

Riverbird distributions and habitat use

John McLaughlin
Western Washington University

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Abstract

Riverbirds are widespread components of river systems. Diverse riverbird species use riparian habitats in differing ways. Riverbirds are mobile, allowing them to respond rapidly to changing river conditions. Most riverbirds are positioned several trophic levels above direct impacts to river systems, facilitating their use as integrative measures of ecosystem responses to anthropogenic and non-anthropogenic impacts. Students can apply riverbird data to evaluate hypotheses about these responses, while gaining research experience, working collaboratively in teams, and contributing data to monitoring programs.

In this module, students determine habitat use by a variety of bird species associated with rivers. The module would be appropriate for students in high school through graduate school, with applications ranging from simple comparisons of species count data to advanced analysis of habitat selection. Students collect data on birds and habitats while traveling downriver in boats. At least two boats and four people are required, but tasks can be divided to accommodate multiple boats and up to 20 people. In addition to boats and river safety gear, equipment needed includes a stopwatch, binoculars, bird identification guide, and either a GPS receiver or a river map. After collecting data, students compare habitats used by each species relative to habitats available by estimating resource selection functions with logistic regression in the R open source statistical environment. This approach is easier to conduct and involves less uncertainty than conventional methods using ratios of random variables (Manly et al. 2002, McDonald et al. 2012). Data and analysis in this module can be used to compare habitat use among species, river reaches, river management regimes. The module can be implemented on multiple river reaches and along diverse rivers to facilitate comparisons or synthesis across river basis. Module results can be applied in diverse contexts to evaluate restoration or riparian management programs.

Keywords

Waterfowl, raptor, kingfisher, heron, indicator species, monitor, habitat selection, riverbank, logistic regression, River Field Studies Network.

Student Learning Objectives

Field Learning Objectives

- Improve field observation skills.
- Develop bird identification skills.
- Recognize habitat categories under field conditions.
- Improve organizational ability in dynamic environments.

Data Analysis Learning Objectives

- Organize raw data into categories for analysis.
- Become familiar with the R statistical environment.
- Understand logistic regression models, resource selection functions, and how to fit them.
- Ability to plot habitat selection functions for different species.
- Understand model uncertainty, in numerical and graphical representations.

Ecology Learning Objectives

- Develop conceptual understanding of riverbird-habitat relationships.
- Develop recognition of species-specific differences in habitat use.
- Develop stronger appreciation of structural diversity in riparian environments.
- Recognize expression of riverbird-habitat relationships in field settings.
(i.e., discern patterns within complexity of nature)

Scientific Learning Objectives

- Increased understanding of scientific inquiry.
- Improved ability to translate questions into hypotheses and predictions.
- Ability to interpret evidence for hypotheses: strong, weak, or contradictory.
- Gain experience working cooperatively in teams.
- Develop experiential knowledge about field science in practice.

Affective Objectives

- Increased sense of belonging, through teamwork and work toward shared goals.
- Stronger self-efficacy, from species identification skill, sampling experience, data analysis, detection of patterns within data, communication of results.
- Comfort outdoors, from field experience and persistence through uncertain conditions.
- Science identity, from developing and testing original hypotheses, and presenting results.
- Service to society, through cooperative problem solving and conducting science to inform and improve human relationships with birds and rivers.

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1 Conceptual Background

Birds are nearly ubiquitous in river systems. River-dependent bird abundances, distributions, and species composition vary across space and time in response to diverse drivers and causal pathways (Figure 1). Riverbird responses reveal changes in river systems and changes in the ecological functions performed by riverbirds. Identifying and delineating these changes are important to understanding riverbirds, river systems, and impacts of natural and anthropogenic drivers (Stevens et al. 1997).

Many riverbird populations are in decline, reflecting anthropocene impacts on river habitats and food sources (Palmer 2004, Vorosmarty et al. 2010, Reid et al. 2018, Rosenberg et al. 2019). Worldwide, nearly 40% of riverbirds and other birds associated with aquatic habitats are declining, a fraction twice as large as the number increasing (Wetlands International 2012). Although waterbird populations are less threatened in North America, a third of species on the continent are declining (Wetlands International 2012), while many waterfowl are increasing (Rosenberg et al. 2019). Future changes in riverbirds are expected to result from changes in land use, riparian development, river restoration, and climate change (Northrup et al. 2018, Rosenberg et al. 2019, Adde et al. 2020a).

Detecting changes in riverbird populations requires collecting data on riverbird locations and abundances. Understanding those changes requires developing knowledge about riverbird habitat use. This research module provides a sampling protocol to collect riverbird and habitat data, and an analytical approach to quantify habitat use for each species. These results can be used to evaluate hypotheses about riverbird habitat relationships, riverbird responses to habitat changes, or effects of river management (Figure 1) at scales ranging from local reaches to multiple basins (Adde et al. 2020b).

Studying riverbird-habitat relationships has relevance beyond ornithology and behavioral ecology. Riverbirds also provide useful measures of effects of river restoration, habitat loss, contaminant impacts, and climate change (Silvy et al. 2012, Ogden et al. 2014a,b, McCaffery et al. 2018, Silverthorn et al. 2018, Adde et al. 2020a,b). Several factors make studying riverbirds broadly useful as measures of river system status and response. First, riverbirds are conspicuous and easy to detect. Second, pre-intervention baseline data often exist for riverbirds due to broad societal and scientific interest. Third, many mechanisms of riverbird habitat use are well-understood, which facilitates interpretation of riverbird responses. Fourth, riverbird habitat requirements correspond to conditions ranging from early to late stages in succession, suggesting that riverbirds may span several temporal scales in restoration or impact. Fifth, many riverbird species potentially occur in multiple river reaches and river basins, facilitating assessments across spatial scales (Weins et al. 2008). Sixth, because riverbirds function two or more trophic levels above primary producers (Figure 1), they represent an integrative measure of ecosystem status. Finally, broad public interest in riverbirds can translate into greater support for river monitoring, conservation, and restoration.

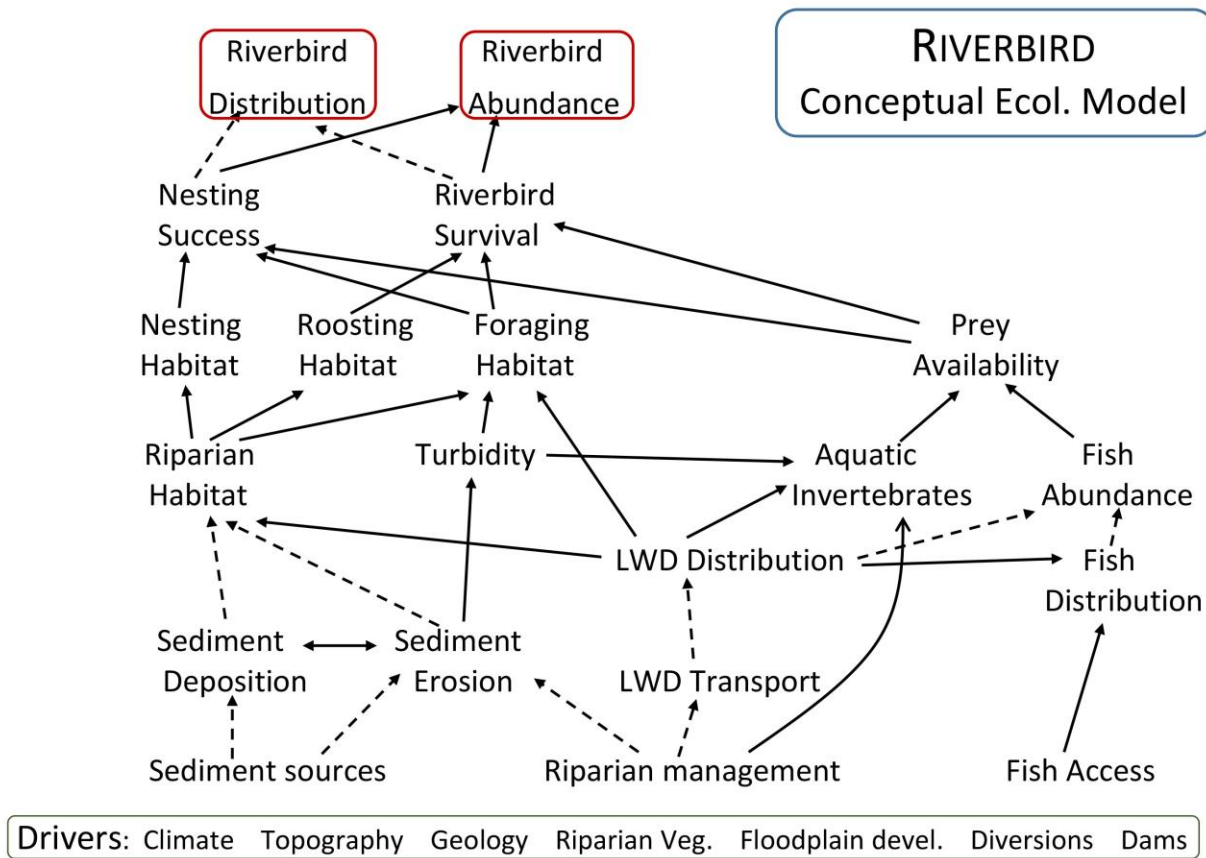


Figure 1. Riverbird conceptual ecological model, linking system drivers to riverbird responses. Direct and indirect links are identified with solid and dashed arrows. Many drivers, components, and links are omitted.

Riverbird and habitat sampling approach in this module

In this project, students record riverbird locations and habitat types while traveling downriver in boats. An observer(s) in the lead boat records riverbird species, abundances, and habitat locations. This sampling method is a form of strip transect, used to estimate relative abundance of birds in linear environments (Sutherland 1996). Observers in following boats record habitat characteristics by category at five minute intervals, initiated at a random starting time. This approach is a linear version of a systematic survey with a random starting point, which supports probabilistic inferences about the proportions of each habitat type throughout the sampled river corridor (Morrison et al. 2001).

With some adaptations, these data also could be collected by observers on land without using boats. These adaptations should include the following.

- (1) Riverbird detection: riverbanks should be carefully observed, to avoid overlooking hidden riverbirds.
- (2) Replace timed habitat sampling with sampling at constant distance intervals. Constant time intervals would not provide a systematic sample of habitat types, because travel time varies with

vegetation type and density, bank sinuosity, and other riverbank characteristics. Replace habitat sampling at 5-minute intervals with constant distance intervals along the bank, initiated from a randomly selected starting point.

(3) While sampling, take care to minimize trampling riparian vegetation or eroding river banks.

These data can be used to estimate the following quantities.

- (1) Counts of each riverbird species, an index of relative abundance for each species.
- (2) Frequency that each riverbird species was detected in association each bank habitat type.
- (3) Frequency that each riverbird species was detected on each water surface type.
- (4) Extent of each bank habitat type and each water surface type in the sampled reach.

These estimates can be used to compare riverbird relative abundances among species, reaches, or river basins. Frequencies of riverbird detections in each habitat type can be compared to extent of habitat available to determine habitat selection, as described in data analysis instructions. Habitat selection values can be used to evaluate hypotheses about riverbird responses to drivers of river system change, as depicted in the Conceptual Ecological Model, Figure 1. These comparisons and analyses require the following assumptions about data collection and riverbird behavior.

Assumptions in habitat use analysis

- (1) Riverbirds are equally visible among habitat types.
- (2) Riverbirds select habitat types independently of each other, within and between species.
- (3) Each riverbird individual is recorded only once.
- (4) Riverbirds have access to the entire study area.
- (5) Observers detect riverbirds before they flush; initial riverbird locations are not affected by observers.

In practice, assumption (2) may be violated when riverbirds occur in pairs, family groups, or flocks. This kind of violation can be addressed by modifying data analysis, using methods beyond the scope of this module. Violations of assumptions (1), (3), and (5) can be minimized through careful application of sampling guidelines described in the next section.

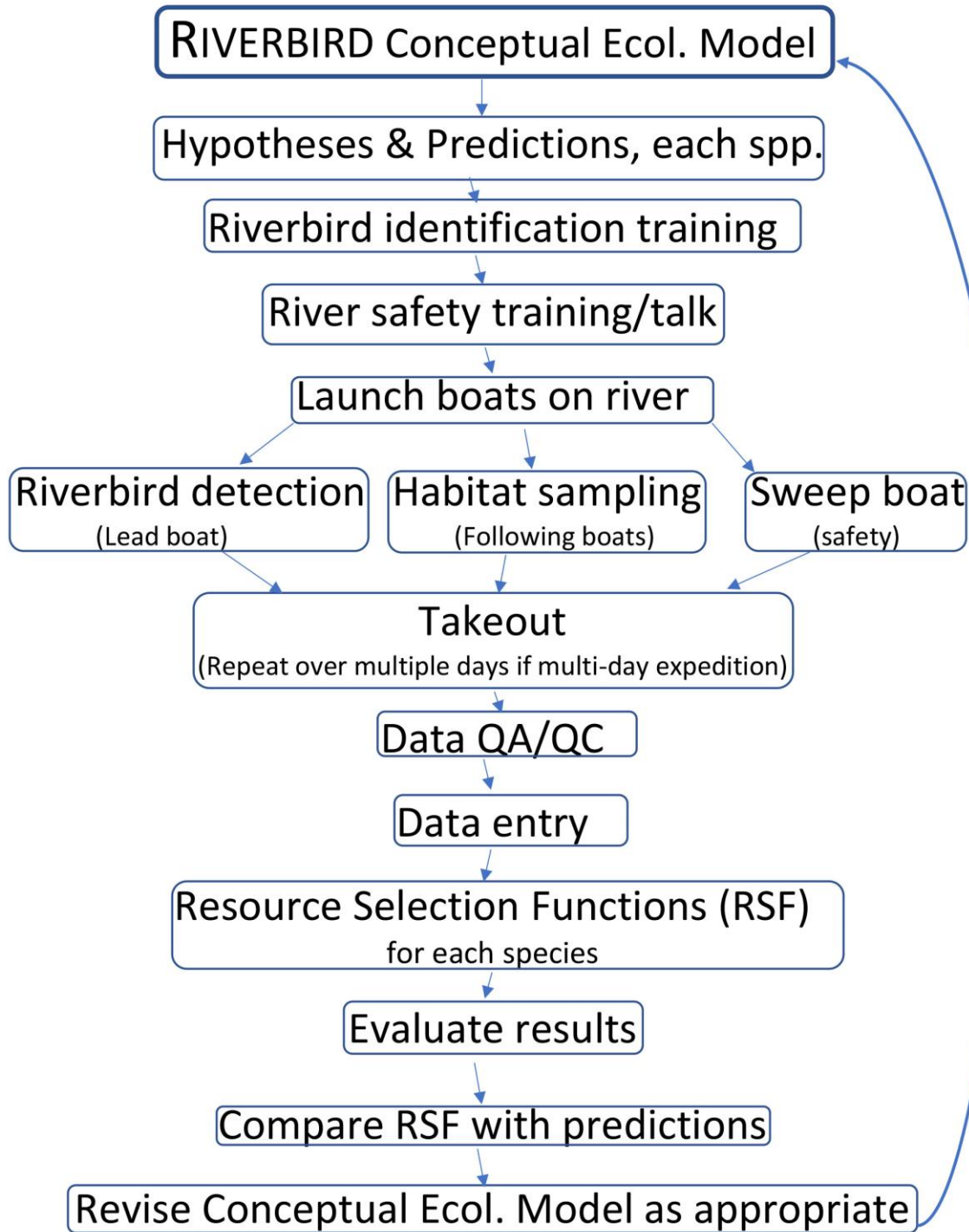


Figure 2. Riverbird research module schematic. The module can be implemented during a single-day sampling period or during multi-day river expeditions. Completing the module across multiple years or river basins facilitates study of temporal or spatial patterns in riverbird-habitat relationships.

2 Field Instructions

Safety Equipment

- 1 Personal Floatation Device (PFD) for each participant, suitable for river use.
- 2 Whistle, attached to PFD.
- 3 Helmet, appropriate for river activities. Optional on flatwater rivers.
- 4 Thermal protection, clothing appropriate for the river and season.
- 5 Footwear appropriate for the river.
- 6 Recommended: knife in accessible position, drinking water, snacks

Group Gear

- 1 Boats capable of transporting the group and suitable for the river
- 2 Paddles or oars appropriate for the boats
- 3 Spare paddles or oars
- 4 First aid kit
- 5 Throw bags
- 6 River rescue kit
- 7 Communication device

Sampling Equipment

- 1 Stopwatch or other timing device
- 2 Data forms (paper or electronic)
- 3 Writing implement, if using paper data forms
- 4 Waterproof case to hold data forms or electronic recorder
- 5 Bird identification guide
- 6 GPS receiver
- 7 Binoculars

Preparation on land

- 1 Review identifying characteristics of each anticipated riverbird species.
Give special attention to characteristics visible to the naked eye, when bird is in flight.
(i.e., prepare to identify flushed birds that fly beyond view within seconds)
- 2 Assign recording tasks to each boat, or multiple observers/recorders within each boat.

The following assignments are needed:

- (1) Riverbird detections
- (2) Left bank habitat characteristics
- (3) Right bank habitat characteristics
- (4) River surface characteristics

Riverbird detections should be assigned to observers in the lead boat, to support accurate determination of original riverbird locations if boats flush birds.

- 3 Prepare all recording gear for use.
- 4 Record information at the top of bird and habitat data forms.
- 5 Group leader or designate gives river safety talk to all participants.

On the water

Riverbird observations

6 As your boat travels downriver, search for riverbirds on the river and along both left and right banks.

7 Whenever observers detect a riverbird, identify the species and note location (river mile, kilometer, GPS point, or other location information). Mark the habitat category on the data form where the bird was first observed. Record both water and bank characteristics. If the bird was detected on the water, record characteristics of the bank closest to the bird. If the bank contains more than one habitat component, mark all relevant categories. For example, if logs lie along a forested bank with grasses at the waters edge, one would mark “LWD,” “Forest,” and “Herb” categories.

If the bird flushes as the boat approaches, try to determine the original location of the bird and record bank and river characteristics at that location.

Do not record “flyovers” – birds first observed flying up or down river.

8 Record each bird once only. If a bird flushes and lands downriver, do not record the bird’s new location.

9 If a group of multiple birds of a species are detected, record only one location for the group. (Locations of birds in a group are not independent. Recording location characteristics for multiple birds in a group would violate assumptions of independence among data points.)

10 Continue searching for riverbirds and recording habitat categories at detection locations until your group stops or decides to cease data collection. You will need at least 30 detections of a focal species, for confidence in results of your data analysis.

Habitat Sampling

11 After launching onto the river, select a random point or starting time (For example, select a 2-digit random number or 100^{ths} of a second on a stopwatch; start that many seconds downriver).

12 When your boat reaches the starting point or time, record (mark) on the habitat data form the water characteristic (calm, riffle, rapid) and habitat categories for left and right banks. Left and right are defined as river left and river right: directions as viewed while facing down river. If a bank contains more than one habitat component, mark all relevant categories. For example, if logs lie along a forested bank with grasses at the waters edge, one would mark “LWD,” “Forest,” and “Herb” categories. Also record the river mile (km) or other location information, if known.

13 While your boat continues to travel downriver, wait five minutes after your starting point or time.

14 After five minutes, record habitat categories (water surface, Left bank, Right bank) at the five minute point.

15 Repeat step 14 every five minutes as you travel downriver. Pause timing whenever your boat stops traveling downriver, e.g., during lunch breaks, scouting rapids, or stopping in eddies to wait for other boats.

3 Data Analysis Instructions

Data analysis in brief

- 1 Review data for accuracy, legibility, and other quality control considerations.
- 2 Sort data on detection locations and habitat categories by riverbird species.
- 3 Enter location data for each riverbird species into R.
- 4 Plot histograms for locations of each riverbird species.
- 5 Tally number of riverbird observations in each habitat, for each species.
- 6 Tally number of observations for each habitat category, recorded at 5-minute intervals.
- 7 Enter tallies of riverbird observations and habitat types into R.
- 8 Create variables consisting of binary values (0,1) for each riverbird species and for each habitat category. Each variable should span all bird detection and habitat sampling locations.
- 9 For each riverbird species, fit logistic regression models for each habitat category.
- 10 Calculate the Resource Selection Function (RSF) for each riverbird species. Exponentiate coefficient values for each habitat category: $\exp(\text{coefficient})$.
- 11 Determine uncertainty in resource selection function values for each habitat type using standard error values for each habitat type coefficient.
- 12 Plot the RSF with standard errors (or confidence intervals) for each riverbird species.

Data Entry

- 1 Review data for accuracy, legibility, and other quality control considerations (Morrison et al. 2001).
For example, proof data by having a team member recite data back to the observer.
- 2 Sort data on detection location and habitat category by riverbird species.
- 3 For each riverbird species, enter location data for each individual bird into R.
- 4 Tally number of riverbird observations in each habitat, for each species.
- 5 Tally number of observations for each habitat category, recorded at 5-minute intervals.
- 6 Enter tallies of riverbird observations and habitat types into R.

Data Analysis

- 1 For each species, plot histograms of location data. The histograms describe longitudinal distributions.
- 2 Create variables consisting of binary values (0,1) for each riverbird species and for each habitat category. Each variable should span all bird detection and habitat sampling locations.
- 3 For each riverbird species, fit logistic regression models for each habitat category.

4 Exponentiate coefficient values for each habitat category: $\exp(\text{coefficient})$.

The set of exponentiated coefficients for each habitat type is the resource selection function (RSF) for that riverbird species.

$$\text{RSF} = \exp(\beta_i) \quad \text{where } \beta_i \text{ is the logistic regression model coefficient for the } i^{\text{th}} \text{ habitat type.}$$

A value of 1 indicates no selection: the riverbird species was detected in that habitat type in equal proportion to the availability of that habitat type. Values larger than one indicate riverbirds selected that habitat type. Values less than one imply riverbirds tended to avoid that habitat type, i.e., they were detected in that habitat at lower proportion than its availability.

5 Determine uncertainty in resource selection function values for each habitat type. RSF values plus or minus one standard error are given by the following expression.

$$\exp(\beta_i \pm s_{\bar{x}}) \quad \text{where } \beta_i \text{ is the logistic regression model coefficient for the } i^{\text{th}} \text{ habitat type,}$$

$$s_{\bar{x}} \text{ is the standard error of } \beta_i$$

95% confidence limits for RSF values are given by the following.

$$\exp(\beta_i \pm 1.96 s_{\bar{x}}) \quad \text{where } \beta_i \text{ is the logistic regression model coefficient for the } i^{\text{th}} \text{ habitat type,}$$

$$s_{\bar{x}} \text{ is the standard error of } \beta_i$$

6 Plot the RSF with standard errors (or confidence intervals) for each riverbird species.

Conducting the Data Analysis

Instructions and R commands for Data Entry and Data Analysis sections, above, are in the data analysis template file. The R commands can be copied from the template and pasted into R to complete the analysis. The commands generate a plot of number of birds of each species detected along the river, similar to Figure 3. They also generate a plot of the RSF, with standard errors, similar to Figure 4.

An example of the entire analysis completed for data on Common Merganser (*Mergus merganser*) and Canada Goose (*Branta canadensis*) is in the data analysis example file.

Interpretation

Riverbird distributions can be interpreted in several ways, appropriate to river and bank conditions, adjacent land use, and other factors relevant to each species. Riverbird detection data are counts that represent minimum estimates of study area abundances. During travel downriver, observers likely overlook some riverbirds. Consequently, count data provide an index of riverbird abundances in the study area. If factors affecting observer ability to detect a given species remain similar along the river, then count data serve as a measure of relative abundance. Then patterns in detection histograms can be interpreted as similarities, differences, or trends in species abundances, providing evidence to evaluate hypotheses about riverbird responses to river conditions. Advanced analyses could fit probability distributions or other functional forms to the histograms.

The habitat selection analysis outlined above (Data Analysis steps 2-6) applies field data to estimate a RSF for a riverbird species in an environment consisting of distinct habitat categories. The RSF is estimated from the data using logistic regression, which determines the ratio of probabilities for each habitat type: the probability that a riverbird species uses a habitat type relative to the probability that it does not use that habitat type (McDonald et al. 2012). When $RSF=1$, the riverbird was found in a given habitat type in the same proportion as that habitat is found in the study area. $RSF=1$ indicates the riverbird neither selects nor avoids that habitat type. RSF values larger than one indicates riverbirds selected that habitat type disproportionately often. Values less than one imply riverbirds tended to avoid a habitat type, i.e., they were detected in that habitat at a lower proportion than its availability. Note that RSF values are determined by exponentiating logistic regression coefficients (β_i). An RSF value of 1 is equivalent to $\beta_i = 0$. The magnitude of RSF values measure the strength of habitat selection or avoidance. If $RSF=10$ for a given habitat type, the riverbird species was found in that habitat ten times more often than would be expected by chance.

Confidence in conclusions about riverbird selection for or avoidance of habitat types depends on the magnitude of RSF values relative to uncertainty. In the context of statistical hypothesis testing, concluding riverbird selection or avoidance of a habitat type with (95%) confidence requires RSF values to be at least two (1.96) standard errors above or below 1. Alternatively, the logistic regression coefficient for a given habitat category must be at least two (1.96) standard errors above or below zero. In graphical form, this equivalent to the height of the RSF bar being at least twice the length of the standard error bar above or below 1. Figure 3 illustrates these results: Canada Geese strongly selected herbaceous habitat, strongly avoided shrub habitat, and were found on bare substrates at a rate that cannot be distinguished from availability with confidence. Similar conclusions can be drawn from logistic regression model results in the example analysis R transcript.

Although statistical hypothesis testing is informative, ecological interpretation of the analysis is more important. One should evaluate the magnitude of RSF values relative to the riverbird natural history, its ecological role in the river system, the distribution of habitat types, and the larger research questions motivating your project.

More information about using logistic regression to estimate Resource Selection Functions is in McDonald et al. (2012).

Additional Analysis to Consider

The analysis described above combines data on riverbird detections and habitat sampling to evaluate riverbird habitat selection. The data also could be used to assess riverbird abundances and distribution of habitat types. Habitat data collected following instructions in this module constitute a systematic sample with a random starting point. Hence the habitat data can be used as a representative sample of riparian habitat types in the study area. These data can be compared among river reaches or between river basins.

If one assumes that riverbird detection probability is equal among rivers, river reaches, or between years, then riverbird count data can be compared across space and time to draw inferences about riverbird responses to ecological differences, restoration programs, riparian management, or other factors. Below are suggestions for additional analyses that could be conducted with riverbird and habitat data.

- (1) Compare riverbird abundances recorded in several river reaches with the amount of preferred habitat types recorded along those reaches.
- (2) Compare abundances of different riverbird species with amounts of their preferred habitat types.
- (3) Compare riverbird abundances and/or habitat type distributions among river reaches with differing riparian management practices.
- (4) Apply data from multiple rivers to conduct (1)-(3) across multiple river basins.
- (5) Apply data on riverbird abundances and habitat distributions collected over multiple years to evaluate effects of riparian restoration or changes in management practices.

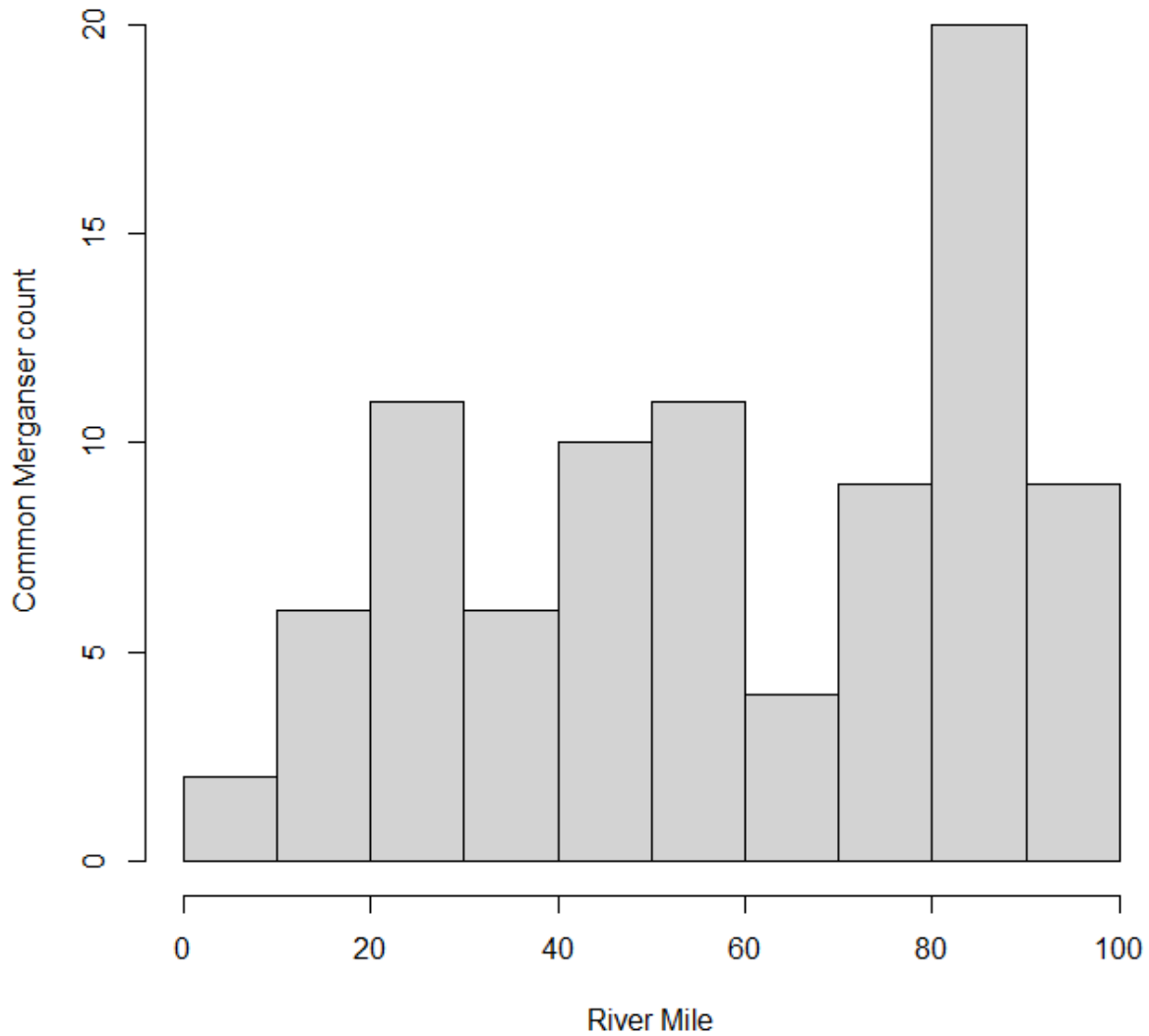


Figure 3. Distribution of Common Merganser (*Mergus merganser*) detections along the Wallowa and Grande Ronde Rivers, April-May 2021. Bar heights are number of Common Merganser individuals detected within each 10-mile reach along the river, from Minam on the Wallowa River (mile 92) to the confluence of the Grande Ronde with the Snake River (mile 0).

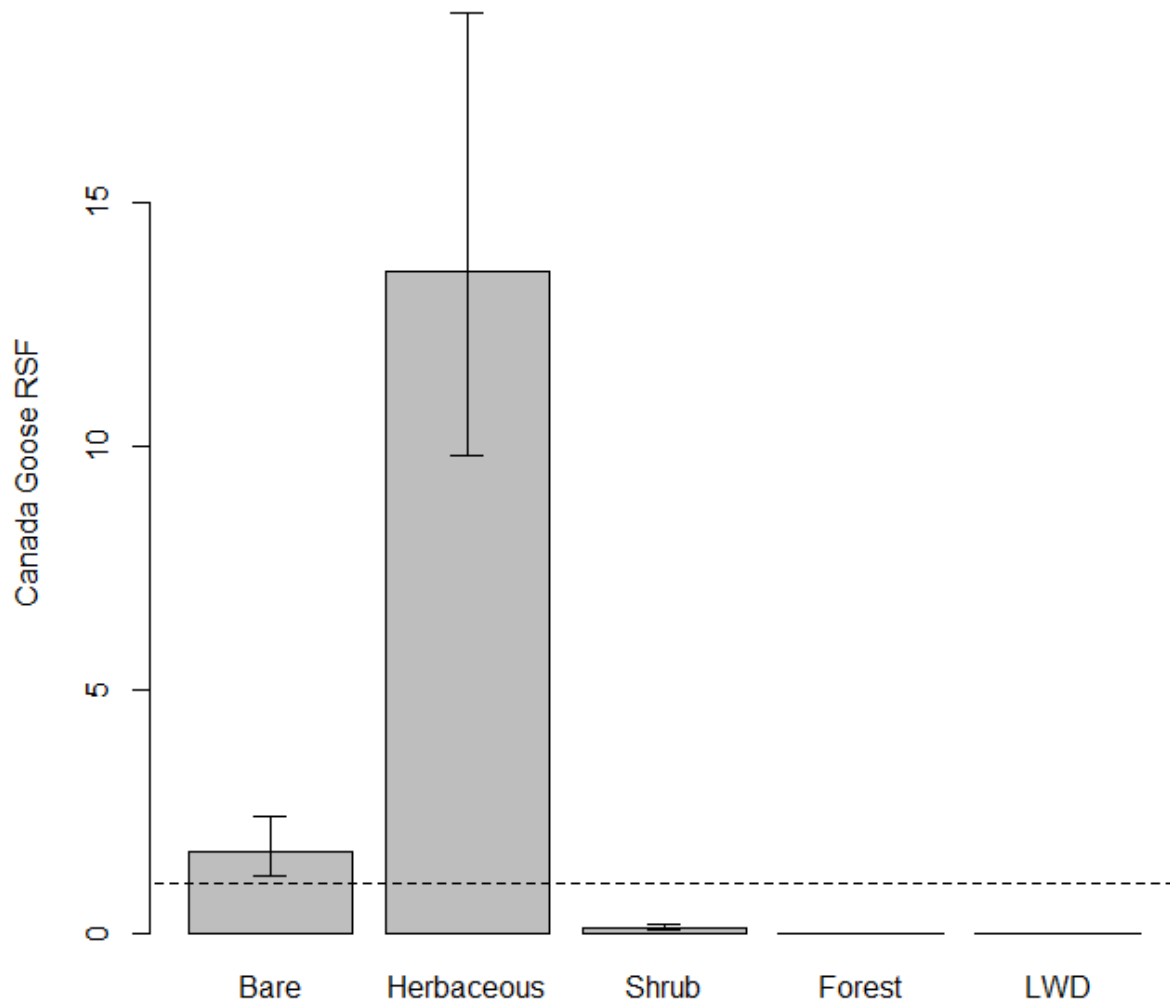


Figure 4. Resource Selection Function (RSF) for Canada Goose (*Branta canadensis*) on the Grande Ronde River, May 2019. Bar heights are RSF values for each habitat type. The dashed line at RSF=1 is equivalent to habitat use at the same proportion as habitat availability, or no selection. Bars above 1 indicate selection for that habitat type, and bars below 1 indicate avoidance. Error bars are one standard error above and below RSF values. Error bars are asymmetric about the RSF bar height because the exponential function expands larger values more than smaller values.

4 Data forms

The following two pages contain data forms for recording riverbird species detections and habitat characteristics for both the river surface and riverbanks.

Riverbird Survey

River _____ Reach _____

Date _____ Observers _____

River flow and conditions _____

Sampling UTM's: Start: N _____ E _____

End: N _____ E _____

Start Time _____ End Time _____

Weather:

Start Temp °C _____ End Temp °C _____ % Cloud cover _____ Wind _____

River Mile	Species*	Water characteristics			Bank Characteristics				
		Rapid	Riffle	Calm	LWD	Bare	Forest	Shrub	Herb.

*Species codes: Canada Goose (CAGO), Mallard (MALL), Canvasback (CANV), Common Goldeneye (COGO), Common Merganser (COME), Hooded Merganser (HOME), Canvasback (CANV), Harlequin Duck (HARD), Osprey (OSPR), Bald Eagle (BAEA), Great Blue Heron (GBHE), Spotted Sandpiper (SPSA), Belted Kingfisher (BEKI), American Dipper (AMDI), Canyon Wren (CANW)

Incidental Sightings:

form_riverbird.pdf

Riverbird Habitat Survey

River _____ Reach _____

Date _____ Observers _____

River flow and conditions _____

Sampling UTM's: Start: N _____ E _____

End: N _____ E _____

Start Time _____ End Time _____

Weather:

Start Temp °C _____ End Temp °C _____ % Cloud cover _____ Wind _____

River Mile	Time	Water characteristics			Left Bank Characteristics					Right Bank Characteristics				
		Rapid	Riffle	Calm	LWD	Bare	Herb.	Shrub	Forest	LWD	Bare	Herb	Shrub	Forest

Incidental Sightings:

form_river_habitat.pdf

5 Data Analysis Template

Commands and code for data analysis using the R software environment.

This document contains raw R commands, suitable for copying and pasting directly into R.

Analysis below is almost entirely automated.

Users need to enter their own numbers in only four places:

- (1) Riverbird location data.
- (2) Number of riverbird detections in each habitat type:
e.g., if 12 birds detected at forested riverbanks, line below would be: `fu <- 12`
- (3) Number of each habitat type detected during 5-minute interval habitat survey.
e.g., if 35 points had forested banks, line below would be: `fa <- 35`
- (4) Standard errors for each habitat type coefficient. These values are given in each model summary, generated by commands below.
If standard errors are not entered, commands below use zero as default values.

Commands below generate numerical results, and plot resource selection function values for each habitat type -- including standard errors.

This analysis should be repeated for each riverbird species.

```
# This is a comment. R ignores anything that follows a pound sign (#).
# To learn more about R, including how to download a copy of R, go to
#   http://cran.R-project.org

# Riverbird distributions
# Below are locations of riverbird detections, for a given species
rm.species <- c( ) # enter locations inside parentheses, divided by commas
rm.species # Check that correct values were entered.
length(rm.species) # Show sample size
hist(rm.species) # Plot histogram, using default plotting parameter values
# Re-plot histogram with breaks every 10 miles
breaks.10 <- 10*c(0:XX) # Replace "XX" with maximum river mile divided by 10
hist(rm.species, breaks = breaks.10, xlab="River Mile",
     ylab="Species Name count", main="") #Replace Species Name with actual name

# Riverbird Habitat Selection
# Below are tallies of riverbird detections in each riverbank habitat
#   type, followed by tallies of habitat types recorded at 5-minute
#   intervals along river.
# Repeat data entry and analysis for each riverbird species.

# Enter number of riverbird detections in each habitat
# (1st letter denotes habitat type; 2nd letter ("u") represents use.)
bu <- # enter no. riverbird detections on bare substrate here
hu <- # enter no. riverbird detections in herbaceous veg. here
su <- # enter no. detections at/in shrubs here
fu <- # enter no. detections at forest here
lu <- # enter no. detections at Large woody debris (LWD) here
```

```

# Enter number of each habitat type recorded at 5-minute intervals
#   = habitat "available"

#   (First letter denotes habitat type;
#   Second letter ("a") represents "available.")

ba <-      # enter no. points w/ bare substrate here
ha <-      # enter no. points w/ herbaceous vegetation here
sa <-      # enter no. points w/ shrubby banks here
fa <-      # enter no. points w/ forested banks here
la <-      # enter no. points w/ LWD here

# Now construct response (bird use) and predictor (habitat) variables
#   for all sampled locations -- both riverbird and habitat sampling.

# For riverbird use, a value of 1 indicates riverbird detected there;
#   0 indicates non-detection.

use.spp <- c(rep(1,bu), rep(0,ba), rep(1,hu), rep(0,ha), rep(1,su),
             rep(0,sa), rep(1,fu), rep(0,fa), rep(1,lu), rep(0,la))

# For habitat variables, 1 indicates location was that habitat type;
#   0 indicates a different habitat.

# Each bare habitat location is assigned value "1" for "bare" category
# Assign 1 and 0 to remaining habitat categories in similar way.

# Variable assignments below include 10 riverbird-habitat
#   combinations, to facilitate error-checking.

# Assignments below use R's repeat function, rep(),
#   to simplify data entry.

bare <- c(rep(1,bu), rep(1,ba), rep(0,hu), rep(0,ha), rep(0,su),
          rep(0,sa), rep(0,fu), rep(0,fa), rep(0,lu), rep(0,la))
herb <- c(rep(0,bu), rep(0,ba), rep(1,hu), rep(1,ha), rep(0,su),
          rep(0,sa), rep(0,fu), rep(0,fa), rep(0,lu), rep(0,la))
shrub <- c(rep(0,bu), rep(0,ba), rep(0,hu), rep(0,ha), rep(1,su),
           rep(1,sa), rep(0,fu), rep(0,fa), rep(0,lu), rep(0,la))
forest <- c(rep(0,bu), rep(0,ba), rep(0,hu), rep(0,ha), rep(0,su),
            rep(0,sa), rep(1,fu), rep(1,fa), rep(0,lu), rep(0,la))
lwd <- c(rep(0,bu), rep(0,ba), rep(0,hu), rep(0,ha), rep(0,su),
         rep(0,sa), rep(0,fu), rep(0,fa), rep(1,lu), rep(1,la))

# Check that Riverbird variable and all habitat variables contain the
#   same number of values.

length(use.spp)
length(bare)
length(herb)
length(shrub)
length(forest)
length(lwd)
#####

```

```

# Fit Generalized Linear Models, glm(), for each categorical habitat variable

spp.bare <- glm(use.spp ~ bare, family=binomial)
summary(spp.bare)

spp.herb <- glm(use.spp ~ herb, family=binomial)
summary(spp.herb)

spp.shrub <- glm(use.spp ~ shrub, family=binomial)
summary(spp.shrub)

spp.for <- glm(use.spp ~ forest, family=binomial)
summary(spp.for)

spp.lwd <- glm(use.spp ~ lwd, family=binomial)
summary(spp.lwd)

#####
# Calculate resource selection function (RSF) values for each habitat
# RSF values for each habitat are glm coefficients,
#   exponentiated (= e^coef)

spp.coef <- c(spp.bare$coef[2], spp.herb$coef[2], spp.shrub$coef[2],
             spp.for$coef[2], spp.lwd$coef[2])

# RSF std errors
spp.err <- c(0, 0, 0, 0, 0) # Replace zeros with coef. std.errors
# Standard errors for each habitat type are in model summaries above

# Function to plot RSF values & standard errors for each habitat type.
# Function adapted from Crawley MJ (2007) The R Book. Wiley. p.56.

error.bar5 <- function(yv, z, nn, yx){
# yv=bar heights, z=error bar heights, nn=labels for each bar,
#   yx=y axis label
xv <-
barplot(exp(yv), ylim=c(0, (max(exp(yv+z)))), names=nn, ylab=yx)
g=(max(xv)-min(xv))/50
for (i in 1:length(xv)) {
  lines(c(xv[i], xv[i]), c(exp(yv[i]+z[i]), exp(yv[i]-z[i]))))
  lines(c(xv[i]-g, xv[i]+g), c(exp(yv[i]+z[i]), exp(yv[i]+z[i]))))
  lines(c(xv[i]-g, xv[i]+g), c(exp(yv[i]-z[i]), exp(yv[i]-z[i]))))
}
}

spp.habitat <- c("Bare", "Herbaceous", "Shrub", "Forest", "LWD")
# x-axis labels
spp.label <- "Riverbird RSF"
# y-axis label: replace "Riverbird" with species name

# Plot RSF values and SE
error.bar5(spp.coef, spp.err, spp.habitat, spp.label)
# Add dashed horizontal line at y=1, or no selection;
#   use in same proportion as availability.
lines(c(0,18), c(1,1), lty=2)

```

6 Example: riverbird data and analysis

Analysis conducted using the R software environment (version 3.6.1).

Upper part of this document contains raw R commands, suitable for copying and pasting directly into R.

The lower part is a transcript of the analysis, including both R commands and results.

```
# This is a comment. R ignores anything that follows a pound sign (#).
# To learn more about R, including how to download a copy of R, go to:
#   http://cran.R-project.org

# Riverbird distributions
# Below is an example for Common Merganser
# Wallowa and Grande Ronde Rivers, 4/28 - 5/6/2021
# Most river guides in US measure distance in miles
# Locations (river miles) where mergansers detected
#   Where multiple individuals detected, use repeat command, rep()
rm.come <- c(91.5, 91.5, 91.25, 91.25, rep(91,5), 90, 90, rep(89, 6),
  88.6, 88.6, rep(86.5,5), 82.5, 82.5, rep(82,3), 78.75, 78.75, 75,
  rep(73,3), 71.5, 71.5, 71, 66, 66, 65, 63, 60, 60, 57.5, 56,
  rep(53.2,7), 49.8, rep(47,3), 46, 43.5, 41.3, rep(40.6,3), 40,
  rep(38,5), 26.5, 26.5, 26, 26, 24.9, 24.7, 20.9, 20.9, rep(20.5,3),
  19, 18.8, 17, 16.5, 16.5, 12.7, 9.8, 8)
rm.come      # Check that correct values were entered.
length(rm.come) # 88 mergansers detected
hist(rm.come)   # Histogram of locations = longitudinal distribution
  # Plot histogram with bars at 10-mile intervals
breaks.come <- 10*c(0:10)
hist(rm.come, breaks = breaks.come, xlab="River Mile",
  ylab="Common Merganser count", main="") # suppress plot title

# Riverbird Habitat Selection
# Below are tallies of Canada Goose (CAGO) detections in each
#   riverbank habitat type, followed by tallies of habitat types
#   recorded at 5-minute intervals along river.
# Grande Ronde River 5/7-10/2019
# CAGO data
# bare 15
# herb 54
# shrub 3
# forest 0
# LWD 0
# total 72

# Assign above tallies to objects for each habitat used
bu <- 15
hu <- 54
su <- 3
fu <- 0
lu <- 0
```

```

# Random sample of habitats
# bare 27
# herb 36
# shrub 61
# forest 73
# LWD 2
# total 199

# Assign above tallies to objects for each habitat "available"
ba <- 27
ha <- 36
sa <- 61
fa <- 73
la <- 2

# A total of 271 (=72+199) bank habitat locations were sampled,
# 72 with geese present and 199 without geese sampled at 5-minute
# intervals along the river.

# Now construct response (CAGO use) and predictor (habitat)
# variables for all 271 locations.
# For CAGO use, a value of 1 indicates CAGO detected there;
# 0 indicates non-detection.

use.cago <- c(rep(1,bu), rep(0,ba), rep(1,hu), rep(0,ha), rep(1,su),
  rep(0,sa), rep(1,fu), rep(0,fa), rep(1,lu), rep(0,la))

# For habitat variables, 1 indicates location was that habitat type;
# 0 indicates a different habitat.
# For "bare" habitat, CAGO detected at 15 locations w/ bare habitat,
# 27 locations in habitat sample were bare.
# Each of those bare habitat locations are assigned value "1" for the
# "bare" category.
# The remaining 229 locations were not "bare" and are assigned "0"
# for the "bare" variable.
# Assign 1 and 0 to remaining habitat categories in similar way.
# Variable assignments below include 10 CAGO-habitat combinations,
# to facilitate error-checking.
# Use R's repeat function, rep(), to simplify data entry.

bare <- c(rep(1,bu), rep(1,ba), rep(0,hu), rep(0,ha), rep(0,su),
  rep(0,sa), rep(0,fu), rep(0,fa), rep(0,lu), rep(0,la))
herb <- c(rep(0,bu), rep(0,ba), rep(1,hu), rep(1,ha), rep(0,su),
  rep(0,sa), rep(0,fu), rep(0,fa), rep(0,lu), rep(0,la))
shrub <- c(rep(0,bu), rep(0,ba), rep(0,hu), rep(0,ha), rep(1,su),
  rep(1,sa), rep(0,fu), rep(0,fa), rep(0,lu), rep(0,la))
forest <- c(rep(0,bu), rep(0,ba), rep(0,hu), rep(0,ha), rep(0,su),
  rep(0,sa), rep(1,fu), rep(1,fa), rep(0,lu), rep(0,la))
lwd <- c(rep(0,bu), rep(0,ba), rep(0,hu), rep(0,ha), rep(0,su),
  rep(0,sa), rep(0,fu), rep(0,fa), rep(1,lu), rep(1,la))

# Check that CAGO and all habitat variables contain the same number
# of values (here n=271).

```

```

length(use.cago)
length(bare)
length(herb)
length(shrub)
length(forest)
length(lwd)

# #####
# Fit Generalized Linear Model, glm(),w/categorical habitat variable
cago.bare <- glm(use.cago ~ bare, family=binomial)
summary(cago.bare)
cago.herb <- glm(use.cago ~ herb, family=binomial)
summary(cago.herb)
cago.shrub <- glm(use.cago ~ shrub, family=binomial)
summary(cago.shrub)
cago.for <- glm(use.cago ~ forest, family=binomial)
summary(cago.for)
cago.lwd <- glm(use.cago ~ lwd, family=binomial)
summary(cago.lwd)
# #####
# Calculate resource selection function (RSF) values for each habitat
# RSF values for each habitat are glm coefficients,
#   exponentiated (= e^coef)

cago.coef <- c(cago.bare$coef[2], cago.herb$coef[2],
              cago.shrub$coef[2], cago.for$coef[2], cago.lwd$coef[2])

# RSF std errors
cago.err <- c(0.3565, 0.3286, 0.6094, 0, 0)
# No detections in forest, LWD, so set std.error forest and LWD
# to zero to suppress unrealistic error bars

# Function to plot RSF values & standard errors for each habitat type.
# Function adapted from Crawley MJ (2007) The R Book. Wiley. p.56.

error.bar5 <- function(yv, z, nn, yx){
# yv=bar heights, z=error bar heights, nn=labels for each bar,
  yx=y axis label
xv <-
barplot(exp(yv), ylim=c(0, (max(exp(yv+z)))),names=nn, ylab=yx)
g=(max(xv)-min(xv))/50
for (i in 1:length(xv)) {
  lines(c(xv[i], xv[i]), c(exp(yv[i]+z[i]),exp(yv[i]-z[i])))
  lines(c(xv[i]-g, xv[i]+g), c(exp(yv[i]+z[i]),exp(yv[i]+z[i]))))
  lines(c(xv[i]-g, xv[i]+g), c(exp(yv[i]-z[i]),exp(yv[i]-z[i]))))
}
}

cago.habitat <- c("Bare", "Herbaceous", "Shrub", "Forest", "LWD")
# x-axis labels
cago.label <- "Canada Goose RSF" # y-axis label

```

```

# Plot RSF values and SE
# Generates Figure 1 in "Data Analysis Instructions" document.

error.bar5(cago.coef, cago.err, cago.habitat, cago.label)
# Add dashed horizontal line at y=1, or no selection;
#     use in same proportion as availability
lines(c(0,18), c(1,1), lty=2)

# *****
# *****

R version 3.6.1 (2019-07-05) -- "Action of the Toes"
Copyright (C) 2019 The R Foundation for Statistical Computing

> # This is a comment. R ignores anything that follows pound sign (#).
> # To learn more about R, including how to download a copy of R, goto
> #   http://cran.R-project.org

> # Riverbird distributions
> # Below is an example for Common Merganser
> # Wallowa and Grande Ronde Rivers, 4/28 - 5/6/2021
> # Most river guides in US measure distance in miles
> # Locations (river miles) where mergansers detected
> #   Where multiple individuals detected, use repeat command, rep()

> rm.come <- c(91.5, 91.5, 91.25, 91.25, rep(91,5), 90, 90, rep(89, 6),
+   88.6, 88.6, rep(86.5,5), 82.5, 82.5, rep(82,3), 78.75, 78.75, 75,
+   rep(73,3), 71.5, 71.5, 71, 66, 66, 65, 63, 60, 60, 57.5, 56,
+   rep(53.2,7), 49.8, rep(47,3), 46, 43.5, 41.3, rep(40.6,3), 40,
+   rep(38,5), 26.5, 26.5, 26, 26, 24.9, 24.7, 20.9, 20.9, rep(20.5,3),
+   19, 18.8, 17, 16.5, 16.5, 12.7, 9.8, 8)
> rm.come
 [1] 91.50 91.50 91.25 91.25 91.00 91.00 91.00 91.00 91.00 90.00 90.00 89.00
[13] 89.00 89.00 89.00 89.00 89.00 88.60 88.60 86.50 86.50 86.50 86.50 86.50
[25] 82.50 82.50 82.00 82.00 82.00 78.75 78.75 75.00 73.00 73.00 73.00 71.50
[37] 71.50 71.00 66.00 66.00 65.00 63.00 60.00 60.00 57.50 56.00 53.20 53.20
[49] 53.20 53.20 53.20 53.20 53.20 49.80 47.00 47.00 47.00 46.00 43.50 41.30
[61] 40.60 40.60 40.60 40.00 38.00 38.00 38.00 38.00 38.00 26.50 26.50 26.00
[73] 26.00 24.90 24.70 20.90 20.90 20.50 20.50 20.50 19.00 18.80 17.00 16.50
[85] 16.50 12.70  9.80  8.00
> length(rm.come) # 88 mergansers detected
[1] 88
> hist(rm.come) # Histogram of locations = longitudinal distribution
> # Plot histogram with bars at 10-mile intervals
> breaks.come <- 10*c(0:10)
> hist(rm.come, breaks = breaks.come2, xlab="River Mile",
+   ylab="Common Merganser count", main="") # suppress plot title

```



```
> # Riverbird Habitat Selection
> # Below are tallies of Canada Goose detections in each
> #   riverbank habitat type, followed by tallies of habitat types
> #   recorded at 5-minute intervals along river.
> # Grande Ronde River 5/7-10/2019
> # CAGO data
> # bare 15
> # herb 54
> # shrub 3
> # forest 0
> # LWD 0
> # total 72

> # Assign above tallies to objects for each habitat used
> bu <- 15
> hu <- 54
> su <- 3
> fu <- 0
> lu <- 0

> # Random sample
> # bare 27
> # herb 36
> # shrub 61
> # forest 73
> # LWD 2
> # total 199

> # Assign above tallies to objects for each habitat "available"
> ba <- 27
> ha <- 36
> sa <- 61
> fa <- 73
> la <- 2

> # A total of 271 (=72+199) bank habitat locations were sampled,
> #   72 with geese present and 199 without geese sampled at 5-minute
> #   intervals along the river.

> # Now construct response (CAGO use) and predictor (habitat)
> #   variables for all 271 locations.
> # For CAGO use, a value of 1 indicates CAGO detected there;
> #   0 indicates non-detection.

> use.cago <- c(rep(1,bu), rep(0,ba), rep(1,hu), rep(0,ha), rep(1,su),
rep(0,sa), rep(1,fu), rep(0,fa), rep(1,lu), rep(0,la))

> # For habitat variables, 1 indicates location was that habitat type;
> #   0 indicates a different habitat.
> # For "bare" habitat, CAGO detected at 15 locations w/ bare habitat,
> #   27 locations in habitat sample were bare.
> # Each of those bare habitat locations are assigned value "1" for
```

```

> # the "bare" category.
> # The remaining 229 locations were not "bare" and are assigned "0"
> # for the "bare" variable.
> # Assign 1 and 0 to remaining habitat categories in similar way.
> # Variable assignments below include 10 CAGO-habitat combinations,
> # to facilitate error-checking.
> # Use R's repeat function, rep(), to simplify data entry.

> bare <- c(rep(1,bu), rep(1,ba), rep(0,hu), rep(0,ha), rep(0,su),
rep(0,sa), rep(0,fu), rep(0,fa), rep(0,lu), rep(0,la))
> herb <- c(rep(0,bu), rep(0,ba), rep(1,hu), rep(1,ha), rep(0,su),
rep(0,sa), rep(0,fu), rep(0,fa), rep(0,lu), rep(0,la))
> shrub <- c(rep(0,bu), rep(0,ba), rep(0,hu), rep(0,ha), rep(1,su),
rep(1,sa), rep(0,fu), rep(0,fa), rep(0,lu), rep(0,la))
> forest <- c(rep(0,bu), rep(0,ba), rep(0,hu), rep(0,ha), rep(0,su),
rep(0,sa), rep(1,fu), rep(1,fa), rep(0,lu), rep(0,la))
> lwd <- c(rep(0,bu), rep(0,ba), rep(0,hu), rep(0,ha), rep(0,su),
rep(0,sa), rep(0,fu), rep(0,fa), rep(1,lu), rep(1,la))

> # Check that CAGO and all habitat variables contain the same number
> # of values (here n=271).
> length(use.cago)
[1] 271
> length(bare)
[1] 271
> length(herb)
[1] 271
> length(shrub)
[1] 271
> length(forest)
[1] 271
> length(lwd)
[1] 271
>
> #####
> # Fit Generalized Linear Model, glm(),w/categorical habitat variable
>
> cago.bare <- glm(use.cago ~ bare, family=binomial)
> summary(cago.bare)

```

Call:

```
glm(formula = use.cago ~ bare, family = binomial)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.9400	-0.7566	-0.7566	1.4350	1.6677

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-1.1044	0.1528	-7.226	4.96e-13 ***
bare	0.5167	0.3565	1.449	0.147

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 313.77 on 270 degrees of freedom
Residual deviance: 311.75 on 269 degrees of freedom
AIC: 315.75

Number of Fisher Scoring iterations: 4

```
>
> cago.herb <- glm(use.cago ~ herb, family=binomial)
> summary(cago.herb)
```

Call:
glm(formula = use.cago ~ herb, family = binomial)

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.3537	-0.4577	-0.4577	1.0108	2.1486

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.2034	0.2484	-8.872	< 2e-16 ***
herb	2.6088	0.3286	7.939	2.03e-15 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 313.77 on 270 degrees of freedom
Residual deviance: 238.38 on 269 degrees of freedom
AIC: 242.38

Number of Fisher Scoring iterations: 4

```
>
> cago.shrub <- glm(use.cago ~ shrub, family=binomial)
> summary(cago.shrub)
```

Call:
glm(formula = use.cago ~ shrub, family = binomial)

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.9005	-0.9005	-0.9005	1.4823	2.4740

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-0.6931	0.1474	-4.701	2.59e-06 ***
shrub	-2.3191	0.6094	-3.805	0.000142 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 313.77 on 270 degrees of freedom
Residual deviance: 287.74 on 269 degrees of freedom
AIC: 291.74

Number of Fisher Scoring iterations: 5

```
>
> cago.for <- glm(use.cago ~ forest, family=binomial)
> summary(cago.for)
```

Call:
glm(formula = use.cago ~ forest, family = binomial)

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.95077	-0.95077	-0.00013	1.42239	1.42239

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-0.5596	0.1477	-3.788	0.000152 ***
forest	-18.0065	763.4171	-0.024	0.981182

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 313.77 on 270 degrees of freedom
Residual deviance: 259.57 on 269 degrees of freedom
AIC: 263.57

Number of Fisher Scoring iterations: 17

```
>
> cago.lwd <- glm(use.cago ~ lwd, family=binomial)
> summary(cago.lwd)
```

Call:
glm(formula = use.cago ~ lwd, family = binomial)

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.7893	-0.7893	-0.7893	1.6236	1.6236

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-1.0065	0.1377	-7.309	2.69e-13 ***
lwd	-14.5595	1029.1215	-0.014	0.989

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 313.77 on 270 degrees of freedom

Residual deviance: 312.53 on 269 degrees of freedom

AIC: 316.53

Number of Fisher Scoring iterations: 14

```
> # #####
> # Calculate resource selection function (RSF) values, each habitat
> # RSF values for each habitat are glm coefficients,
> #     exponentiated (= e^coef)

> cago.coef <- c(cago.bare$coef[2], cago.herb$coef[2],
+             cago.shrub$coef[2], cago.for$coef[2], cago.lwd$coef[2])

> # RSF std errors
> cago.err <- c(0.3565, 0.3286, 0.6094, 0, 0)
>     # No detections in forest, LWD, so set std.error forest and LWD
>     # to zero to suppress unrealistic error bars

> # Function to plot RSF values and std. errors for each habitat type
> # Function adapted from Crawley MJ (2007) The R Book. Wiley. p.56.

> error.bar5 <- function(yv, z, nn, yx){
+ # yv=bar heights, z=error bar heights, nn=labels for each bar,
+   yx=y axis label
+ xv <-
+ barplot(exp(yv), ylim=c(0, (max(exp(yv+z))))), names=nn, ylab=yx)
+ g=(max(xv)-min(xv))/50
+ for (i in 1:length(xv)) {
+   lines(c(xv[i], xv[i]), c(exp(yv[i]+z[i]), exp(yv[i]-z[i])))
+   lines(c(xv[i]-g, xv[i]+g), c(exp(yv[i]+z[i]), exp(yv[i]+z[i])))
+   lines(c(xv[i]-g, xv[i]+g), c(exp(yv[i]-z[i]), exp(yv[i]-z[i])))
+ }
+ }

> cago.habitat <- c("Bare", "Herbaceous", "Shrub", "Forest", "LWD")
+   # x-axis labels
> cago.label <- "Canada Goose RSF"     # y-axis label

> # Plot RSF values and SE
> # Generates Figure 1 in "Data Analysis Instructions" document.

> error.bar5(cago.coef, cago.err, cago.habitat, cago.label)
> # Add dashed horizontal line at y=1, or no selection;
> #     use in same proportion as availability
> lines(c(0,18), c(1,1), lty=2)
```

7 Further Reading

All About Birds. Cornell Laboratory of Ornithology, Ithaca, New York.

<https://www.allaboutbirds.org/guide/>

Ehrlich P.R., D.S. Dobkin, D. Wheye. 1988. *The Birder's Handbook: A Field Guide to the Natural History of North American Birds*. Simon & Schuster, Inc., New York.

Rosenberg K.V., A.M. Dokter, P.J. Blancher, J.R. Sauer, A.C. Smith, P.A. Smith, J.C. Stanton, A. Panjabi, L. Helft, M. Parr, P.P. Marra. 2019. Decline of the North American avifauna. *Science* 366:120-124. doi: 10.1126/science.aaw1313

Sibley D.A. 2009. *The Sibley Guide to Bird Life and Behavior*. Alfred A. Knopf, New York.

Sibley D.A. 2011. *The Sibley Guide to Birds, Second ed.* Alfred A. Knopf, New York.

Stevens L.E., K.A. Buck, B.T. Brown, N.C. Kline. 1997. Dam and geomorphological influences on Colorado River waterbird distribution, Grand Canyon, Arizona. *Regulated Rivers: Res. & Manage.* 13:151-169.

8 References Cited

Adde A., D. Stralberg, T. Logan, C. Lepage, S. Cumming, and M. Darveau. 2020a. Projected effects of climate change on the distribution and abundance of breeding waterfowl in Eastern Canada. *Climatic Change* 162:2339-2358. doi: 10.1007/s10584-020-02829-9

Adde A., M. Darveau, N. Barker, L. Imbeau, and S. Cumming. 2020b. Environmental covariates for modelling the distribution and abundance of breeding ducks in northern North America: a review. *Écoscience* 1-20. doi: 10.1080/11956860.2020.1802933

Hill, A. F., M. Jacquemart, A. U. Gold, and K. Tiampo. 2021. Changing the culture of fieldwork in the geosciences. *Eos* 102 doi: 10.1029/2021EO158013.

Manly B.F.J., L.L. McDonald, D.L. Thomas, T.L. McDonald, and W.P. Erickson. 2002. *Resource Selectin by Animals: Statistical Design and Analysis for Field Studies*. 2nd ed. Kluwer Academic, Dordrecht, The Netherlands.

McCaffery R., J. McLaughlin, K. Sager-Fradkin, and K.J. Jenkins. 2018. Terrestrial fauna are agents and endpoints in ecosystem restoration following dam removal. *Ecological Restoration* 36: 97-107. doi: 10.3368/er.36.2.97

McDonald, L.L., W.P. Erickson, M.S. Boyce, and J.R. Alldredge. 2012. Modeling vertebrate use of terrestrial resources. Pp.410-428 in N.J. Silvy, editor. *The Wildlife Techniques Manual, Volume 1: Research*, 7th ed. Johns Hopkins Univ. Press, Baltimore, MD.

Morrison M.L., W.M. Block, M.D. Strickland, and W.L. Kendall. 2001. *Wildlife Study Design*. Springer-Verlag, New York, NY.

NASEM (National Academies of Sciences, Engineering, and Medicine). 2018. *How People Learn II: Learners, Contexts, and Cultures*. National Academies Press, Washington, D.C.

- Northrup J.M., J.W. Rivers, Z. Yang, and M.G. Betts. 2018. Synergistic effects of climate and land-use change influence broad-scale avian population declines. *Global Change Biology* 25: 1561-1575. doi: 10.1111/gcb.14571
- O'Connell K., K.L. Hoke, M. Giamellaro, A.R. Berkowitz, and J. Branchaw. 2021. A Tool for Designing and Studying Student-Centered Undergraduate Field Experiences: The UFERN Model. *BioScience* XX:XXXX-XXXX doi: 10.1093/biosci/biab112
- Ogden J.C., J.D. Baldwin, O.L. Bass, J.A. Browder, M.I. Cook, P.C. Frederick, P.E. Frezza, R.A. Galvez, A.B. Hodgson, K.D. Meyer, L.D. Oberhofer, A.F. Paul, P.J. Fletcher, S.M. Davis, and J.J. Lorenz. 2014a. Waterbirds as indicators of ecosystem health in the coastal marine habitats of southern Florida: 1. Selection and justification for a suite of indicator species. *Ecological Indicators* 44:148-163.
- Ogden J.C., J.D. Baldwin, O.L. Bass, J.A. Browder, M.I. Cook, P.C. Frederick, P.E. Frezza, R.A. Galvez, A.B. Hodgson, K.D. Meyer, L.D. Oberhofer, A.F. Paul, P.J. Fletcher, S.M. Davis, and J.J. Lorenz. 2014b. Waterbirds as indicators of ecosystem health in the coastal marine habitats of Southern Florida: 2. Conceptual ecological models. *Ecological Indicators* 44:128-147.
- Palmer, T. 2004. *Lifelines: The Case for River Conservation*, 2nd ed. Rowman & Littlefield Pub.
- Puritty, C., L. R. Strickland, E. Alia, B. Blonder, E. Klein, M. T. Kohl, E. McGee, M. Quintana, R. E. Ridley, B. Tellman, L. R. Gerber. 2017. Without inclusion, diversity initiatives may not be enough. *Science* 357:1101-1102. doi: 10.1126/science.aai9054
- R Core Team. 2019. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL: <https://www.R-project.org/>.
- Reid A.J., A.K. Carlson, I.F. Creed, E.J. Eliason, P.A. Gell, P.T. Johnson, K.A. Kidd, T.J. MacCormack, J.D. Olden, S.J. Ormerod, J.P. Smol, W.W. Taylor, K. Tockner, J.C. Vermaire, D. Dudgeon, and S.J. Cooke. 2018. Emerging threats and persistent conservation challenges for freshwater biodiversity. *Biological Reviews* 94:849-873. doi:10.1111/brv.12480
- Rosenberg K.V., A.M. Dokter, P.J. Blancher, J.R. Sauer, A.C. Smith, P.A. Smith, J.C. Stanton, A. Panjabi, L. Helft, M. Parr, and P.P. Marra. 2019. Decline of the North American avifauna. *Science* 366: 120-124. doi: 10.1126/science.aaw1313
- Shortlidge, E. E., A. Jolley, S. Shaulskiy, E. G. Ward, C. N. Lorentz, and K. O'Connell. 2021. A resource for understanding and evaluating outcomes of undergraduate field experiences. *Ecology and Evolution* 11:16387-16408. doi: 10.1002/ece3.8241
- Silverthorn V.M., C.A. Bishop, J.E. Elliott, and C.A. Morrissey. 2018. An assessment of run-of-river hydroelectric dams on mountain stream ecosystems using the American dipper as an avian indicator. *Ecological Indicators* 93: 942-951. doi: 10.1016/j.ecolind.2018.05.086
- Silvy, N.J., editor. 2012. *The Wildlife Techniques Manual, Volume 1: Research*, 7th ed. Johns Hopkins Univ. Press, Baltimore, MD.
- Stevens L.E., K.A. Buck, B.T. Brown, N.C. Kline. 1997. Dam and geomorphological influences on Colorado River waterbird distribution, Grand Canyon, Arizona. *Regulated Rivers: Res. & Manage.* 13:151-169.
- Sutherland W.J., ed. 1996. *Ecological Census Techniques: A Handbook*. Cambridge University Press, Cambridge, UK.

Vorosmarty C.J., P.B. McIntyre, M.O. Gessner, D. Dudgeon, A. Prusevich, P. Green, S. Glidden, S.E. Bunn, C.A. Sullivan, C.R. Liermann, and P.M. Davies, 2010. Global threats to human water security and river biodiversity. *Nature* 467:555–561.

Wetlands International. 2012. Waterbird Population Estimates, Fifth Edition. Summary Report. Wetlands International, Wageningen, The Netherlands.

Wiens J., G.D. Hayward, R.S. Holthausen, and M.J. Wisdom. 2008. Using surrogate species and groups for conservation planning and management. *BioScience* 58, 241–252.