

# **Report on the use of passive acoustic monitoring for analysis of bird trends in Jasper National Park**

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## Note

This report is dynamically generated, meaning its results may evolve with the addition of new data or further analyses. For the most recent updates, refer to the publication date and feel free to reach out to the authors.

## 1 Abstract

Since 2007, Jasper National Park has conducted passive acoustic monitoring as part of its ecological integrity monitoring program. The 18 years of data were analyzed to identify trends and extract insights that inform ongoing monitoring and strengthen future species monitoring practices. The analysis assessed whether species and guild abundances shifted by  $\pm 2.5\%$  in the alpine and montane ecoregions. Data were managed and processed in WildTrax, combining and harmonizing legacy datasets from multiple methodologies. Sampling locations were tested for independence, and trend analyses quantified changes in species counts over time across guilds and ecoregions.

## 2 Land Acknowledgement

We respectfully acknowledge that Jasper National Park is located in Treaty 6 and 8 as well as the traditional lands of the Anishinabe, Aseniwuche Winewak, Dene-zaa, Nêhiyawak, Secwépemc, Stoney Nakoda, Mountain Métis and Métis. We acknowledge the past, present, and future generations of these nations who continue to steward the land.

## 3 Introduction

Human activities have been identified as key pressures and contributors to the global decline in forest wildlife (Allan et al. (2017)). The repercussions of habitat fragmentation (Fahrig (2003)) and loss (Hanski (2011)), climate change (Mantyka-pringle, Martin, and Rhodes (2012), Sattar et al. (2021), Abrahms et al. (2023)), and increased access to sensitive areas exert direct and indirect pressures on forest biodiversity, particularly in managed regions in Canada (Lemieux et al. (2011)). Climate change and increasing wildfire activity in Alberta's Rocky Mountain Natural Region have significantly impacted montane bird monitoring; in 2023, two of the park's three long-term montane monitoring transects were affected by wildfires, while the third is currently undergoing wildfire risk reduction measures. Since 2007, Jasper National Park initiated a program incorporating passive acoustic monitoring of the Park's vocalizing wildlife. ARUs are compact environmental sensors that are designed to passively record the environment (Shonfield and Bayne (2017)), capturing vocalizing species like birds and amphibians, which is growing in use across the globe (Sugai et al. (2018)). This technology enables resource managers to conduct prolonged surveys with minimal human interference, but also to create a permanent, archiveable recording of the soundscape. The subsequent data collected by these units contribute valuable information to ecological integrity metrics such as species richness, diversity, occupancy, and trends of species and human activities in National Parks over time. This data can aid in decision-making and management within the Park.

Given the rapid and ease of accumulating data from these units, maintaining a high standard of data integrity is paramount to ensure future data interoperability and sharing.

This project aims to analyze Jasper's passive acoustic monitoring data from 2007 to 2024, assessing trends in species and guild abundance while accounting for the clustering of survey points within transects. Separate analyses will be conducted for montane and sub-alpine and alpine ecoregions to align with Ecological Integrity reporting requirements, determining time-to-first-detection usability in analysis. To enhance accessibility and reproducibility, the findings will be presented in this online report with fully documented code, allowing future updates as data collection methods become standardized. Additionally, recommendations will be developed to refine data transcription priorities, improve annual reporting methods, and evaluate species guild classifications for long-term monitoring. The objectives of this report are to:

- Describe the data management and processing procedures for the acoustic data collected from 2007 to 2025;
- Comparing data processing methods on count of species and individuals heard on recordings;
- Report on transects in montane/sub-alpine and alpine ecoregions, including time-to-first-detection where possible, with key metrics such as the percentage of bird species and guilds declining by 2.5% in both montane/sub-alpine and alpine regions.
- Recommendations for prioritizing previous years' data for re-transcription to 1SPT, determine the best approach for annual reporting, e.g. baseline comparisons or 10-year trend assessments, adjust methods for evaluating species trends against thresholds, and review guilds and traits used in assessments
- Facilitate data publication to the public, resource managers, academic institutions, and any other relevant agencies

## 4 Methods

### 4.1 Data collection

Songbird data was collected using autonomous recording units (ARUs), deployed by field staff to capture one 10-minute recordings per point count annually. Surveys were scheduled consistently each breeding season in June and early July, starting at dawn. Technicians walked transects containing ten points, each spaced at least 300 m apart to prevent duplicate detections and ensure independence of locations. At each location, the ARU is set up, and technicians move 10–20 m away to minimize disturbance, allowing at least 11 minutes of recording for voice notes and activation and de-activation of the units.

```
datatable(locs_summary,
    options = list(
        searching = TRUE,
        paging = TRUE,
        pageLength = 10
    )) |>
formatStyle(columns = colnames(locs_summary),
    backgroundColor = styleEqual(c("NA"), "lightgray"))
```

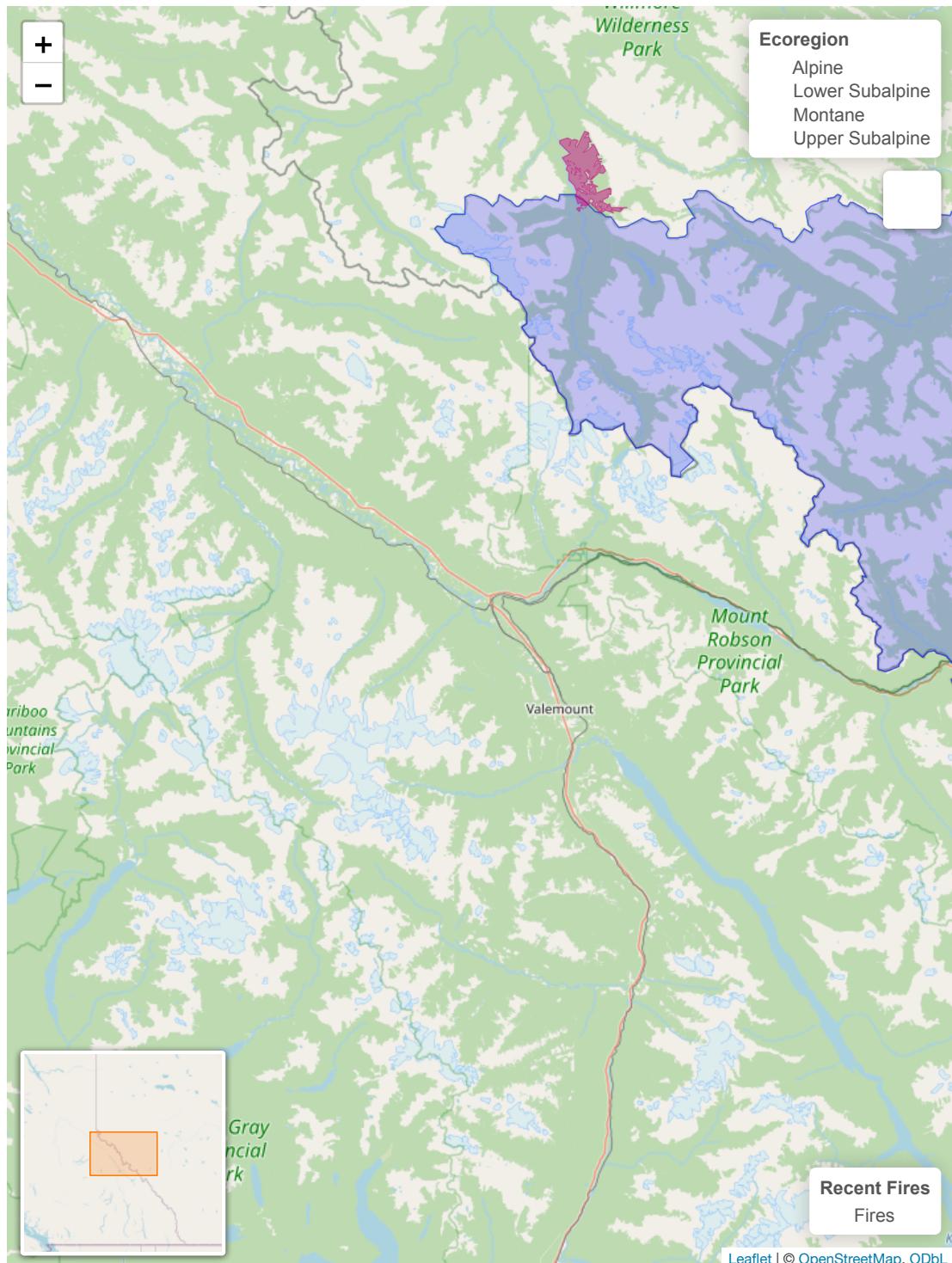


Figure 1: Locations from Jasper National Park ARU EI Monitoring Program.

Table 1: Locations surveyed across years. Ones indicated a deployment in that year for that location.

Show <input type="button" value="10"/> entries			Search: <input type="text"/>											
	Location	ecoregion	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018
1	CAVELL-1	Upper Subalpine	1	1	1	1	1	0	1	1	1	1	0	1
2	CAVELL-2	Alpine	1	1	1	1	1	0	1	1	1	1	0	1
3	CAVELL-3	Alpine	1	1	1	1	1	0	1	1	1	1	0	1
4	CAVELL-4	Alpine	1	1	1	1	1	0	1	1	1	1	0	1
5	CAVELL-5	Alpine	1	1	1	1	1	0	1	1	1	1	0	1
6	ELYSIUM-1	Montane	1	1	1	1	1	0	1	1	1	1	1	1
7	ELYSIUM-10	Lower Subalpine	1	1	1	1	1	0	1	1	1	1	1	1
8	ELYSIUM-2	Montane	1	1	1	1	1	0	1	1	1	1	1	1
9	ELYSIUM-3	Montane	1	1	1	1	1	0	1	1	1	1	1	1
10	ELYSIUM-4	Montane	1	1	1	1	1	0	1	1	1	1	1	1

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## 4.2 Data management, processing and quality control

Recordings were clipped and organized to only include the 10-minute count. Before adopting WildTrax in 2021, processing analysts excluded the initial 20 seconds to 1.5 minutes of recordings to reduce human impact on detection probability, then logged the first detection time per species. Recordings are now uploaded as clean 10-minute files with the voice note and observer notes removed. In WildTrax, individuals were counted by users scanning both the spectrogram and listening to the audio output. Tags were then drawn to encompass the signal within the methods indicated in each project (see Table 2 and Figure 2). Transcribers also had site photos available (see Figure 3) to optimize their species identification by having habitat context while processing.

```
transcription_table <- tibble(
  Years = c("2007-2020", "2021-2022", "2023-2025", "2007-2011"),
  `Transcription Method` = c(
    "0-3.33, 3.33-6.66, 6.66-10 min",
    "1 SPT - Species per task or recording (Every new individual is tagged within the 10 minute period)",
    "1 SPT - Species per task or recording (Every new individual is tagged within the 10 minute period)",
    "1 SPT - Species per task or recording (Every new individual is tagged within the 10 minute period)",
  ),
  `Bin Method` = c(
    "Abundance re-starts for each 3.33-minute bin",
    "Time of first detection over 10 minute period",
    "Time of first detection over 10 minute period",
    "Time of first detection over 10 minute period. Re-transcription."
  ),
  `Method Details` = c(
    "No cap on abundance; abundance re-starts for each bin, no total abundance for the 10-minute period",
    "Time of first detection over 10 minute period",
    "Time of first detection over 10 minute period",
    "Time of first detection over 10 minute period. Re-transcription."
  ),
  `Max # of Individuals` = c(
    "No cap",
    "Maximum of 3 individuals per 10-minute recording",
    "No cap",
    "No cap. Re-transcription."
  )
)

transcription_table
## # A tibble: 4 x 5
##   Years      `Transcription Method`          `Bin Method` `Method Details` 
##   <chr>      <chr>                      <chr>         <chr>        
## 1 2007-2020 0-3.33, 3.33-6.66, 6.66-10 min Abundance r~ No cap on abunda~ 
## 2 2021-2022 1 SPT - Species per task or recording~ Time of fir~ Time of first d~ 
## 3 2023-2025 1 SPT - Species per task or recording~ Time of fir~ Time of first d~ 
## 4 2007-2011 1 SPT - Species per task or recording~ Time of fir~ Time of first d~ 
## # i 1 more variable: `Max # of Individuals` <chr>
```

```
# Render the datatable
datatable(transcription_table,
  options = list(
    searching = TRUE,
    paging = TRUE,
    pageLength = 10
  )) |>
formatStyle(columns = colnames(transcription_table),
  backgroundColor = styleEqual(c("NA"), "lightgray"))
```

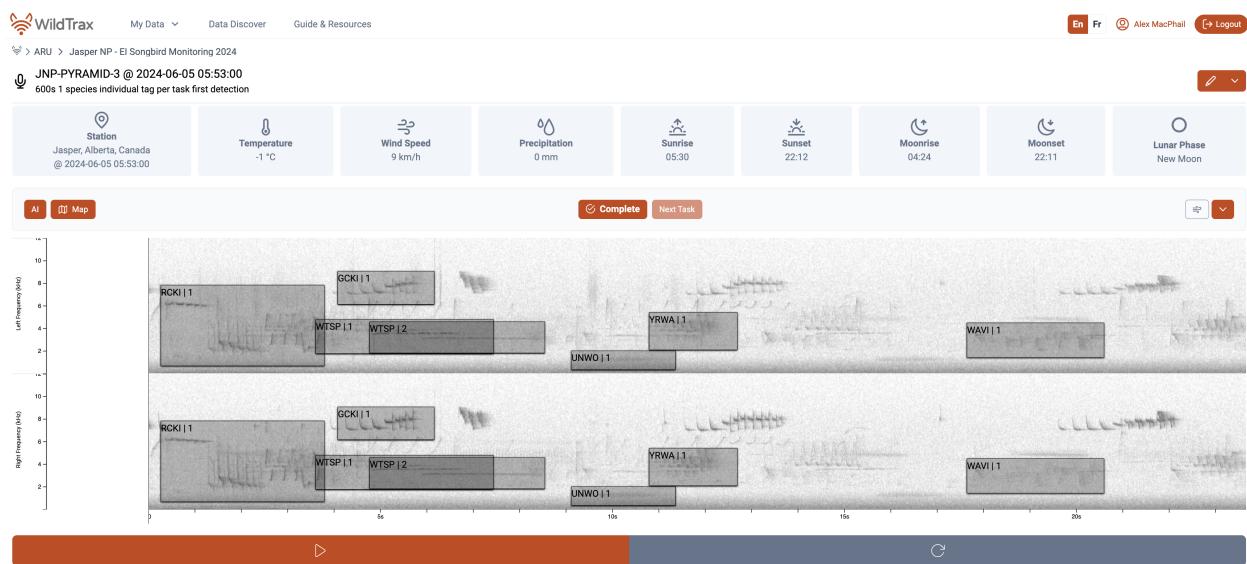


Figure 2: WildTrax Acoustic Processing Interface (Version 2)

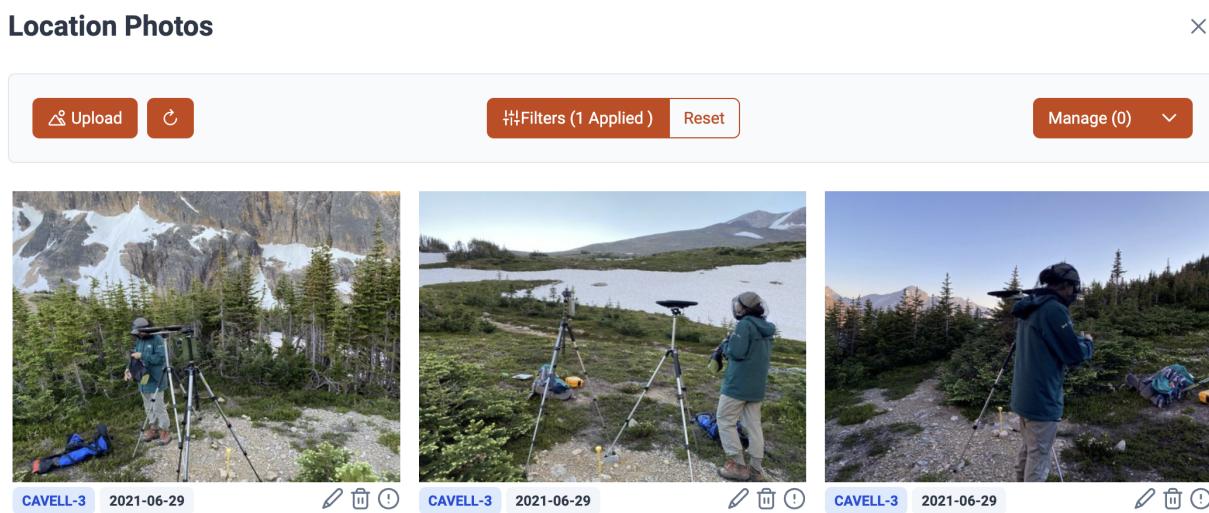


Figure 3: Visit photos at CAVELL-3

Table 2: Transcription method by year with re-transcribed data being conducted from 2007 - 2024.

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Years	Transcription Method	Bin Method	Method Details	Max # of Individuals
1 2007-2020	0-3.33, 3.33-6.66, 6.66-10 min	Abundance restarts for each 3.33-minute bin	No cap on abundance; abundance restarts for each bin, no total abundance for the 10-min recording	No cap
2 2021-2022	1 SPT - Species per task or recording (Every new individual is tagged within the 10 minute recording).	Time of first detection over 10 minute period	Time of first detection over 10 minute period	Maximum of 3 individuals per 10-minute recording
3 2023-2025	1 SPT - Species per task or recording (Every new individual is tagged within the 10 minute recording).	Time of first detection over 10 minute period	Time of first detection over 10 minute period	No cap
4 2007-2011	1 SPT - Species per task or recording (Every new individual is tagged within the 10 minute recording). Re-transcription.	Time of first detection over 10 minute period. Re-transcription.	Time of first detection over 10 minute period. Re-transcription.	No cap. Re-transcription.

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## 4.3 Analyses

### i Note

For the purpose of these analyses abundance was defined as the count of individuals detected during point counts, rather than as a density x area relationship. All analyses took place in R 4.5.1 ‘Great Square Root’.

### 4.3.1 Location correlation

To assess spatial autocorrelation among bird survey locations across years, we examined the spatial relationship between survey points based on total species abundance per location and year in order to determine whether spatial clustering or spatial dependence exists in the species abundance data. Given that survey points are typically 300 meters apart, we used the `knearneigh()` function to identify the nearest neighbours within this threshold. This function calculates the closest neighboring survey points for each location. We then constructed a spatial weight matrix using the `knn2nb()` function. To evaluate whether spatial proximity among sampling locations influenced annual count estimates, we tested for spatial autocorrelation using Moran’s *I*. Annual minimum counts were calculated for each location by estimating the maximum number of individuals per species detected within a year and summing across species. Spatial coordinates for each location were derived from geographic point data and used to construct spatial neighbor relationships. Global spatial autocorrelation was assessed using Moran’s *I* under a randomization assumption. Neighbors were defined using a k-nearest-neighbor approach ( $k = 1$ ) based on great-circle distances, and row-standardized spatial weights were applied. Non-finite values were excluded prior to analysis to ensure valid estimation. To assess whether spatial dependence was driven by localized clusters, we further calculated Local Indicators of Spatial Association (LISA) using local Moran’s *I*. Local statistics were used to identify potential high–high, low–low, and spatial outlier patterns, with statistical significance evaluated at  $\alpha = 0.05$ . While global Moran’s *I* indicated significant positive spatial autocorrelation, local Moran’s *I* did not identify statistically significant local clusters. This suggests that spatial dependence in counts was diffuse across the study area.

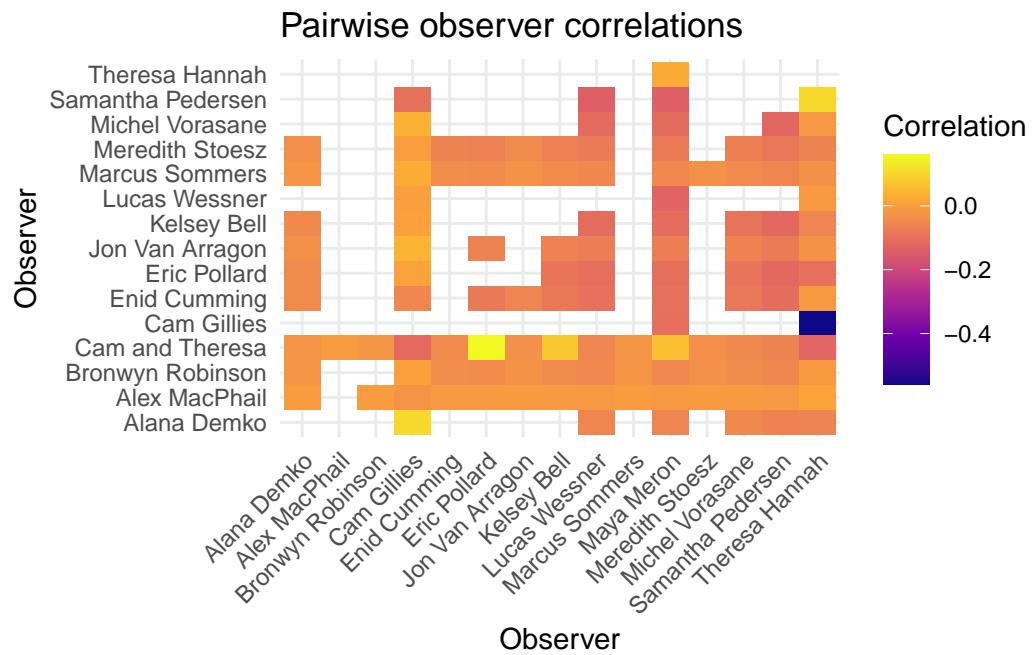
### 4.3.2 Site comparisons

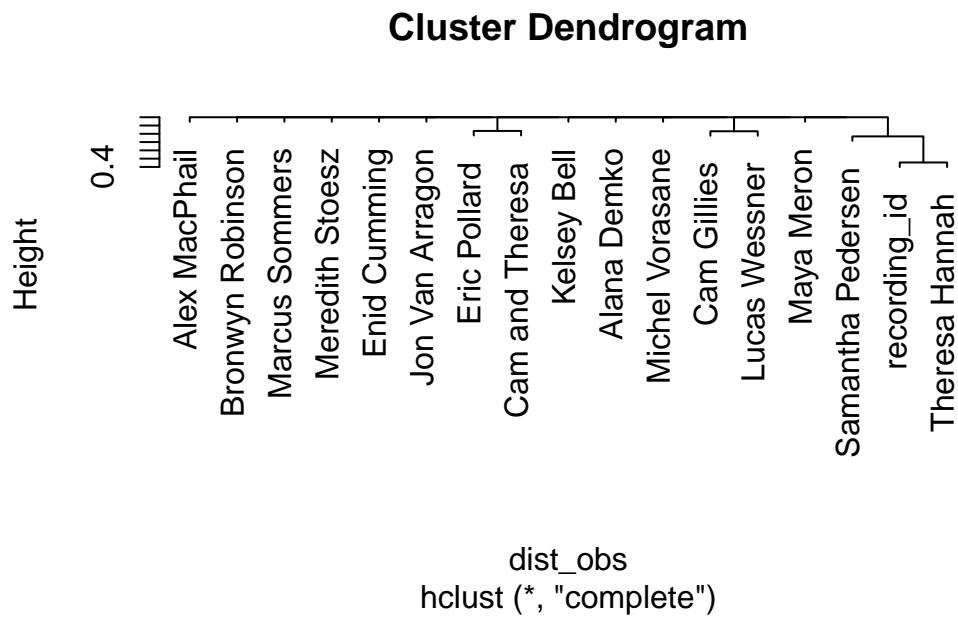
The 2024 Jasper Fire destroyed two established acoustic transects (VALLEY5 and TEKKARA). These transects were replaced in 2025 with two new montane transects (COTTONWOOD and MUSHROOM). To assess whether the replacement transects were appropriate proxies for the original sites, we evaluated how similar their species assemblages were to those observed at other existing montane transects.

Specifically, we compared species detections from COTTONWOOD and MUSHROOM to the distribution of detections across all other montane transects to quantify their compositional similarity and degree of departure from the montane baseline. We assessed whether replacement transects were representative of montane communities using a multivariate dispersion analysis (PERMDISP) based on Bray–Curtis dissimilarity. Distances of replacement transects to the montane centroid were compared against the distribution of distances observed among existing montane transects.

### 4.3.3 Observer and methodological comparisons

To compare species observations between the legacy dataset and those recorded in WildTrax, we first filtered the dataset to include only recordings processed twice. For each recording and species, we summarized the maximum count of individuals recorded by each observer. We then computed pairwise Pearson correlations between all observers to quantify agreement in species detection and abundance. The resulting correlations were visualized as a heatmap to provide an overview of inter-observer consistency. Additionally, the observer-by-species matrix was binarized (presence/absence) and used to compute Bray–Curtis dissimilarities between observers. Hierarchical clustering of these dissimilarities provided an alternative visualization of observer similarity based on species composition.





#### 4.3.4 Community analysis

A redundancy analysis (RDA) was conducted using the `vegan` package (Oksanen et al. (2025)) to quantify the variation in community composition explained by ecoregions and to visualize species–ecoregion relationships with ordination plots (C. Radhakrishna Rao (1964)). Species-level observations were aggregated into a species-by-location matrix, with abundances recorded as the maximum count of each species at each location. Ecoregions were categorized into Alpine and Montane with the Montaine ecoregions that can be further sub-divided into Upper Subalpine, Lower Subalpine, and Montane proper ecozones for all subsequent analyses. Differences in composition between Alpine and Montane groups were tested using permutational multivariate analysis of variance (PERMANOVA; Anderson (2001)) on Bray–Curtis dissimilarities with 999 permutations under a reduced model.

#### 4.3.5 Functional and community-level diversity

To evaluate community-level ecological responses, we examined temporal changes in functional diversity, species richness, and community evenness. Functional diversity was quantified using Rao's Q (C. R. Rao (1982); Laliberté and Legendre (2010)) via the `dbFD()` function in the `FD` package (Laliberté, Legendre, and Shipley (2014)). We also calculated species richness (number of unique species per location per year) and Shannon's diversity index, which integrates richness and evenness to describe community structure. These metrics were modeled through time using linear, mixed-effects, and segmented regression models to detect both gradual and threshold-type changes. Results were summarized graphically by ecoregion and functional guild to highlight spatial variation in diversity trajectories.

```

guilds <- read_csv("./assets/jasper_guilds.csv")

guild_activity <- janp_main |>
  filter(!grepl('COTTONWOOD|MUSHROOM', location)) |>
  filter(data_type %in% c("legacy", "single_visit_3_max", "single_visit_0_max")) |>
  filter(!(data_type == "single_visit_0_max" & year < 2023)) |>
  wt_tidy_species(remove = c("mammal", "amphibian", "abiotic", "insect", "unknown"), zerofill = F) |>
  dplyr::select(location, recording_date_time, species_common_name, species_code, abundance) |>
  mutate(julian = lubridate::yday(recording_date_time),
        month = month(recording_date_time),
        year = factor(year(recording_date_time))) |>
  inner_join(guilds, by = "species_code") |>
  group_by(species_code) |>
  add_tally() |>
  ungroup() |>
  group_by(julian, species_code) |>
  add_tally() |>
  ungroup() |>
  arrange(species_code) |>
  mutate(recording_date_time = as.POSIXct(recording_date_time)) |>
  mutate(species_code = factor(species_code, levels = sort(unique(species_code)))) |>
  inner_join(locs_summary, by = c("location" = "Location")) |>
  mutate(ecoregion = case_when(ecoregion %in% c("Alpine") ~ "Alpine",
                               ecoregion %in% c("Upper Subalpine", "Lower Subalpine", "Montane") ~ "Montane"))

datatable(guilds,
         options = list(
           searching = TRUE,
           paging = TRUE,
           pageLength = 10
         ))

```

```

shannon_d <- janp_main |>
  filter(!grepl('COTTONWOOD|MUSHROOM', location)) |>
  mutate(ecoregion = case_when(ecoregion %in% c("Alpine") ~ "Alpine",
                               ecoregion %in% c("Upper Subalpine", "Lower Subalpine", "Montane") ~ "Montane"))

wt_tidy_species(remove = c("mammal", "amphibian", "abiotic", "insect", "unknown"), zerofill = F) |>
  inner_join(wt_get_species() |> dplyr::select(species_code, species_class, species_order), by = "species_code") |>
  dplyr::select(location, ecoregion, recording_date_time, species_code, species_common_name, individual_order) |>
  distinct() |>
  group_by(location, ecoregion, recording_date_time, species_code, species_common_name) |>
  summarise(count = max(individual_order)) |>
  ungroup() |>
  pivot_wider(names_from = species_code, values_from = count, values_fill = 0) |>
  pivot_longer(cols = -(location:species_common_name), names_to = "species", values_to = "count") |>
  group_by(location, ecoregion, year = year(recording_date_time), species) |>
  summarise(total_count = sum(count)) |>

```

Table 3: Guilds

Species Guilds							
	species_code	species_common_name	trait	dietary_guild	habitat_guild	migratory_guild	continental_importance
1	AGOL	American Goldfinch	PlantSeed	Granivore-insectivore	Forest Generalist	Short-distance migrants	
2	AGOS	American Goshawk	VertFishScav	Carnivore	Forest Generalist	Winter residents	
3	ALFL	Alder Flycatcher	Invertebrate	Aerial insectivore	Forest Generalist	Long-distance migrants	
4	AMBI	American Bittern	VertFishScav	Aquatic	Wetland	Short-distance migrant	
5	AMCO	American Coot	PlantSeed	Aquatic	Wetland	Short-distance migrants	
6	AMCR	American Crow	Omnivore	Omnivore	Habitat Generalist	Short-distance migrants	
7	AMKE	American Kestrel	Invertebrate	Insect gleaner	Forest Generalist	Long-distance migrants	
8	AMPI	American Pipit	Invertebrate	Insect gleaner	Grassland-shrubland-alpine	Short-distance migrants	Common Bird in Steep Decline
9	AMRE	American Redstart	Invertebrate	Insect gleaner	Forest Generalist	Long-distance migrants	
10	AMRO	American Robin	Omnivore	Omnivore	Habitat Generalist	Short-distance migrants	

Show  entries Search:

Showing 1 to 10 of 158 entries

Previous 1 2 3 4 5 ... 16 Next

```

ungroup() |>
group_by(location, ecoregion, year) |>
summarise(shannon_index = diversity(total_count, index = "shannon")) |>
ungroup() |>
filter(!(year == 2012 & ecoregion == "Montane")) |>
ggplot(aes(x = factor(year), y = shannon_index, fill = factor(year))) +
geom_boxplot() +
geom_point(alpha = 0.6, colour = "grey") +
labs(x = "Year",
y = "Shannon diversity index per location") +
theme_bw() +
guides(fill = guide_legend(title = "Year")) +
scale_fill_viridis_d(alpha = 0.8, option = "cividis") +
facet_wrap(~ecoregion, ncol = 1)

```

## 4.3.6 Trend analysis

To quantify temporal changes in bird populations and community composition from 2007 to 2025, we analyzed trends in species-specific abundance, forest and alpine assemblages, and functional guilds. Analyses were designed to separate biological change from potential sampling and methodological effects, ensuring that observed patterns represented genuine ecological responses. This was achieved through a multi-step framework that (1) modeled detection probability and methodological variability, (2) estimated detection-corrected abundance, and (3) evaluated long-term directional trends and associated shifts in functional and community-level diversity.

### 4.3.6.1 Detection-corrected abundance estimation

Temporal trends in abundance were estimated using single-visit abundance models implemented in the `detect::svabu()` function (Sólymos, Lele, and Bayne (2012)). This framework jointly models site-level abundance and detection probability from single-visit counts, providing unbiased estimates without requiring repeated surveys. In the models, year, ecoregion and landcover type and proportion at a 150 meter buffer were included as observation covariates with julian date, hour of day and observer included in the detection covariates to account for within-season and diurnal variation in detectability. The resulting detection-corrected expected abundance per site-visit () was then aggregated by year to produce mean annual abundance indices. These indices were subsequently used to evaluate temporal trends in species abundance.

### 4.3.6.2 Trend estimation

Temporal trends were quantified using the Mann–Kendall test (Mann (1945a); Hamed (2009)), which detects monotonic directional change, and Sen’s Slope (Pranab Kumar Sen (1968)) to estimate the magnitude of those trends. Both tests were implemented via the `modifiedmk` package (Hamed and Rao (1998)) and applied to the detection-corrected abundance estimates (). Sen’s slope provides an estimate of the median annual rate of change in the abundance index over the time series. To express this rate in a standardized and interpretable way, we converted Sen’s slope to a percent change per year by dividing the estimated slope by the mean annual abundance index across the

full time series and multiplying by 100. This metric represents the average proportional change in abundance per year, relative to the long-term mean abundance of the species in that ecoregion. Positive values indicate increasing abundance, while negative values indicate declining abundance.

## 5 Results

### i Note

Some of these analyses are still a work-in-progress. Check back soon for updates and additional details.

### 5.1 Ecoregions

Figure 4 shows the relationship between species and ecoregion. The PERMANOVA test was performed using Bray-Curtis dissimilarity to assess whether community composition significantly differed between ecoregion groups. The analysis revealed a significant difference in community composition between alpine and montane groups. The ecoregion grouping explained approximately 27.85% of the variation in community composition, while residual variation accounted for 72.15%. These findings indicate a substantial divergence in species composition between ecoregion groups and helps to justify subsequent analyses looking at trend differences between these areas.

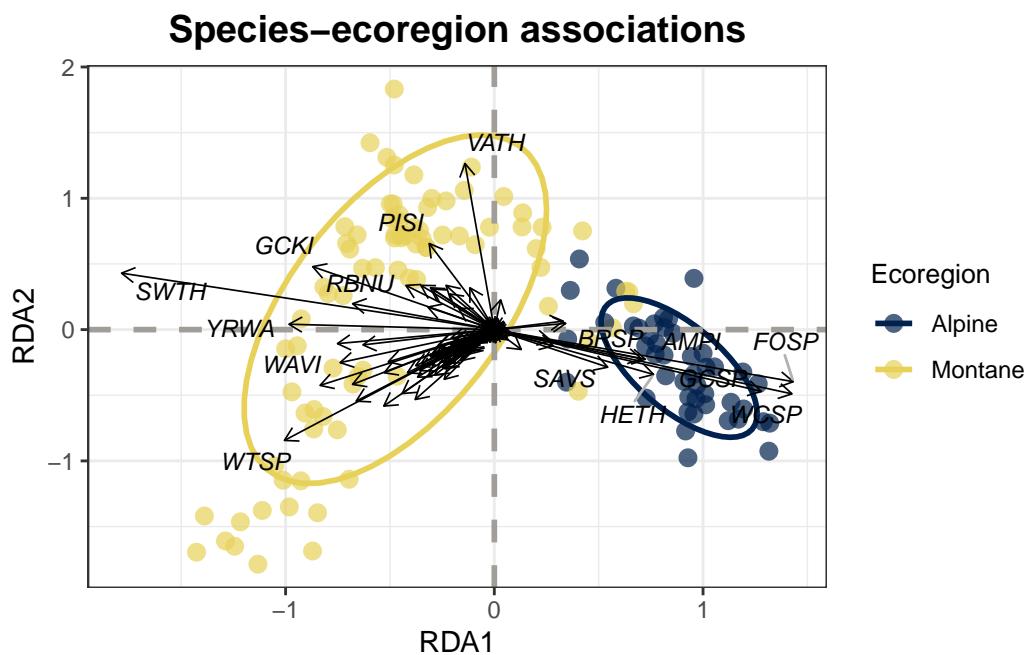


Figure 4

## 5.2 Species richness and functional diversity

Activity patterns across nesting, dietary and migratory guilds are illustrated in Figure 5 onwards. A notable pattern emerges across all four guilds of the proportion of tags detected being detected later in the alpine ecoregion compared to the montane ecoregion. Species richness per location is at Figure 10 and Shannon's diversity index over years at Figure 11. Overall, both richness and diversity were stable across years. Rao's Q averaged between about 8.2 and 10.5 across survey locations, with a clear upward tendency over time (Figure 9). The non-parametric Mann–Kendall test gave a Kendall's  $\tau$  of 0.32 ( $p = 0.07$ ), indicating a positive but marginally non-significant monotonic increase in functional diversity. A simple linear regression of mean Rao's Q against year yielded a slope of 0.051 units per year ( $p = 0.06$ ), again suggesting an upward trend that narrowly misses the conventional 0.05 significance threshold. When we account for repeated measures at each location via a mixed-effects model (random intercepts by location), the year effect becomes highly significant (slope = 0.058 Rao's Q units per year;  $t = 4.3$ ), demonstrating that functional diversity has increases when location-level variation is considered. Finally, breakpoint analysis identifies a shift around 2009, suggesting that functional diversity was relatively low and stable from 2007–2009, then rose to more variable but generally higher values from 2010 onward.

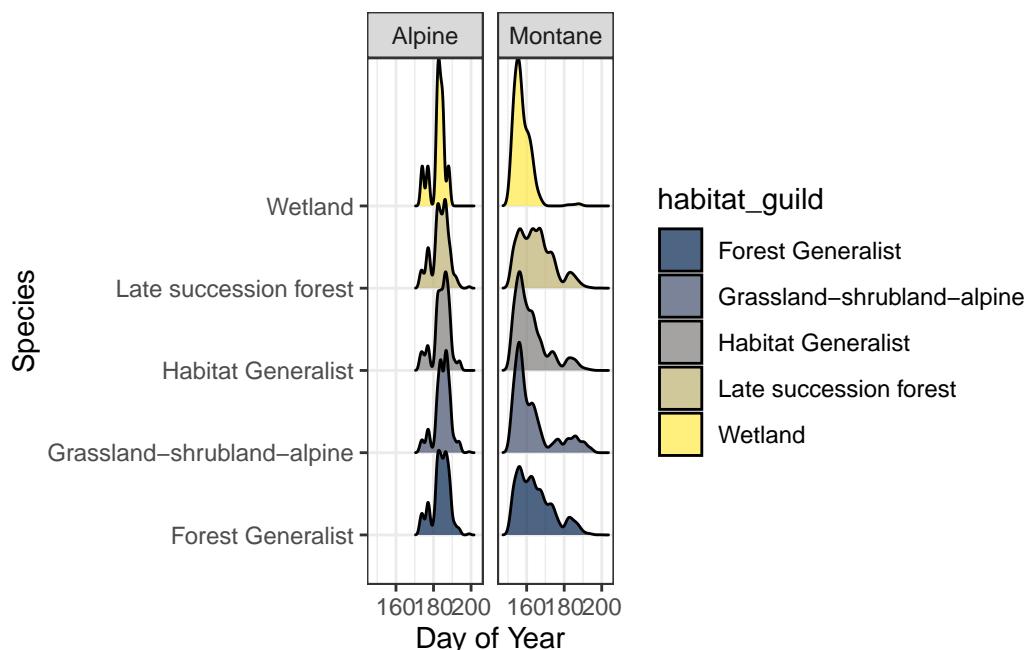


Figure 5:  
Seasonal  
detection  
activity of by  
nesting guild  
and ecoregion

```
spp_rich_location <- janp_main |>
  filter(!grepl('COTTONWOOD|MUSHROOM', location)) |>
  filter(data_type %in% c("legacy", "single_visit_3_max", "single_visit_0_max")) |>
  filter(!(data_type == "single_visit_0_max" & year < 2023)) |>
  wt_tidy_species(remove = c("mammal", "amphibian", "abiotic", "insect", "unknown"), zerofill = F)
  dplyr::select(location, year, species_code) |>
  distinct() |>
  group_by(location, year) |>
  summarise(species_count = n_distinct(species_code)) |>
  ungroup() |>
```

Figure 6:  
Seasonal detection activity of by migratory guild and ecoregion

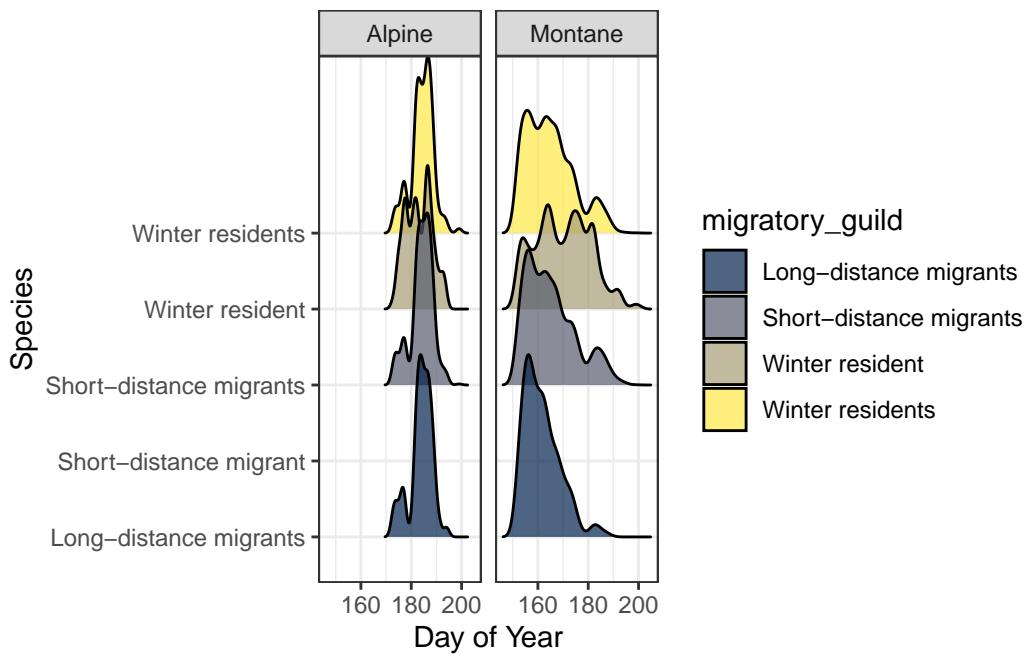


Figure 7:  
Seasonal detection activity of by trait and ecoregion

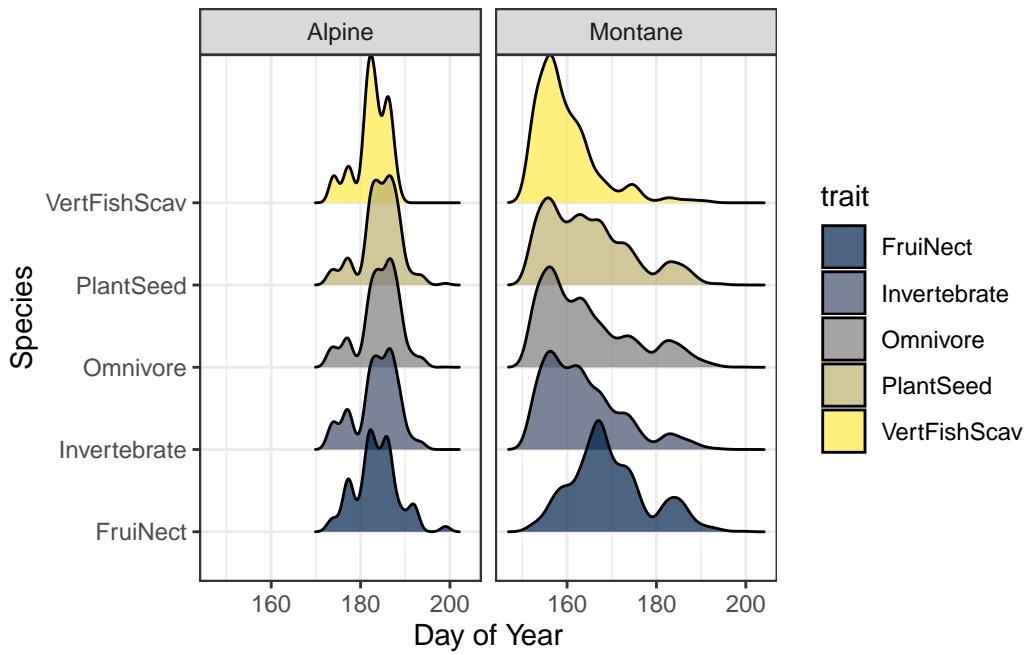


Figure 8:  
Seasonal detection activity of by dietary guild and ecoregion

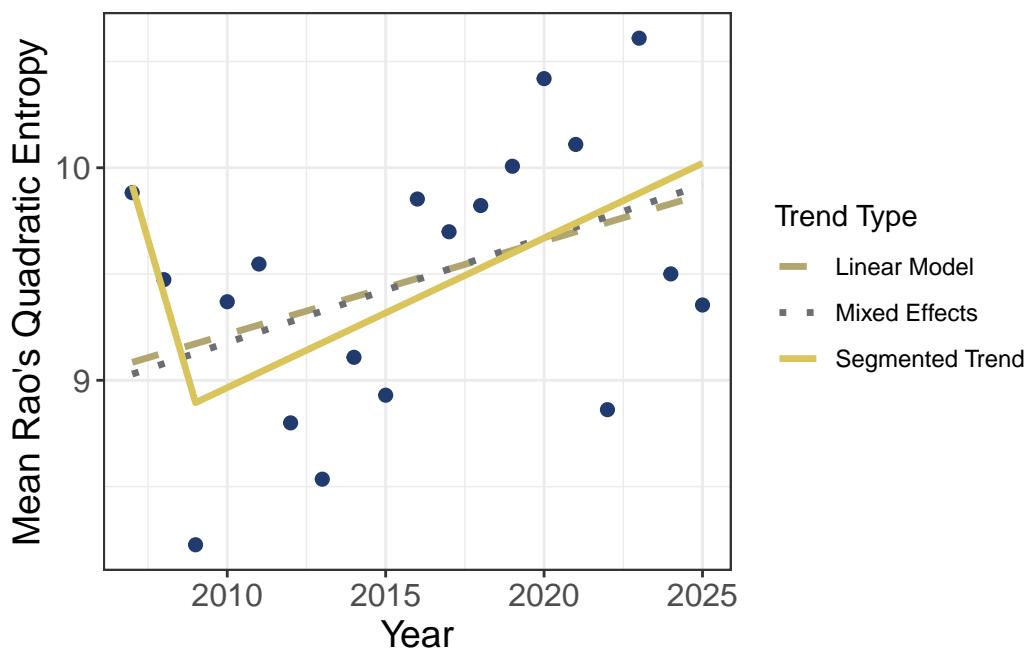
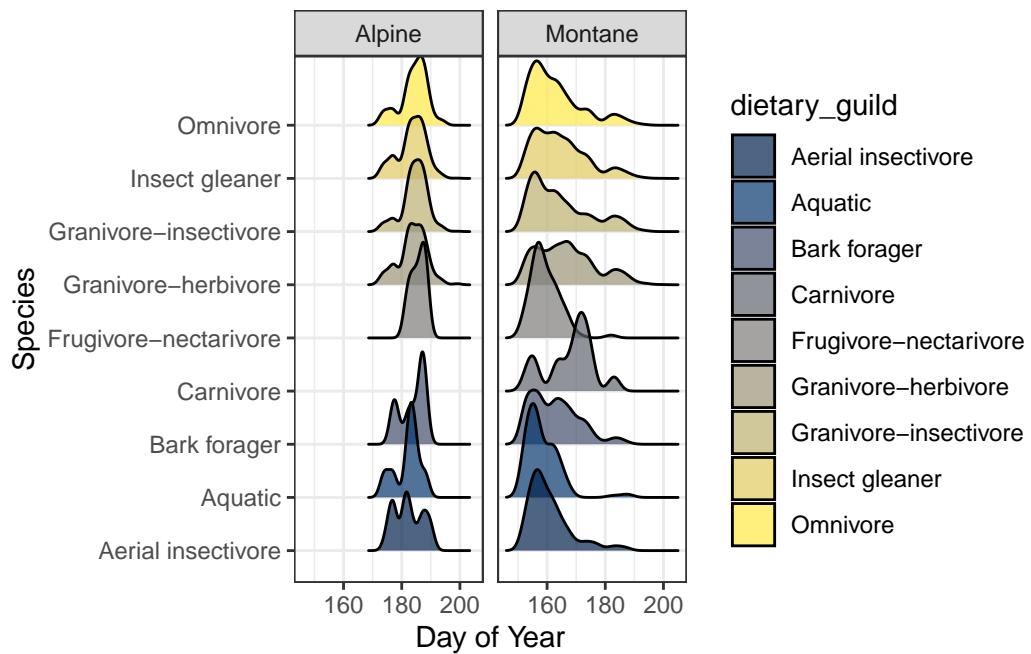


Figure 9:  
Mean functional diversity (Rao's Q) over time

```

inner_join(locs_summary, by = c("location" = "Location")) |>
  mutate(ecoregion = case_when(ecoregion %in% c("Alpine") ~ "Alpine",
                               ecoregion %in% c("Upper Subalpine", "Lower Subalpine", "Montane"))
        filter(!(year == 2012 & ecoregion == "Montane"))

spp_rich_location |>
  ggplot(aes(x=as.factor(year), y=species_count, fill=year)) +
  geom_boxplot() +
  geom_point(alpha = 0.7, colour = "grey") +
  geom_smooth(method = "lm") +
  theme_bw() +
  facet_wrap(~ecoregion, ncol = 1) +
  scale_fill_viridis_c(option = "cividis") +
  xlab('Year') + ylab('Species richness per location') +
  guides(fill = guide_legend(title = "Year"))

```

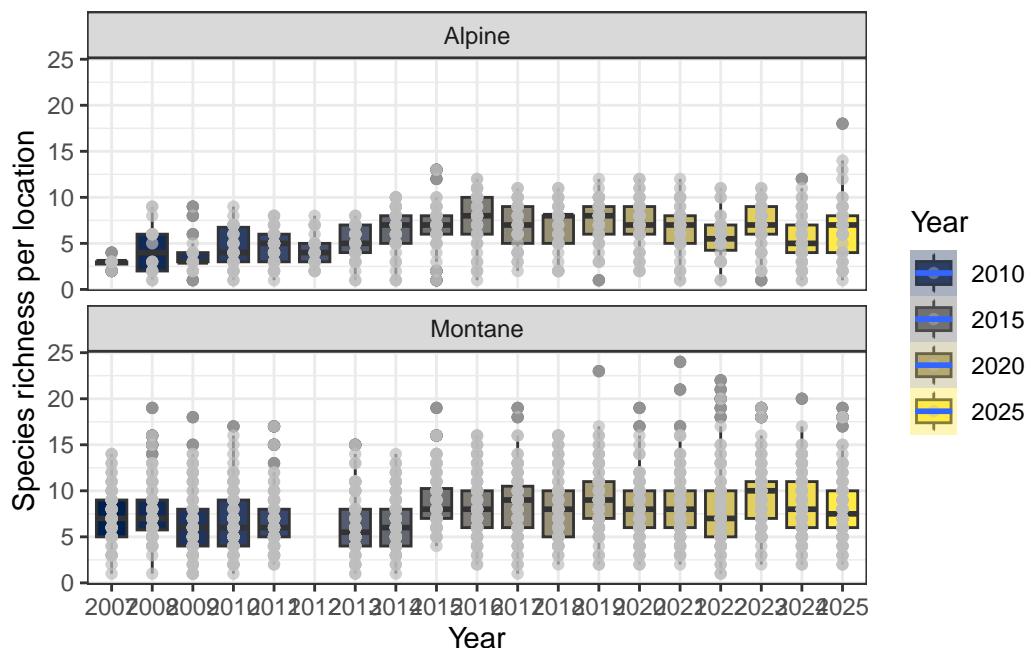


Figure 10: Species richness by year

```
shannon_d
```

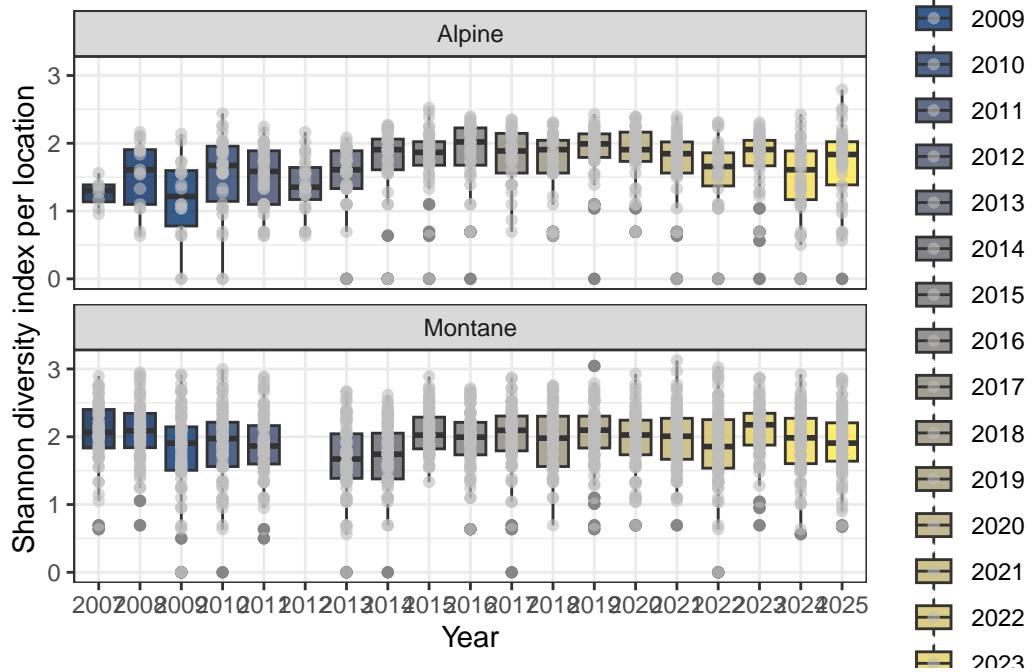


Figure 11: Shannon diversity index over years

### 5.3 Trends

```

janp_ready_trend <- janp_main |>
  inner_join(lc_150m, by = c("location" = "Point_ID")) |>
  mutate(landcover = case_when(grepl('TEKARRA|VALLEY5', location) & year > 2024 ~ "Burned", TRU
  distinct()

# Trend
run_trend <- function(spp) {

  # 1. Summarize per site-visit using max()
  janp_trend <- janp_ready_trend |>
    filter(!(data_type == "single_visit_0_max" & year < 2021)) |>
    filter(ecoregion %in% c("Alpine")) |>
    mutate(year = year(recording_date_time),
           hour = hour(recording_date_time),
           julian = yday(recording_date_time)) |>
    dplyr::select(organization, project_id, longitude, latitude, location,
                  location_id, task_id, ecoregion, landcover, prop_cover,
                  VEGETATION_DENSITY, recording_date_time, observer, species_code,
                  individual_order, abundance, detection_time) |>
    distinct() |>
    wt_tidy_species(remove = c("mammal", "amphibian", "abiotic", "insect", "human", "unknown"), z
  
```

```

# 2. Combine with zero sites
base_zero <- janp_trend |>
  dplyr::select(location, ecoregion, landcover, prop_cover, VEGETATION_DENSITY, recording_date_time)
  distinct()

spp_max <- janp_trend |>
  filter(species_code == spp) |>
  group_by(location, ecoregion, landcover, prop_cover, VEGETATION_DENSITY, recording_date_time)
  summarise(individual_order = max(individual_order, na.rm = TRUE)) |>
  ungroup()

if (nrow(spp_max) < 20) {
  message(paste0("Probably an error in Alpine with ", spp))
}

jpt <- base_zero |>
  left_join(spp_max, by = c("location", "ecoregion", "landcover", "prop_cover", "VEGETATION_DENSITY"))
  mutate(individual_order = tidyr::replace_na(individual_order, 0)) |>
  mutate(year = year(recording_date_time),
         hour = hour(recording_date_time),
         julian = yday(recording_date_time)) |>
  filter(!is.infinite(individual_order)) |>
  mutate(lc_group = case_when(landcover %in% c("Tree Coniferous", "Shrub Low", "Herbaceous Mixed") ~ "Coniferous",
                             landcover %in% c("Shrub Low", "Herbaceous Mixed") ~ "Shrub Low",
                             landcover %in% c("Herbaceous Mixed", "Other") ~ "Herbaceous Mixed",
                             landcover == "Other" ~ "Other"))
  dplyr::select(-c(landcover, VEGETATION_DENSITY)) |>
  group_by(location, ecoregion, recording_date_time, observer, individual_order, year, hour)
  pivot_wider(names_from = lc_group, values_from = prop_cover, values_fill = 0, values_fn = sum) |>
  ungroup() |>
  rename(shrub = `Shrub Low`) |>
  rename(conf = `Tree Coniferous`) |>
  rename(herb = `Herbaceous Mixed`) |>
  rename(other = Other) |>
  mutate(across(c(shrub, conf, herb, other, julian, hour), scale))

fit <- svabu(individual_order ~ year + shrub + herb + conf + julian + hour + observer, data = jpt)

ref_vals <- jpt |>
  summarise(observer = first(observer),
            julian = mean(julian, na.rm = TRUE),
            hour = mean(hour, na.rm = TRUE))

jpt$lambda_hat <- predict(fit, newdata = jpt |>
  mutate(julian = ref_vals$julian,
        hour = ref_vals$hour,
        observer = ref_vals$observer),
  type = "response")

lambda_year <- jpt |>

```

```

group_by(year) |>
  summarise(lambda_hat = mean(lambda_hat, na.rm = TRUE)) |>
  ungroup() |>
  arrange(year)

# 6. Run Mann-Kendall + Sen's slope
x <- lambda_year$lambda_hat
mk <- mmkh(x)
tau       <- mk[6]
sen_slope <- mk[7]
p_value   <- mk[2]
pct_change <- mk[["Sen's slope"]] / mean(x) * 100
trend_class <- dplyr::case_when(pct_change > 2.5 ~ "Increasing",
                                 pct_change < -2.5 ~ "Decreasing",
                                 TRUE                ~ "Stable")

trend_result_alpine <- tibble(
  ecoregion = "Alpine",
  tau        = tau,
  p_value    = p_value,
  sen_slope  = sen_slope,
  pct_change = pct_change,
  trend      = trend_class
)

janp_trend <- janp_ready_trend |>
  filter(!(data_type == "single_visit_0_max" & year < 2021)) |>
  filter(ecoregion %in% c("Montane", "Upper Subalpine", "Lower Subalpine"), !grepl('COTTON', species_code)) |>
  mutate(year = year(recording_date_time),
         hour = hour(recording_date_time),
         julian = yday(recording_date_time)) |>
  dplyr::select(organization, project_id, longitude, latitude, location, location_id, task,
                recording_date_time, observer, species_code, individual_order, abundance, abundance_zeta) |>
  distinct() |>
  wt_tidy_species(remove = c("mammal", "amphibian", "abiotic", "insect", "human", "unknown"), zero_weight = TRUE)

base_zero <- janp_trend |>
  dplyr::select(location, ecoregion, landcover, prop_cover, VEGETATION_DENSITY, recording_date_time) |>
  distinct()

spp_max <- janp_trend |>
  filter(species_code == spp) |>
  group_by(location, ecoregion, landcover, prop_cover, VEGETATION_DENSITY, recording_date_time) |>
  summarise(individual_order = max(individual_order, na.rm = TRUE)) |>
  ungroup()

if (nrow(spp_max) < 20) {message(paste0("Probably an error in Forested with ", spp))}
```

```

jpt <- base_zero |>
  left_join(spp_max, by = c("location", "ecoregion", "landcover", "prop_cover", "VEGETATION_DENSITY")) |>
  mutate(individual_order = tidyr::replace_na(individual_order, 0)) |>
  mutate(year = year(recording_date_time),
         hour = hour(recording_date_time),
         julian = yday(recording_date_time)) |>
  filter(!is.infinite(individual_order)) |>
  mutate(lc_group = case_when(landcover %in% c("Tree Coniferous", "Shrub Low", "Herbaceous Mixed") ~ "Coniferous", TRUE ~ "Other")) |>
  dplyr::select(-c(landcover, VEGETATION_DENSITY)) |>
  group_by(location, ecoregion, recording_date_time, observer, individual_order, year, hour) |>
  pivot_wider(names_from = lc_group, values_from = prop_cover, values_fill = 0, values_fn = sum) |>
  ungroup() |>
  rename(shrub = `Shrub Low`) |>
  rename(conf = `Tree Coniferous`) |>
  rename(herb = `Herbaceous Mixed`) |>
  rename(other = Other) |>
  mutate(across(c(shrub, conf, herb, other, julian, hour), scale))

fit <- svabu(individual_order ~ year + shrub + conf + herb + other | julian + hour + observer)

ref_vals <- jpt |>
  summarise(observer = first(observer),
            julian = mean(julian, na.rm = TRUE),
            hour = mean(hour, na.rm = TRUE))

jpt$lambda_hat <- predict(fit, newdata = jpt |> mutate(julian = ref_vals$julian, hour = ref_vals$hour))

lambda_year <- jpt |>
  group_by(year) |>
  summarise(lambda_hat = mean(lambda_hat, na.rm = TRUE),
            .groups = "drop") |>
  arrange(year)

x <- lambda_year$lambda_hat
mk <- mmkh(x)
tau      <- mk[6]
sen_slope <- mk[7]
p_value   <- mk[2]
pct_change <- mk[["Sen's slope"]] / mean(x) * 100
trend_class <- dplyr::case_when(pct_change > 2.5 ~ "Increasing",
                                 pct_change < -2.5 ~ "Decreasing",
                                 TRUE ~ "Stable")

trend_result_forested <- tibble(
  ecoregion = "Forested",
  tau        = tau,
  p_value    = p_value,

```

```

        sen_slope    = sen_slope,
        pct_change   = pct_change,
        trend        = trend_class
    )

    return(bind_rows(trend_result_alpine, trend_result_forested))
}

```

```

trendz <- janp_main |>
  group_by(species_code) |>
  tally() |>
  arrange(-n) |>
  filter(!species_code == "NONE") |>
  slice(1:10) |>
  mutate(trend = map(.x = species_code, .f = ~run_trend(.x))) |>
  unnest_wider(trend) |>
  unnest()

```

```
kable(trendz)
```

species_code	n	ecoregion	tau	p_value	sen_slope	pct_change	trend
YRWA	2012	Alpine	0.9766082	0.0000126	0.0318282	7.0116287	Increasing
YRWA	2012	Forested	1.0000000	0.0000000	0.0141453	1.5555426	Stable
CHSP	1801	Alpine	0.9883041	0.0000000	0.0463486	7.0403381	Increasing
CHSP	1801	Forested	1.0000000	0.0000000	0.0181844	2.4521958	Stable
PISI	1696	Alpine	0.7777778	0.0000039	0.0375699	1.2499726	Stable
PISI	1696	Forested	1.0000000	0.0002347	0.0608479	10.5744214	Increasing
SWTH	1558	Alpine	0.9766082	0.0002905	0.0000000	13.3633393	Increasing
SWTH	1558	Forested	0.9869281	0.0000000	0.0321601	3.1727561	Increasing
AMRO	1474	Alpine	1.0000000	0.0000318	0.0286273	4.2136212	Increasing
AMRO	1474	Forested	1.0000000	0.0000000	0.0151263	3.4488914	Increasing
DEJU	1119	Alpine	0.9883041	0.0002862	0.0316479	8.2327021	Increasing
DEJU	1119	Forested	1.0000000	0.0000537	0.0239635	5.9547718	Increasing
VATH	1111	Alpine	1.0000000	0.0002605	0.0453672	9.2984333	Increasing
VATH	1111	Forested	0.9738562	0.0000000	0.0446191	5.4265248	Increasing
HETH	935	Alpine	1.0000000	0.0000000	0.0533295	5.0483559	Increasing
HETH	935	Forested	0.8692810	0.0000000	0.0087057	1.4106653	Stable
FOSP	879	Alpine	1.0000000	0.0001074	0.0574620	5.9240858	Increasing
FOSP	879	Forested	1.0000000	0.0003212	0.0226203	7.8894049	Increasing
RCKI	770	Alpine	0.8713450	0.0000002	0.1263787	5.5749058	Increasing
RCKI	770	Forested	0.9738562	0.0000000	0.0025375	0.9767556	Stable

```

trend_guild <- trendz |>
  inner_join(guilds, by = "species_code")

```

```

kable(trend_guild |>
  group_by(ecoregion) |>
  summarise(
    total_species = n_distinct(species_code),
    declining_species = n_distinct(species_code[pct_change <= -2.5]),
    percent_declining = declining_species / total_species * 100
  ))

```

ecoregion	total_species	declining_species	percent_declining
Alpine	10	0	0
Forested	10	0	0

```

kable(trend_guild |>
  group_by(ecoregion, habitat_guild) |>  # or another guild column if desired
  summarise(
    total_guild_species = n_distinct(species_code),
    declining_guild_species = n_distinct(species_code[pct_change <= -2.5]),
    percent_declining = declining_guild_species / total_guild_species * 100
  ) |>
  ungroup() |>
  group_by(ecoregion) |>
  summarise(
    total_guilds = n_distinct(habitat_guild),
    guilds_with_decline = sum(percent_declining > 0),
    percent_guilds_declining = guilds_with_decline / total_guilds * 100
  ))

```

ecoregion	total_guilds	guilds_with_decline	percent_guilds_declining
Alpine	3	0	0
Forested	3	0	0

## 5.4 Discussion and recommendations

The Discussion and Recommendations.

- Abrahms, Briana, Neil H Carter, TJ Clark-Wolf, Kaitlyn M Gaynor, Erik Johansson, Alex McInturff, Anna C Nisi, Kasim Rafiq, and Leigh West. 2023. “Climate Change as a Global Amplifier of Human–Wildlife Conflict.” *Nature Climate Change* 13 (3): 224–34.
- Ackleh, Azmy S, Jacoby Carter, Lauren Cole, Tom Nguyen, Jay Monte, and Claire Pettit. 2010. “Measuring and Modeling the Seasonal Changes of an Urban Green Treefrog (*Hyla Cinerea*) Population.” *Ecological Modelling* 221 (2): 281–89.
- Akaike, Hirotugu. 1974. “A New Look at the Statistical Model Identification.” *IEEE Transactions on Automatic Control* 19 (6): 716–23. <https://doi.org/10.1109/TAC.1974.1100705>.

- Allan, James R, Oscar Venter, Sean Maxwell, Bastian Bertzky, Kendall Jones, Yichuan Shi, and James EM Watson. 2017. "Recent Increases in Human Pressure and Forest Loss Threaten Many Natural World Heritage Sites." *Biological Conservation* 206: 47–55.
- Anderson, Marti J. 2001. "A New Method for Non-Parametric Multivariate Analysis of Variance." *Austral Ecology* 26 (1): 32–46. <https://doi.org/10.1111/j.1442-9993.2001.01070.pp.x>.
- Bates, Douglas, Reinhold Kliegl, Shravan Vasishth, and Harald Baayen. 2015. "Parsimonious Mixed Models." *arXiv Preprint arXiv:1506.04967*.
- Bates, Douglas, Martin Mächler, Ben Bolker, and Steve Walker. 2015. "Fitting Linear Mixed-Effects Models Using lme4." *Journal of Statistical Software* 67 (1): 1–48. <https://doi.org/10.18637/jss.v067.i01>.
- Cameron, J., A. Crosby, C. Paszkowski, and E. Bayne. 2020. "Visual Spectrogram Scanning Paired with an Observation–Confirmation Occupancy Model Improves the Efficiency and Accuracy of Bioacoustic Anuran Data." *Canadian Journal of Zoology* 98 (11): 733–42. <https://doi.org/10.1139/cjz-2020-0103>.
- Dawood, Muhammad. 2017. "Spatio-Statistical Analysis of Temperature Fluctuation Using Mann–Kendall and Sen's Slope Approach." *Climate Dynamics* 48 (3): 783–97.
- Devarajan, Kadambari, Toni Lyn Morelli, and Simone Tenan. 2020. "Multi-Species Occupancy Models: Review, Roadmap, and Recommendations." *Ecography* 43 (11): 1612–24.
- Fahrig, Lenore. 2003. "Effects of Habitat Fragmentation on Biodiversity." *Annual Review of Ecology, Evolution, and Systematics* 34 (1): 487–515.
- Farnsworth, George L, Kenneth H Pollock, James D Nichols, Theodore R Simons, James E Hines, and John R Sauer. 2002. "A Removal Model for Estimating Detection Probabilities from Point-Count Surveys." *The Auk* 119 (2): 414–25.
- Gahbauer, Marcel A, Scott R Parker, Joanna X Wu, Cavan Harpur, Brooke L Bateman, Darroch M Whitaker, Douglas P Tate, Lotem Taylor, and Denis Lepage. 2022. "Projected Changes in Bird Assemblages Due to Climate Change in a Canadian System of Protected Areas." *Plos One* 17 (1): e0262116.
- Garland, Laura, Andrew Crosby, Richard Hedley, Stan Boutin, and Erin Bayne. 2020. "Acoustic Vs. Photographic Monitoring of Gray Wolves (*Canis lupus*): A Methodological Comparison of Two Passive Monitoring Techniques." *Canadian Journal of Zoology* 98 (3): 219–28. <https://doi.org/10.1139/cjz-2019-0081>.
- Hamed, K. H. 2009. "Exact Distribution of the Mann-Kendall Trend Test Statistic for Persistent Data." *Journal of Hydrology* 365 (1): 86–94. <https://doi.org/10.1016/j.jhydrol.2009.01.040>.
- Hamed, K. H., and A. Ramachandra Rao. 1998. "A Modified Mann-Kendall Trend Test for Autocorrelated Data." *Journal of Hydrology* 204 (1): 182–96. [https://doi.org/10.1016/S0022-1694\(97\)00125-X](https://doi.org/10.1016/S0022-1694(97)00125-X).
- Handel, C. M., and M. N. Cady. 2004. "Alaska Landbird Monitoring Survey: Protocol for Setting up and Conducting Point Count Surveys." Technical Report 2004-3. Alaska Science Center: U.S. Geological Survey.
- Hanski, Ilkka. 2011. "Habitat Loss, the Dynamics of Biodiversity, and a Perspective on Conservation." *Ambio* 40 (3): 248–55.
- Kendall, Maurice G. 1975. *Multivariate Analysis*. Charles Griffin & Company Ltd.
- Knight, Elly C, and Erin M Bayne. 2019. "Classification Threshold and Training Data Affect the Quality and Utility of Focal Species Data Processed with Automated Audio-Recognition Software." *Bioacoustics* 28 (6): 539–54.
- Laliberté, Etienne, and Pierre Legendre. 2010. "A Distance-Based Framework for Measuring Functional Diversity from Multiple Traits." *Ecology* 91: 299–305.
- Laliberté, Etienne, Pierre Legendre, and Bill Shipley. 2014. *FD: Measuring Functional Diversity*

- from Multiple Traits, and Other Tools for Functional Ecology.*
- Lemieux, Christopher J., Thomas J Beechey, Daniel J Scott, and Paul A Gray. 2011. “The State of Climate Change Adaptation in Canada’s Protected Areas Sector.” *The Canadian Geographer/Le Géographe Canadien* 55 (3): 301–17.
- Loeb, Susan C., Thomas J. Rodhouse, Laura E. Ellison, Cori L. Lausen, Jonathan D. Reichard, Kathryn M. Irvine, Thomas E. Ingersoll, et al. 2015. *A Plan for the North American Bat Monitoring Program (NABat)*. U.S. Department of Agriculture, Forest Service, Southern Research Station. <https://doi.org/10.2737/srs-gtr-208>.
- Loeb, Susan C., Thomas J. Rodhouse, Lee E. Ellison, et al. 2015. *A Plan for the North American Bat Monitoring Program (NABat)*. Asheville, NC: U.S. Department of Agriculture, Forest Service, Southern Research Station. <https://doi.org/10.1898/NWN21-10>.
- Lovett, Gary M. 2013. “When Do Peepers Peep? Climate and the Date of First Calling in the Spring Peeper (*Pseudacris Crucifer*) in Southeastern New York State.” *Northeastern Naturalist* 20 (2): 333–40.
- MacKenzie, Darryl I., and Larissa L. Bailey. 2004. “Assessing the Fit of Site-Occupancy Models.” *Journal of Agricultural, Biological, and Environmental Statistics* 9 (3): 300–318. <http://www.jstor.org/stable/1400484>.
- MacKenzie, Darryl I., James D. Nichols, James E. Hines, Melinda G. Knutson, and Alan B. Franklin. 2003. “ESTIMATING SITE OCCUPANCY, COLONIZATION, AND LOCAL EXTINCTION WHEN a SPECIES IS DETECTED IMPERFECTLY.” *Ecology* 84 (8): 2200–2207. <https://doi.org/https://doi.org/10.1890/02-3090>.
- MacKenzie, Darryl I., James D Nichols, Gideon B Lachman, Sam Droege, J Andrew Royle, and Catherine A Langtimm. 2002. “Estimating Site Occupancy Rates When Detection Probabilities Are Less Than One.” *Ecology* 83 (8): 2248–55.
- MacKenzie, Darryl I., James D Nichols, Mark E Seamans, and RJ Gutiérrez. 2009. “Modeling Species Occurrence Dynamics with Multiple States and Imperfect Detection.” *Ecology* 90 (3): 823–35.
- Mann, H. B. 1945a. “Non-Parametric Tests Against Trend.” *Econometrica: Journal of the Econometric Society* 13 (3): 245–59.
- . 1945b. “Nonparametric Tests Against Trend.” *Econometrica* 13 (3): 245–59. <https://doi.org/10.1017/CBO9781107415324.004>.
- Mantyka-pringle, Chrystal S, Tara G Martin, and Jonathan R Rhodes. 2012. “Interactions Between Climate and Habitat Loss Effects on Biodiversity: A Systematic Review and Meta-Analysis.” *Global Change Biology* 18 (4): 1239–52.
- Muggeo, Vito M. R. 2008. “Segmented: An r Package to Fit Regression Models with Broken-Line Relationships.” *R News* 8 (1): 20–25. <https://cran.r-project.org/doc/Rnews/>.
- Oksanen, Jari, Frank G Blanchet, Roeland Kindt, Pierre Legendre, Peter R Minchin, Robert B O’Hara, Gavin L Simpson, et al. 2010. “Canonical Analysis of Principal Coordinates: A Useful Method of Constrained Ordination for Ecology.” *Ecology* 92 (3): 597–611. <https://doi.org/10.1890/10-0340.1>.
- Oksanen, Jari, Gavin L. Simpson, F. Guillaume Blanchet, Roeland Kindt, Pierre Legendre, Peter R. Minchin, R. B. O’Hara, et al. 2025. *Vegan: Community Ecology Package*. <https://vegandevs.github.io/vegan/>.
- Önöz, B., and M. Bayazit. 2012. “The Power of Statistical Tests for Trend Detection.” *Hydrological Processes* 26 (17): 2809–14. <https://doi.org/10.1002/hyp.8438>.
- Petrikeev, Michael. 2019. “Forest Breeding Bird Abundance and Composition, Kluane National Park Reserve.”
- Rao, C. R. 1982. “Diversity and Dissimilarity Coefficients: A Unified Approach.” *Theoretical*

- Population Biology* 21 (1): 24–43.
- Rao, C. Radhakrishna. 1964. “The Use and Interpretation of Principal Component Analysis in Applied Research.” *Sankhya: The Indian Journal of Statistics, Series A* 26 (4): 329–58.
- Reichert, B., C. Lausen, S. Loeb, et al. 2018. *A Guide to Processing Bat Acoustic Data for the North American Bat Monitoring Program (NABat)*. U.S. Geological Survey. <https://doi.org/10.1898/NWN21-10>.
- Reichert, Brian, Cori Lausen, Susan Loeb, Ted Weller, Ryan Allen, Eric Britzke, Tara Hohoff, et al. 2018. “A Guide to Processing Bat Acoustic Data for the North American Bat Monitoring Program (NABat).” US Geological Survey.
- Sattar, Q, ME Maqbool, R Ehsan, S Akhtar, Q Sattar, ME Maqbool, R Ehsan, and S Akhtar. 2021. “Review on Climate Change and Its Effect on Wildlife and Ecosystem.” *Open J Environ Biol* 6 (1): 008–14.
- Sen, P. K. 1968. “Estimates of the Regression Coefficient Based on Kendall’s Tau.” *Journal of the American Statistical Association* 63 (324): 1379–89. <https://doi.org/10.2307/2285891>.
- Sen, Pranab Kumar. 1968. “Estimates of the Regression Coefficient Based on Kendall’s Tau.” *Journal of the American Statistical Association* 63 (324): 1379–89. <https://doi.org/10.1080/01621459.1968.10480934>.
- Shannon, Claude Elwood. 1948. “A Mathematical Theory of Communication.” *The Bell System Technical Journal* 27 (3): 379–423.
- Shonfield, Julia, and Erin M Bayne. 2017. “Autonomous Recording Units in Avian Ecological Research: Current Use and Future Applications.” *Avian Conservation & Ecology* 12 (1).
- Shonfield, Julia, Sarah Heemskerk, and Erin M Bayne. 2018. “Utility of Automated Species Recognition for Acoustic Monitoring of Owls.” *Journal of Raptor Research* 52 (1): 42–55.
- Slough, B., C. Lausen, B. Paterson, et al. 2022. “New Records about the Diversity, Distribution, and Seasonal Activity Patterns by Bats in Yukon and Northwestern British Columbia.” *Northwest Naturalist* 103: 162–82. <https://doi.org/10.1898/NWN21-10>.
- Slough, Brian G, Donald G Reid, Dafna S Schultz, and Maria C-Y Leung. 2023. “Little Brown Bat Activity Patterns and Conservation Implications in Agricultural Landscapes in Boreal Yukon, Canada.” *Ecosphere* 14 (3): e4446.
- Smith, Adam C, Marie-Anne R Hudson, Constance M Downes, and Charles M Francis. 2015. “Change Points in the Population Trends of Aerial-Insectivorous Birds in North America: Synchronized in Time Across Species and Regions.” *PloS One* 10 (7): e0130768.
- Solick, Daniel I. 2022. “Bat Acoustic Species-Pair Matrix for Western u.s./Canada.” Colorado: Vesper Bat Detection Services.
- Solick, Donald I, and Robert MR Barclay. 2022. “Coat Color of Western Long-Eared Bats (*Myotis Evotis*) Living in Different Environments: A Test of Gloger’s Rule.” *Northwestern Naturalist* 103 (2): 183–89.
- Sólymos, Péter, Subhash Lele, and Erin Bayne. 2012. “Conditional Likelihood Approach for Analyzing Single Visit Abundance Survey Data in the Presence of Zero Inflation and Detection Error.” *Environmetrics* 23 (2): 197–205. <https://doi.org/https://doi.org/10.1002/env.1149>.
- Sólymos, Péter, Steven M Matsuoka, Erin M Bayne, Subhash R Lele, Patricia Fontaine, Steve G Cumming, Diana Stralberg, Fiona KA Schmiegelow, and Samantha J Song. 2013. “Calibrating Indices of Avian Density from Non-Standardized Survey Data: Making the Most of a Messy Situation.” *Methods in Ecology and Evolution* 4 (11): 1047–58.
- Sólymos, Péter, Steven M. Matsuoka, Steven G. Cumming, Diana Stralberg, Patricia Fontaine, Fiona K. A. Schmiegelow, Samantha J. Song, and Erin M. Bayne. 2018. “Evaluating time-removal models for estimating availability of boreal birds during point count surveys: Sample size requirements and model complexity.” *The Condor* 120 (4): 765–86. <https://doi.org/10.1650>

**CONDOR-18-32.1.**

- Sonobat. n.d. "Western North America Bat Acoustic Table." [https://sonobat.com/download/Western\\_NA\\_Bat\\_Acoustic\\_Table.pdf](https://sonobat.com/download/Western_NA_Bat_Acoustic_Table.pdf).
- Sugai, Larissa Sayuri Moreira, Thiago Sanna Freire Silva, Jr Ribeiro José Wagner, and Diego Llusia. 2018. "Terrestrial Passive Acoustic Monitoring: Review and Perspectives." *BioScience* 69 (1): 15–25. <https://doi.org/10.1093/biosci/biy147>.
- Suthar, Akshit R., Alan R. Biggs, and James T. Anderson. 2025. "A Decadal Change in Shorebird Populations in Response to Temperature, Wind, and Precipitation at Hilton Head Island, South Carolina, USA." *Birds* 6 (1). <https://www.mdpi.com/2673-6004/6/1/14>.
- Szewczak, Joe. 2018. "Acoustic Features of Western US Bats." Arcata, California: Humboldt State University.
- Turgeon, Patrick, Steven L. Van Wilgenburg, and Kiel L. Drake. 2017. "Microphone Variability and Degradation: Implications for Monitoring Programs Employing Autonomous Recording Units." *Avian Conservation and Ecology* 12. <https://api.semanticscholar.org/CorpusID:89959184>.
- Ware, Lena, C. Lisa Mahon, Logan McLeod, and Jean-François Jetté. 2023. "Artificial Intelligence (BirdNET) Supplements Manual Methods to Maximize Bird Species Richness from Acoustic Data Sets Generated from Regional Monitoring." *Canadian Journal of Zoology* 101 (12): 1031–51. <https://doi.org/10.1139/cjz-2023-0044>.