
Automating the annotation and stacking of JV rasters

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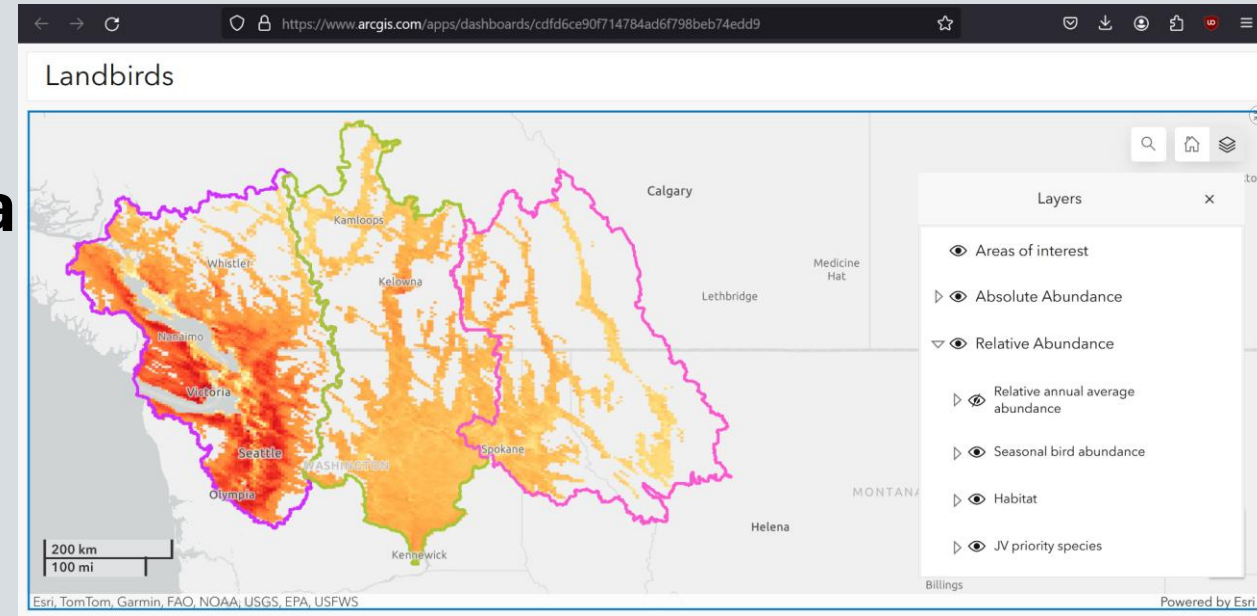
Impact Assessment Fellow

Boreal Avian Modelling Project, UofA

Problems:

(1) How can we efficiently attach ecological and management data to rasters scattered across multiple folders?

(2) How can we automate the sorting of these raster data by ecological or management variables of interest?

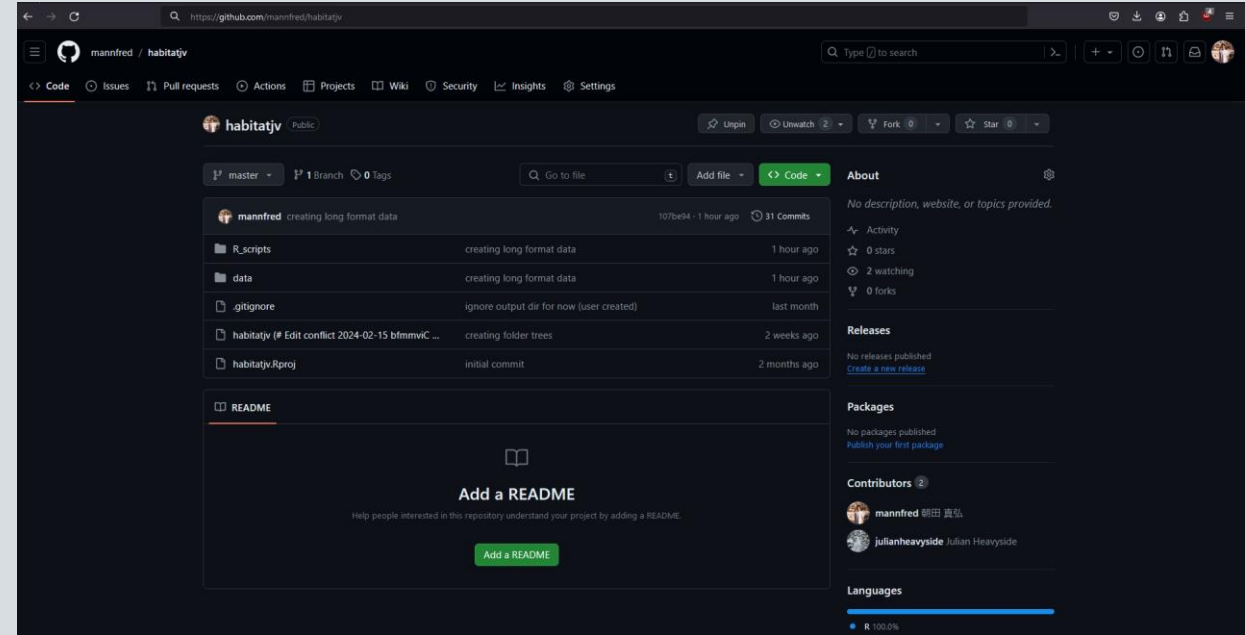


Lili Simon, Devin de Zwaan

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github.com/mannfred/habitatjv

Problems:

(1) How can we efficiently attach ecological and management data to raster files scattered across multiple folders?

> sourcing ecological data from Rosenberg et al (2019) *Science*

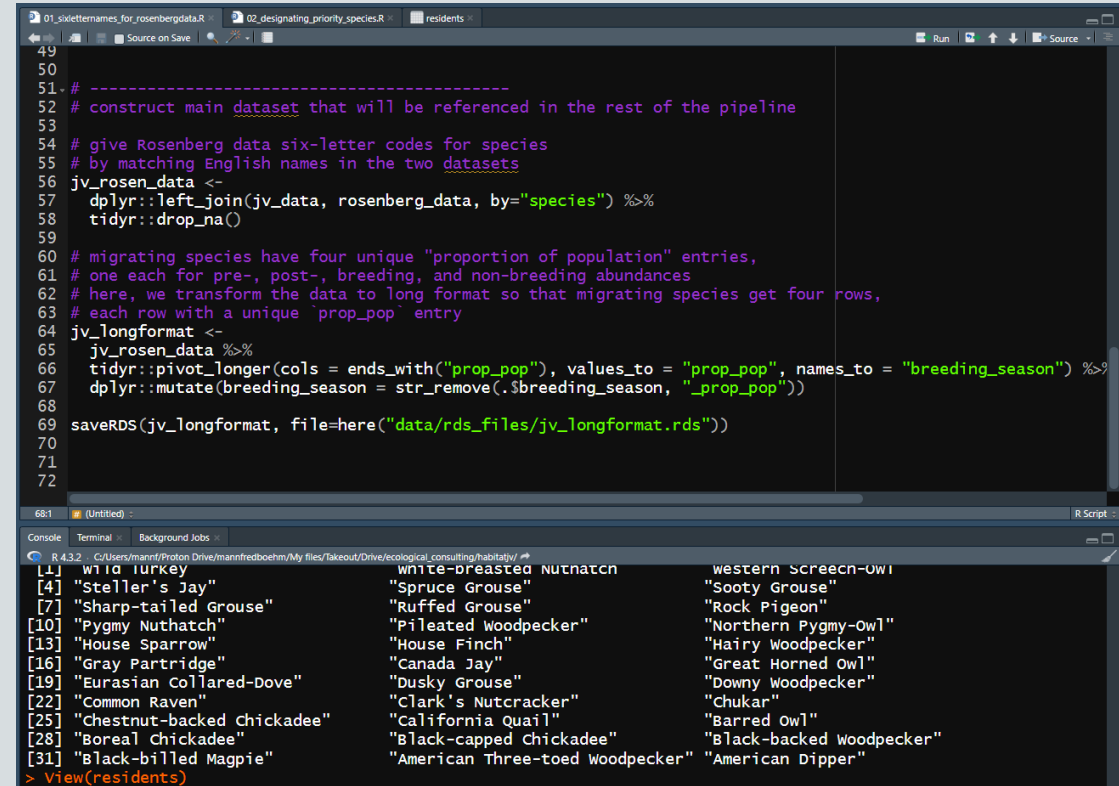
> `joining` to JV abundance data



Problems:

(1) How can we efficiently attach ecological and management data to raster files scattered across multiple folders?

> generating a long format
`data.frame` that treats breeding season as an observation of the smallest sampling unit (species)



```
49  
50  
51 # -----  
52 # construct main dataset that will be referenced in the rest of the pipeline  
53  
54 # give Rosenberg data six-letter codes for species  
55 # by matching English names in the two datasets  
56 jv_rosen_data <-  
57   dplyr::left_join(jv_data, rosenberg_data, by="species") %>%  
58   tidyr::drop_na()  
59  
60 # migrating species have four unique "proportion of population" entries,  
61 # one each for pre-, post-, breeding, and non-breeding abundances  
62 # here, we transform the data to long format so that migrating species get four rows,  
63 # each row with a unique 'prop_pop' entry  
64 jv_longformat <-  
65   jv_rosen_data %>%  
66   tidyr::pivot_longer(cols = ends_with("prop_pop"), values_to = "prop_pop", names_to = "breeding_season") %>%  
67   dplyr::mutate(breeding_season = str_remove(.$breeding_season, "_prop_pop"))  
68  
69 saveRDS(jv_longformat, file=here("data/rds_files/jv_longformat.rds"))  
70  
71  
72
```

Console

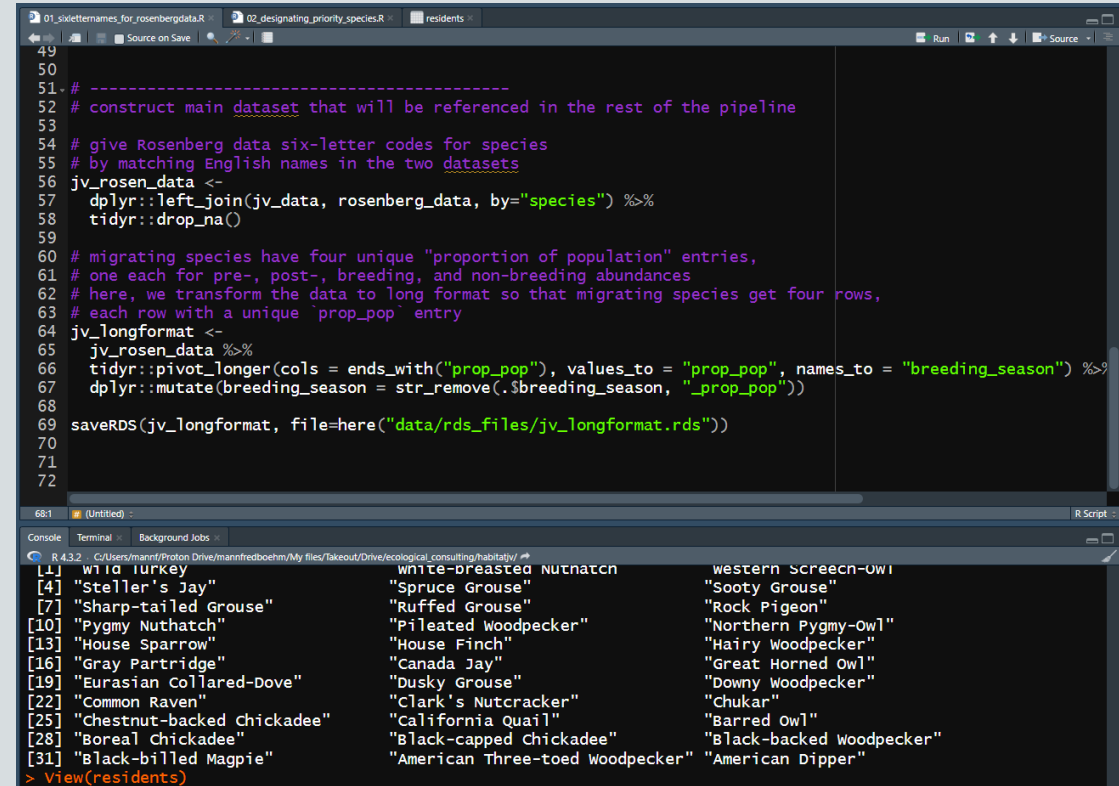
[1] wild turkey	white-breasted nuthatch	western screech-owl
[4] "Steller's Jay"	"Spruce Grouse"	"Sooty Grouse"
[7] "Sharp-tailed Grouse"	"Ruffed Grouse"	"Rock Pigeon"
[10] "Pygmy Nuthatch"	"Pileated Woodpecker"	"Northern Pygmy-Owl"
[13] "House Sparrow"	"House Finch"	"Hairy Woodpecker"
[16] "Gray Partridge"	"Canada Jay"	"Great Horned Owl"
[19] "Eurasian Collared-Dove"	"Dusky Grouse"	"Downy Woodpecker"
[22] "Common Raven"	"Clark's Nutcracker"	"chukar"
[25] "Chestnut-backed chickadee"	"California Quail"	"Barred Owl"
[28] "Boreal Chickadee"	"Black-capped chickadee"	"Black-backed woodpecker"
[31] "Black-billed Magpie"	"American Three-toed Woodpecker"	"American Dipper"

> View(residents)

Problems:

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> assigning stewardship responsibility (logical) to each observation (row) using a threshold of >0.90 proportion of global population



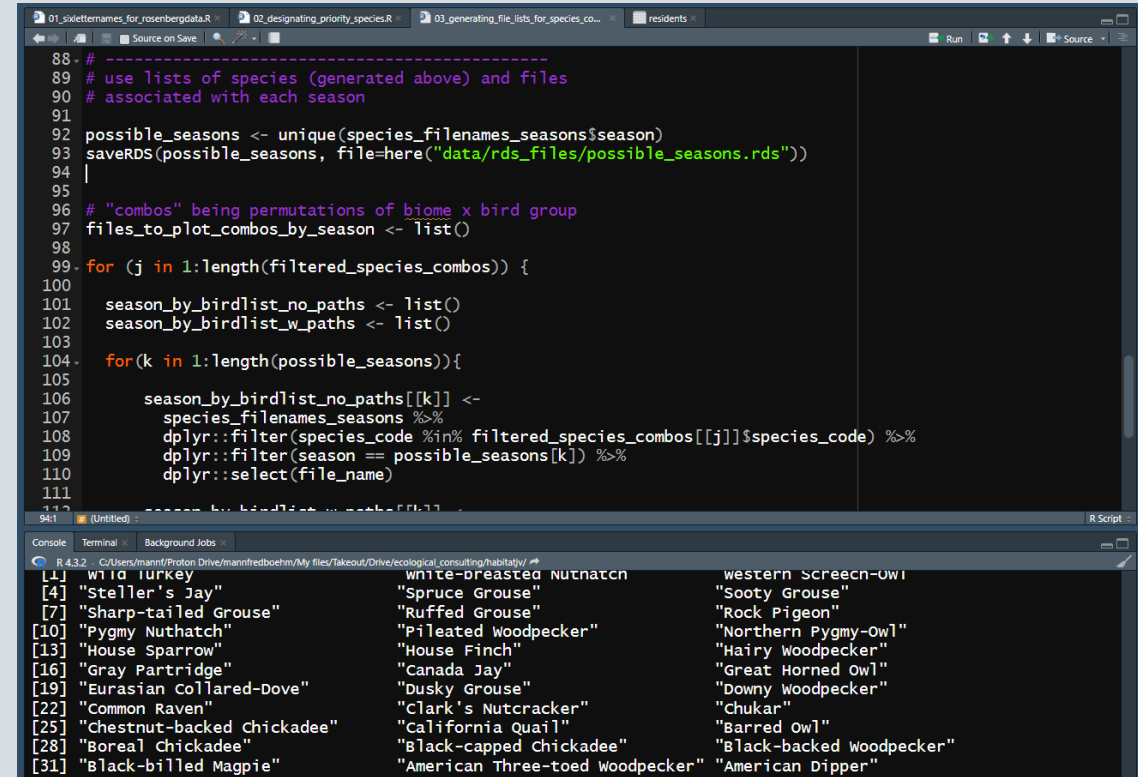
```
01_sixletternames_for_rosenbergdata.R 02_designating_priority_species.R residents
# -----
# construct main dataset that will be referenced in the rest of the pipeline
# give Rosenberg data six-letter codes for species
# by matching English names in the two datasets
jv_rosen_data <-
  dplyr::left_join(jv_data, rosenberg_data, by="species") %>%
  tidyr::drop_na()
# migrating species have four unique "proportion of population" entries,
# one each for pre-, post-, breeding, and non-breeding abundances
# here, we transform the data to long format so that migrating species get four rows,
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jv_longformat <-
  jv_rosen_data %>%
  tidyr::pivot_longer(cols = ends_with("prop_pop"), values_to = "prop_pop", names_to = "breeding_season") %>%
  dplyr::mutate(breeding_season = str_remove(.$breeding_season, "_prop_pop"))
saveRDS(jv_longformat, file=here("data/rds_files/jv_longformat.rds"))

68:1 (Untitled) R Script
Console Terminal Background Jobs
R 4.3.2 - C:\Users\marnf\Proton Drive\mannfredboehm\My files\Takeout\Drive\ecological_consulting\habitatjv
[1] wild turkey white-breasted Nuthatch western Screech-Owl
[4] "Steller's Jay" "Spruce Grouse" "Sooty Grouse"
[7] "Sharp-tailed Grouse" "Ruffed Grouse" "Rock Pigeon"
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> View(residents)
```


Problems:

(2) How can we automate the sorting of these raster data by ecological or management variables of interest?

> generating lists of file paths that capture every permutation of the variables of interest (breeding biome, bird group, stewardship responsibility, JV, etc.)



```
88 # -----
89 # use lists of species (generated above) and files
90 # associated with each season
91
92 possible_seasons <- unique(species_filenames_seasons$season)
93 saveRDS(possible_seasons, file=here("data/rds_files/possible_seasons.rds"))
94
95
96 # "combos" being permutations of biome x bird group
97 files_to_plot_combos_by_season <- list()
98
99 for (j in 1:length(filtered_species_combos)) {
100
101   season_by_birdlist_no_paths <- list()
102   season_by_birdlist_w_paths <- list()
103
104   for(k in 1:length(possible_seasons)){
105
106     season_by_birdlist_no_paths[[k]] <-
107       species_filenames_seasons %>%
108       dplyr::filter(species_code %in% filtered_species_combos[[j]]$species_code) %>%
109       dplyr::filter(season == possible_seasons[k]) %>%
110       dplyr::select(file_name)
111
112     season_by_birdlist_w_paths[[k]] <-
113       species_filenames_seasons %>%
114       dplyr::filter(species_code %in% filtered_species_combos[[j]]$species_code) %>%
115       dplyr::filter(season == possible_seasons[k]) %>%
116       dplyr::select(file_name)
```

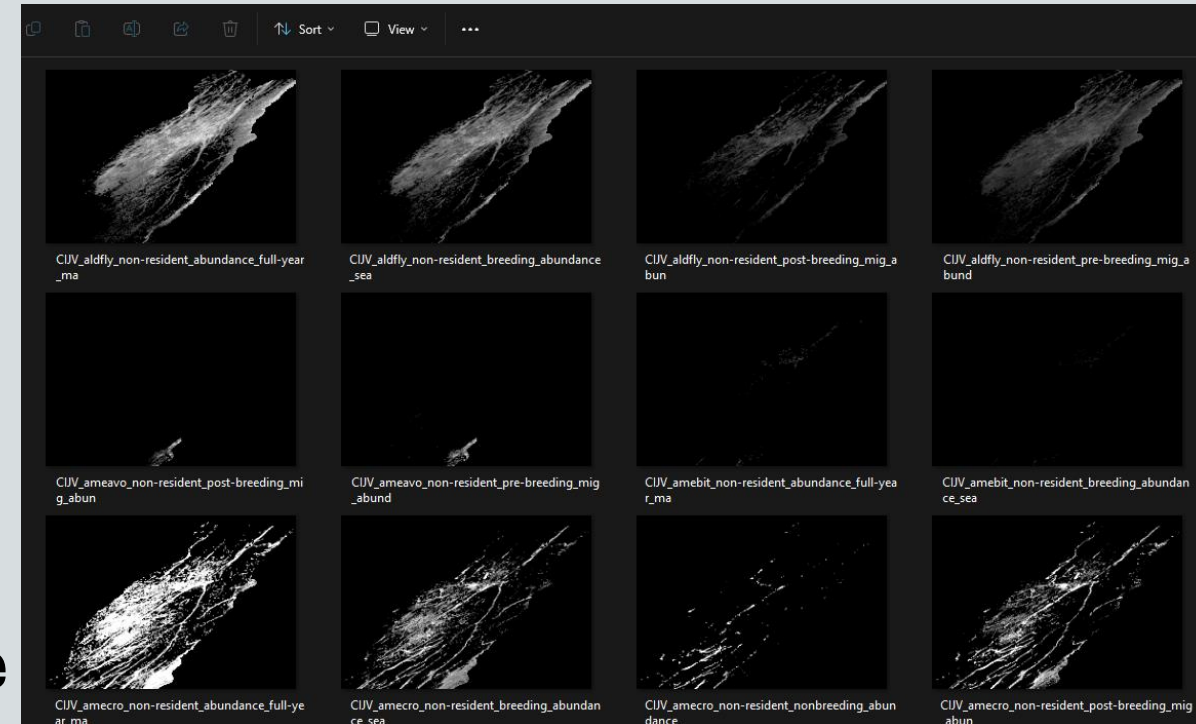
Console

[1] "wild turkey"	"white-breasted Nuthatch"	"western Screech-Owl"
[4] "Steller's Jay"	"Spruce Grouse"	"Sooty Grouse"
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Problems:

(2) How can we automate the sorting of these raster data by ecological or management variables of interest?

> generating a local folder tree that can house the sorted data, and automating the copying of the right files to the right folders

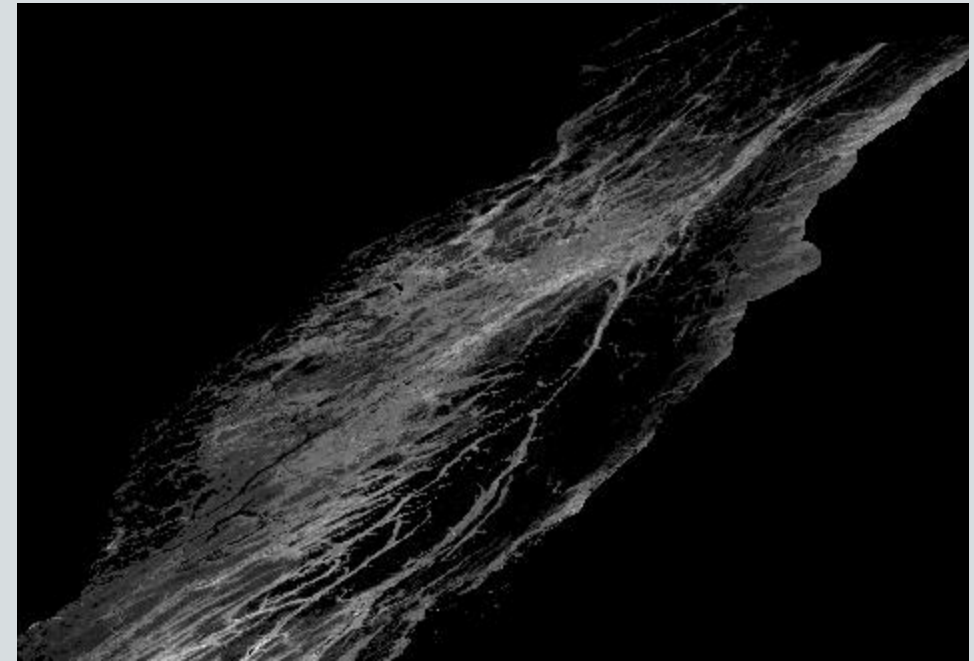


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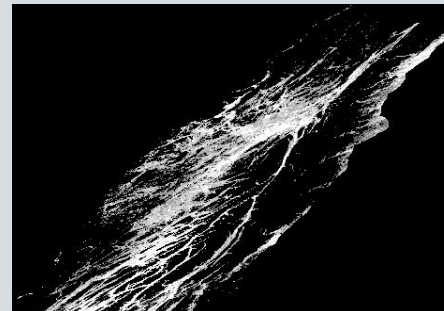
(2) How can we automate the sorting of these raster data by ecological or management variables of interest?

> `CIJV` & `Forest_Generalist` &
`landbird` & `Resident` &
`seasonal_mean`

> 7 spp: dowwoo, haiwoo,
rufgro, whbnut, ...



bkcchi



brdowl



wiltur

