

Source code for *Using citizen science to parse climatic and landcover influences on bird occupancy within a tropical biodiversity hotspot*

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65 1 Introduction

66 This is the readable version containing analysis that models associations between environmental predictors (climate and
67 landcover) and citizen science observations of birds across the Nilgiri and Anamalai Hills of the Western Ghats Biodiversity
68 Hotspot.

69 Methods and format are derived from Strimas-Mackey et al..

70 1.1 Attribution

71 Please contact the following in case of interest in the project.

- 72 • Vijay Ramesh (lead author)
- 73 – PhD student, Columbia University
- 74 • Pratik Gupte (repo maintainer)
- 75 – PhD student, University of Groningen

76 1.2 Data access

77 The data used in this work are available from eBird.

78 1.3 Data processing

79 The data processing for this project is described in the following sections. Navigate through them using the links in the
80 sidebar.

1.4 Main Text Figure 1

Figure prepared in QGIS 3.10.

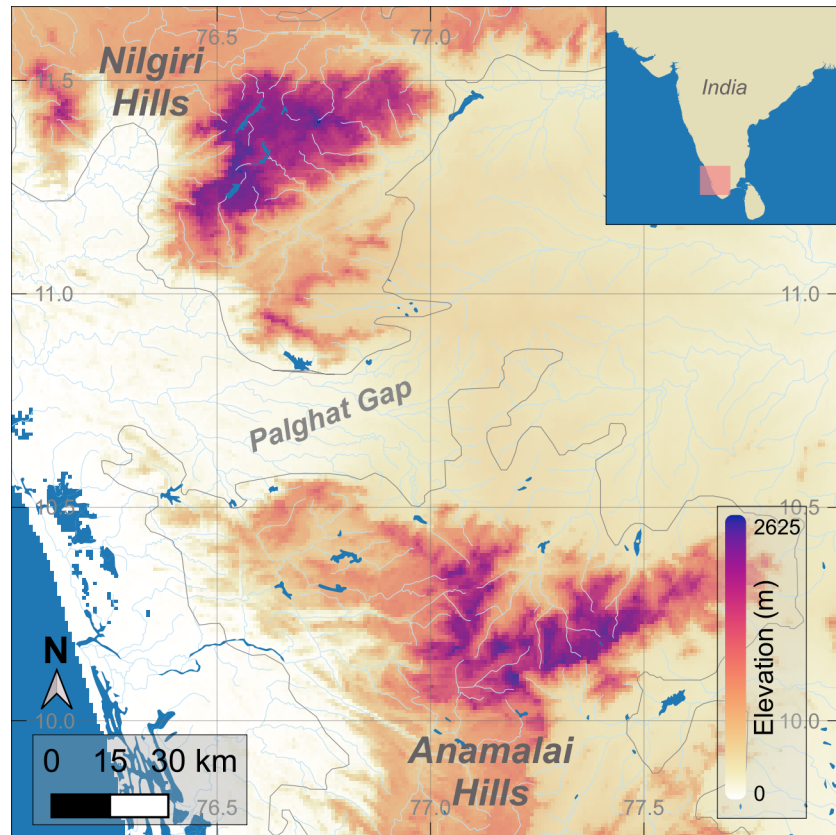


Figure 1: A shaded relief of the study area - the Nilgiri and the Anamalai hills are shown in this figure. This map was made using the SRTM digital elevation model at a spatial resolution of 1km and data from Natural Earth were used to outline boundaries of water bodies.

2 Preparing eBird Data

2.1 Prepare libraries and data sources

Here, we will load the necessary libraries required for preparing the eBird data. Please download the latest versions of the eBird Basic Dataset (for India) and the eBird Sampling dataset from <https://ebird.org/data/download>.

```
# load libraries
library(tidyverse)
library(readr)
library(sf)
library(auk)
library(readxl)

# custom sum function
sum.no.na <- function(x) {
  sum(x, na.rm = T)
}
```

```

13 # set file paths for auk functions
14 # To use these two datasets, please download the latest versions from https://ebird.org/data/download and set the f
15
16 f_in_ebd <- file.path("data/ebd_IN_relApr-2020.txt")
17 f_in_sampling <- file.path("data/ebd_sampling_relApr-2020.txt")

```

87 2.2 Filter data

88 Insert the list of species that we will be analyzing in this study. We initially chose those species that occurred in at least
89 5% of all checklists across 50% of the 25 x 25 km cells from where they have been reported, resulting in a total of 93
90 species. To arrive at this final list of species, we carried out further pre-processing which can be found in Section 2 of the
91 Supplementary material.

```

1 # add species of interest
2 specieslist <- read.csv("data/species_list.csv")
3 speciesOfInterest <- as.character(specieslist$scientific_name)

```

92 Here, we set broad spatial filters for the states of Kerala, Tamil Nadu and Karnataka and keep only those checklists for our
93 list of species that were reported between 1st Jan 2013 and 31st Dec 2019.

```

1 # run filters using auk packages
2 ebd_filters <- auk_ebd(f_in_ebd, f_in_sampling) %>%
3   auk_species(speciesOfInterest) %>%
4   auk_country(country = "IN") %>%
5   auk_state(c("IN-KL", "IN-TN", "IN-KA")) %>% # Restricting geography to TamilNadu, Kerala & Karnataka
6   auk_date(c("2013-01-01", "2019-12-31")) %>%
7   auk_complete()

```

```

8
9 # check filters
10 ebd_filters

```

94 Below code need not be run if it has been filtered once already and the above path leads to the right dataset. NB: This is a
95 computation heavy process, run with caution.

```

1 # specify output location and perform filter
2 f_out_ebd <- "data/01_ebird-filtered-EBD-westernGhats.txt"
3 f_out_sampling <- "data/01_ebird-filtered-sampling-westernGhats.txt"
4
5 ebd_filtered <- auk_filter(ebd_filters,
6   file = f_out_ebd,
7   file_sampling = f_out_sampling, overwrite = TRUE
8 )

```

96 2.3 Process filtered data

97 The data has been filtered above using the auk functions. We will now work with the filtered checklist observations (Please
98 note that we have not yet spatially filtered the checklists to the confines of our study area, which is the Nilgiris and the
99 Anamalai hills. This step is carried out further on).

```

1 # read in the data
2 ebd <- read_ebd(f_out_ebd)

```

100 eBird checklists only suggest whether a species was reported at a particular location. To arrive at absence data, we use a
101 process known as zero-filling (Johnston et al. 2019), wherein a new dataframe is created with a 0 marked for each checklist
102 when the bird was not observed.

```

1 # fill zeroes
2 zf <- auk_zerofill(f_out_ebd, f_out_sampling)
3 new_zf <- collapse_zerofill(zf)

```

103 Let us now choose specific columns necessary for further analysis.

```
1 # choose columns of interest
2 columnsOfInterest <- c(
3   "checklist_id", "scientific_name", "common_name",
4   "observation_count", "locality", "locality_id",
5   "locality_type", "latitude", "longitude",
6   "observation_date", "time_observations_started",
7   "observer_id", "sampling_event_identifier",
8   "protocol_type", "duration_minutes",
9   "effort_distance_km", "effort_area_ha",
10  "number_observers", "species_observed",
11  "reviewed"
12 )
13
14 # make list of presence and absence data and choose cols of interest
15 data <- list(ebd, new_zf) %>%
16   map(function(x) {
17     x %>% select(one_of(columnsOfInterest))
18   })
19
20 # remove zerofills to save working memory
21 rm(zf, new_zf)
22 gc()
23
24 # check for presences and absence in absences df, remove essentially the presences df which may lead to erroneous a
25 data[[2]] <- data[[2]] %>% filter(species_observed == F)
```

104 2.4 Spatial filter

105 A spatial filter is now supplied to further restrict our list of observations to the confines of the Nilgiris and the Anamalai
106 hills of the Western Ghats biodiversity hotspot.

```
1 # load shapefile of the study area
2 library(sf)
3 hills <- st_read("data/spatial/hillsShapefile/Nil_Ana_Pal.shp")
4
5 # write a prelim filter by bounding box
6 box <- st_bbox(hills)
7
8 # get data spatial coordinates
9 dataLocs <- data %>%
10   map(function(x) {
11     select(x, longitude, latitude) %>%
12     filter(between(longitude, box["xmin"], box["xmax"]) &
13           between(latitude, box["ymin"], box["ymax"]))
14   }) %>%
15   bind_rows() %>%
16   distinct() %>%
17   st_as_sf(coords = c("longitude", "latitude")) %>%
18   st_set_crs(4326) %>%
19   st_intersection(hills)
20
21 # get simplified data and drop geometry
22 dataLocs <- mutate(dataLocs, spatialKeep = T) %>%
```

```

23   bind_cols(., as_tibble(st_coordinates(dataLocs))) %>%
24   st_drop_geometry()
25
26   # bind to data and then filter
27   data <- data %>%
28     map(function(x) {
29       left_join(x, dataLocs, by = c("longitude" = "X", "latitude" = "Y")) %>%
30       filter(spatialKeep == T) %>%
31       select(-Id, -spatialKeep)
32     })
107  Save temporary data created so far.
1
1   # save a temp data file
2   save(data, file = "data/01_data_temp.rdata")

```

108 2.5 Handle presence data

109 Further pre-processing is required in the case of many checklists where species abundance is often unknown and an ‘X’
110 is denoted in such cases. Here, we convert all ‘X’ notations to a 1, suggesting a presence (as we are not concerned with
111 abundance data in this analysis). We also removed those checklists where the duration in minutes is either not recorded or
112 listed as zero. Lastly, we added an sampling effort based filter following (Johnston et al. 2019), wherein we considered
113 only those checklists with duration in minutes is less than 300 and distance in kilometres traveled is less than 5km. Lastly,
114 we excluded those group checklists where the number of observers was greater than 10.

```

1   # in the first set, replace X, for presences, with 1
2   data[[1]] <- data[[1]] %>%
3     mutate(observation_count = ifelse(observation_count == "X",
4       "1", observation_count
5     ))
6
7   # remove records where duration is 0
8   data <- map(data, function(x) filter(x, duration_minutes > 0))
9
10  # group data by site and sampling event identifier
11  # then, summarise relevant variables as the sum
12  dataGrouped <- map(data, function(x) {
13    x %>%
14      group_by(sampling_event_identifier) %>%
15      summarise_at(
16        vars(
17          duration_minutes, effort_distance_km,
18          effort_area_ha
19        ),
20        list(sum.no.na)
21      )
22  })
23
24  # bind rows combining data frames, and filter
25  dataGrouped <- bind_rows(dataGrouped) %>%
26    filter(
27      duration_minutes <= 300,
28      effort_distance_km <= 5,
29      effort_area_ha <= 500
30    )
31

```

```

32 # get data identifiers, such as sampling identifier etc
33 dataConstants <- data %>%
34   bind_rows() %>%
35   select(
36     sampling_event_identifier, time_observations_started,
37     locality, locality_type, locality_id,
38     observer_id, observation_date, scientific_name,
39     observation_count, protocol_type, number_observers,
40     longitude, latitude
41   )
42
43 # join the summarised data with the identifiers,
44 # using sampling_event_identifier as the key
45 dataGrouped <- left_join(dataGrouped, dataConstants,
46   by = "sampling_event_identifier"
47 )
48
49 # remove checklists or seis with more than 10 observers
50 count(dataGrouped, number_observers > 10) # count how many have 10+ obs
51 dataGrouped <- filter(dataGrouped, number_observers <= 10)

```

115 2.6 Add decimal time

116 We added a column where time is denoted in decimal hours since midnight.

```

1 # assign present or not, and get time in decimal hours since midnight
2 library(lubridate)
3 time_to_decimal <- function(x) {
4   x <- hms(x, quiet = TRUE)
5   hour(x) + minute(x) / 60 + second(x) / 3600
6 }
7
8 # will cause issues if using time obs started as a linear effect and not quadratic
9 dataGrouped <- mutate(dataGrouped,
10   pres_abs = observation_count >= 1,
11   decimalTime = time_to_decimal(time_observations_started)
12 )
13
14 # check class of dataGrouped, make sure not sf
15 assertthat::assert_that(!"sf" %in% class(dataGrouped))

```

117 The above data is saved to a file.

```

1
2 # save a temp data file
3 save(dataGrouped, file = "data/01_data_prelim_processing.rdata")

```

118 3 Preparing Environmental Predictors

119 In this script, we processed climatic and landscape predictors for occupancy modeling.

120 All climatic data was obtained from <https://chelsa-climate.org/bioclim/> All landscape data was derived from a high resolution Sentinel-2 composite image that was classified using Google Earth Engine. This code can be accessed in Section 3 of the Supplementary Material and here: <https://code.earthengine.google.com/ec69fc4ffad32a532b25202009243d42>.

123 The goal here is to resample all rasters so that they have the same resolution of 1km cells. We also tested for spatial
124 autocorrelation among climatic predictors, which can be found in Section 4 of the Supplementary Material.

125 3.1 Prepare libraries

126 We load some common libraries for raster processing and define a custom mode function.

```
1 # load libs
2 library(raster)
3 library(stringi)
4 library(glue)
5 library(gdalUtils)
6 library(purrr)
7
8
9 # prep mode function to aggregate
10 funcMode <- function(x, na.rm = T) {
11   ux <- unique(x)
12   ux[which.max(tabulate(match(x, ux)))]
13 }
14
15 # a basic test
16 assertthat::assert_that(funcMode(c(2, 2, 2, 2, 3, 3, 3, 4)) == as.character(2),
17   msg = "problem in the mode function"
18 ) # works
```

127 3.2 Prepare spatial extent

128 We prepare a 30km buffer around the boundary of the study area. This buffer will be used to mask the landscape rasters. The
129 buffer procedure is done on data transformed to the UTM 43N CRS to avoid distortions.

```
1 # load hills
2 library(sf)
3 hills <- st_read("data/spatial/hillsShapefile/Nil_Ana_Pal.shp")
4 hills <- st_transform(hills, 32643)
5 buffer <- st_buffer(hills, 3e4) %>%
6   st_transform(4326)
```

130 3.3 Prepare terrain rasters

131 We prepare the elevation data which is an SRTM raster layer, and derive the slope and aspect from it after cropping it to the
132 extent of the study site buffer. Please download the latest version of the SRTM raster layer from <https://www.worldclim.org/data/worldclim21.html>
133

```
1 # load elevation and crop to hills size, then mask by hills
2 alt <- raster("data/spatial/Elevation/alt") # this layer is not added to github as a result of its large size and c
3 alt.hills <- crop(alt, as(buffer, "Spatial"))
4 rm(alt)
5 gc()
6
7 # get slope and aspect
8 slopeData <- terrain(x = alt.hills, opt = c("slope", "aspect"))
9 elevData <- raster::stack(alt.hills, slopeData)
10 rm(alt.hills)
11 gc()
```


3.4 Prepare CHELSA rasters

We prepare the CHELSA rasters for annual temperature and annual precipitation in the same way, reading them in, cropping them to the study site buffer extent, and handling the temperature layer values which we divide by 10. The CHELSA rasters can be downloaded from <https://chelsa-climate.org/bioclim/>

```
1 # list chelsa files
2 # the chelsa data for Annual mean temperature and annual precipitation can be downloaded from the aforementioned li
3 chelsaFiles <- list.files("data/chelsa/",
4   full.names = TRUE,
5   pattern = "*.tif"
6 )
7
8 # gather chelsa rasters
9 chelsaData <- purrr::map(chelsaFiles, function(chr) {
10   a <- raster(chr)
11   crs(a) <- crs(elevData)
12   a <- crop(a, as(buffer, "Spatial"))
13   return(a)
14 })
15
16 # divide temperature by 10
17 chelsaData[[1]] <- chelsaData[[1]] / 10
18
19 # stack chelsa data
20 chelsaData <- raster::stack(chelsaData)
```

We stack the terrain and climatic rasters.

```
1 # stack rasters for efficient reprojection later
2 env_data <- stack(elevData, chelsaData)
```

3.5 Resample landcover from 10m to 1km

We read in a land cover classified image and resample that using the mode function to a 1km resolution. Please note that the resampling process need not be carried out as it has been done already and the resampled raster can be loaded with the subsequent code chunk.

The classified image can be obtained from: <https://code.earthengine.google.com/ec69fc4ffad32a532b25202009243d42>.

```
1 # read in landcover raster location
2 landcover <- "data/landUseClassification/classifiedImage-UTM.tif"
3
4 # get extent
5 e <- bbox(raster(landcover))
6
7 # init resolution
8 res_init <- res(raster(landcover))
9
10 # res to transform to 1000m
11 res_final <- res_init * 100
12
13 # use gdalutils gdalwarp for resampling transform
14 # to 1km from 10m
15 gdalUtils::gdalwarp(
16   srcfile = landcover,
17   dstfile = "data/landUseClassification/lc_01000m.tif",
```

```

18   tr = c(res_final), r = "mode", te = c(e)
19 )

```

144 We compare the frequency of landcover classes between the original 10m and the resampled 1km raster to be certain that
 145 the resampling has not resulted in drastic misrepresentation of the frequency of any landcover type. This comparison is
 146 made using the figure below.

147 3.6 Resample other rasters to 1km

148 We now resample all other rasters to a resolution of 1km.

149 3.6.1 Read in resampled landcover

150 Here, we read in the 1km landcover raster and set 0 to NA.

```

1   lc_data <- raster("data/landUseClassification/lc_01000m.tif")
2   lc_data[lc_data == 0] <- NA

```

151 3.6.2 Reproject environmental data using landcover as a template

```

1
2   # resample to the corresponding landcover data
3   env_data_resamp <- projectRaster(
4     from = env_data, to = lc_data,
5     crs = crs(lc_data), res = res(lc_data)
6   )
7
8   # export as raster stack
9   land_stack <- stack(env_data_resamp, lc_data)
10
11  # get names
12  land_names <- glue('data/spatial/landscape_resamp{c("01")}km.tif')
13
14  # write to file
15  writeRaster(land_stack, filename = as.character(land_names), overwrite = TRUE)

```

152 3.7 Temperature and rainfall in relation to elevation

153 3.7.1 Prepare libraries and CI function

```

1   # load libs
2   library(dplyr)
3   library(tidyr)
4
5   library(scales)
6   library(ggplot2)
7
8   # get ci func
9   ci <- function(x) {
10     qnorm(0.975) * sd(x, na.rm = T) / sqrt(length(x))
11   }

```

154 3.7.2 Load resampled environmental rasters

```

1   # read landscape prepare for plotting
2   landscape <- stack("data/spatial/landscape_resamp01_km.tif")
3

```

```

4 # get proper names
5 elev_names <- c("elev", "slope", "aspect")
6 chelsea_names <- c("bio_01", "bio_12")
7
8 names(landscape) <- as.character(glue('{c(elev_names, chelsea_names, "landcover")}'))
9
10 # make duplicate stack
11 land_data <- landscape[[c("elev", chelsea_names)]]
12
13 # convert to list
14 land_data <- as.list(land_data)
15
16 # map get values over the stack
17 land_data <- purrr::map(land_data, getValues)
18 names(land_data) <- c("elev", chelsea_names)
19
20 # conver to dataframe and round to 100m
21 land_data <- bind_cols(land_data)
22 land_data <- drop_na(land_data) %>%
23   mutate(elev_round = plyr::round_any(elev, 200)) %>%
24   dplyr::select(-elev) %>%
25   pivot_longer(
26     cols = contains("bio"),
27     names_to = "clim_var"
28   ) %>%
29   group_by(elev_round, clim_var) %>%
30   summarise_all(.funs = list(~ mean(.), ~ ci(.)))

```

Figure code is hidden in versions rendered as HTML or PDF.

3.8 Land cover type in relation to elevation

```

1 # get data from landscape rasters
2 lc_elev <- tibble(
3   elev = getValues(landscape[["elev"]]),
4   landcover = getValues(landscape[["landcover"]])
5 )
6
7 # process data for proportions
8 lc_elev <- lc_elev %>%
9   filter(!is.na(landcover), !is.na(elev)) %>%
10  mutate(elev = plyr::round_any(elev, 100)) %>%
11  count(elev, landcover) %>%
12  group_by(elev) %>%
13  mutate(prop = n / sum(n))
14
15 # fill out lc elev
16 lc_elev_canon <- crossing(
17   elev = unique(lc_elev$elev),
18   landcover = unique(lc_elev$landcover)
19 )
20
21 # bind with lcelelev
22 lc_elev <- full_join(lc_elev, lc_elev_canon)
23

```

```

24 # convert NA to zero
25 lc_elev <- replace_na(lc_elev, replace = list(n = 0, prop = 0))
157 Figure code is hidden in versions rendered as HTML and PDF.

```

3.9 Main Text Figure 2

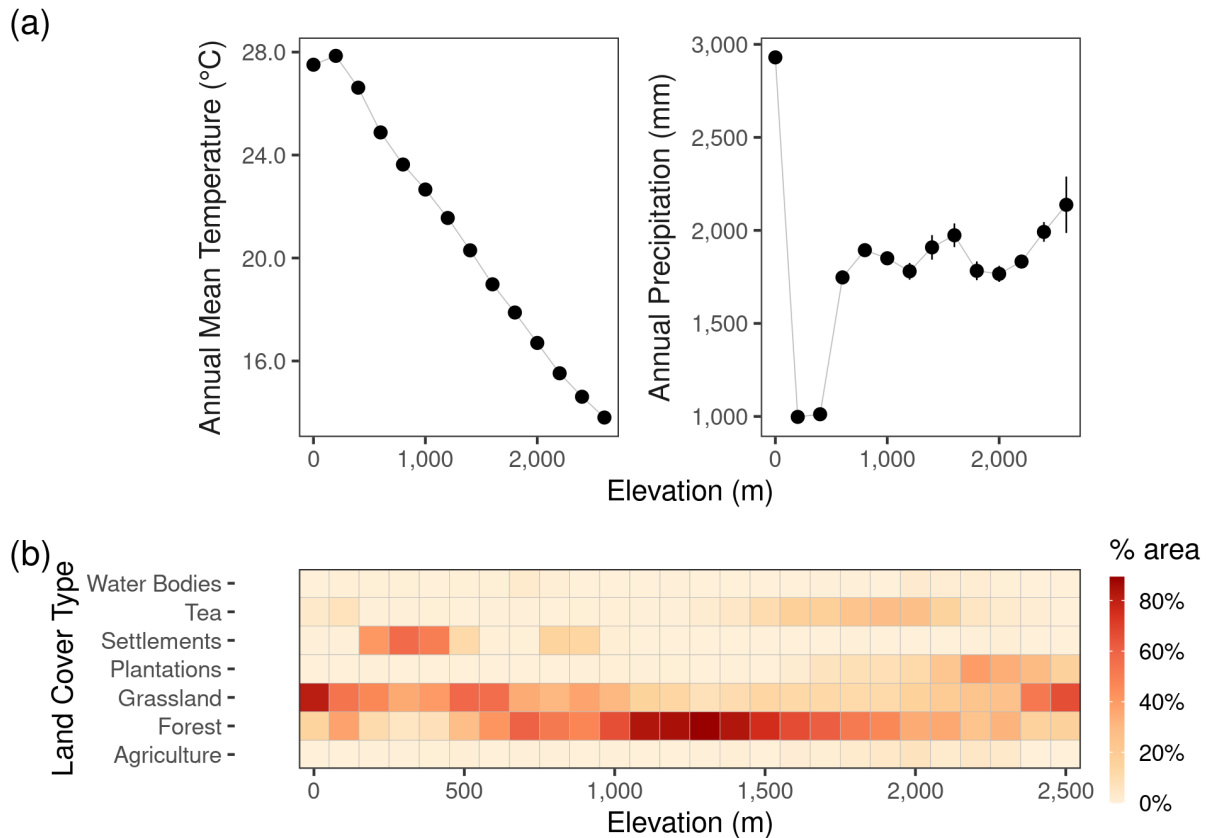


Figure 2: Annual Mean Temperature varied from ~28C in the plains to <14C at higher elevations. Annual precipitation increased at lower elevations (in the plains) to ~3000mm and ranged between 1500mm and 2200mm at mid- and high elevations across the Nilgiri and the Anamalai hills. (b) The proportion of land cover types varied across the study area as shown in this panel (1 = agriculture; 2 = forests; 3 = grasslands; 4 = plantations; 5 = settlements; 6 = tea; 7 = water bodies).

4 Preparing Observer Expertise Scores

Differences in local avifaunal expertise among citizen scientists can lead to biased species detection when compared with data collected by a consistent set of trained observers (van Strien, van Swaay, and Termaat 2013). Including observer expertise as a detection covariate in occupancy models using eBird data can help account for this variation (Johnston et al. 2018). Observer-specific expertise in local avifauna was calculated following (Kelling et al. 2015) as the normalized predicted number of species reported by an observer after 60 minutes of sampling across the most common land cover type within the study area. This score was calculated by examining checklists from anonymized observers across the study area. We modified Kelling et al. (2015) formulation by including only observations of the 93 species of interest in our calculations. An observer with a higher number of species of interest reported within 60 minutes would have a higher observer-specific expertise score, with respect to the study area.

169 Plots with respect to how observer expertise varied over time (2013-2019) for the list of species considered in this study
170 (across the study area alone) can be accessed in Section 7 of the Supplementary Material.

171 4.1 Prepare libraries

```
1
2 # load libs
3 library(data.table)
4 library(readxl)
5 library(magrittr)
6 library(stringr)
7 library(dplyr)
8 library(tidyr)
9 library(auk)
10
11 # get decimal time function
12 library(lubridate)
13 time_to_decimal <- function(x) {
14   x <- lubridate::hms(x, quiet = TRUE)
15   lubridate::hour(x) + lubridate::minute(x) / 60 + lubridate::second(x) / 3600
16 }
```

172 4.2 Prepare data

173 Here, we go through the data preparation process again because we might want to assess observer expertise over a larger
174 area than the study site.

```
1 # Read in shapefile of study area to subset by bounding box
2 library(sf)
3 wg <- st_read("data/spatial/hillsShapefile/Nil_Ana_Pal.shp") %>%
4   st_transform(32643)
5
6 # set file paths for auk functions
7 f_in_ebd <- file.path("data/01_ebird-filtered-EBD-westernGhats.txt")
8 f_in_sampling <- file.path("data/01_ebird-filtered-sampling-westernGhats.txt")
9
10 # run filters using auk packages
11 ebd_filters <- auk_ebd(f_in_ebd, f_in_sampling) %>%
12   auk_country(country = "IN") %>%
13   auk_state(c("IN-KL", "IN-TN", "IN-KA")) %>%
14   # Restricting geography to TamilNadu, Kerala & Karnataka
15   auk_date(c("2013-01-01", "2019-12-31")) %>%
16   auk_complete()
17
18 # check filters
19 ebd_filters
20
21 # specify output location and perform filter
22 f_out_ebd <- "data/ebird_for_expertise.txt"
23 f_out_sampling <- "data/ebird_sampling_for_expertise.txt"
24
25 ebd_filtered <- auk_filter(ebd_filters,
26   file = f_out_ebd,
27   file_sampling = f_out_sampling, overwrite = TRUE
28 )
```

175 Load in the filtered data and columns of interest.

```
1 ## Process filtered data
2 # read in the data
3 ebd <- fread(f_out_ebd)
4 names <- names(ebd) %>%
5   stringr::str_to_lower() %>%
6   stringr::str_replace_all(" ", "_")
7
8 setnames(ebd, names)
9 # choose columns of interest
10 columnsOfInterest <- c(
11   "checklist_id", "scientific_name", "observation_count",
12   "locality", "locality_id", "locality_type", "latitude",
13   "longitude", "observation_date",
14   "time_observations_started", "observer_id",
15   "sampling_event_identifer", "protocol_type",
16   "duration_minutes", "effort_distance_km", "effort_area_ha",
17   "number_observers", "species_observed", "reviewed"
18 )
19
20 ebd <- setDF(ebd) %>%
21   as_tibble() %>%
22   dplyr::select(one_of(columnsOfInterest))
23
24 setDT(ebd)
```

176 4.3 Spatially explicit filter on checklists

```
1 # get checklist locations
2 ebd_locs <- ebd[, .(longitude, latitude)]
3 ebd_locs <- setDF(ebd_locs) %>% distinct()
4 ebd_locs <- st_as_sf(ebd_locs,
5   coords = c("longitude", "latitude")
6 ) %>%
7   `st_crs<-`(4326) %>%
8   bind_cols(as_tibble(st_coordinates(.))) %>%
9   st_transform(32643) %>%
10  mutate(id = 1:nrow(.))
11
12 # check whether to include
13 to_keep <- unlist(st_contains(wg, ebd_locs))
14
15 # filter locs
16 ebd_locs <- filter(ebd_locs, id %in% to_keep) %>%
17   bind_cols(as_tibble(st_coordinates(st_as_sf(.)))) %>%
18   st_drop_geometry()
19
20 ebd <- ebd[longitude %in% ebd_locs$X & latitude %in% ebd_locs$Y, ]
```

177 4.4 Prepare species of interest

```
1 # read in species list
2 specieslist <- read.csv("data/species_list.csv")
3
```

```

4 # set species of interest
5 soi <- specieslist$scientific_name
6
7 ebdSpSum <- ebd[, .(
8   nSp = .N,
9   totSoiSeen = length(intersect(scientific_name, soi))
10 ),
11 by = list(sampling_event_identifier)
12 ]
13
14 # write to file and link with checklist id later
15 fwrite(ebdSpSum, file = "data/03_data-nspp-per-chk.csv")

```

178 4.5 Prepare checklists for observer score

```

1 # 1. add new columns of decimal time and julian date
2 ebd[, `:=`(
3   decimalTime = time_to_decimal(time_observations_started),
4   julianDate = yday(as.POSIXct(observation_date))
5 )]
6
7 ebdEffChk <- setDF(ebd) %>%
8   mutate(year = year(observation_date)) %>%
9   distinct(
10     sampling_event_identifier, observer_id,
11     year,
12     duration_minutes, effort_distance_km, effort_area_ha,
13     longitude, latitude,
14     locality, locality_id,
15     decimalTime, julianDate, number_observers
16 ) %>%
17 # drop rows with NAs in cols used in the model
18 tidyr::drop_na(
19   sampling_event_identifier, observer_id,
20   duration_minutes, decimalTime, julianDate
21 ) %>%
22
23 # drop years below 2013
24 filter(year >= 2013)
25
26 # 3. join to covariates and remove large groups (> 10)
27 ebdChkSummary <- inner_join(ebdEffChk, ebdSpSum)
28
29 # remove ebird data
30 rm(ebd)
31 gc()

```

179 4.6 Get landcover

180 Read in land cover type data resampled at 1km resolution.

```

1 # read in 1km landcover and set 0 to NA
2 library(raster)
3 landcover <- raster::raster("data/landUseClassification/lc_01000m.tif")
4 landcover[landcover == 0] <- NA

```

```

5
6 # get locs in utm coords
7 locs <- distinct(
8   ebdChkSummary, sampling_event_identifier, longitude, latitude,
9   locality, locality_id
10 )
11 locs <- st_as_sf(locs, coords = c("longitude", "latitude")) %>%
12   `st_crs<-`(4326) %>%
13   st_transform(32643) %>%
14   st_coordinates()
15
16 # get for unique points
17 landcoverVec <- raster::extract(
18   x = landcover,
19   y = locs
20 )
21
22 # assign to df and overwrite
23 setDT(ebdChkSummary)[, landcover := landcoverVec]

```

181 4.7 Filter checklist data

```

1 # change names for easy handling
2 setnames(ebdChkSummary, c(
3   "sei", "observer", "year", "duration", "distance",
4   "area", "longitude", "latitude", "locality",
5   "locality_id", "decimalTime",
6   "julianDate", "nObs", "nSp", "nSoi", "landcover"
7 ))
8
9 # count data points per observer
10 obscount <- count(ebdChkSummary, observer) %>%
11   filter(n >= 10)
12
13 # make factor variables and remove obs not in obscount
14 # also remove 0 durations
15 ebdChkSummary <- ebdChkSummary %>%
16   mutate(
17     distance = ifelse(is.na(distance), 0, distance),
18     duration = if_else(is.na(duration), 0.0, as.double(duration))
19   ) %>%
20   filter(
21     observer %in% obscount$observer,
22     duration > 0,
23     duration <= 300,
24     nSoi >= 0,
25     distance <= 5,
26     !is.na(nSoi)
27   ) %>%
28   mutate(
29     landcover = as.factor(landcover),
30     observer = as.factor(observer)
31   ) %>%
32   drop_na(landcover)

```



```

33
34
35 # save to file for later reuse
36 fwrite(ebdChkSummary, file = "data/03_data-covars-perChklist.csv")

```

182 4.8 Model observer expertise

183 Our observer expertise model aims to include the random intercept effect of observer identity, with a random slope effect
 184 of duration. This models the different rate of species accumulation by different observers, as well as their different starting
 185 points.

```

1 # uses either a subset or all data
2 library(lmerTest)
3
4 # here we specify a glmm with random effects for observer
5 # time is considered a fixed log predictor and a random slope
6 modObsExp <- glmer(nSoi ~ sqrt(duration) +
7   landcover +
8   sqrt(decimalTime) +
9   I((sqrt(decimalTime))^2) +
10  log(julianDate) +
11  I((log(julianDate)^2)) +
12  (1 | observer) + (0 + duration | observer),
13  data = ebdChkSummary, family = "poisson"
14 )
15
16 # make dir if absent
17 if (!dir.exists("data/modOutput")) {
18   dir.create("data/modOutput")
19 }
20
21 # write model output to text file
22 {
23   writeLines(R.utils::captureOutput(list(Sys.time(), summary(modObsExp))),
24     con = "data/modOutput/03_model-output-expertise.txt"
25   )
26 }
27
28 # make df with means
29 observer <- unique(ebdChkSummary$observer)
30
31 # predict at 60 mins on the most common landcover
32 dfPredict <- ebdChkSummary %>%
33   summarise_at(vars(duration, decimalTime, julianDate), list(~ mean(.))) %>%
34   mutate(duration = 60, landcover = as.factor(6)) %>%
35   tidyr::crossing(observer)
36
37 # run predict from model on it
38 dfPredict <- mutate(dfPredict,
39   score = predict(modObsExp,
40     newdata = dfPredict,
41     type = "response",
42     allow.new.levels = TRUE
43   )
44 ) %>%
45   mutate(score = scales::rescale(score))

```

```

1 fwrite(dfPredict %>% dplyr::select(observer, score),
2   file = "data/03_data-obsExpertise-score.csv"
3 )

```

186 5 Examining Spatial Sampling Bias

187 The goal of this section is to determine how far each checklist location is from the nearest road, and how far each site is from
 188 its nearest neighbour. This involves finding the pairwise distance between a large number of unique checklist locations to
 189 a vast number of roads, as well as to each other.

190 Parts of this section are thus implemented in Python, using the R-Python interface package, reticulate.

191 5.1 Prepare libraries

```

1 # load libraries
2 library(reticulate)
3 library(sf)
4 library(dplyr)
5 library(scales)
6 library(readr)
7 library(purrr)
8
9 library(ggplot2)
10 library(ggthemes)
11 library(ggspatial)
12 library(scico)
13
14 # round any function
15 round_any <- function(x, accuracy = 20000) {
16   round(x / accuracy) * accuracy
17 }
18 # ci function
19 ci <- function(x) {
20   qnorm(0.975) * sd(x, na.rm = TRUE) / sqrt(length(x))
21 }
22
23 # set python path
24 use_python("/usr/bin/python3")

```

192 Importing python libraries. These libraries need to be installed before use.

```

1 # import classic python libs
2 import itertools
3 from operator import itemgetter
4 import numpy as np
5 import matplotlib.pyplot as plt
6 import math
7
8 # libs for dataframes
9 import pandas as pd
10
11 # import libs for geodata
12 from shapely.ops import nearest_points
13 import geopandas as gpd
14 import rasterio

```

```

15
16 # import ckdtree
17 from scipy.spatial import cKDTree
18 from shapely.geometry import Point, MultiPoint, LineString, MultiLineString

```

193 5.2 Prepare data for processing

194 First we read in the roads shapefile, which is obtained from the Open Street Map database. Then we read in the checklist
 195 covariates, and extract the unique coordinate pairs. All data are reprojected to be in the UTM 43N coordinate system.

196 We define a custom Python function to separate multi-feature geometries (here, roads which are in parts) into single feature
 197 geometries. Then we define a function to use the K-dimensional trees method from scipy to find the distance between two
 198 geometries, here, the distance between the locations and the nearest road. We define another function to find the distance
 199 between checklist locations and all other checklist locations.

200 We use these functions to find the distance between each checklist location and the nearest road and the next nearest site.

201 5.2.1 Python functions and distance calculations

```

1 # read in roads shapefile
2 roads = gpd.read_file("data/spatial/roads_studysite_2019/roads_studysite_2019.shp")
3 roads.head()
4
5 # read in checklist covariates for conversion to gpd
6 # get unique coordinates, assign them to the df
7 # convert df to geo-df
8 chkCovars = pd.read_csv("data/03_data-covars-perChklist.csv")
9 unique_locs = chkCovars.drop_duplicates(subset=['longitude',
10                                             'latitude'])[['longitude', 'latitude']]
11 unique_locs['coordId'] = np.arange(1, unique_locs.shape[0]+1)
12 chkCovars = chkCovars.merge(unique_locs, on=['longitude', 'latitude'])
13
14 unique_locs = gpd.GeoDataFrame(
15     unique_locs,
16     geometry = gpd.points_from_xy(unique_locs.longitude, unique_locs.latitude))
17 unique_locs.crs = {'init' : 'epsg:4326'}
18
19 # reproject spatial to 43n epsg 32643
20
21 roads = roads.to_crs({'init': 'epsg:32643'})
22 unique_locs = unique_locs.to_crs({'init': 'epsg:32643'})
23
24 # function to simplify multilinestrings
25 def simplify_roads(complex_roads):
26     simpleRoads = []
27     for i in range(len(complex_roads.geometry)):
28         feature = complex_roads.geometry.iloc[i]
29         if feature.geom_type == "LineString":
30             simpleRoads.append(feature)
31         elif feature.geom_type == "MultiLineString":
32             for road_level2 in feature:
33                 simpleRoads.append(road_level2)
34     return simpleRoads
35
36 # function to use ckd trees to find the nearest road

```

```

37 def ckdnearest(gdfA, gdfB):
38     A = np.concatenate(
39         [np.array(geom.coords) for geom in gdfA.geometry.to_list()])
40     simplified_features = simplify_roads(gdfB)
41     B = [np.array(geom.coords) for geom in simplified_features]
42     B = np.concatenate(B)
43     ckd_tree = cKDTree(B)
44     dist, idx = ckd_tree.query(A, k=1)
45     return dist
46
47 # function to use ckd trees for nearest other checklist point
48 def ckdnearest_point(gdfA, gdfB):
49     A = np.concatenate(
50         [np.array(geom.coords) for geom in gdfA.geometry.to_list()])
51     #simplified_features = simplify_roads(gdfB)
52     B = np.concatenate(
53         [np.array(geom.coords) for geom in gdfB.geometry.to_list()])
54     #B = np.concatenate(B)
55     ckd_tree = cKDTree(B)
56     dist, idx = ckd_tree.query(A, k=[2])
57     return dist
58
59 # get distance to nearest road
60 unique_locs['dist_road'] = ckdnearest(unique_locs, roads)
61
62 # get distance to nearest other site
63 unique_locs['nnb'] = ckdnearest_point(unique_locs, unique_locs)
64
65 # write to file
66 unique_locs = pd.DataFrame(unique_locs.drop(columns='geometry'))
67 unique_locs['dist_road'] = unique_locs['dist_road']
68 unique_locs['nnb'] = unique_locs['nnb']
69 unique_locs.to_csv(path_or_buf = "data/locs_dist_to_road.csv", index=False)
70
71 # merge unique locs with chkCovars
72 chkCovars = chkCovars.merge(unique_locs, on=['latitude',
73                                     'longitude', 'coordId'])

```

202 5.2.2 Spatially explicit filter on checklists

203 We filter the checklists by the boundary of the study area. This is *not* the extent.

```

1 # extract data from python
2 chkCovars <- py$chkCovars
3 chkCovars <- st_as_sf(chkCovars, coords = c("longitude", "latitude")) %>%
4   `st_crs`->`(4326) %>%
5   st_transform(32643)
6
7 # read wg
8 wg <- st_read("data/spatial/hillsShapefile/Nil_Ana_Pal.shp") %>%
9   st_transform(32643)
10
11 # spatial subset
12 chkCovars <- chkCovars %>%
13   mutate(id = 1:nrow(.)) %>%

```

```
14 filter(id %in% unlist(st_contains(wg, chkCovars)))
```

204 5.3 Main Text Figure 3

205 5.3.1 Prepare histogram of distance to roads

206 Figure code is hidden in versions rendered as HTML or PDF.

207 5.3.2 Table: Distance to roads

```
1 # write the mean and ci95 to file
2 chkCovars %>%
3   st_drop_geometry() %>%
4   select(dist_road, nnb) %>%
5   tidyr::pivot_longer(
6     cols = c("dist_road", "nnb"),
7     names_to = "variable"
8   ) %>%
9   group_by(variable) %>%
10  summarise_at(
11    vars(value),
12    list(~ mean(.), ~ sd(.), ~ min(.), ~ max(.))
13  ) %>%
14  write_csv("data/results/distance_roads_sites.csv")
```

208 5.4 Distance to nearest neighbouring site

```
1 # get unique locations
2 locs <- py$unique_locs
```

209 Figure code is hidden in versions rendered as HTML and PDF.

210 5.5 Main Text Figure 3

```
1 roads <- st_read("data/spatial/roads_studysite_2019/roads_studysite_2019.shp") %>%
2   st_transform(32643)
3 points <- chkCovars %>%
4   bind_cols(as_tibble(st_coordinates(.))) %>%
5   st_drop_geometry() %>%
6   mutate(X = round_any(X, 2500), Y = round_any(Y, 2500))
7
8 points <- count(points, X, Y)
9
10 # add land
11 library(rnaturalearth)
12 land <- ne_countries(
13   scale = 50, type = "countries", continent = "asia",
14   country = "india",
15   returnclass = c("sf")
16 ) %>%
17   st_transform(32643)
18
19 bbox <- st_bbox(wg)
```

211 Figure code is hidden in versions rendered as HTML and PDF.

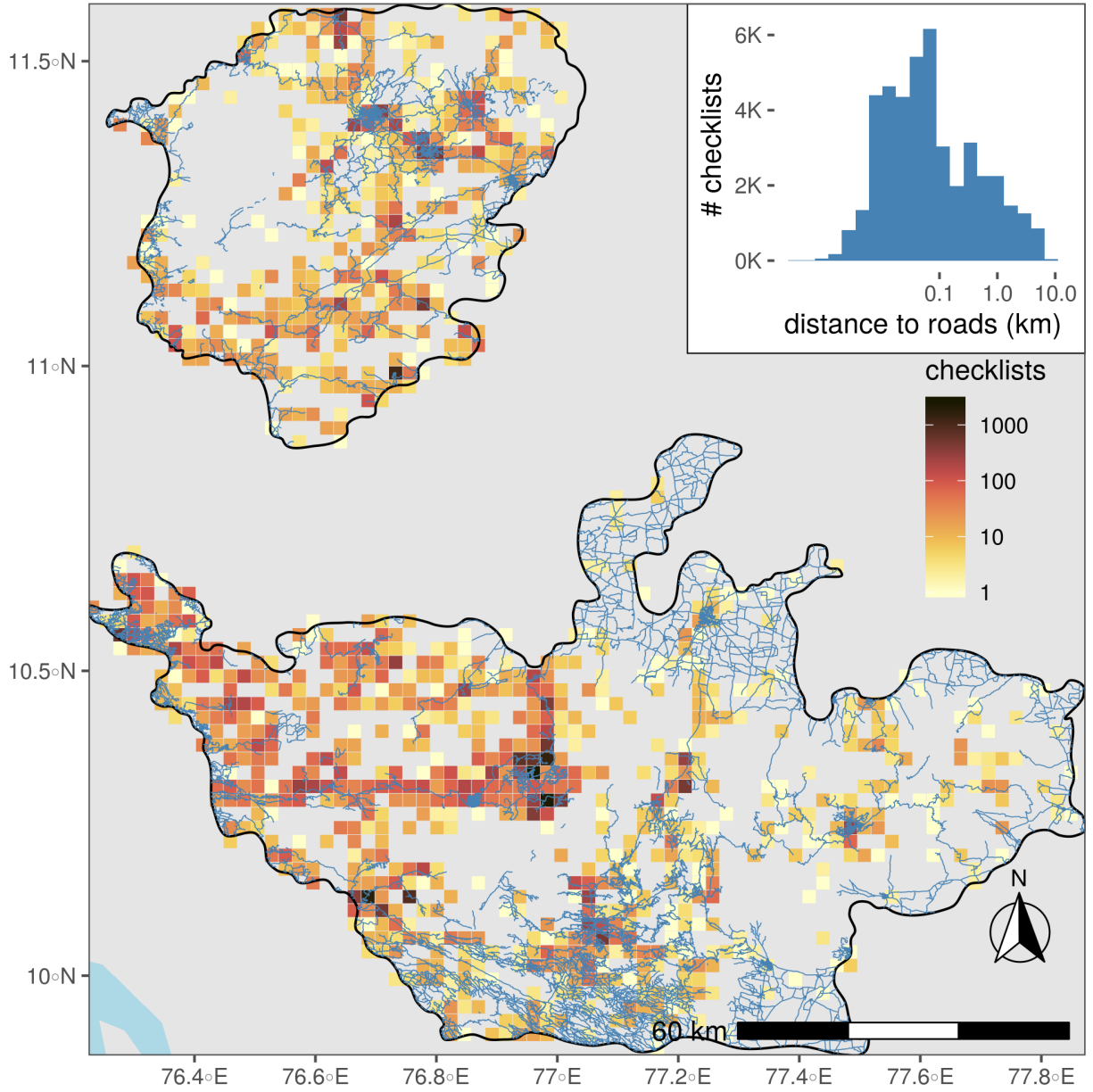


Figure 3: Spatial sampling bias of eBird observations across the Nilgiri and the Anamalai hills. A large proportion of localities/sites were next to roads and were on average only ~300m from another locality/site. Each cell here is 2.5km x 2.5km

6 Adding Covariates to Checklist Data

In this section, we prepare a final list of covariates, after taking into account spatial sampling bias (examined in the previous section), temporal bias and observer expertise scores.

6.1 Prepare libraries and data

```
1
2 # load libs
3 library(dplyr)
4 library(readr)
5 library(stringr)
6 library(purrr)
7 library(raster)
8 library(glue)
9 library(velox)
10 library(tidyr)
11 library(sf)
12
13 # load saved data object
14 load("data/01_ebird_data_prelim_processing.rdata")
```

6.2 Spatial subsampling

Sampling bias can be introduced into citizen science due to the often ad-hoc nature of data collection (Sullivan et al. 2014). For eBird, this translates into checklists reported when convenient, rather than at regular or random points in time and space, leading to non-independence in the data if observations are spatio-temporally clustered (Johnston et al. 2019). Spatio-temporal autocorrelation in the data can be reduced by sub-sampling at an appropriate spatial resolution, and by avoiding temporal clustering. We estimated two simple measures of spatial clustering: the distance from each site to the nearest road (road data from OpenStreetMap; (OpenStreetMap contributors 2019)), and the nearest-neighbor distance for each site. Sites were strongly tied to roads (mean distance to road \pm SD = 390.77 \pm 859.15 m; range = 0.28 m – 7.64 km) and were on average only 297 m away from another site (SD = 553 m; range = 0.14 m – 12.85 km) (Figure 3). This analysis was done in the previous section.

Here, to further reduce spatial autocorrelation, we divided the study area into a grid of 1km wide square cells and picked checklists from one site at random within each grid cell.

Prior to running this analysis, we checked how many checklists/data would be retained given a particular value of distance to account for spatial independence. This analysis can be accessed in Section 8 of the Supplementary Material. We show that over 80% of checklists are retained with a distance cutoff of 1km. In addition, a number of thinning approaches were tested to determine which method retained the highest proportion of points, while accounting for sampling effort (time and distance). This analysis can be accessed in Section 9 of the Supplementary Material.

```
1 # grid based spatial thinning
2 gridsize <- 1000 # grid size in metres
3 effort_distance_max <- 1000 # removing checklists with this distance
4
5 # make grids across the study site
6 hills <- st_read("data/spatial/hillsShapefile/Nil_Ana_Pal.shp") %>%
7   st_transform(32643)
8 grid <- st_make_grid(hills, cellsize = gridsize)
9
10 # split data by species
11 data_spatial_thin <- split(x = dataGrouped, f = dataGrouped$scientific_name)
12
13 # spatial thinning on each species retains
```

```

14 # site with maximum visits per grid cell
15 data_spatial_thin <- map(data_spatial_thin, function(df) {
16
17   # count visits per locality
18   df <- group_by(df, locality) %>%
19     mutate(tot_effort = length(sampling_event_identifiers)) %>%
20     ungroup()
21
22   # remove sites with distances above spatial independence
23   df <- df %>%
24     filter(effort_distance_km <= effort_distance_max) %>%
25     st_as_sf(coords = c("longitude", "latitude")) %>%
26     `st_crs<-`(4326) %>%
27     st_transform(32643) %>%
28     mutate(coordId = 1:nrow(.)) %>%
29     bind_cols(as_tibble(st_coordinates(.)))
30
31   # which cell has which coords
32   grid_contents <- st_contains(grid, df) %>%
33     as_tibble() %>%
34     rename(cell = row.id, coordId = col.id)
35
36   # what's the max point in each grid
37   points_max <- left_join(df %>% st_drop_geometry(),
38     grid_contents,
39     by = "coordId"
40   ) %>%
41     group_by(cell) %>%
42     filter(tot_effort == max(tot_effort))
43
44   return(points_max)
45 })
46
47 # remove old data
48 rm(dataGrouped)

```

233 6.3 Temporal subsampling

234 Additionally, from each selected site, we randomly selected a maximum of 10 checklists, which reduced temporal autocor-
235 relation.

```

1 # subsample data for random 10 observations
2 dataSubsample <- map(data_spatial_thin, function(df) {
3   df <- ungroup(df)
4   df_to_locality <- split(x = df, f = df$locality)
5   df_samples <- map_if(
6     .x = df_to_locality,
7     .p = function(x) {
8       nrow(x) > 10
9     },
10    .f = function(x) sample_n(x, 10, replace = FALSE)
11  )
12
13   return(bind_rows(df_samples))
14 })

```



```

15
16 # bind all rows for data frame
17 dataSubsample <- bind_rows(dataSubsample)
18
19 # remove previous data
20 rm(data_spatial_thin)

```

236 6.4 Add checklist calibration index

237 Load the CCI computed in the previous section. The CCI was the lone observer's expertise score for single-observer
 238 checklists, and the highest expertise score among observers for group checklists.

```

1 # read in obs score and extract numbers
2 expertiseScore <- read_csv("data/03_data-obsExpertise-score.csv") %>%
3   mutate(numObserver = str_extract(observer, "\\d+")) %>%
4   dplyr::select(-observer)
5
6 # group seis consist of multiple observers
7 # in this case, seis need to have the highest expertise observer score
8 # as the associated covariate
9
10 # get unique observers per sei
11 dataSeiScore <- distinct(
12   dataSubsample, sampling_event_identifider,
13   observer_id
14 ) %>%
15   # make list column of observers
16   mutate(observers = str_split(observer_id, ",")) %>%
17   unnest(cols = c(observers)) %>%
18   # add numeric observer id
19   mutate(numObserver = str_extract(observers, "\\d+")) %>%
20   # now get distinct sei and observer id numeric
21   distinct(sampling_event_identifider, numObserver)
22
23 # now add expertise score to sei
24 dataSeiScore <- left_join(dataSeiScore, expertiseScore,
25   by = "numObserver"
26 ) %>%
27   # get max expertise score per sei
28   group_by(sampling_event_identifider) %>%
29   summarise(expertise = max(score))
30
31 # add to dataCovar
32 dataSubsample <- left_join(dataSubsample, dataSeiScore,
33   by = "sampling_event_identifider"
34 )
35
36 # remove data without expertise score
37 dataSubsample <- filter(dataSubsample, !is.na(expertise))

```

239 6.5 Add climatic and landscape covariates

240 Reload climate and land cover predictors prepared previously.

```

1
2 # list landscape covariate stacks
3 landscape_files <- "data/spatial/landscape_resamp01_km.tif"
4
5 # read in as stacks
6 landscape_data <- stack(landscape_files)
7
8 # get proper names
9 elev_names <- c("elev", "slope", "aspect")
10 chelsea_names <- c("bio1", "bio12")
11
12 names(landscape_data) <- as.character(glue('{c(elev_names, chelsea_names, "landcover")}'))

```

241 6.6 Spatial buffers around selected checklists

242 Every checklist on eBird is associated with a latitude and longitude. However, the coordinates entered by an observer may
243 not accurately depict the location at which a species was detected. This can occur for two reasons: first, traveling checklists
244 are often associated with a single location along the route travelled by observers; and second, checklist locations could be
245 assigned to a 'hotspot' – a location that is marked by eBird as being frequented by multiple observers. In many cases, an
246 observation might be assigned to a hotspot even though the observation was not made at the precise location of the hotspot
247 (J. 2017). Johnston et al., (2019) showed that a large proportion of observations occurred within a 3km grid, even for those
248 checklists up to 5km in length. Hence to adjust for spatial precision, we considered a minimum radius of 2.5km around
249 each unique locality when sampling environmental covariate values.

```

1 # assign neighbourhood radius in m
2 sample_radius <- 2.5 * 1e3
3
4 # get distinct points and make buffer
5 ebird_buff <- dataSubsample %>%
6   ungroup() %>%
7   distinct(X, Y) %>%
8   mutate(id = 1:nrow(.)) %>%
9   crossing(sample_radius) %>%
10  arrange(id) %>%
11  group_by(sample_radius) %>%
12  nest() %>%
13  ungroup()
14
15
16 # convert to spatial features
17 ebird_buff <- mutate(ebird_buff,
18   data = map2(
19     data, sample_radius,
20     function(df, rd) {
21       df_sf <- st_as_sf(df, coords = c("X", "Y"), crs = 32643) %>%
22         # add long lat
23         bind_cols(as_tibble(st_coordinates(.))) %>%
24         # rename(longitude = X, latitude = Y) %>%
25         # # transform to modis projection
26         # st_transform(crs = 32643) %>%
27         # buffer to create neighborhood around each point
28         st_buffer(dist = rd)
29     }
30   )
31 )

```

6.7 Spatial buffer-wide covariates

6.7.1 Mean climatic covariates

All climatic covariates are sampled by considering the mean values within a 2.5km radius as discussed above and prefixed “am_”.

```
1 # get area mean for all preds except landcover, which is the last one
2 env_area_mean <- purrr::map(ebird_buff$data, function(df) {
3   stk <- landscape_data[[-dim(landscape_data)[3]]] # removing landcover here
4   velstk <- velox(stk)
5   dextr <- velstk$extract(
6     sp = df, df = TRUE,
7     fun = function(x) mean(x, na.rm = T)
8   )
9
10  # assign names for joining
11  names(dextr) <- c("id", names(stk))
12  return(as_tibble(dextr))
13 })
14
15 # join to buffer data
16 ebird_buff <- ebird_buff %>%
17   mutate(data = map2(data, env_area_mean, inner_join, by = "id"))
```

6.7.2 Proportions of land cover type

All land cover covariates were sampled by considering the proportion of each land cover type within a 2.5km radius.

```
1 # get the last element of each stack from the list
2 # this is the landcover at that resolution
3 lc_area_prop <- purrr::map(ebird_buff$data, function(df) {
4   lc <- landscape_data[[dim(landscape_data)[3]]] # accessing landcover here
5   lc_velox <- velox(lc)
6   lc_vals <- lc_velox$extract(sp = df, df = TRUE)
7   names(lc_vals) <- c("id", "lc")
8
9   # get landcover proportions
10  lc_prop <- count(lc_vals, id, lc) %>%
11    group_by(id) %>%
12    mutate(
13      lc = glue('lc_{str_pad(lc, 2, pad = "0")}',
14      prop = n / sum(n)
15    ) %>%
16    dplyr::select(-n) %>%
17    tidyr::pivot_wider(
18      names_from = lc,
19      values_from = prop,
20      values_fill = list(prop = 0)
21    ) %>%
22    ungroup()
23
24  return(lc_prop)
25 })
26
27 # join to data
```

```

28 ebird_buff <- ebird_buff %>%
29   mutate(data = map2(data, lc_area_prop, inner_join, by = "id"))

```

256 6.7.3 Link environmental covariates to checklists

```

1   # duplicate scale data
2   data_at_scale <- ebird_buff
3
4   # join the full data to landscape samples at each scale
5   data_at_scale$data <- map(data_at_scale$data, function(df) {
6     df <- st_drop_geometry(df)
7     df <- inner_join(dataSubsample, df, by = c("X", "Y"))
8     return(df)
9   })

```

257 Save data to file.

```

1   # write to file
2   pmap(data_at_scale, function(sample_radius, data) {
3     write_csv(data, path = glue('data/04_data-covars-{str_pad(sample_radius/1e3, 2, pad = "0")}km.csv'))
4     message(glue('export done: data/04_data-covars-{str_pad(sample_radius/1e3, 2, pad = "0")}km.csv'))
5   })

```

258 7 Modelling Species Occupancy

259 7.0.1 Load necessary libraries

```

1   # Load libraries
2   library(auk)
3   library(lubridate)
4   library(sf)
5   library(unmarked)
6   library(raster)
7   library(ebirdst)
8   library(MuMIn)
9   library(AICcmodavg)
10  library(fields)
11  library(tidyverse)
12  library(doParallel)
13  library(snow)
14  library(openxlsx)
15  library(data.table)
16  library(dplyr)
17  library(ecodist)
18
19  # Source necessary functions
20  source("code/fun_screen_cor.R")
21  source("code/fun_model_estimate_collection.r")

```

260 7.1 Load dataframe and scale covariates

261 Here, we load the required dataframe that contains 10 random visits to a site and environmental covariates that were prepared
 262 at a spatial scale of 2.5 sq.km. We also scaled all covariates (mean around 0 and standard deviation of 1). Next, we ensured
 263 that only Traveling and Stationary checklists were considered. Even though stationary counts have no distance traveled,
 264 we defaulted all stationary accounts to an effective distance of 100m, which we consider the average maximum detection

265 radius for most bird species in our area. Following this, we excluded predictors with a Pearson coefficient > 0.5 which
266 resulted in the removal of grasslands as it was highly negatively correlated with forests ($r = -0.77$).

267 Please note that species-specific plots of probabilities of occupancy as a function of environmental data can be accessed in
268 Section 10 of the Supplementary Material.

```
1  # Load in the prepared dataframe that contains 10 random visits to each site
2  dat <- fread("data/04_data-covars-2.5km.csv", header = T)
3  setDF(dat)
4  head(dat)
5
6  # Some more pre-processing to get the right data structures
7
8  # Ensuring that only Traveling and Stationary checklists were considered
9  names(dat)
10 dat <- dat %>% filter(protocol_type %in% c("Traveling", "Stationary"))
11
12 # We take all stationary counts and give them a distance of 100 m (so 0.1 km),
13 # as that's approximately the max normal hearing distance for people doing point counts.
14 dat <- dat %>%
15   mutate(effort_distance_km = replace(
16     effort_distance_km,
17     which(effort_distance_km == 0 &
18       protocol_type == "Stationary"),
19     0.1
20   ))
21
22 # Converting time observations started to numeric and adding it as a new column
23 # This new column will be minute_observations_started
24 dat <- dat %>%
25   mutate(min_obs_started = strtoi(as.difftime(time_observations_started,
26     format = "%H:%M:%S", units = "mins"
27   )))
28
29 # Adding the julian date to the dataframe
30 dat <- dat %>% mutate(julian_date = lubridate::yday(dat$observation_date))
31
32 # Removing other unnecessary columns from the dataframe and creating a clean one without the rest
33 names(dat)
34 dat <- dat[, -c(1, 4, 5, 16, 18, 21, 23, 24, 25, 26, 28:37, 39:45, 47)]
35
36 # Rename column names:
37 names(dat) <- c(
38   "duration_minutes", "effort_distance_km", "locality",
39   "locality_type", "locality_id", "observer_id",
40   "observation_date", "scientific_name", "observation_count",
41   "protocol_type", "number_observers", "pres_abs", "tot_effort",
42   "longitude", "latitude", "expertise", "bio_1.y", "bio_12.y",
43   "lc_02.y", "lc_06.y", "lc_01.y", "lc_07.y", "lc_04.y",
44   "lc_05.y", "min_obs_started", "julian_date"
45 )
46
47 dat.1 <- dat %>%
48   mutate(
49     year = year(observation_date),
```

```

50     pres_abs = as.integer(pres_abs)
51   ) # occupancy modeling requires an integer response
52
53   # Dividing Annual Mean Temperature by 10 to arrive at accurate values of temperature
54   dat.1$bio_1.y <- dat.1$bio_1.y / 10
55
56   # Scaling detection and occupancy covariates
57   dat.scaled <- dat.1
58   dat.scaled[, c(1, 2, 11, 16:25)] <- scale(dat.scaled[, c(1, 2, 11, 16:25)]) # Scaling and standardizing detection and occupancy covariates
59   fwrite(dat.scaled, file = "data/05_scaled-covars-2.5km.csv")
60
61   # Reload the scaled covariate data
62   dat.scaled <- fread("data/05_scaled-covars-2.5km.csv", header = T)
63   setDF(dat.scaled)
64   head(dat.scaled)
65
66   # Ensure observation_date column is in the right format
67   dat.scaled$observation_date <- format(
68     as.Date(
69       dat.scaled$observation_date,
70       "%m/%d/%Y"
71     ),
72     "%Y-%m-%d"
73   )
74
75   # Testing for correlations before running further analyses
76   # Most are uncorrelated since we decided to keep only 2 climatic and 6 land cover predictors
77   source("code/screen_cor.R")
78   names(dat.scaled)
79   screen.cor(dat.scaled[, c(1, 2, 11, 16:25)], threshold = 0.5)

```

269 7.2 Running a null model

```

1   # All null models are stored in lists below
2   all_null <- list()
3
4   # Add a progress bar for the loop
5   pb <- txtProgressBar(
6     min = 0,
7     max = length(unique(dat.scaled$scientific_name)),
8     style = 3
9   ) # text based bar
10
11   for (i in 1:length(unique(dat.scaled$scientific_name))) {
12     data <- dat.scaled %>%
13       filter(dat.scaled$scientific_name == unique(dat.scaled$scientific_name)[i])
14
15     # Preparing data for the unmarked model
16     occ <- filter_repeat_visits(data,
17       min_obs = 1, max_obs = 10,
18       annual_closure = FALSE,
19       n_days = 2600, # 7 years is considered a period of closure
20       date_var = "observation_date",
21       site_vars = c("locality_id")

```

```

22 )
23
24 obs_covs <- c(
25   "min_obs_started",
26   "duration_minutes",
27   "effort_distance_km",
28   "number_observers",
29   "protocol_type",
30   "expertise",
31   "julian_date"
32 )
33
34 # format for unmarked
35 occ_wide <- format_unmarked_occu(occ,
36   site_id = "site",
37   response = "pres_abs",
38   site_covs = c("locality_id", "lc_01.y", "lc_02.y", "lc_04.y",
39     "lc_05.y", "lc_06.y", "lc_07.y", "bio_1.y", "bio_12.y"),
40   obs_covs = obs_covs
41 )
42
43 # Convert this dataframe of observations into an unmarked object to start fitting occupancy models
44 occ_um <- formatWide(occ_wide, type = "unmarkedFrameOccu")
45
46 # Set up the model
47 all_null[[i]] <- occu(~1 ~ 1, data = occ_um)
48 names(all_null)[i] <- unique(dat.scaled$scientific_name)[i]
49 setTxtProgressBar(pb, i)
50 }
51 close(pb)
52
53 # Store all the model outputs for each species
54 capture.output(all_null, file = "data\\results\\null_models.csv")

```

270 7.3 Identifying covariates necessary to model the detection process

271 Here, we use the unmarked package in R (Fiske and Chandler 2011) to identify detection level covariates that are important
 272 for each species. We use AIC criteria to select top models (Burnham, Anderson, and Huyvaert 2011).

```

1
2 # All models are stored in lists below
3 det_dred <- list()
4
5 # Subsetting those models whose deltaAIC<2 (Burnham et al., 2011)
6 top_det <- list()
7
8 # Getting model averaged coefficients and relative importance scores
9 det_avg <- list()
10 det_imp <- list()
11
12 # Getting model estimates
13 det_modelEst <- list()
14
15 # Add a progress bar for the loop
16 pb <- txtProgressBar(min = 0,

```

```

17   max = length(unique(dat.scaled$scientific_name)), style = 3) # text based bar
18
19   for (i in 1:length(unique(dat.scaled$scientific_name))) {
20     data <- dat.scaled %>%
21       filter(dat.scaled$scientific_name == unique(dat.scaled$scientific_name)[i])
22
23     # Preparing data for the unmarked model
24     occ <- filter_repeat_visits(data,
25       min_obs = 1, max_obs = 10,
26       annual_closure = FALSE,
27       n_days = 2600, # 6 years is considered a period of closure
28       date_var = "observation_date",
29       site_vars = c("locality_id")
30   )
31
32   obs_covs <- c(
33     "min_obs_started",
34     "duration_minutes",
35     "effort_distance_km",
36     "number_observers",
37     "protocol_type",
38     "expertise",
39     "julian_date"
40   )
41
42   # format for unmarked
43   occ_wide <- format_unmarked_occu(occ,
44     site_id = "site",
45     response = "pres_abs",
46     site_covs = c("locality_id", "lc_01.y", "lc_02.y", "lc_04.y",
47       "lc_05.y", "lc_06.y", "lc_07.y", "bio_1.y", "bio_12.y"),
48     obs_covs = obs_covs
49   )
50
51   # Convert this dataframe of observations into an unmarked object to start fitting occupancy models
52   occ_um <- formatWide(occ_wide, type = "unmarkedFrameOccu")
53
54   # Fit a global model with all detection level covariates
55   global_mod <- occu(~ min_obs_started +
56     julian_date +
57     duration_minutes +
58     effort_distance_km +
59     number_observers +
60     protocol_type +
61     expertise ~ 1, data = occ_um)
62
63   # Set up the cluster
64   clusterType <- if (length(find.package("snow", quiet = TRUE))) "SOCK" else "PSOCK"
65   clust <- try(makeCluster(getOption("cl.cores", 6), type = clusterType))
66
67   clusterEvalQ(clust, library(unmarked))
68   clusterExport(clust, "occ_um")
69
70   det_dred[[i]] <- pdredge(global_mod, clust)

```



```

71 names(det_dred)[i] <- unique(dat.scaled$scientific_name)[i]
72
73 # Get the top models, which we'll define as those with deltaAICc < 2
74 top_det[[i]] <- get.models(det_dred[[i]], subset = delta < 2, cluster = clust)
75 names(top_det)[i] <- unique(dat.scaled$scientific_name)[i]
76
77 # Obtaining model averaged coefficients
78 if (length(top_det[[i]]) > 1) {
79   a <- model.avg(top_det[[i]], fit = TRUE)
80   det_avg[[i]] <- as.data.frame(a$coefficients)
81   names(det_avg)[i] <- unique(dat.scaled$scientific_name)[i]
82
83   det_modelEst[[i]] <- data.frame(
84     Coefficient = coefTable(a, full = T)[, 1],
85     SE = coefTable(a, full = T)[, 2],
86     lowerCI = confint(a)[, 1],
87     upperCI = confint(a)[, 2],
88     z_value = (summary(a)$coefmat.full)[, 3],
89     Pr_z = (summary(a)$coefmat.full)[, 4]
90   )
91
92   names(det_modelEst)[i] <- unique(dat.scaled$scientific_name)[i]
93
94   det_imp[[i]] <- as.data.frame(MuMIn::importance(a))
95   names(det_imp)[i] <- unique(dat.scaled$scientific_name)[i]
96 } else {
97   det_avg[[i]] <- as.data.frame(unmarked::coef(top_det[[i]][[1]]))
98   names(det_avg)[i] <- unique(dat.scaled$scientific_name)[i]
99
100   lowDet <- data.frame(lowerCI = confint(top_det[[i]][[1]], type = "det")[, 1])
101   upDet <- data.frame(upperCI = confint(top_det[[i]][[1]], type = "det")[, 2])
102   zDet <- data.frame(summary(top_det[[i]][[1]])$det[, 3])
103   Pr_zDet <- data.frame(summary(top_det[[i]][[1]])$det[, 4])
104
105   Coefficient <- coefTable(top_det[[i]][[1]])[, 1]
106   SE <- coefTable(top_det[[i]][[1]])[, 2]
107
108   det_modelEst[[i]] <- data.frame(
109     Coefficient = Coefficient[2:9],
110     SE = SE[2:9],
111     lowerCI = lowDet,
112     upperCI = upDet,
113     z_value = zDet,
114     Pr_z = Pr_zDet
115   )
116
117   names(det_modelEst)[i] <- unique(dat.scaled$scientific_name)[i]
118 }
119 setTxtProgressBar(pb, i)
120 stopCluster(clust)
121 }
122 close(pb)
123
124 ## Storing output from the above models in excel sheets

```

```

125
126 # 1. Store all the model outputs for each species (variable: det_dred() - see above)
127 write.xlsx(det_dred, file = "data\\results\\det-dred.xlsx")
128
129 # 2. Store all the model averaged outputs for each species and the relative importance score
130 write.xlsx(det_avg, file = "data\\results\\det-avg.xlsx", rowNames = T, colNames = T)
131 write.xlsx(det_imp, file = "data\\results\\det-imp.xlsx", rowNames = T, colNames = T)
132
133 write.xlsx(det_modelEst, file = "data\\results\\det-modelEst.xlsx", rowNames = T, colNames = T)

```

273 7.4 Land Cover and Climate

274 Occupancy models estimate the probability of occurrence of a given species while controlling for the probability of detection
 275 and allow us to model the factors affecting occurrence and detection independently (Johnston et al. 2018; MacKenzie et al.
 276 2002). The flexible eBird observation process contributes to the largest source of variation in the likelihood of detecting
 277 a particular species (Johnston et al. 2019); hence, we included seven covariates that influence the probability of detection
 278 for each checklist: ordinal day of year, duration of observation, distance travelled, protocol type, time observations started,
 279 number of observers and the checklist calibration index (CCI).

280 Using a multi-model information-theoretic approach, we tested how strongly our occurrence data fit our candidate set of
 281 environmental covariates (Burnham and Anderson 2002). We fitted single-species occupancy models for each species,
 282 to simultaneously estimate a probability of detection (p) and a probability of occupancy (ψ) (Fiske and Chandler 2011;
 283 MacKenzie et al. 2002). For each species, we fit 256 models, each with a unique combination of the eight (climate and
 284 land cover) occupancy covariates and all seven detection covariates (Appendix S5).

285 Across the 256 models tested for each species, the model with highest support was determined using AICc scores. However,
 286 across the majority of the species, no single model had overwhelming support. Hence, for each species, we examined those
 287 models which had $\Delta AICc < 2$, as these top models were considered to explain a large proportion of the association between
 288 the species-specific probability of occupancy and environmental drivers (Burnham, Anderson, and Huyvaert 2011; Elsen
 289 et al. 2017). Using these restricted model sets for each species; we created a model-averaged coefficient estimate for each
 290 predictor and assessed its direction and significance (Bartoń 2020). We considered a predictor to be significantly associated
 291 with occupancy if the range of the 95% confidence interval around the model-averaged coefficient did not contain zero.
 292 Next, we obtained a measure of relative importance of climatic and landscape predictors by calculating cumulative variable
 293 importance scores. These scores were calculated by obtaining the sum of model weights (AIC weights) across all models
 294 (including the top models) for each predictor across all species.

```

1 # All models are stored in lists below
2 lc_clim <- list()
3
4 # Subsetting those models whose deltaAIC<2 (Burnham et al., 2011)
5 top_lc_clim <- list()
6
7 # Getting model averaged coefficients and relative importance scores
8 lc_clim_avg <- list()
9 lc_clim_imp <- list()
10
11 # Storing Model estimates
12 lc_clim_modelEst <- list()
13
14 # Add a progress bar for the loop
15 pb <- txtProgressBar(min = 0, max = length(unique(dat.scaled$scientific_name)), style = 3) # text based bar
16
17 for (i in 1:length(unique(dat.scaled$scientific_name))) {
18   data <- dat.scaled %>% filter(dat.scaled$scientific_name == unique(dat.scaled$scientific_name)[1])
19
20   # Preparing data for the unmarked model

```

```

21 occ <- filter_repeat_visits(data,
22   min_obs = 1, max_obs = 10,
23   annual_closure = FALSE,
24   n_days = 2600, # 6 years is considered a period of closure
25   date_var = "observation_date",
26   site_vars = c("locality_id")
27 )
28
29 obs_covs <- c(
30   "min_obs_started",
31   "duration_minutes",
32   "effort_distance_km",
33   "number_observers",
34   "protocol_type",
35   "expertise",
36   "julian_date"
37 )
38
39 # format for unmarked
40 occ_wide <- format_unmarked_occu(occ,
41   site_id = "site",
42   response = "pres_abs",
43   site_covs = c("locality_id", "lc_01.y", "lc_02.y", "lc_04.y", "lc_05.y",
44     "lc_06.y", "lc_07.y", "bio_1.y", "bio_12.y"),
45   obs_covs = obs_covs
46 )
47
48 # Convert this dataframe of observations into an unmarked object to start fitting occupancy models
49 occ_um <- formatWide(occ_wide, type = "unmarkedFrameOccu")
50
51 model_lc_clim <- occu(~ min_obs_started +
52   julian_date +
53   duration_minutes +
54   effort_distance_km +
55   number_observers +
56   protocol_type +
57   expertise ~ lc_01.y + lc_02.y + lc_04.y +
58   lc_05.y + lc_06.y + lc_07.y + bio_1.y + bio_12.y, data = occ_um)
59
60 # Set up the cluster
61 clusterType <- if (length(find.package("snow", quiet = TRUE))) "SOCK" else "PSOCK"
62 clust <- try(makeCluster(getOption("cl.cores", 6), type = clusterType))
63
64 clusterEvalQ(clust, library(unmarked))
65 clusterExport(clust, "occ_um")
66
67 # Detection terms are fixed
68 det_terms <- c(
69   "p(duration_minutes)", "p(effort_distance_km)", "p(expertise)",
70   "p(julian_date)", "p(min_obs_started)",
71   "p(number_observers)", "p(protocol_type)"
72 )
73
74 lc_clim[[i]] <- pdredge(model_lc_clim, clust, fixed = det_terms)

```

```

75 names(lc_clim)[i] <- unique(dat.scaled$scientific_name)[i]
76
77 # Identifying top subset of models based on deltaAIC scores being less than 2 (Burnham et al., 2011)
78 top_lc_clim[[i]] <- get.models(lc_clim[[i]], subset = delta < 2, cluster = clust)
79
80 names(top_lc_clim)[i] <- unique(dat.scaled$scientific_name)[i]
81
82 # Obtaining model averaged coefficients for both candidate model subsets
83 if (length(top_lc_clim[[i]]) > 1) {
84   a <- model.avg(top_lc_clim[[i]], fit = TRUE)
85   lc_clim_avg[[i]] <- as.data.frame(a$coefficients)
86   names(lc_clim_avg)[i] <- unique(dat.scaled$scientific_name)[i]
87
88   lc_clim_modelEst[[i]] <- data.frame(
89     Coefficient = coefTable(a, full = T)[, 1],
90     SE = coefTable(a, full = T)[, 2],
91     lowerCI = confint(a)[, 1],
92     upperCI = confint(a)[, 2],
93     z_value = (summary(a)$coefmat.full)[, 3],
94     Pr_z = (summary(a)$coefmat.full)[, 4]
95   )
96
97   names(lc_clim_modelEst)[i] <- unique(dat.scaled$scientific_name)[i]
98
99   lc_clim_imp[[i]] <- as.data.frame(MuMIn::importance(a))
100   names(lc_clim_imp)[i] <- unique(dat.scaled$scientific_name)[i]
101 } else {
102   lc_clim_avg[[i]] <- as.data.frame(unmarked::coef(top_lc_clim[[i]][[1]]))
103   names(lc_clim_avg)[i] <- unique(dat.scaled$scientific_name)[i]
104
105   lowSt <- data.frame(lowerCI = confint(top_lc_clim[[i]][[1]]), type = "state")[, 1]
106   lowDet <- data.frame(lowerCI = confint(top_lc_clim[[i]][[1]]), type = "det")[, 1]
107   upSt <- data.frame(upperCI = confint(top_lc_clim[[i]][[1]]), type = "state")[, 2]
108   upDet <- data.frame(upperCI = confint(top_lc_clim[[i]][[1]]), type = "det")[, 2]
109   zSt <- data.frame(z_value = summary(top_lc_clim[[i]][[1]])$state[, 3])
110   zDet <- data.frame(z_value = summary(top_lc_clim[[i]][[1]])$det[, 3])
111   Pr_zSt <- data.frame(Pr_z = summary(top_lc_clim[[i]][[1]])$state[, 4])
112   Pr_zDet <- data.frame(Pr_z = summary(top_lc_clim[[i]][[1]])$det[, 4])
113
114   lc_clim_modelEst[[i]] <- data.frame(
115     Coefficient = coefTable(top_lc_clim[[i]][[1]]), 1],
116     SE = coefTable(top_lc_clim[[i]][[1]]), 2],
117     lowerCI = rbind(lowSt, lowDet),
118     upperCI = rbind(upSt, upDet),
119     z_value = rbind(zSt, zDet),
120     Pr_z = rbind(Pr_zSt, Pr_zDet)
121   )
122
123   names(lc_clim_modelEst)[i] <- unique(dat.scaled$scientific_name)[i]
124 }
125 setTxtProgressBar(pb, i)
126 stopCluster(clust)
127 }
128 close(pb)

```



```

40     julian_date +
41     duration_minutes +
42     effort_distance_km +
43     number_observers +
44     protocol_type +
45     expertise ~ lc_01.y + lc_02.y + lc_04.y +
46     lc_05.y + lc_06.y + lc_07.y + bio_1.y + bio_12.y, data = occ_um)
47
48     occ_gof <- mb.gof.test(model_lc_clim, nsim = 5000, plot.hist = FALSE)
49
50     p.value <- occ_gof$p.value
51     c.hat <- occ_gof$c.hat.est
52     scientific_name <- unique(data$scientific_name)
53
54     a <- data.frame(scientific_name, p.value, c.hat)
55
56     goodness_of_fit <- rbind(a, goodness_of_fit)
57
58     setTxtProgressBar(pb, i)
59 }
60 close(pb)
61
62 write.csv(goodness_of_fit, "data\\results\\05_goodness-of-fit-2.5km.csv")

```

298 8 Visualizing Occupancy Predictor Effects

299 In this section, we will visualize the cumulative AIC weights and the magnitude and direction of species-specific probability
300 of occupancy.

301 To get cumulative AIC weights, we first obtained a measure of relative importance of climatic and landscape predictors by
302 calculating cumulative variable importance scores. These scores were calculated by obtaining the sum of model weights
303 (AIC weights) across all models (including the top models) for each predictor across all species. We then calculated the
304 mean cumulative variable importance score and a standard deviation for each predictor (Burnham and Anderson 2002).

305 8.1 Prepare libraries

```

1 # to load data
2 library(readxl)
3
4 # to handle data
5 library(dplyr)
6 library(readr)
7 library(forcats)
8 library(tidyr)
9 library(purrr)
10 library(stringr)
11 library(data.table)
12
13 # to wrangle models
14 source("code/fun_model_estimate_collection.r")
15 source("code/fun_make_resp_data.r")
16
17 # nice tables
18 library(knitr)

```

```

19 library(kableExtra)
20
21 # plotting
22 library(ggplot2)
23 library(patchwork)
24 source("code/fun_plot_interaction.r")

```

306 8.2 Load species list

```

1 # list of species
2 species <- read_csv("data/species_list.csv")
3 list_of_species <- as.character(species$scientific_name)

```

307 8.3 Show AIC weight importance

308 8.3.1 Read in AIC weight data

```

1 # which files to read
2 file_names <- c("data/results/lc-clim-imp.xlsx")
3
4 # read in sheets by species
5 model_imp <- map(file_names, function(f) {
6   md_list <- map(list_of_species, function(sn) {
7
8     # some sheets are not found
9
10    tryCatch(
11      {
12        readxl::read_excel(f, sheet = sn) %>%
13        `colnames<-`(c("predictor", "AIC_weight")) %>%
14        filter(str_detect(predictor, "psi")) %>%
15        mutate(
16          predictor = stringr::str_extract(predictor,
17            pattern = stringr::regex("\\((.*?)\\)")
18          ),
19          predictor = stringr::str_replace_all(predictor, "[/(//)]", ""),
20          predictor = stringr::str_remove(predictor, "\\..y")
21        )
22      },
23      error = function(e) {
24        message(as.character(e))
25      }
26    )
27  })
28   names(md_list) <- list_of_species
29
30   return(md_list)
31 })

```

309 8.3.2 Prepare cumulative AIC weight data

```

1 # assign scale - minimum spatial scale at which the analysis was carried out to account for observer effort
2 names(model_imp) <- c("2.5km")
3 model_imp <- imap(model_imp, function(.x, .y) {
4   .x <- bind_rows(.x)

```

```

5   .x$scale <- .y
6   return(.x)
7 })
8
9 # bind rows
10 model_imp <- map(model_imp, bind_rows) %>%
11   bind_rows()
12
13 # convert to numeric
14 model_imp$AIC_weight <- as.numeric(model_imp$AIC_weight)
15 model_imp$scale <- as.factor(model_imp$scale)
16 levels(model_imp$scale) <- c("2.5km")
17
18 # Let's get a summary of cumulative variable importance
19 model_imp <- group_by(model_imp, predictor) %>%
20   summarise(
21     mean_AIC = mean(AIC_weight),
22     sd_AIC = sd(AIC_weight),
23     min_AIC = min(AIC_weight),
24     max_AIC = max(AIC_weight),
25     med_AIC = median(AIC_weight)
26   )
27
28 # write to file
29 write_csv(model_imp,
30   file = "data/results/cumulative_AIC_weights.csv"
31 )
310 Read data back in.
311
312 # read data and make factor
313 model_imp <- read_csv("data/results/cumulative_AIC_weights.csv")
314 model_imp$predictor <- as_factor(model_imp$predictor)
315
316 # make nice names
317 predictor_name <- tibble(
318   predictor = levels(model_imp$predictor),
319   pred_name = c(
320     "Annual Mean Temperature (°C)",
321     "Annual Precipitation (mm)",
322     "% Agriculture", "% Forests",
323     "% Plantations", "% Settlements",
324     "% Tea", "% Water Bodies"
325   )
326 )
327
328 # rename predictor
329 model_imp <- left_join(model_imp, predictor_name)
330
331 Prepare figure for cumulative AIC weight. Figure code is hidden in versions rendered as HTML and PDF.
332
333 fig_aic <-
334   ggplot(model_imp) +
335     geom_pointrange(aes(
336       x = reorder(predictor, mean_AIC),
337       y = mean_AIC,

```



```

6     ymin = mean_AIC - sd_AIC,
7     ymax = mean_AIC + sd_AIC
8   )) +
9   geom_text(aes(
10     x = predictor,
11     y = 0.2,
12     label = pred_name
13   ),
14   angle = 0,
15   hjust = "inward",
16   vjust = 2
17 ) +
18 # scale_y_continuous(breaks = seq(45, 75, 10))+
19 scale_x_discrete(labels = NULL) +
20 # scale_color_brewer(palette = "RdBu", values = c(0.5, 1))+
21 coord_flip(
22   # ylim = c(45, 75)
23 ) +
24 theme_test() +
25 theme(legend.position = "none") +
26 labs(
27   x = "Predictor",
28   y = "Cumulative AIC weight"
29 )
30
31 ggsave(fig_aic,
32   filename = "figs/fig_aic_weight.png",
33   device = png(),
34   dpi = 300,
35   width = 79, height = 120, units = "mm"
36 )

```

312 8.4 Prepare model coefficient data

313 For each species, we examined those models which had $\Delta AIC_c < 2$, as these top models were considered to explain a large
314 proportion of the association between the species-specific probability of occupancy and environmental drivers (Burnham,
315 Anderson, and Huyvaert 2011; Elsen et al. 2017). Using these restricted model sets for each species; we created a model-
316 averaged coefficient estimate for each predictor and assessed its direction and significance (Bartoń 2020). We considered
317 a predictor to be significantly associated with occupancy if the range of the 95% confidence interval around the model-
318 averaged coefficient did not contain zero.

```

1 file_read <- c("data/results/lc-clim-modelEst.xlsx")
2
3 # read data as list column
4 model_est <- map(file_read, function(fr) {
5   md_list <- map(list_of_species, function(sn) {
6     readxl::read_excel(fr, sheet = sn)
7   })
8   names(md_list) <- list_of_species
9   return(md_list)
10 })
11
12 # prepare model data
13 scales <- c("2.5km")
14 model_data <- tibble(

```

```

15   scale = scales,
16   scientific_name = list_of_species
17 ) %>%
18   arrange(desc(scale))
19
20 # rename model data components and separate predictors
21 names <- c(
22   "predictor", "coefficient", "se", "ci_lower",
23   "ci_higher", "z_value", "p_value"
24 )
25
26 # get data for plotting:
27 model_est <- map(model_est, function(l) {
28   map(l, function(df) {
29     colnames(df) <- names
30     df <- separate_interaction_terms(df)
31     df <- make_response_data(df)
32     return(df)
33   })
34 })
35
36 # add names and scales
37 model_est <- map(model_est, function(l) {
38   imap(l, function(.x, .y) {
39     mutate(.x, scientific_name = .y)
40   })
41 })
42
43 # add names to model estimates
44 names(model_est) <- scales
45 model_est <- imap(model_est, function(.x, .y) {
46   bind_rows(.x) %>%
47     mutate(scale = .y)
48 })
49
50 # remove modulators
51 model_est <- bind_rows(model_est) %>%
52   select(-matches("modulator"))
53
54 # join data to species name
55 model_data <- model_data %>%
56   left_join(model_est)
57
58 # Keep only those predictors whose p-values are significant:
59 model_data <- model_data %>%
60   filter(p_value < 0.05)
319 Export predictor effects.
6
1 # get predictor effect data
2 data_predictor_effect <- distinct(
3   model_data,
4   scientific_name,
5   se,
6   predictor, coefficient

```

```

7   )
8
9   # write to file
10  write_csv(data_predictor_effect,
11            path = "data/results/data_predictor_effect.csv"
12  )
320 Export model data.
1   model_data_to_file <- model_data %>%
2     select(
3       predictor, data,
4       scientific_name, scale
5     ) %>%
6     unnest(cols = "data")
7
8   # remove .y
9   model_data_to_file <- model_data_to_file %>%
10     mutate(predictor = str_remove(predictor, "\\..y"))
11
12  write_csv(
13    model_data_to_file,
14    "data/results/data_occupancy_predictors.csv"
15  )
321 Read in data after clearing R session.
1   # read from file
2   model_data <- read_csv("data/results/data_predictor_effect.csv")
322 Fix predictor name.
1   # remove .y from predictors
2   model_data <- model_data %>%
3     mutate_at(.vars = c("predictor"), .funs = function(x) {
4       stringr::str_remove(x, ".y")
5     })

```

323 8.5 Get predictor effects

```

1   # is the coeff positive? how many positive per scale per predictor per axis of split?
2   data_predictor <- mutate(model_data,
3     direction = coefficient > 0
4   ) %>%
5     count(
6       predictor,
7       direction
8     ) %>%
9     mutate(mag = n * (if_else(direction, 1, -1)))
10
11  # wrangle data to get nice bars
12  data_predictor <- data_predictor %>%
13    select(-n) %>%
14    drop_na(direction) %>%
15    mutate(direction = ifelse(direction, "positive", "negative")) %>%
16    pivot_wider(values_from = "mag", names_from = "direction") %>%
17    mutate_at(

```

```

18     vars(positive, negative),
19     ~ if_else(is.na(.), 0, .)
20   )
21
22 data_predictor_long <- data_predictor %>%
23   pivot_longer(
24     cols = c("negative", "positive"),
25     names_to = "effect",
26     values_to = "magnitude"
27   )
28
29 # write
30 write_csv(data_predictor_long,
31   path = "data/results/data_predictor_direction_nSpecies.csv"
32 )

```

324 Prepare data to determine the direction (positive or negative) of the effect of each predictor. How many species are affected
 325 in either direction?

```

1 # join with predictor names and relative AIC
2 data_predictor_long <- left_join(data_predictor_long, model_imp)

```

326 Prepare figure of the number of species affected in each direction. Figure code is hidden in versions rendered as HTML
 327 and PDF.

328 **8.6 Main Text Figure 4**

329 Figure code is hidden in versions rendered as HTML and PDF.

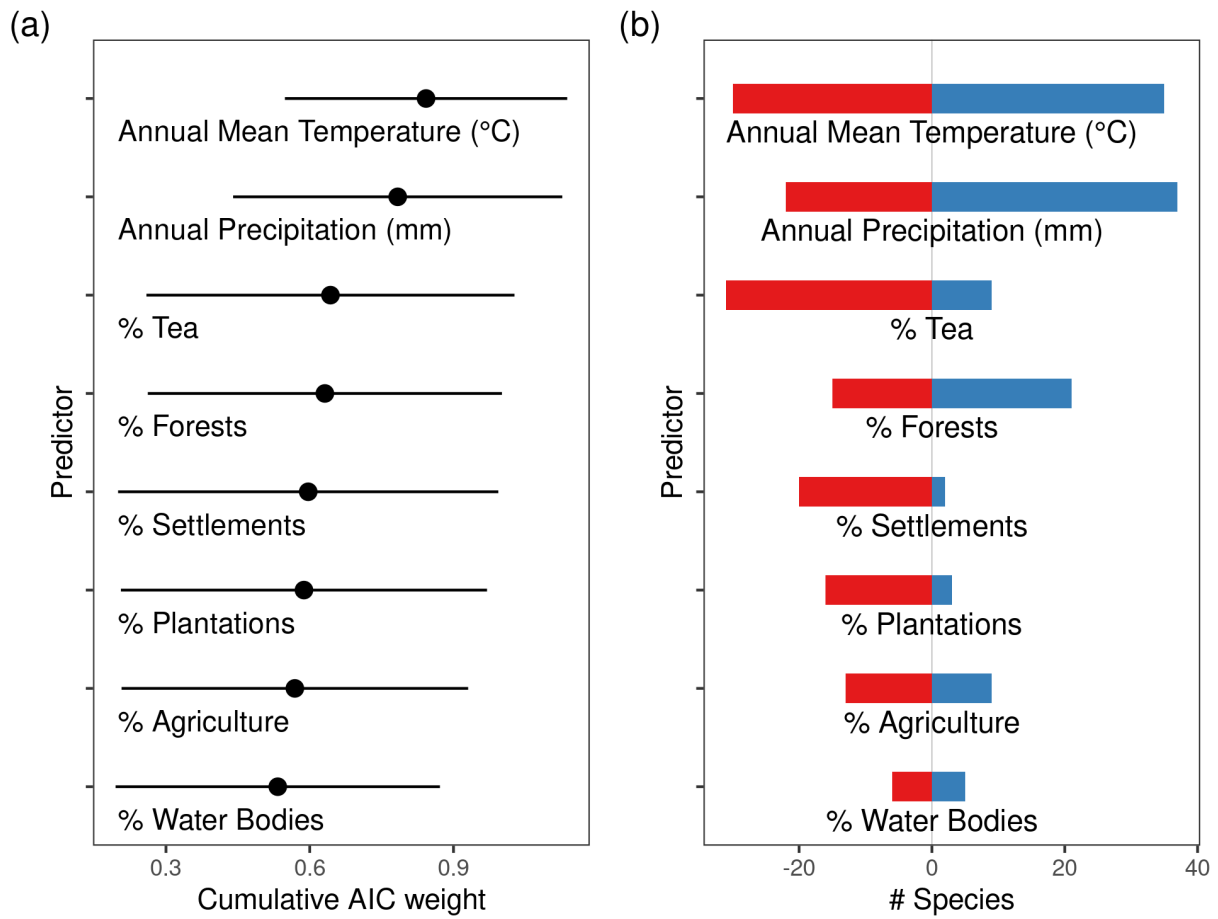


Figure 4: (a) Cumulative AIC weights suggest that climatic predictors have higher relative importance when compared to landscape predictors. (b) The direction of association between species-specific probability of occupancy and climatic and landscape is shown here. While climatic predictors were both positively and negatively associated with the probability of occupancy for a number of species, human-associated land cover types were largely negatively associated with species-specific probability of occupancy.

9 References

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