

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

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Table of contents

1 Abstract	2
2 Land Acknowledgement	2
3 Introduction	2
4 Methods	3
4.1 Data collection	3
4.2 Data management, processing and quality control	6
4.3 Analyses	9
4.3.1 Location correlation	9
4.3.2 Site comparisons	9
4.3.3 Observer and methodological comparisons	10
4.3.4 Community analysis	12
4.3.5 Functional and community-level diversity	12
4.3.6 Trend analysis	14
5 Results	15
5.1 Jasper 2024 Fire	15
5.2 Species-region associations	15
5.3 Species richness and functional diversity	16
5.4 Trends	21
Discussion and recommendations	29



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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 forested 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 2025, 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 recording per point count annually. Surveys were scheduled consistently each breeding season in June and early July, starting 30 minutes before sunrise. Technicians walked transects containing ten points, each spaced at least 300 m apart to prevent duplicate detections and ensure independence of locations. At each monumented 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"))
```

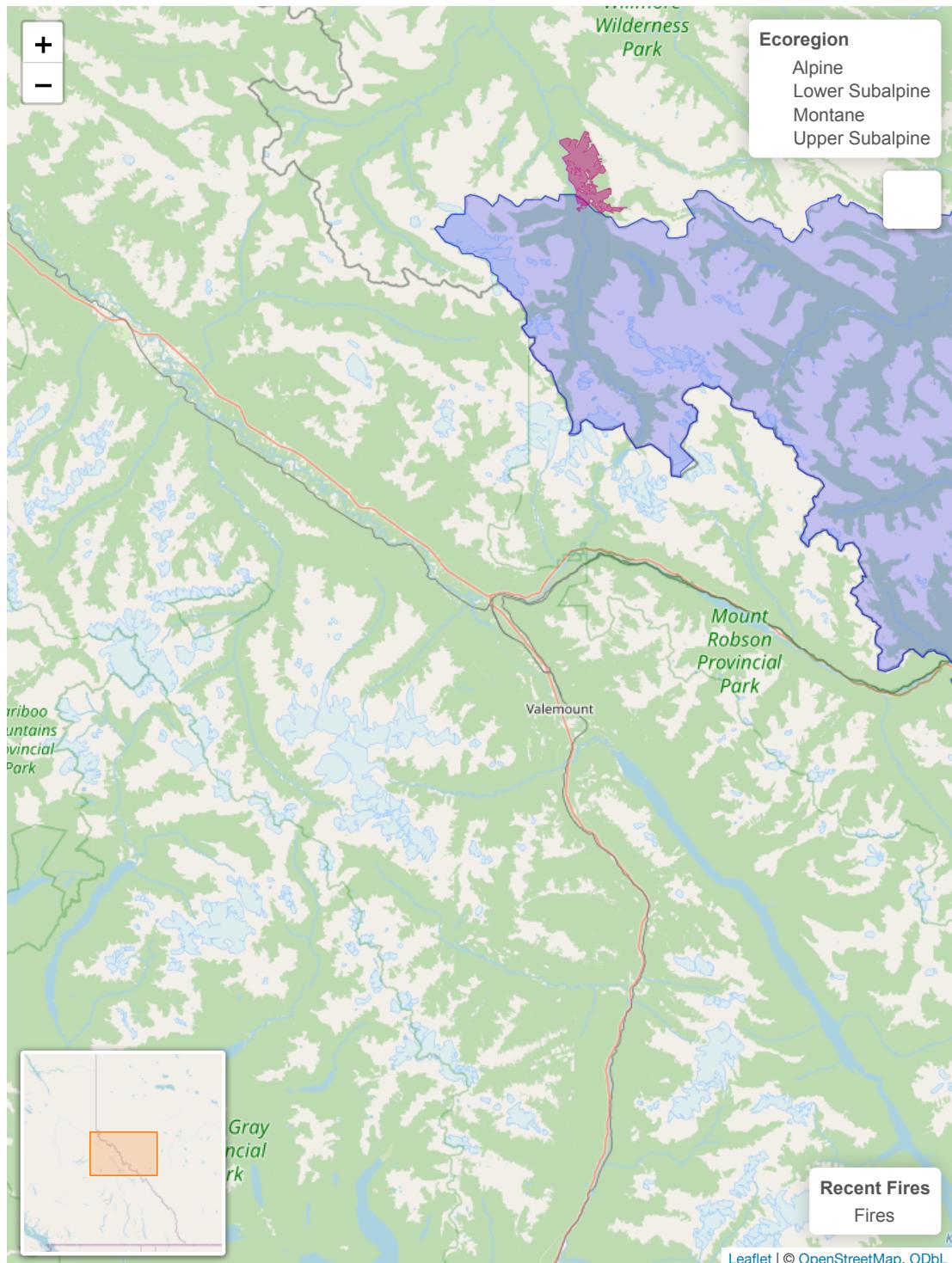


Figure 1: Locations from Jasper National Park ARU EI Monitoring Program.

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

Show entries Search:

	Location	ecoregion	2023	2024	2025
1	CAVELL-1	Upper Subalpine	1	1	1
2	CAVELL-10	Upper Subalpine	1	1	1
3	CAVELL-2	Alpine	1	1	1
4	CAVELL-3	Alpine	1	1	1
5	CAVELL-4	Alpine	1	1	1
6	CAVELL-5	Alpine	1	1	1
7	CAVELL-6	Alpine	1	1	1
8	CAVELL-7	Alpine	1	1	1
9	CAVELL-8	Upper Subalpine	1	1	1
10	CAVELL-9	Upper Subalpine	1	1	1

Showing 1 to 10 of 148 entries

Previous	1	2	3	4	5	...	15	Next
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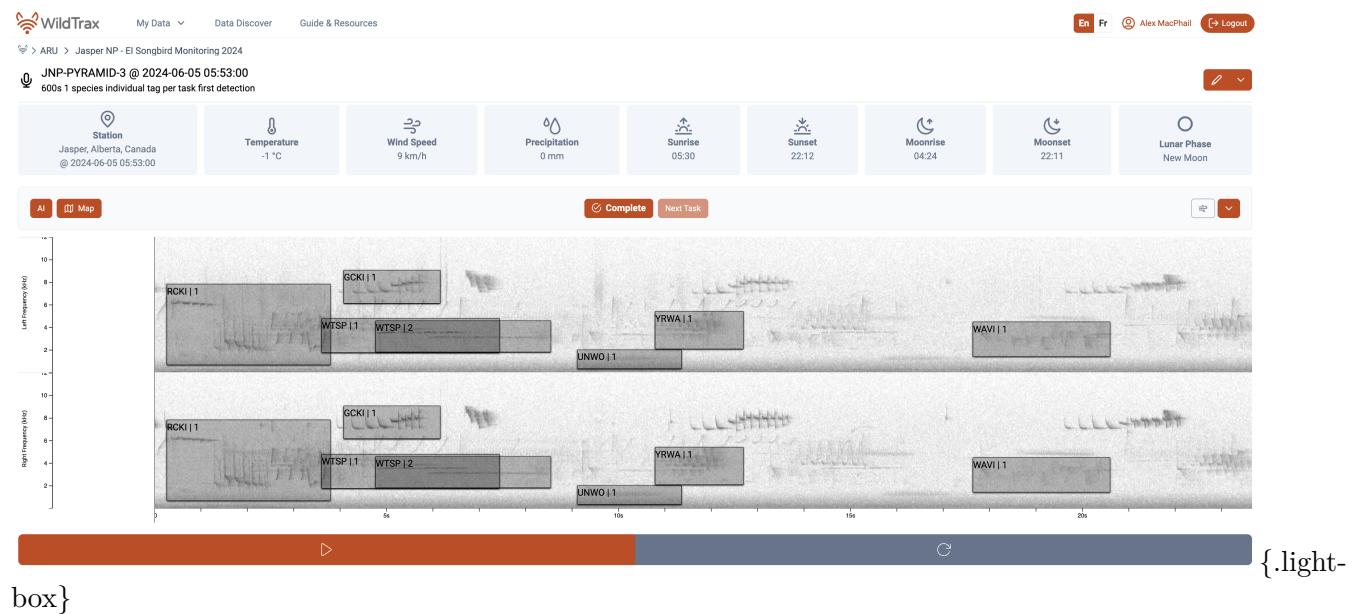
4.2 Data management, processing and quality control

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 (MacPhail 2026, *In Review*). Tags were then drawn to encompass the signal within the methods indicated in each project (see Table 2). Transcribers also had site photos available 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 abund~
## 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"))
```



Location Photos

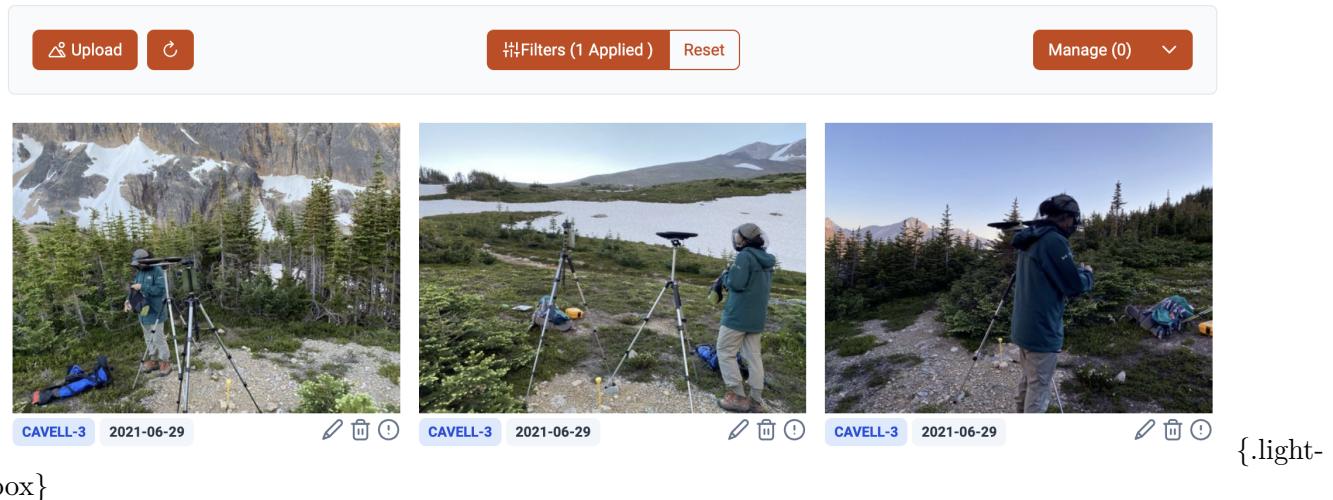


Table 2: Transcription method by year with re-transcribed data being conducted from 2007 - 2025.

Show <input type="button" value="10"/> entries		Search: <input type="text"/>		
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.

Showing 1 to 4 of 4 entries

Previous Next

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’.

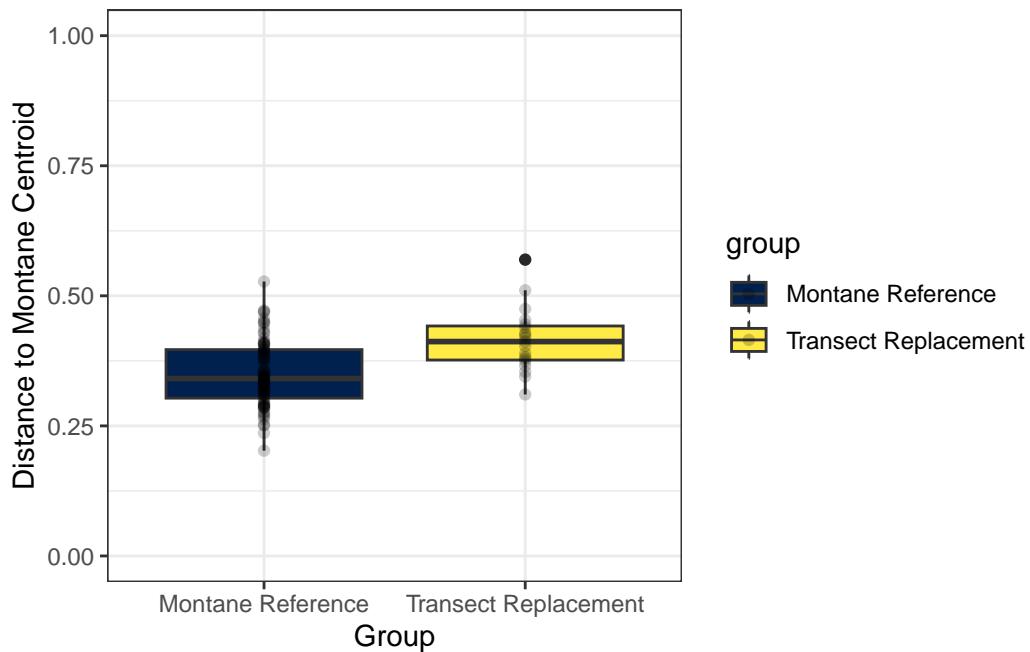
4.3.1 Location correlation

To inform our subsequent modeling choices, we first evaluated the bird survey data for spatial autocorrelation (e.g., survey points close to one another exhibit similar bird counts). To test for this, we calculated a total abundance index for each location and year by summing the maximum number of individuals detected, representing the minimum number of individuals known to be present. Because survey points were typically spaced 300 m apart, we defined spatial neighbor relationships using a 1-nearest-neighbor approach ($k = 1$) based on great-circle distances. We derived spatial coordinates from geographic point data, excluding non-finite values to ensure valid estimation. Using the `knearneigh()` and `knn2nb()` functions in R, we constructed a spatial weights matrix with row-standardized weights to reflect immediate adjacency between points. We assessed global spatial autocorrelation in total abundance using Moran’s I under a randomization assumption. This statistic evaluates whether the landscape is spatially structured—specifically, whether nearby locations tend to have similar abundance values more often than expected by chance. To determine if this dependence was driven by localized clustering, we further calculated Local Indicators of Spatial Association (LISA) using local Moran’s I . This allowed for the identification of 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 across the study area, local Moran’s I revealed no statistically significant clusters. This pattern suggests that similarities in bird counts among nearby survey locations were spread broadly rather than concentrated in distinct hotspots, consistent with spatial dependence arising from gradual, landscape-scale ecological processes rather than localized aggregations. Therefore, in the following analyses we X, Y and Z...

4.3.2 Site comparisons

The 2024 Jasper Fire severely burned two established acoustic transects (VALLEY5 and TEKKARA). We added two control transects in 2025 in the montane (COTTONWOOD and MUSHROOM), and we plan to continue to monitor both the burned and control transects. Monitoring aims to assess the condition of the bird community in the park, so it is important to monitor bird communities in burned and unburned habitats. While only 50% of montane habitat was burned since 2023, two of three transects were severely burned so it was important to add control transects. 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 control 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.



We summarized bird community composition on the VALLEY5 and TEKARRA transects using a species–by–site community matrix and applied redundancy analysis (RDA) to test whether community structure differed between pre-fire and post-fire periods (Figure 2). The ordination visualizes shifts in species associations attributable to fire, with site scores grouped by fire period and species vectors indicating taxa contributing most strongly to observed differences.

4.3.3 Observer and methodological comparisons

To evaluate consistency between the legacy dataset and the modern WildTrax workflow, we analyzed a subset of recordings processed using both approaches. This included re-processing legacy recordings using new observers in WildTrax, allowing for direct comparison of individual observer performance between the legacy and modern protocols. For each dual-processed recording, we derived the maximum count of individuals per species identified by each specific observer. We used two different metrics to verify data continuity. First, to quantify consistency in abundance estimates, we calculated pairwise Pearson correlations between all individual observers. These relationships were visualized using a heatmap to identify any systematic deviations in counting between legacy contractors and current WildTrax observers. Second, to evaluate consistency in species detection (composition), we binarized the data to presence/absence and calculated Bray–Curtis dissimilarities between individual observers. We then applied hierarchical clustering to these dissimilarity scores to verify that the transition to WildTrax did not introduce observer-specific biases in species identification or community composition.

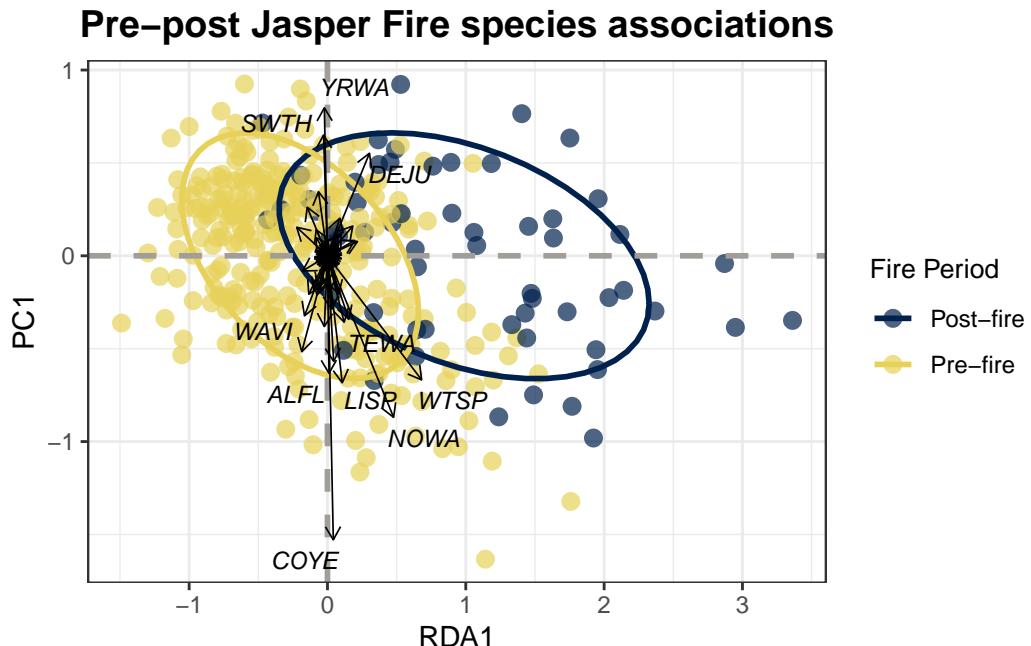
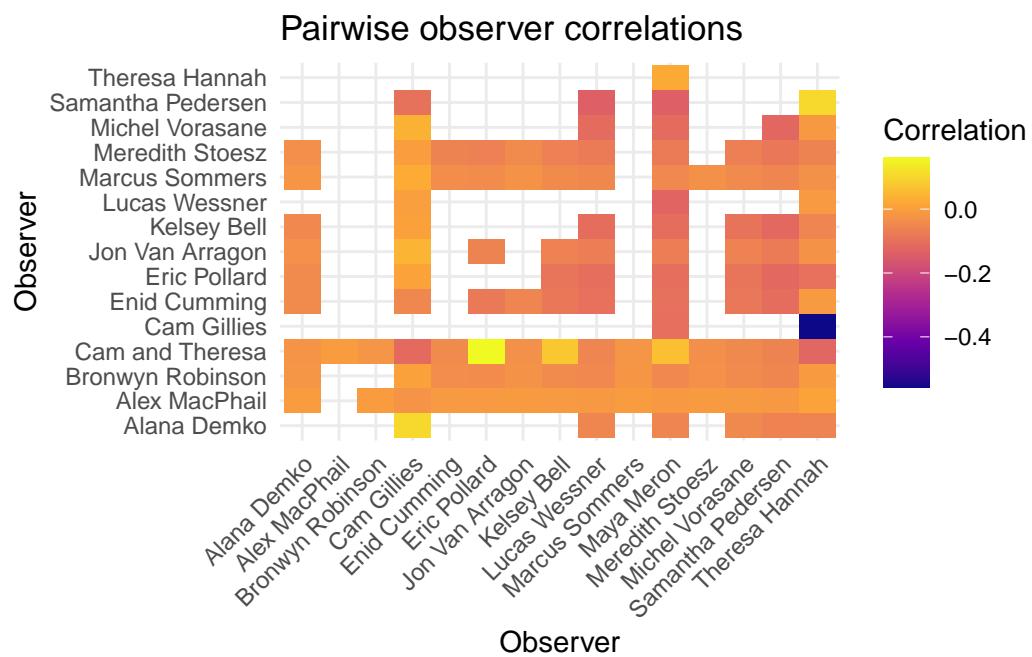
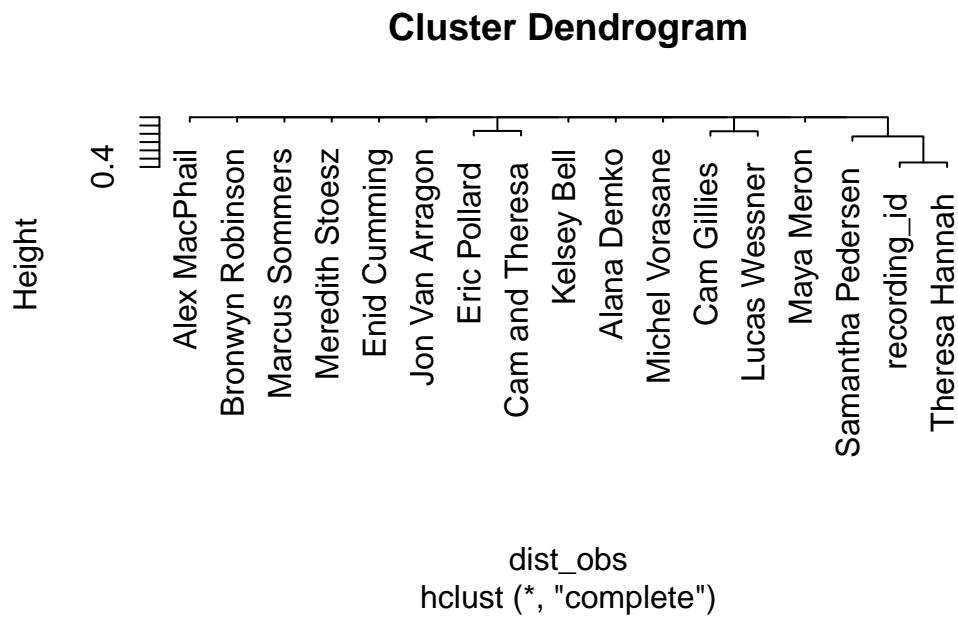


Figure 2: Community matrix of species associations before and after the Jasper 2024 fire on the VALLEY5 and TEKARRA transects.





4.3.4 Community analysis

To characterize bird community composition, we first aggregated species-level observations into a species-by-location matrix, populated with the maximum count of each species at each location. Survey points were then classified into two primary ecoregions: alpine and forested. For the purpose of this analysis, the forested category served as a broad aggregate, grouping the upper subalpine, lower subalpine, and montane ecoregions into a single unit. We quantified the variation in community composition explained by these two ecoregions using Redundancy Analysis (RDA) in the vegan package ((Oksanen2025?)) and visualized species–ecoregion relationships with ordination plots (C. Radhakrishna Rao (1964)). Finally, to test for statistical differences in composition between the Alpine and Montane groups, we performed a permutational multivariate analysis of variance (PERMANOVA; Anderson (2001)). This test was conducted on Bray–Curtis dissimilarities using 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.

Table 3: Guilds

Show <input type="button" value="10"/> entries							Search: <input type="text"/>
	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	

Showing 1 to 10 of 158 entries

Previous 1 2 3 4 5 ... 16 Next

```

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") ~ "Subalpine/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 = c("species_code", "species_class", "species_order")) |>
  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)) |>
  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 Jasper 2024 Fire

Multivariate dispersion differed significantly between replacement and reference montane transects (PERMDISP; $F_{\text{adj}} = 16.44$, $p = 0.001$). Replacement transects exhibited greater distances to the montane centroid (mean = 0.415) than existing montane reference transects (mean = 0.350), indicating higher compositional variability and a greater degree of departure from the montane baseline. This elevated dispersion suggests that species assemblages at the replacement transects were less tightly clustered around typical montane community structure and may reflect more heterogeneous or transitional assemblages relative to long-established montane sites. Consequently, while the replacement transects occur within montane environments, they appear to be less representative of the central tendency of montane species composition observed across the broader transect network.

5.2 Species-region associations

Figure 3 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.

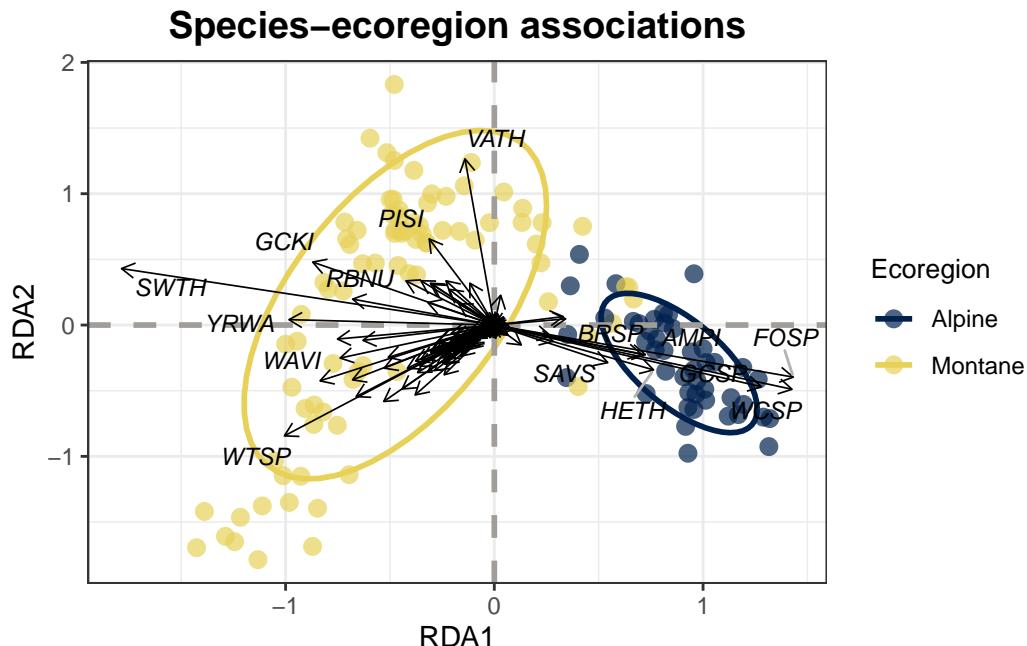


Figure 3

5.3 Species richness and functional diversity

Activity patterns across nesting, dietary and migratory guilds are illustrated in Figure 4 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 9 and Shannon's diversity index over years at Figure 10. 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 8). The non-parametric Mann–Kendall test gave a Kendall's τ 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 increased 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.

```
spp_rich_location <- janp_main |>
  filter(!grepl('COTTONWOOD|MUSHROOM', location)) |>
```

Figure 4:
Seasonal detection activity of by nesting guild and ecoregion

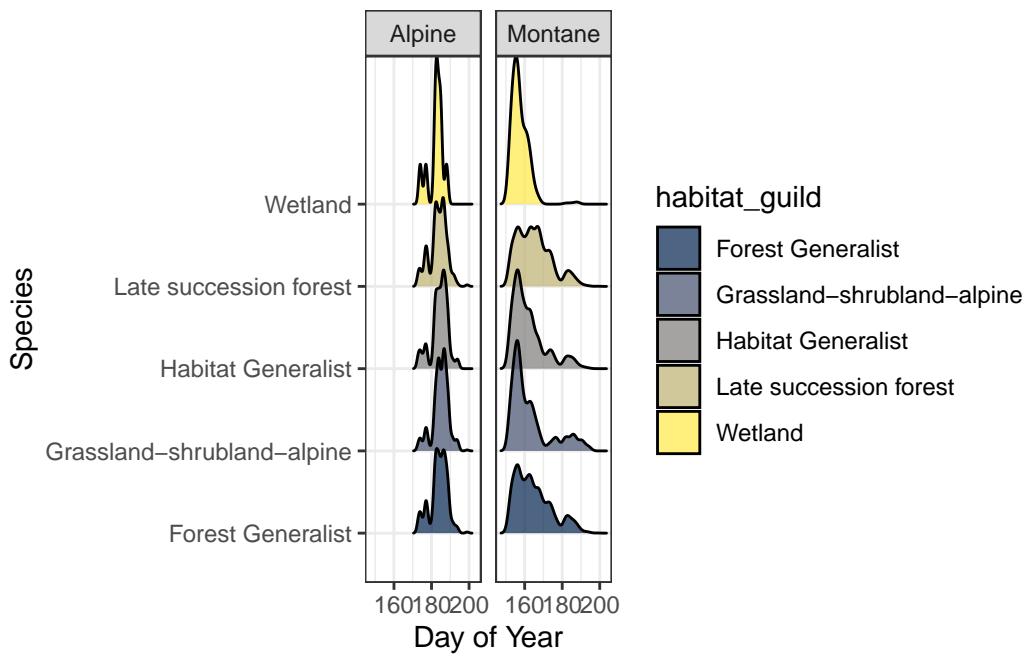


Figure 5:
Seasonal detection activity of by migratory guild and ecoregion

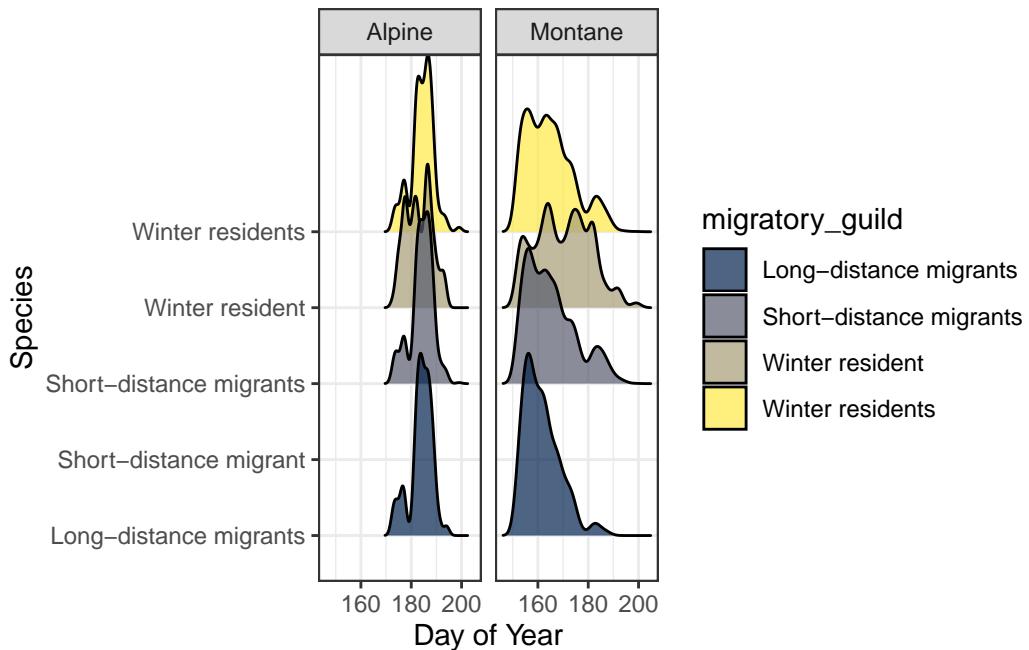


Figure 6:
Seasonal detection activity of by trait and ecoregion

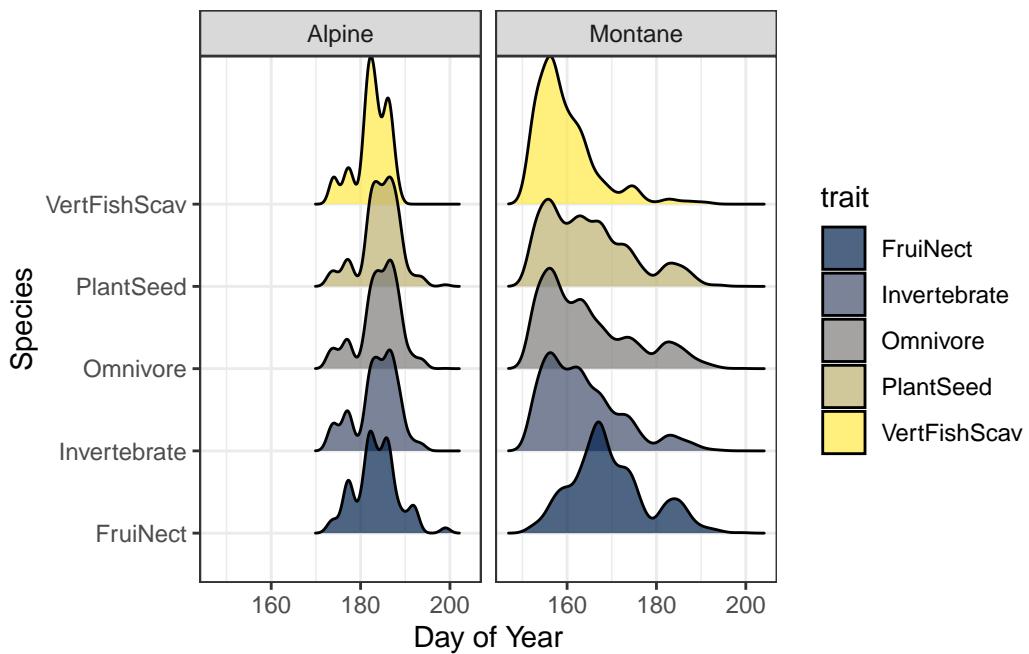


Figure 7:
Seasonal detection activity of by dietary guild and ecoregion

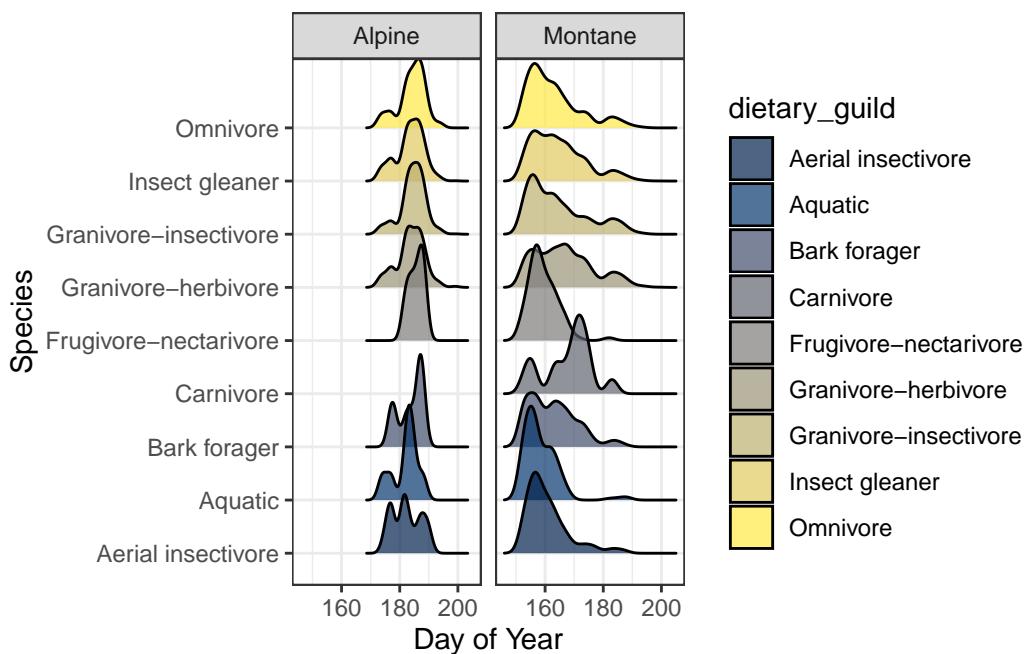
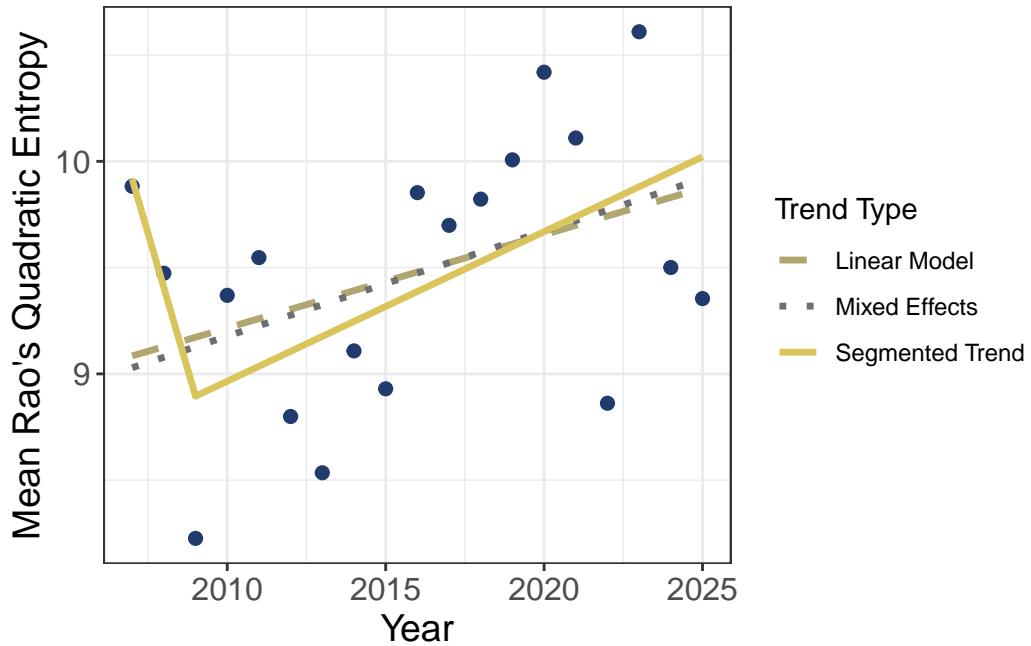


Figure 8:
Mean functional diversity
(Rao's Q)
over time



```

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() |>
  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"))

```

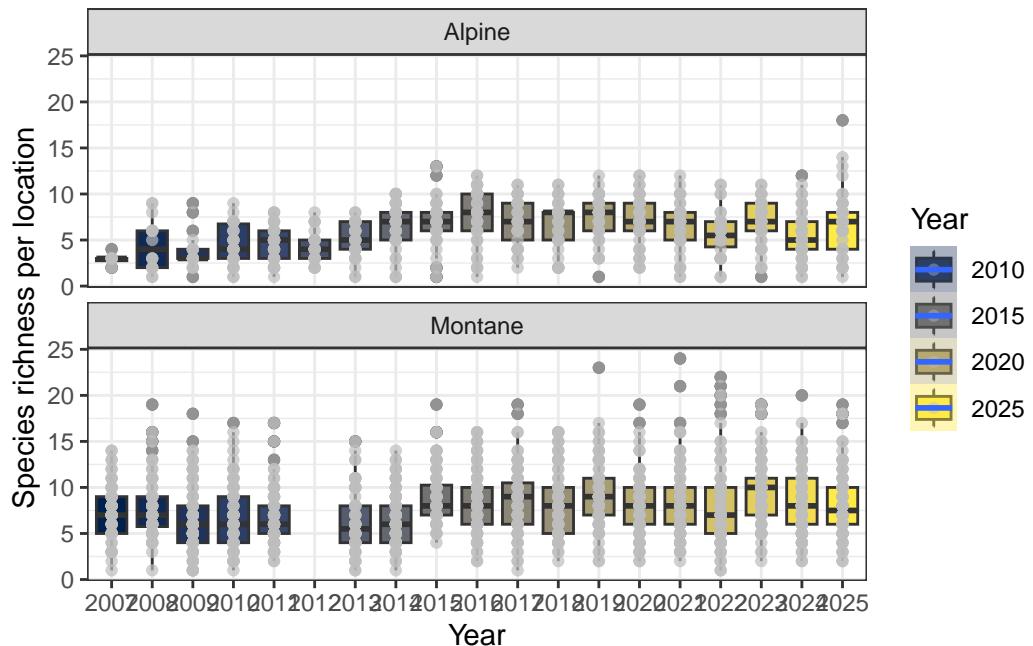


Figure 9: Species richness by year

shannon_d

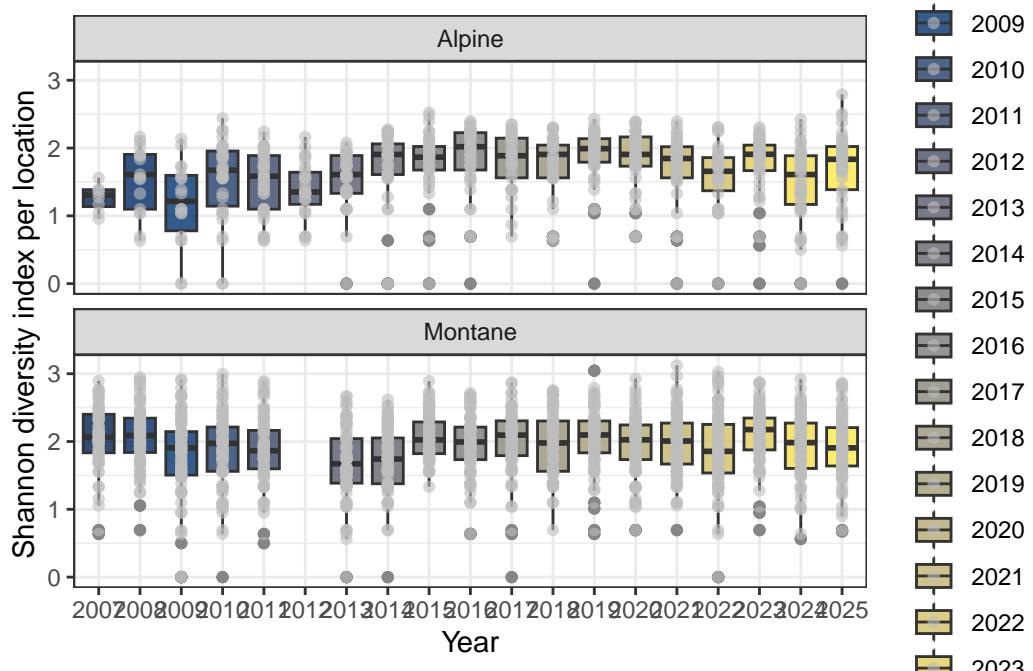


Figure 10: Shannon diversity index over years

5.4 Trends

```
janp_ready_trend <- janp_main |>
  inner_join(lc_150m, by = c("location" = "Point_ID")) |>
  inner_join(canopy_150m, by = c("location" = "Point_ID")) |>
  inner_join(understory_150m, by = c("location" = "Point_ID")) |>
  mutate(landcover = case_when(grepl('TEKARRA|VALLEY5', location) & year > 2024 ~ "Burned", TRUE ~ "Unburned")) |>
  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, canopy_species, canopy_cover, avg_height, recording_date_time,
                  individual_order, abundance, detection_time) |>
    distinct() |>
    wt_tidy_species(remove = c("mammal", "amphibian", "abiotic", "insect", "human", "unknown"), zero = TRUE)

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

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

  if (nrow(spp_max) < 20) {
    next(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
dplyr::select(-c(landcover, VEGETATION_DENSITY)) |>
  group_by(location, ecoregion, canopy_species, canopy_cover, avg_height, recording_date_t
pivot_wider(names_from = lc_group, values_from = prop_cover, values_fill = 0, values_fn =
ungroup() |>
  rename(shrub = `Shrub Low`) |>
  rename(conf = `Tree Coniferous`) |>
  rename(herb = `Herbaceous Mixed`) |>
  rename(bedrock = `Bedrock`) |>
  rename(other = Other) |>
  mutate(across(c(shrub, conf, herb, other, bedrock, julian, hour), scale)) |>
  distinct()

fit <- svabu(individual_order ~ year + shrub + herb + conf + bedrock + julian + hour + obs

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', ecoregion)) |>
  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, count) |>
  distinct() |>
  wt_tidy_species(remove = c("mammal", "amphibian", "abiotic", "insect", "human", "unknown"), zero = 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) {stop(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") ~ lc_group)) |>
  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))
}


```

```

safe_run_trend <- possibly(run_trend, otherwise = NA)

trendz <- janp_main |>
  group_by(species_code) |>
  tally() |>
  arrange(-n) |>
  filter(species_code != "NONE") |>
  mutate(trend = map(species_code, safe_run_trend))
unnest_wider(trend) |>

```

```

unnest()

kable(trendz)

```

species_code	n	trend
YRWA	2012	NA
CHSP	1801	NA
PISI	1696	NA
SWTH	1558	NA
AMRO	1474	NA
DEJU	1119	NA
VATH	1111	NA
HETH	935	NA
FOSP	879	NA
RCKI	770	NA
GCKI	707	NA
WCSP	698	NA
GCSP	611	NA
WTSP	489	NA
RBNU	453	NA
WAVI	430	NA
LISP	333	NA
RESQ	330	NA
OCWA	325	NA
BRSP	304	NA
CAJA	298	NA
AMPI	288	NA
MOCH	288	NA
CORA	278	NA
WIWA	262	NA
TEWA	247	NA
COYE	239	NA
UNPA	227	NA
HAFL	223	NA
NOWA	196	NA
WWCR	186	NA
SAVS	156	NA
RECR	155	NA
CLNU	154	NA
RUGR	143	NA
CEDW	132	NA
PAWR	132	NA
CAVI	126	NA
BLPW	120	NA
WETA	118	NA
TOWA	117	NA

species_code	n	trend
ALFL	110	NA
BOCH	103	NA
TOSO	102	NA
AMCR	93	NA
AMRE	83	NA
NOFL	77	NA
UNBI	73	NA
YEWA	73	NA
BHCO	64	NA
LEFL	62	NA
GCRF	61	NA
CANG	55	NA
MGWA	55	NA
OSFL	55	NA
PIGR	55	NA
COLO	54	NA
HOLA	54	NA
ATTW	53	NA
BCCH	52	NA
WISN	51	NA
CCSP	47	NA
BRCR	46	NA
UNMA	46	NA
UNWO	46	NA
AMPK	44	NA
UNKN	41	NA
WIFL	41	NA
PIWO	33	NA
RNSA	30	NA
UNTR	29	NA
WEWP	29	NA
MAWA	27	NA
SWSP	24	NA
DUFL	22	NA
HAWO	22	NA
SOSP	21	NA
VESP	21	NA
SORA	20	NA
UNSP	20	NA
MOBL	19	NA
WEFL	18	NA
EVGR	17	NA
RWBL	17	NA
SPECOL	17	NA
UNWA	15	NA
SPSA	14	NA

species_code	n	trend
UNTH	14	NA
BBMA	12	NA
DOWO	11	NA
BBWO	9	NA
TRES	9	NA
AMCO	8	NA
BHVI	8	NA
ROWR	8	NA
YBFL	8	NA
MALL	7	NA
UNFL	7	NA
VGSW	7	NA
LCSP	6	NA
RBGR	6	NA
UNFI	6	NA
UROPAR	6	NA
WTPT	6	NA
YBSA	6	NA
MODO	5	NA
NOPO	5	NA
NRWS	5	NA
PUFI	5	NA
UGRS	5	NA
UNVI	5	NA
UPCH	5	NA
CONI	4	NA
DUGR	4	NA
GBHE	4	NA
GRYE	4	NA
GWTE	4	NA
MERL	4	NA
NOGO	4	NA
REVI	4	NA
RUHU	4	NA
AGOS	3	NA
ATSP	3	NA
BLJA	3	NA
CAFI	3	NA
HOMA	3	NA
SOSA	3	NA
UNDU	3	NA
UNSA	3	NA
BAEA	2	NA
BAGO	2	NA
BAWW	2	NA
BTNW	2	NA

species_code	n	trend
CAHU	2	NA
CMWA	2	NA
ELKK	2	NA
HOAMAR	2	NA
HOFI	2	NA
KILL	2	NA
NHWR	2	NA
REDP	2	NA
SPGR	2	NA
UCRS	2	NA
UCTH	2	NA
UNBL	2	NA
UNFR	2	NA
UNQK	2	NA
AMBI	1	NA
AMKE	1	NA
BADO	1	NA
BAOW	1	NA
BEKI	1	NA
BHGR	1	NA
BLSW	1	NA
BLTE	1	NA
COHA	1	NA
DOGG	1	NA
GHOW	1	NA
HORS	1	NA
HOWR	1	NA
LEYE	1	NA
MOWA	1	NA
NAWA	1	NA
NHOW	1	NA
OSPR	1	NA
OVEN	1	NA
PBGR	1	NA
PSFL	1	NA
RTHA	1	NA
SAPH	1	NA
SSHA	1	NA
STJA	1	NA
STSA	1	NA
UGOL	1	NA
UNAM	1	NA
UNBT	1	NA
UNCV	1	NA
UNHA	1	NA
UNHU	1	NA

species_code	n	trend
UNWR	1	NA
VEER	1	NA
VIRA	1	NA
WBNU	1	NA
WIPT	1	NA
WTDE	1	NA

```

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
  ))

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
  ))

```

Discussion and recommendations

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