filter(TIME=="Repeat") %>% pull(LANDCOVE
```

```
## [1] 0.04447595
```

Given these outputs, we can see which land cover types changed. We can also be confident that the landscape diversity declined between the historical photos and the repeat photos.

Examine bird diversity change

Run paired t-tests for each bird species and for bird diversity. We chose paired t-tests because the samples (photographs) are not independent - it's the same landscape at two different times.

```r
birddata  <- data %>%
  select(STATION, TIME, SPECIES, SPECIES_OCCURRENCE) %>%
  unique()

for (spp in species$CODE) {
  print(species$NAME[which(species$CODE==spp)])
  print(t.test(birddata %>% filter(SPECIES==spp, TIME=="Historic") %>% pull(SPECIES_OCCURRENCE),
               birddata %>% filter(SPECIES==spp, TIME=="Repeat") %>% pull(SPECIES_OCCURRENCE),
               paired=T))
}
```

```
## [1] "Gray Jay"
##
##  Paired t-test
##
## data:  birddata %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE) and bird
## t = 3.8312, df = 45, p-value = 0.0003928
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.02374718 0.07639195
## sample estimates:
## mean difference
##      0.05006956
##
## [1] "Wilson's Warbler"
##
##  Paired t-test
##
## data:  birddata %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE) and bird
## t = 0.40219, df = 45, p-value = 0.6894
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.01739597  0.02607694
## sample estimates:
## mean difference
##      0.004340486
##
## [1] "Savannah Sparrow"
##
##  Paired t-test
##
## data:  birddata %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE) and bird
## t = -3.514, df = 45, p-value = 0.001019
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.18669617 -0.05065448
## sample estimates:
## mean difference
##      -0.1186753
##
## [1] "Golden-crowned Kinglet"
##
##  Paired t-test
##
## data:  birddata %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE) and bird
## t = 4.5144, df = 45, p-value = 4.543e-05
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.01242143 0.03243330
## sample estimates:
## mean difference
##      0.02242736
##
## [1] "Ruby-crowned Kinglet"
##
```

```
##  Paired t-test
##
## data:  birddata %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE) and bird
## t = 3.0555, df = 45, p-value = 0.00377
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.004442516 0.021626548
## sample estimates:
## mean difference
##      0.01303453
##
## [1] "Dark-eyed Junco"
##
##  Paired t-test
##
## data:  birddata %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE) and bird
## t = 5.8957, df = 45, p-value = 4.459e-07
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.01882403 0.03835902
## sample estimates:
## mean difference
##      0.02859153
##
## [1] "American Robin"
##
##  Paired t-test
##
## data:  birddata %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE) and bird
## t = -3.907, df = 45, p-value = 0.0003112
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.04997135 -0.01597497
## sample estimates:
## mean difference
##      -0.03297316
##
## [1] "Hermit Thrush"
##
##  Paired t-test
##
## data:  birddata %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE) and bird
## t = 2.8944, df = 45, p-value = 0.00584
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.007576746 0.042247916
## sample estimates:
## mean difference
##      0.02491233
##
## [1] "Pine Siskin"
##
##  Paired t-test
##
```

```
## data:  birddata %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE) and bird
## t = 4.1807, df = 45, p-value = 0.0001323
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.02617540 0.07484153
## sample estimates:
## mean difference
##      0.05050846
##
## [1] "American Pipit"
##
##  Paired t-test
##
## data:  birddata %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE) and bird
## t = -2.0487, df = 45, p-value = 0.04635
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.0741438345 -0.0006321223
## sample estimates:
## mean difference
##      -0.03738798
##
## [1] "Golden-crowned Sparrow"
##
##  Paired t-test
##
## data:  birddata %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE) and bird
## t = -1.9743, df = 45, p-value = 0.05451
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.0692928547  0.0006916874
## sample estimates:
## mean difference
##      -0.03430058
##
## [1] "Swainson's Thrush"
##
##  Paired t-test
##
## data:  birddata %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE) and bird
## t = 0.46603, df = 45, p-value = 0.6434
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.008776938  0.014061380
## sample estimates:
## mean difference
##      0.002642221
##
## [1] "Yellow-rumped Warbler"
##
##  Paired t-test
##
## data:  birddata %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE) and bird
## t = 6.7136, df = 45, p-value = 2.713e-08
```

```
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.1167426 0.2168094
## sample estimates:
## mean difference
##        0.166776
##
## [1] "Chipping Sparrow"
##
##  Paired t-test
##
## data:  birddata %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE) and birdd
## t = -2.8055, df = 45, p-value = 0.007394
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.054107230 -0.008884972
## sample estimates:
## mean difference
##      -0.0314961
##
## [1] "Varied Thrush"
##
##  Paired t-test
##
## data:  birddata %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE) and birdd
## t = -0.8566, df = 45, p-value = 0.3962
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.03186980  0.01285023
## sample estimates:
## mean difference
##    -0.009509786
```

```r
# Overall bird diversity
print(t.test(data %>% select(STATION, TIME, SPECIES_DIV) %>% unique() %>% filter(TIME=="Historic") %>% p
             data %>% select(STATION, TIME, SPECIES_DIV) %>% unique() %>% filter(TIME=="Repeat") %>% pul
             paired=T))
```

```
##
##  Paired t-test
##
## data:  data %>% select(STATION, TIME, SPECIES_DIV) %>% unique() %>% filter(TIME == "Historic") %>% pu
## t = -0.1605, df = 45, p-value = 0.8732
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.006930295  0.005907297
## sample estimates:
## mean difference
##    -0.000511499
```

At the species level, many species were affected and changed in probability of occurrence between the two
time points. However, we cannot say that the species diversity changed significantly between the two time
periods.

Plot bird diversity changes

Create a data frame with the t-test outputs to make it easier to plot.

```
birddata  <- data %>%
  select(STATION, TIME, SPECIES, SPECIES_OCCURRENCE) %>%
  unique()

df <- data.frame(CODE=NA, ESTIMATE=NA, CI_LOW=NA, CI_HIGH=NA)
for (spp in species$CODE) {
  testoutput <- t.test(birddata %>% filter(SPECIES==spp, TIME=="Historic") %>% pull(SPECIES_OCCURRENCE)
                       birddata %>% filter(SPECIES==spp, TIME=="Repeat") %>% pull(SPECIES_OCCURRENCE),
                       paired=T)
  row <- c(spp, testoutput$estimate, testoutput$conf.int[1], testoutput$conf.int[2])
  df <- rbind(df, row)
}
df <- df[-1,]# remove the NA row
```

Link to external data on each species:

- Breeding habitat
- Non-breeding habitat
- Conservation concern

Source: State of North America's Birds 2016 Report

```
sonab <- read_xlsx(here("SupplementaryData","assessment-table-full.xlsx"), sheet="SONAB database for di
  filter(`English Name` %in% species$NAME) %>%
  select(`English Name`, `Breeding Habitats`, `Non-breeding Habitats`, CCSmax) %>%
  rename(NAME = `English Name`)

# Regroup habitats based on classes that match the categories we used in our analysis
sonab <- sonab %>%
  rename(BREEDING = `Breeding Habitats`,
         NONBREEDING = `Non-breeding Habitats`,
         CONSERVATION = CCSmax) %>%
  mutate(BREEDING = gsub("Arctic tundra", "", BREEDING), # remove classes that don't exist in our study
         BREEDING = gsub("Temperate western forest", "", BREEDING),
         BREEDING = gsub("Temperate eastern forest", "", BREEDING),
         BREEDING = gsub("Mexican highland forest", "", BREEDING),
         BREEDING = gsub("Mexican pine and oak forest", "", BREEDING),
         BREEDING = gsub("Temperate grassland", "", BREEDING),
         BREEDING = gsub("Agricultural", "", BREEDING),
         BREEDING = gsub("Alpine tundra", "Herbaceous", BREEDING), # rename to match our class names
         BREEDING = gsub("Boreal forest", "Forest", BREEDING),
         BREEDING = gsub(";", "", BREEDING),
         BREEDING = trimws(BREEDING)) %>%
  mutate(NONBREEDING = gsub("Beach and estuary", "", NONBREEDING), # remove classes that don't exist in
         NONBREEDING = gsub("Agricultural", "", NONBREEDING),
         NONBREEDING = gsub("Coastal saltmarsh", "", NONBREEDING),
         NONBREEDING = gsub("Tropical highland forest", "", NONBREEDING),
         NONBREEDING = gsub("Temperate grassland", "Herbaceous", NONBREEDING), # rename to match our cl
         NONBREEDING = gsub("Temperate western forest", "Forest", NONBREEDING),
         NONBREEDING = gsub("Tropical evergreen forest", "Herbaceous", NONBREEDING),
         NONBREEDING = gsub("Boreal forest", "Forest", NONBREEDING),
         NONBREEDING = gsub(";", "", NONBREEDING),
         NONBREEDING = trimws(NONBREEDING)) %>%
```

```
    mutate(CONSERVATION = replace(CONSERVATION, which(CONSERVATION %in% as.character(5:8)), "Low"), # cut
           CONSERVATION = replace(CONSERVATION, which(CONSERVATION %in% as.character(9:13)), "Moderate"))
    left_join(species, by="NAME")

df <- left_join(df, sonab, by="CODE")

df$ESTIMATE <- as.numeric(df$ESTIMATE)
df$CI_LOW <- as.numeric(df$CI_LOW)
df$CI_HIGH <- as.numeric(df$CI_HIGH)
df$NAME <- factor(df$NAME)
df$BREEDING <- factor(df$BREEDING)
df$NONBREEDING <- factor(df$NONBREEDING)
df$CONSERVATION <- factor(df$CONSERVATION)
df$NAMESEP <- factor(df$NAMESEP)

speciesorder <- levels(reorder(df$NAMESEP, df$ESTIMATE)) # we want to use this specific order for all p
df$NAMESEP <- factor(df$NAMESEP, speciesorder)
```
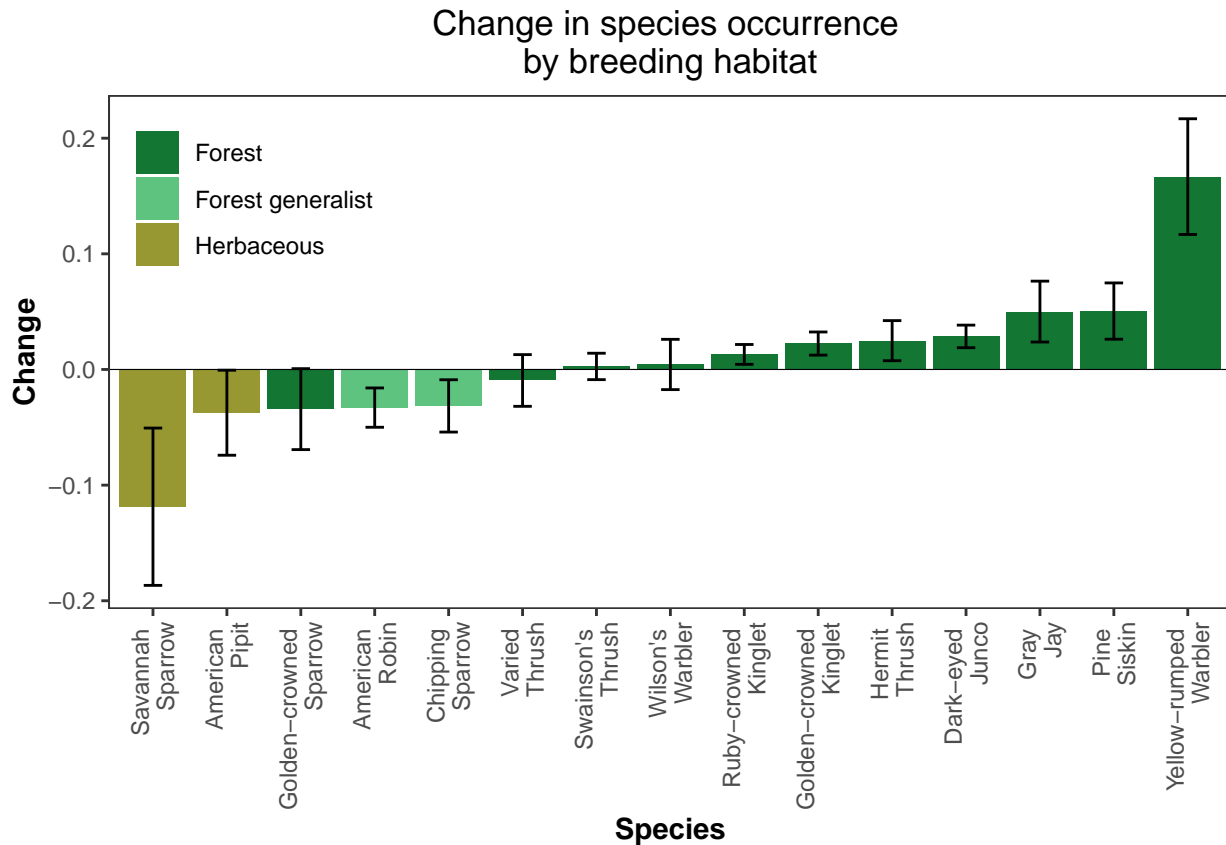
Make plots used in manuscript.

```
plot1 <- ggplot(data=df, aes(x=NAMESEP, y=ESTIMATE, fill=BREEDING)) +
  theme_bw() +
  geom_bar(stat="identity",position=position_dodge(0.9)) +
  geom_errorbar(aes(ymax=CI_HIGH, ymin=CI_LOW) ,position=position_dodge(0.9),width=0.25) +
  scale_fill_manual("Legend", values = c("Forest" = rgb(19/256,119/256,51/256),
                                         "Herbaceous" = rgb(153/256,153/256,50/256),
                                         "Forest generalist" = rgb(95/256,196/256,128/256))) +
  labs(x="Species",y="Change") +
  ggtitle("Change in species occurrence \nby breeding habitat") +
  theme(plot.title = element_text(hjust = 0.5),
        axis.text  = element_text(),
        axis.text.x = element_text(angle=90, vjust=0.5, hjust=1),
        axis.title = element_text(face="bold"),
        text       = element_text(),
        panel.background = element_rect(fill="transparent", colour=NA), # transparent background for gr
        plot.background = element_rect(fill="transparent", colour=NA),
        panel.grid.minor = element_blank(),
        panel.grid.major = element_blank(),
        legend.title = element_blank(),
        legend.position = c(0.01,0.99),
        legend.background = element_blank(),
        legend.justification = c("left","top"))+
  geom_hline(yintercept = 0, linewidth=0.2)

plot1
```

Change in species occurrence
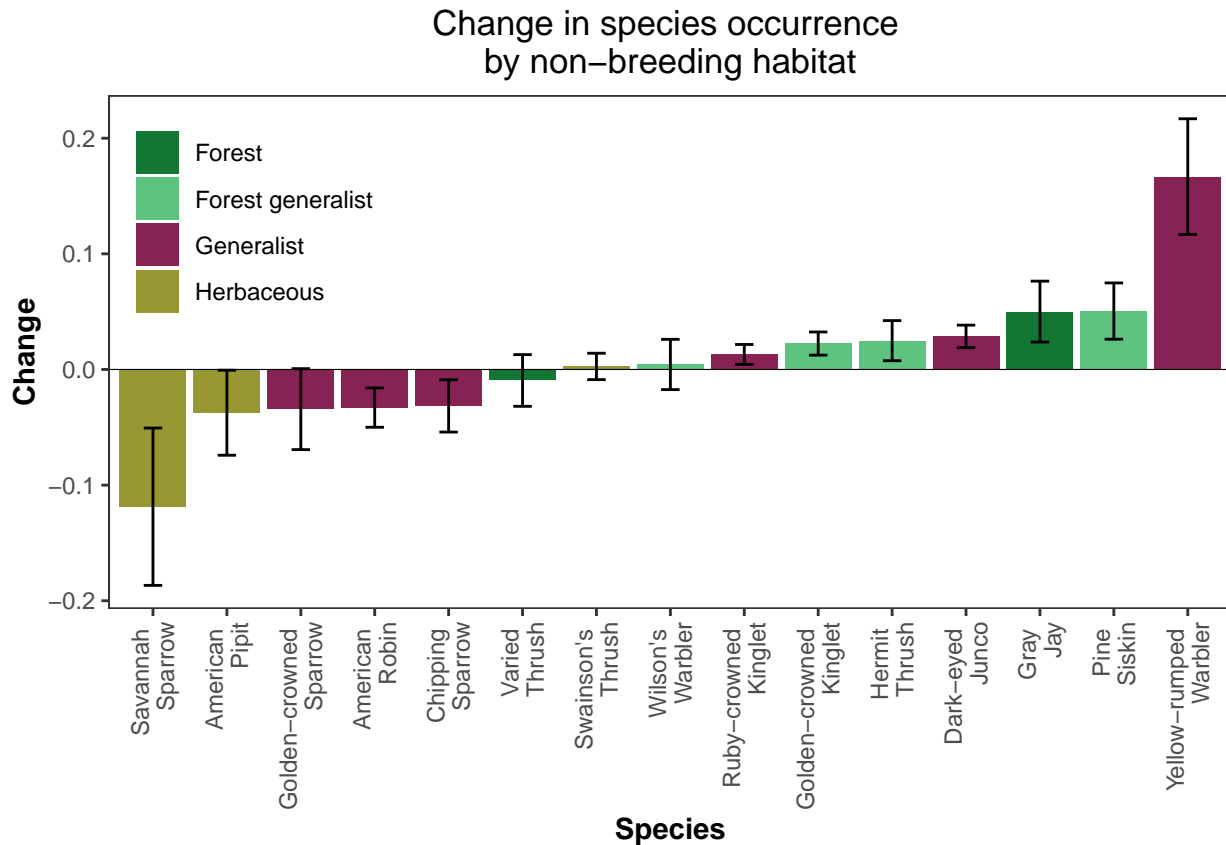by breeding habitat

As we can see from this plot, species whose main breeding habitat is not forest have declined more than species that breed in forest.

```
plot2 <- ggplot(data=df, aes(x=NAMESEP, y=ESTIMATE, fill=NONBREEDING)) +
  theme_bw() +
  geom_bar(stat="identity",position=position_dodge(0.9)) +
  geom_errorbar(aes(ymax=CI_HIGH, ymin=CI_LOW) ,position=position_dodge(0.9),width=0.25) +
  scale_fill_manual("Legend", values = c("Forest" = rgb(19/256,119/256,51/256),
                                        "Herbaceous" = rgb(153/256,153/256,50/256),
                                        "Forest generalist" = rgb(95/256,196/256,128/256),
                                        "Generalist" = rgb(136/256,35/256,84/256))) +
  labs(x="Species",y="Change") +
  ggtitle("Change in species occurrence \nby non-breeding habitat") +
  theme(plot.title = element_text(hjust = 0.5),
        axis.text  = element_text(),
        axis.text.x = element_text(angle=90, vjust=0.5, hjust=1),
        axis.title = element_text(face="bold"),
        text       = element_text(),
        panel.grid.minor = element_blank(),
        panel.grid.major = element_blank(),
        legend.title = element_blank(),
        legend.position = c(0.01,0.99),
        legend.background = element_blank(),
        legend.justification = c("left","top"))+
  geom_hline(yintercept = 0, linewidth=0.2)

plot2
```

Change in species occurrence
by non–breeding habitat

As we can see from this plot, species' non-breeding habitat does not show a clear correlation with direction of change. Generally, forest-dwelling species are positively affected and herbaceous-dwelling species are negatively affected.

```
plot3 <- ggplot(data=df, aes(x=NAMESEP, y=ESTIMATE, fill=CONSERVATION)) +
  theme_bw() +
  geom_bar(stat="identity",position=position_dodge(0.9)) +
  geom_errorbar(aes(ymax=CI_HIGH, ymin=CI_LOW) ,position=position_dodge(0.9),width=0.25) +
  scale_fill_manual("Legend", values = c("Low" = rgb(136/256,205/256,238/256),
                                         "Moderate" = rgb(188/256,94/256,109/256))) +
  labs(x="Species",y="Change") +
  ggtitle("Change in species occurrence \nby level of conservation concern") +
  theme(plot.title = element_text(hjust = 0.5),
        axis.text  = element_text(),
        axis.text.x = element_text(angle=90, vjust=0.5, hjust=1),
        axis.title = element_text(face="bold"),
        text       = element_text(),
        panel.grid.minor = element_blank(),
        panel.grid.major = element_blank(),
        legend.title = element_blank(),
        legend.position = c(0.01,0.99),
        legend.background = element_blank(),
        legend.justification = c("left","top"))+
  geom_hline(yintercept = 0, linewidth=0.2)

plot3
```

Change in species occurrence
by level of conservation concern
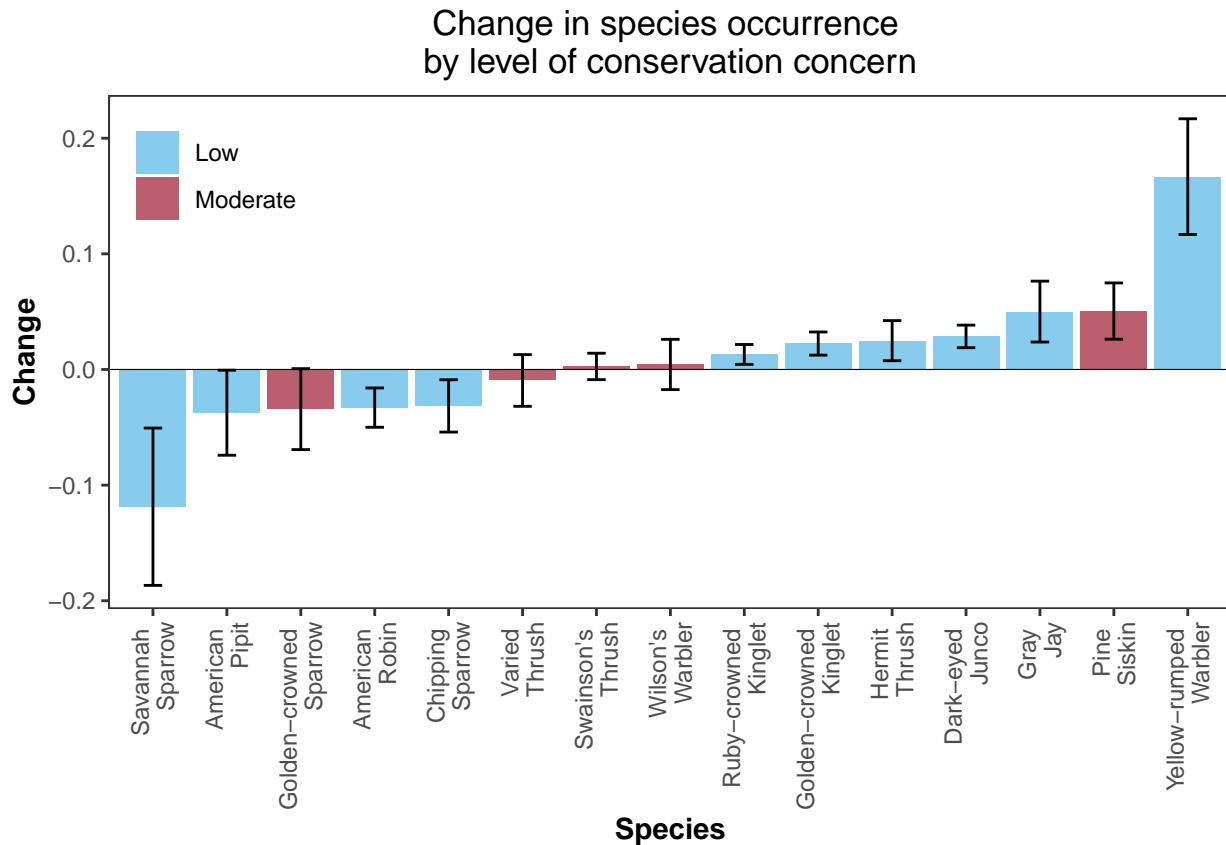
As we can see from this plot, the level of conservation concern of the species does not show a clear correlation with direction of change.

Sensitivity Analysis

Our species distribution models report coefficients as well as standard errors (SE). To ensure we are dealing with error propagation, we run a sensitivity analysis. The results we produced for the main text show the model predictions using the mean coefficients. Here we also show the predictions using coefficient-SE and coefficient+SE and evaluate whether our conclusions change.

Load the lower bound (coefficient-SE) and upper bound (coefficient+SE) data.

```
historicdata_lb <- read_xlsx(here("SupplementaryData","ImageAnalysis_SensitivityAnalysis_MinusSE.xlsx")
  mutate(TIME = "Historic")
repeatdata_lb <- read_xlsx(here("SupplementaryData","ImageAnalysis_SensitivityAnalysis_MinusSE.xlsx"), 
  mutate(TIME = "Repeat")
data_lb <- rbind(historicdata_lb, repeatdata_lb) %>%
  pivot_longer(cols=CF:SN, names_to="LANDCOVER", values_to="LANDCOVER_PERCENT") %>%
  pivot_longer(cols=GRAJ:VATH, names_to="SPECIES", values_to="SPECIES_OCCURRENCE_LB") %>%
  mutate(across(c(STATION, TIME, LANDCOVER, SPECIES), as.factor)) %>%
  select(STATION, TIME, SPECIES, SPECIES_OCCURRENCE_LB) %>%
  distinct()

data_lb <- data_lb %>%
  group_by(STATION, TIME) %>%
  mutate(SPECIES_DIV = diversity(SPECIES_OCCURRENCE_LB, index="shannon")) %>%
  ungroup()
```

```r
# Historical bird diversity, lower bound
data_lb %>% select(STATION, TIME, SPECIES_DIV) %>% unique() %>% filter(TIME=="Historic") %>% pull(SPECI
```

```
## [1] 2.695998
```

```r
# Repeat bird diversity, lower bound
data_lb %>% select(STATION, TIME, SPECIES_DIV) %>% unique() %>% filter(TIME=="Repeat") %>% pull(SPECIES_
```

```
## [1] 2.699622
```

```r
historicdata_ub <- read_xlsx(here("SupplementaryData","ImageAnalysis_SensitivityAnalysis_PlusSE.xlsx"),
  mutate(TIME = "Historic")
repeatdata_ub <- read_xlsx(here("SupplementaryData","ImageAnalysis_SensitivityAnalysis_PlusSE.xlsx"), sh
  mutate(TIME = "Repeat")
data_ub <- rbind(historicdata_ub, repeatdata_ub) %>%
  pivot_longer(cols=CF:SN, names_to="LANDCOVER", values_to="LANDCOVER_PERCENT") %>%
  pivot_longer(cols=GRAJ:VATH, names_to="SPECIES", values_to="SPECIES_OCCURRENCE_UB") %>%
  mutate(across(c(STATION, TIME, LANDCOVER, SPECIES), as.factor)) %>%
  select(STATION, TIME, SPECIES, SPECIES_OCCURRENCE_UB) %>%
  distinct()

data_ub <- data_ub %>%
  group_by(STATION, TIME) %>%
  mutate(SPECIES_DIV = diversity(SPECIES_OCCURRENCE_UB, index="shannon")) %>%
  ungroup()

# Historical bird diversity, upper bound
data_ub %>% select(STATION, TIME, SPECIES_DIV) %>% unique() %>% filter(TIME=="Historic") %>% pull(SPECI
```

```
## [1] 2.619888
```

```r
# Repeat bird diversity, upper bound
data_ub %>% select(STATION, TIME, SPECIES_DIV) %>% unique() %>% filter(TIME=="Repeat") %>% pull(SPECIES_
```

```
## [1] 2.606102
```

Re-run the paired t-tests with the lower bound (coefficient-SE) and upper bound (coefficient+SE) on individual species and on species diversity.

```r
birddata_lb  <- data_lb %>%
  select(STATION, TIME, SPECIES, SPECIES_OCCURRENCE_LB) %>%
  unique()

for (spp in species$CODE) {
  print(species$NAME[which(species$CODE==spp)])
  print(t.test(birddata_lb %>% filter(SPECIES==spp, TIME=="Historic") %>% pull(SPECIES_OCCURRENCE_LB),
               birddata_lb %>% filter(SPECIES==spp, TIME=="Repeat") %>% pull(SPECIES_OCCURRENCE_LB),
               paired=T))
}
```

```
## [1] "Gray Jay"
##
##  Paired t-test
##
## data:  birddata_lb %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_LB) and
## t = 4.2679, df = 45, p-value = 0.0001003
## alternative hypothesis: true mean difference is not equal to 0
```

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```
## 95 percent confidence interval:
##  0.006546118 0.018245967
## sample estimates:
## mean difference
##      0.01239604
##
## [1] "Wilson's Warbler"
##
##  Paired t-test
##
## data:  birddata_lb %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_LB) an
## t = 2.3318, df = 45, p-value = 0.02425
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.001323701 0.018107324
## sample estimates:
## mean difference
##      0.009715512
##
## [1] "Savannah Sparrow"
##
##  Paired t-test
##
## data:  birddata_lb %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_LB) an
## t = -3.0426, df = 45, p-value = 0.003906
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.1399712 -0.0284692
## sample estimates:
## mean difference
##      -0.08422019
##
## [1] "Golden-crowned Kinglet"
##
##  Paired t-test
##
## data:  birddata_lb %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_LB) an
## t = 4.6025, df = 45, p-value = 3.411e-05
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.0009320615 0.0023825733
## sample estimates:
## mean difference
##      0.001657317
##
## [1] "Ruby-crowned Kinglet"
##
##  Paired t-test
##
## data:  birddata_lb %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_LB) an
## t = 3.5842, df = 45, p-value = 0.0008274
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.0004912145 0.0017514509
```

```
## sample estimates:
## mean difference
##     0.001121333
##
## [1] "Dark-eyed Junco"
##
##  Paired t-test
##
## data:  birddata_lb %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_LB) and
## t = 7.5834, df = 45, p-value = 1.402e-09
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.01801018 0.03103671
## sample estimates:
## mean difference
##     0.02452345
##
## [1] "American Robin"
##
##  Paired t-test
##
## data:  birddata_lb %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_LB) and
## t = -3.3546, df = 45, p-value = 0.001621
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.036494291 -0.009112119
## sample estimates:
## mean difference
##     -0.02280321
##
## [1] "Hermit Thrush"
##
##  Paired t-test
##
## data:  birddata_lb %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_LB) and
## t = 2.4257, df = 45, p-value = 0.01935
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.001058028 0.011412449
## sample estimates:
## mean difference
##     0.006235238
##
## [1] "Pine Siskin"
##
##  Paired t-test
##
## data:  birddata_lb %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_LB) and
## t = 3.7199, df = 45, p-value = 0.0005508
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.01105227 0.03715161
## sample estimates:
## mean difference
```

```
##      0.02410194
##
## [1] "American Pipit"
##
##  Paired t-test
##
## data:  birddata_lb %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_LB) and
## t = -1.6827, df = 45, p-value = 0.09937
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.056933203  0.005104453
## sample estimates:
## mean difference
##      -0.02591437
##
## [1] "Golden-crowned Sparrow"
##
##  Paired t-test
##
## data:  birddata_lb %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_LB) and
## t = -1.6666, df = 45, p-value = 0.1025
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.048403947  0.004570439
## sample estimates:
## mean difference
##      -0.02191675
##
## [1] "Swainson's Thrush"
##
##  Paired t-test
##
## data:  birddata_lb %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_LB) and
## t = 1.7669, df = 45, p-value = 0.08403
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -1.922358e-05  2.940224e-04
## sample estimates:
## mean difference
##    0.0001373994
##
## [1] "Yellow-rumped Warbler"
##
##  Paired t-test
##
## data:  birddata_lb %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_LB) and
## t = 6.9286, df = 45, p-value = 1.3e-08
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.05164396 0.09397432
## sample estimates:
## mean difference
##      0.07280914
##
```

```
## [1] "Chipping Sparrow"
##
##  Paired t-test
##
## data:  birddata_lb %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_LB) and
## t = -1.9406, df = 45, p-value = 0.05858
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.0513965814  0.0009549555
## sample estimates:
## mean difference
##     -0.02522081
##
## [1] "Varied Thrush"
##
##  Paired t-test
##
## data:  birddata_lb %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_LB) and
## t = -0.51179, df = 45, p-value = 0.6113
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.003558681  0.002116589
## sample estimates:
## mean difference
##    -0.0007210462
```

```r
# Overall bird diversity
print(t.test(data_lb %>% select(STATION, TIME, SPECIES_DIV) %>% unique() %>% filter(TIME=="Historic") %>
             data_lb %>% select(STATION, TIME, SPECIES_DIV) %>% unique() %>% filter(TIME=="Repeat") %>%
             paired=T))
```

```
##
##  Paired t-test
##
## data:  data_lb %>% select(STATION, TIME, SPECIES_DIV) %>% unique() %>% filter(TIME == "Historic") %>%
## t = -1.9687, df = 45, p-value = 0.05517
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -7.331250e-03  8.357808e-05
## sample estimates:
## mean difference
##     -0.003623836
```

```r
birddata_ub  <- data_ub %>%
  select(STATION, TIME, SPECIES, SPECIES_OCCURRENCE_UB) %>%
  unique()

for (spp in species$CODE) {
  print(species$NAME[which(species$CODE==spp)])
  print(t.test(birddata_ub %>% filter(SPECIES==spp, TIME=="Historic") %>% pull(SPECIES_OCCURRENCE_UB),
               birddata_ub %>% filter(SPECIES==spp, TIME=="Repeat") %>% pull(SPECIES_OCCURRENCE_UB),
               paired=T))
}
```

```
## [1] "Gray Jay"
##
```

```
##  Paired t-test
##
## data:  birddata_ub %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_UB) and
## t = 3.8584, df = 45, p-value = 0.0003613
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.05388656 0.17158307
## sample estimates:
## mean difference
##       0.1127348
##
## [1] "Wilson's Warbler"
##
##  Paired t-test
##
## data:  birddata_ub %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_UB) and
## t = -0.48626, df = 45, p-value = 0.6291
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.04559386  0.02786020
## sample estimates:
## mean difference
##     -0.008866828
##
## [1] "Savannah Sparrow"
##
##  Paired t-test
##
## data:  birddata_ub %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_UB) and
## t = -4.2372, df = 45, p-value = 0.0001106
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.24056787 -0.08555097
## sample estimates:
## mean difference
##      -0.1630594
##
## [1] "Golden-crowned Kinglet"
##
##  Paired t-test
##
## data:  birddata_ub %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_UB) and
## t = 4.4154, df = 45, p-value = 6.256e-05
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.06276711 0.16806013
## sample estimates:
## mean difference
##       0.1154136
##
## [1] "Ruby-crowned Kinglet"
##
##  Paired t-test
##
```

```
## data:  birddata_ub %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_UB) and
## t = 2.9396, df = 45, p-value = 0.005172
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.02246134 0.12022453
## sample estimates:
## mean difference
##      0.07134293
##
## [1] "Dark-eyed Junco"
##
##  Paired t-test
##
## data:  birddata_ub %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_UB) and
## t = 2.9979, df = 45, p-value = 0.004414
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.009185672 0.046795689
## sample estimates:
## mean difference
##      0.02799068
##
## [1] "American Robin"
##
##  Paired t-test
##
## data:  birddata_ub %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_UB) and
## t = -3.9614, df = 45, p-value = 0.0002629
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.05735872 -0.01869235
## sample estimates:
## mean difference
##     -0.03802554
##
## [1] "Hermit Thrush"
##
##  Paired t-test
##
## data:  birddata_ub %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_UB) and
## t = 3.1896, df = 45, p-value = 0.002595
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.02080370 0.09209571
## sample estimates:
## mean difference
##       0.0564497
##
## [1] "Pine Siskin"
##
##  Paired t-test
##
## data:  birddata_ub %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_UB) and
## t = 4.1697, df = 45, p-value = 0.000137
```

```
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.03425685 0.09827318
## sample estimates:
## mean difference
##      0.06626501
##
## [1] "American Pipit"
##
##  Paired t-test
##
## data:  birddata_ub %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_UB) and
## t = -2.5867, df = 45, p-value = 0.013
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.09428341 -0.01173342
## sample estimates:
## mean difference
##     -0.05300842
##
## [1] "Golden-crowned Sparrow"
##
##  Paired t-test
##
## data:  birddata_ub %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_UB) and
## t = -2.4368, df = 45, p-value = 0.01884
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.089564645 -0.008505613
## sample estimates:
## mean difference
##     -0.04903513
##
## [1] "Swainson's Thrush"
##
##  Paired t-test
##
## data:  birddata_ub %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_UB) and
## t = 2.6335, df = 45, p-value = 0.01154
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.02289099 0.17176561
## sample estimates:
## mean difference
##      0.0973283
##
## [1] "Yellow-rumped Warbler"
##
##  Paired t-test
##
## data:  birddata_ub %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_UB) and
## t = 4.717, df = 45, p-value = 2.346e-05
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
```

```
##   0.07389142 0.18401529
## sample estimates:
## mean difference
##        0.1289534
##
## [1] "Chipping Sparrow"
##
##   Paired t-test
##
## data:  birddata_ub %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_UB) and
## t = -3.7159, df = 45, p-value = 0.0005576
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##   -0.03720057 -0.01104835
## sample estimates:
## mean difference
##      -0.02412446
##
## [1] "Varied Thrush"
##
##   Paired t-test
##
## data:  birddata_ub %>% filter(SPECIES == spp, TIME == "Historic") %>% pull(SPECIES_OCCURRENCE_UB) and
## t = -1.0155, df = 45, p-value = 0.3153
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##   -0.06735026  0.02219903
## sample estimates:
## mean difference
##      -0.02257561
```

```
# Overall bird diversity
print(t.test(data_ub %>% select(STATION, TIME, SPECIES_DIV) %>% unique() %>% filter(TIME=="Historic") %>%
             data_ub %>% select(STATION, TIME, SPECIES_DIV) %>% unique() %>% filter(TIME=="Repeat") %>%
             paired=T))
```

```
##
##   Paired t-test
##
## data:  data_ub %>% select(STATION, TIME, SPECIES_DIV) %>% unique() %>% filter(TIME == "Historic") %>%
## t = 2.369, df = 45, p-value = 0.02219
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##   0.002065134 0.025506872
## sample estimates:
## mean difference
##        0.013786
```

At the species level, many species were affected and changed in probability of occurrence between the two time points; some positively, some negatively. This is true for both the lower bound and upper bound predictions. Overall, based on the lower bound predictions, we cannot say that species diversity changed between the time steps (mean difference -0.004, CI=[-0.007,0.00008], t=-1.969, df=45, p-value=0.055). However, using the upper bound predictions, species diversity decreased slightly (mean difference 0.013, CI=[0.002,0.026], t=2.369, df=45, p-value=0.022).

Create a data frame with the t-test outputs to make it easier to compare.

```
birddata_lb  <- data_lb %>%
  select(STATION, TIME, SPECIES, SPECIES_OCCURRENCE_LB) %>%
  unique()

df_lb <- data.frame(CODE=NA, ESTIMATE=NA, CI_LOW=NA, CI_HIGH=NA)
for (spp in species$CODE) {
  testoutput <- t.test(birddata_lb %>% filter(SPECIES==spp, TIME=="Historic") %>% pull(SPECIES_OCCURREN(
                       birddata_lb %>% filter(SPECIES==spp, TIME=="Repeat") %>% pull(SPECIES_OCCURRENCE_
                       paired=T)
  row <- c(spp, testoutput$estimate, testoutput$conf.int[1], testoutput$conf.int[2])
  df_lb <- rbind(df_lb, row)
}
df_lb <- df_lb[-1,] %>% # remove the NA row
  mutate(DIRECTION_LB=ifelse(ESTIMATE<0 & CI_LOW<0 & CI_HIGH<0, "NEGATIVE",
                      ifelse(ESTIMATE>0 & CI_LOW>0 & CI_HIGH>0, "POSITIVE",
                         "NULL")))

birddata_ub  <- data_ub %>%
  select(STATION, TIME, SPECIES, SPECIES_OCCURRENCE_UB) %>%
  unique()

df_ub <- data.frame(CODE=NA, ESTIMATE=NA, CI_LOW=NA, CI_HIGH=NA)
for (spp in species$CODE) {
  testoutput <- t.test(birddata_ub %>% filter(SPECIES==spp, TIME=="Historic") %>% pull(SPECIES_OCCURREN(
                       birddata_ub %>% filter(SPECIES==spp, TIME=="Repeat") %>% pull(SPECIES_OCCURRENCE_
                       paired=T)
  row <- c(spp, testoutput$estimate, testoutput$conf.int[1], testoutput$conf.int[2])
  df_ub <- rbind(df_ub, row)
}
df_ub <- df_ub[-1,] %>% # remove the NA row
  mutate(DIRECTION_UB=ifelse(ESTIMATE<0 & CI_LOW<0 & CI_HIGH<0, "NEGATIVE",
                        ifelse(ESTIMATE>0 & CI_LOW>0 & CI_HIGH>0, "POSITIVE",
                            "NULL")))

df_mean <- df %>%
  select(CODE, ESTIMATE, CI_LOW, CI_HIGH) %>%
  mutate(DIRECTION_MEAN=ifelse(ESTIMATE<0 & CI_LOW<0 & CI_HIGH<0, "NEGATIVE",
                        ifelse(ESTIMATE>0 & CI_LOW>0 & CI_HIGH>0, "POSITIVE",
                            "NULL")))

df_merge <- left_join(df_mean, df_lb, by="CODE") %>%
  left_join(df_ub, by="CODE") %>%
  select(CODE, DIRECTION_LB, DIRECTION_MEAN, DIRECTION_UB) %>%
  distinct()

df_merge
```

```
##     CODE DIRECTION_LB DIRECTION_MEAN DIRECTION_UB
## 1  GRAJ     POSITIVE       POSITIVE     POSITIVE
## 2  WIWA     POSITIVE           NULL         NULL
## 3  SAVS     NEGATIVE       NEGATIVE     NEGATIVE
## 4  GCKI     POSITIVE       POSITIVE     POSITIVE
## 5  RCKI     POSITIVE       POSITIVE     POSITIVE
## 6  DEJU     POSITIVE       POSITIVE     POSITIVE
```

```
## 7  AMRO       NEGATIVE       NEGATIVE       NEGATIVE
## 8  HETH       POSITIVE       POSITIVE       POSITIVE
## 9  PISI       POSITIVE       POSITIVE       POSITIVE
## 10 AMPI           NULL       NEGATIVE       NEGATIVE
## 11 GCSP           NULL           NULL       NEGATIVE
## 12 SWTH           NULL           NULL       POSITIVE
## 13 YRWA       POSITIVE       POSITIVE       POSITIVE
## 14 CHSP           NULL       NEGATIVE       NEGATIVE
## 15 VATH           NULL           NULL           NULL
```

As we can see from the above table, for most species (10/15), there was no difference in conclusions. For 5 of the 15 species, the result changed from "no evidence of change" to either positive or negative. That being said, there are no situations in which the direction of change switched from "negative" to "positive" or vice-versa between the lower, mean and upper bound predictions.

Let's prep for plotting.

```r
df_lb <- left_join(df_lb, sonab, by="CODE")

df_lb$ESTIMATE <- as.numeric(df_lb$ESTIMATE)
df_lb$CI_LOW <- as.numeric(df_lb$CI_LOW)
df_lb$CI_HIGH <- as.numeric(df_lb$CI_HIGH)
df_lb$NAME <- factor(df_lb$NAME)
df_lb$BREEDING <- factor(df_lb$BREEDING)
df_lb$NONBREEDING <- factor(df_lb$NONBREEDING)
df_lb$CONSERVATION <- factor(df_lb$CONSERVATION)
df_lb$NAMESEP <- factor(df_lb$NAMESEP, levels=speciesorder)
```

```r
df_ub <- left_join(df_ub, sonab, by="CODE")

df_ub$ESTIMATE <- as.numeric(df_ub$ESTIMATE)
df_ub$CI_LOW <- as.numeric(df_ub$CI_LOW)
df_ub$CI_HIGH <- as.numeric(df_ub$CI_HIGH)
df_ub$NAME <- factor(df_ub$NAME)
df_ub$BREEDING <- factor(df_ub$BREEDING)
df_ub$NONBREEDING <- factor(df_ub$NONBREEDING)
df_ub$CONSERVATION <- factor(df_ub$CONSERVATION)
df_ub$NAMESEP <- factor(df_ub$NAMESEP, levels=speciesorder)
```

Recreate Figure 4 from the main text with the lower and upper bound values to visualize these differences.

```r
plot4 <- ggplot(data=df_lb, aes(x=NAMESEP, y=ESTIMATE, fill=BREEDING)) +
  theme_bw() +
  geom_bar(stat="identity",position=position_dodge(0.9)) +
  geom_errorbar(aes(ymax=CI_HIGH, ymin=CI_LOW) ,position=position_dodge(0.9),width=0.25) +
  scale_fill_manual("Legend", values = c("Forest" = rgb(19/256,119/256,51/256),
                                         "Herbaceous" = rgb(153/256,153/256,50/256),
                                         "Forest generalist" = rgb(95/256,196/256,128/256))) +
  labs(x="Species",y="Change") +
  ggtitle("Change in species occurrence \nby breeding habitat (lower bound)") +
  theme(plot.title = element_text(hjust = 0.5),
        axis.text  = element_text(),
        axis.text.x = element_text(angle=90, vjust=0.5, hjust=1),
        axis.title = element_text(face="bold"),
        text       = element_text(),
        panel.background = element_rect(fill="transparent", colour=NA), # transparent background for gr
```
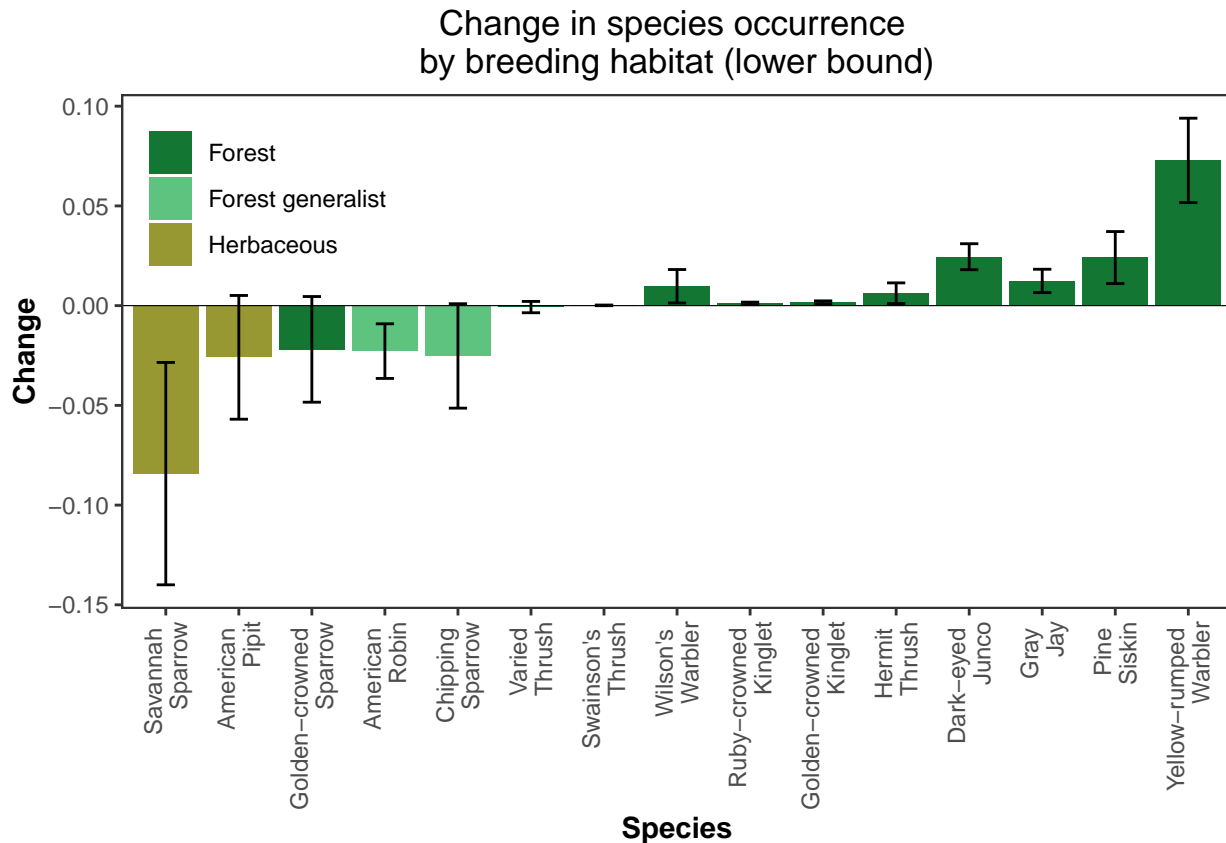
```
        plot.background = element_rect(fill="transparent", colour=NA),
        panel.grid.minor = element_blank(),
        panel.grid.major = element_blank(),
        legend.title = element_blank(),
        legend.position = c(0.01,0.99),
        legend.background = element_blank(),
        legend.justification = c("left","top"))+
  geom_hline(yintercept = 0, linewidth=0.2)

plot4
```


Change in species occurrence
by breeding habitat (lower bound)

```
plot5 <- ggplot(data=df_ub, aes(x=NAMESEP, y=ESTIMATE, fill=BREEDING)) +
  theme_bw() +
  geom_bar(stat="identity",position=position_dodge(0.9)) +
  geom_errorbar(aes(ymax=CI_HIGH, ymin=CI_LOW) ,position=position_dodge(0.9),width=0.25) +
  scale_fill_manual("Legend", values = c("Forest" = rgb(19/256,119/256,51/256),
                                          "Herbaceous" = rgb(153/256,153/256,50/256),
                                          "Forest generalist" = rgb(95/256,196/256,128/256))) +
  labs(x="Species",y="Change") +
  ggtitle("Change in species occurrence \nby breeding habitat (upper bound)") +
  theme(plot.title = element_text(hjust = 0.5),
        axis.text  = element_text(),
        axis.text.x = element_text(angle=90, vjust=0.5, hjust=1),
        axis.title = element_text(face="bold"),
        text       = element_text(),
        panel.background = element_rect(fill="transparent", colour=NA), # transparent background for gr
        plot.background = element_rect(fill="transparent", colour=NA),
```

```
      panel.grid.minor = element_blank(),
      panel.grid.major = element_blank(),
      legend.title = element_blank(),
      legend.position = c(0.01,0.99),
      legend.background = element_blank(),
      legend.justification = c("left","top"))+
  geom_hline(yintercept = 0, linewidth=0.2)

plot5
```


Change in species occurrence
by breeding habitat (upper bound)