Main figures and analyses for the manuscript

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This notebook estimates the indicators based on the raw clean data and perfomrs the main analyses and figures used in the manuscript of the multicountry paper. The input is the “clean kobo output” that was first cleaned by 2\_cleaning.Rmd. Besides the plots and statistics shown below, the output is are the indicators data ready to be used to estimate the indicators (ind[1-3]\_data.csv), a single file with the indicators already calculated (indicators\_full.csv) and metadata.

## Packages and functions

Load required libraries:

library(tidyr)  
library(dplyr)  
library(readr)  
library(utile.tools)  
library(stringr)  
library(ggplot2)  
library(ggsankey)  
library(ggnewscale)  
library(alluvial)  
library(viridis)  
library(cowplot)  
library(lme4)  
library(knitr)  
library(glmmTMB)

Load required functions. These custom fuctions are available at: <https://github.com/AliciaMstt/GeneticIndicators>

source("get\_indicator1\_data.R")  
source("get\_indicator2\_data.R")  
source("get\_indicator3\_data.R")  
source("get\_metadata.R")  
source("transform\_to\_Ne.R")  
source("estimate\_indicator1.R")

Other custom functions:

### not in  
'%!in%' <- function(x,y)!('%in%'(x,y))  
  
  
#' Duplicates data to create additional facet. Thanks to https://stackoverflow.com/questions/18933575/easily-add-an-all-facet-to-facet-wrap-in-ggplot2  
#' @param df a dataframe  
#' @param col the name of facet column  
#'   
CreateAllFacet <- function(df, col){  
 df$facet <- df[[col]]  
 temp <- df  
 temp$facet <- "all"  
 merged <-rbind(temp, df)  
  
 # ensure the facet value is a factor  
 merged[[col]] <- as.factor(merged[[col]])  
  
 return(merged)  
}

Custom colors:

## IUCN official colors  
# Assuming order of levels is: "re", "cr", "en", "vu", "nt", "lc", "dd", "not\_assessed", "unknown" (for regional, and w/o "re" for global). Make sure to change the levels to that order before plotting. Note: NE should be "#FFFFFF" but since that means white I'm suing azure2  
IUCNcolors<-c("#FF0000", "#FFA500", "#FFFF00", "#ADFF2F", "#008000", "#808080", "azure2", "bisque1")  
IUCNcolors\_regional<-c("darkorchid2", "#FF0000", "#FFA500", "#FFFF00", "#ADFF2F", "#008000", "#808080", "azure2", "bisque1")  
  
## nice soft ramp for taxonomic groups  
taxoncolors<-cividis(12) # same than using cividis(length(levels(as.factor(metadata$taxonomic\_group))))  
  
## Colors for simplified methods to define populations   
# assuming the levels (see how this was created in the section "Simplify combinations of methods to define populations"): of running levels(as.factor(ind2\_data$defined\_populations\_simplified)) (after new order)  
  
# get a set of colors to highlight genetic and geographic with similar colors  
  
simplifiedmethods\_colors<-c("#FFA07A", #"dispersal\_buffer"  
 "#7f611b", # "eco\_biogeo\_proxies"  
 "#668cd1", # "genetic\_clusters"   
 "#668cd1", # "genetic\_clusters eco\_biogeo\_proxies"   
 "#45c097", # "genetic\_clusters geographic\_boundaries"   
 "#d4b43e", # "geographic\_boundaries"  
 "#d4b43e", # "geographic\_boundaries eco\_biogeo\_proxies"  
 "#d4b43e", # "geographic\_boundaries management\_units"   
 "#b34656", # "management\_units"   
 "#be72c9", # "other"   
 "#be72c9")# "other\_combinations"   
  
grouped\_taxon\_colors<-c("#9f43c8", "#91c637", "#e5463c")

## Get data

Get indicators and metadata data from clean kobo output

# Get data:  
kobo\_clean<-read.csv(file="kobo\_output\_clean.csv", header=TRUE)  
  
# Extract indicator 1 data from kobo output, show most relevant columns  
ind1\_data<-get\_indicator1\_data(kobo\_output=kobo\_clean)

## [1] "the data already contained a taxon column, that was used instead of creating a new one"

head(ind1\_data[,c(1:3, 12:14)])

## # A tibble: 6 × 6  
## country\_assessm… taxonomic\_group taxon X\_validation\_st… X\_uuid multiassessment  
## <chr> <chr> <chr> <chr> <chr> <chr>   
## 1 sweden mammal Alce… validation\_stat… 87eb6… single\_assessm…  
## 2 sweden mammal Alce… validation\_stat… 87eb6… single\_assessm…  
## 3 sweden mammal Alce… validation\_stat… 87eb6… single\_assessm…  
## 4 sweden fish Silu… <NA> 54f0c… single\_assessm…  
## 5 sweden fish Silu… <NA> 54f0c… single\_assessm…  
## 6 sweden fish Silu… <NA> 54f0c… single\_assessm…

# Extract Proportion of maintained populations (indicator) data from kobo output, show most relevant columns  
ind2\_data<-get\_indicator2\_data(kobo\_output=kobo\_clean)

## [1] "the data already contained a taxon column, that was used instead of creating a new one"

head(ind2\_data[,c(1:3, 9:10,13)])

## country\_assessment taxonomic\_group taxon  
## 1 sweden mammal Alces alces  
## 2 sweden fish Siluris glanis  
## 3 sweden bird Dendrocopos leucotos  
## 4 south\_africa gymnosperm Encephalartos latrifrons  
## 5 south\_africa amphibian Capensibufo rosei  
## 6 france mammal Galemys pyrenaicus  
## n\_extant\_populations n\_extint\_populations  
## 1 3 0  
## 2 6 6  
## 3 5 12  
## 4 1 0  
## 5 2 4  
## 6 3 0  
## defined\_populations  
## 1 genetic\_clusters  
## 2 genetic\_clusters geographic\_boundaries  
## 3 geographic\_boundaries  
## 4 genetic\_clusters  
## 5 genetic\_clusters  
## 6 genetic\_clusters eco\_biogeo\_proxies

# Extract indicator 3 data from kobo output, show most relevant columns  
ind3\_data<-get\_indicator3\_data(kobo\_output=kobo\_clean)

## [1] "the data already contained a taxon column, that was used instead of creating a new one"

head(ind3\_data[,c(1:3, 9:11)])

## country\_assessment taxonomic\_group taxon gen\_studies  
## 1 sweden mammal Alces alces pop  
## 2 sweden fish Siluris glanis phylo\_pop  
## 3 sweden bird Dendrocopos leucotos phylo\_pop  
## 4 south\_africa gymnosperm Encephalartos latrifrons pop  
## 5 south\_africa amphibian Capensibufo rosei phylo\_pop  
## 6 france mammal Galemys pyrenaicus phylo\_pop  
## temp\_gen\_monitoring gen\_monitoring\_years  
## 1 yes 1839-2020  
## 2 yes 1980-2018  
## 3 no <NA>  
## 4 no <NA>  
## 5 yes 2008;2015  
## 6 yes 2011-2013

# extract metadata, show most relevant columns  
metadata<-get\_metadata(kobo\_output=kobo\_clean)

## [1] "the data already contained a taxon column, that was used instead of creating a new one"

head(metadata[,c(1:3, 12, 25,26, 64)])

## country\_assessment taxonomic\_group taxon  
## 1 sweden mammal Alces alces  
## 2 sweden fish Siluris glanis  
## 3 sweden bird Dendrocopos leucotos  
## 4 south\_africa gymnosperm Encephalartos latrifrons  
## 5 south\_africa amphibian Capensibufo rosei  
## 6 france mammal Galemys pyrenaicus  
## X\_uuid popsize\_data ne\_pops\_exists  
## 1 87eb6bd2-58cb-4def-9b0c-fbea85304e41 yes ne\_available  
## 2 54f0cd8f-0932-4d62-8dd7-b62c98732999 yes ne\_available  
## 3 24b389e0-fe5c-46d4-a00d-5dcc83e948fe yes other\_genetic\_info  
## 4 79e2d9df-8e43-424e-9794-376b9e63b604 data\_for\_species <NA>  
## 5 461e2dd7-b7a3-4497-8b5a-a51ce8d73ad4 yes ne\_available  
## 6 3b87c40f-b7d7-4edd-9779-915db57bf975 yes ne\_available  
## sources\_life\_history  
## 1 https://www.iucnredlist.org/species/56003281/22157381 ; https://artfakta.se/artbestamning/taxon/alces-alces-206046  
## 2 https://artfakta.se/artbestamning/taxon/silurus-glanis-100131;https://www.iucnredlist.org/species/40713/10356149  
## 3 https://artfakta.se/naturvard/taxon/100046\nÅtgärdsprogram för vitryggig hackspett 2017-2021. Naturvårdsverket Rapport 6770, maj 2017  
## 4 Bösenberg, J.D. 2022. Encephalartos latifrons. The IUCN Red List of Threatened Species 2022: e.T41892A51052295.\nhttps://dx.doi.org/10.2305/IUCN.UK.2022-1.RLTS.T41892A51052295.en. Accessed on 19 October 2022; John Donaldson personal communication 31 October 2022.  
## 5 Becker. 2014. Searching for answers to a silent decline: first estimates of survival and recruitment for the critically endangered Rose’s mountain toadlet, Capensibufo rosei. Hons. thesis. University of Cape Town.  
## 6 Poncet, E., Némoz, M., & Blanc, F. (2017). Outils techniques pour la prise en compte du Desman des Pyrénées dans les procédures d’évaluations environnementales. Livret 1 - Etat des connaissances. Conservatoire d’espaces naturels de Midi-Pyrénées, 20p.

Get population data for those species assessed using the tabular text template instead of Kobo. This file was produced by the script 1.2\_cleaning.Rmd

ind1\_data\_from\_templates<-read.csv(file="ind1\_data\_from\_templates.csv")

Add data recorded using the population template to the ind1\_data already in the nice format.

ind1\_data<-rbind(ind1\_data, ind1\_data\_from\_templates)

## Estimate indicators

### Indicator 1 or Ne 500 indicator (proportion of populations with Ne >500):

Show most relevant columns of indicator 1 data

ind1\_data %>% select(country\_assessment, taxon, population, Name, Ne, NeLower, NeUpper, NeYear, GeneticMarkers, NcType, NcMethod, NcRange)

## # A tibble: 5,652 × 12  
## country\_assessment taxon population Name Ne NeLower NeUpper NeYear  
## <chr> <chr> <chr> <chr> <dbl> <dbl> <dbl> <chr>   
## 1 sweden Alces alces pop1 North 4950 NA NA 2020   
## 2 sweden Alces alces pop2 South 194 NA NA 1980   
## 3 sweden Alces alces pop3 Tran… 11519 NA NA 2020   
## 4 sweden Siluris gla… pop1 Båven 12 6 33 2004   
## 5 sweden Siluris gla… pop2 lowe… 13 7 31 2004   
## 6 sweden Siluris gla… pop3 Uppe… 11 5 26 2010   
## 7 sweden Siluris gla… pop4 Möck… 13 7 30 2010   
## 8 sweden Siluris gla… pop5 Förs… 9 4 26 2006   
## 9 sweden Siluris gla… pop6 Helg… 11 6 26 2010   
## 10 sweden Dendrocopos… pop1 Värm… NA NA NA <NA>   
## # … with 5,642 more rows, and 4 more variables: GeneticMarkers <chr>,  
## # NcType <chr>, NcMethod <chr>, NcRange <chr>

Remember what the function to transform NcRange and NcPoint data into Ne does:

# check what the custom funciton does  
transform\_to\_Ne

## function (ind1\_data, ratio = 0.1)   
## {  
## ratio = ratio  
## if (!is.numeric(ratio) || ratio < 0 || ratio > 1) {  
## stop("Invalid argument. Please provide a number within the range 0 to 1, using `.` to delimit decimals.")  
## }  
## else {  
## ind1\_data = ind1\_data  
## ind1\_data <- ind1\_data %>% mutate(Nc\_from\_range = case\_when(NcRange ==   
## "more\_5000\_bymuch" ~ 10000, NcRange == "more\_5000" ~   
## 5500, NcRange == "less\_5000\_bymuch" ~ 500, NcRange ==   
## "less\_5000" ~ 4050, NcRange == "range\_includes\_5000" ~   
## 5001)) %>% mutate(Ne\_from\_Nc = case\_when(!is.na(NcPoint) ~   
## NcPoint \* ratio, !is.na(Nc\_from\_range) ~ Nc\_from\_range \*   
## ratio)) %>% mutate(Ne\_combined = if\_else(is.na(Ne),   
## Ne\_from\_Nc, Ne)) %>% mutate(Ne\_calculated\_from = if\_else(is.na(Ne),   
## if\_else(!is.na(NcPoint), "NcPoint ratio", if\_else(!is.na(Nc\_from\_range),   
## "NcRange ratio", NA\_character\_)), "genetic data"))  
## print(ind1\_data)  
## }  
## }

Use function to get Ne data from NcRange or NcPoint data, and their combination (Ne estimated from Ne if Ne is available, otherwise, from Nc)

ind1\_data<-transform\_to\_Ne(ind1\_data = ind1\_data, ratio = 0.1)

## # A tibble: 5,652 × 40  
## country\_assessme… taxonomic\_group taxon scientific\_auth… genus year\_assesment  
## <chr> <chr> <chr> <chr> <chr> <chr>   
## 1 sweden mammal Alce… (Linnaeus, 1758) Alces 2023   
## 2 sweden mammal Alce… (Linnaeus, 1758) Alces 2023   
## 3 sweden mammal Alce… (Linnaeus, 1758) Alces 2023   
## 4 sweden fish Silu… (Linnaeus, 1758) Silu… 2023   
## 5 sweden fish Silu… (Linnaeus, 1758) Silu… 2023   
## 6 sweden fish Silu… (Linnaeus, 1758) Silu… 2023   
## 7 sweden fish Silu… (Linnaeus, 1758) Silu… 2023   
## 8 sweden fish Silu… (Linnaeus, 1758) Silu… 2023   
## 9 sweden fish Silu… (Linnaeus, 1758) Silu… 2023   
## 10 sweden bird Dend… Bechstein 1803 Dend… 2022   
## # … with 5,642 more rows, and 34 more variables: name\_assessor <chr>,  
## # email\_assessor <chr>, kobo\_tabular <chr>, defined\_populations <chr>,  
## # time\_populations <chr>, X\_validation\_status <chr>, X\_uuid <chr>,  
## # multiassessment <chr>, population <chr>, Name <chr>, Origin <chr>,  
## # IntroductionYear <chr>, Ne <dbl>, NeLower <dbl>, NeUpper <dbl>,  
## # NeYear <chr>, GeneticMarkers <chr>, GeneticMarkersOther <chr>,  
## # MethodNe <chr>, SourceNe <chr>, NcType <chr>, NcYear <chr>, …

Check transformation in example:

ind1\_data %>% select(country\_assessment, taxon, population, Name, Ne, NeLower, NeUpper, NeYear, GeneticMarkers, NcType, NcMethod, NcRange, Nc\_from\_range, Ne\_from\_Nc, Ne\_combined)

## # A tibble: 5,652 × 15  
## country\_assessment taxon population Name Ne NeLower NeUpper NeYear  
## <chr> <chr> <chr> <chr> <dbl> <dbl> <dbl> <chr>   
## 1 sweden Alces alces pop1 North 4950 NA NA 2020   
## 2 sweden Alces alces pop2 South 194 NA NA 1980   
## 3 sweden Alces alces pop3 Tran… 11519 NA NA 2020   
## 4 sweden Siluris gla… pop1 Båven 12 6 33 2004   
## 5 sweden Siluris gla… pop2 lowe… 13 7 31 2004   
## 6 sweden Siluris gla… pop3 Uppe… 11 5 26 2010   
## 7 sweden Siluris gla… pop4 Möck… 13 7 30 2010   
## 8 sweden Siluris gla… pop5 Förs… 9 4 26 2006   
## 9 sweden Siluris gla… pop6 Helg… 11 6 26 2010   
## 10 sweden Dendrocopos… pop1 Värm… NA NA NA <NA>   
## # … with 5,642 more rows, and 7 more variables: GeneticMarkers <chr>,  
## # NcType <chr>, NcMethod <chr>, NcRange <chr>, Nc\_from\_range <dbl>,  
## # Ne\_from\_Nc <dbl>, Ne\_combined <dbl>

Remember what the function to estimate indicator 1 does:

# check what the custom function does  
estimate\_indicator1

## function (ind1\_data)   
## {  
## indicator1 <- ind1\_data %>% group\_by(X\_uuid, ) %>% summarise(n\_pops = n(),   
## n\_pops\_Ne\_data = sum(!is.na(Ne\_combined)), n\_pops\_more\_500 = sum(Ne\_combined >   
## 500, na.rm = TRUE), indicator1 = n\_pops\_more\_500/n\_pops\_Ne\_data) %>%   
## left\_join(metadata)  
## print(indicator1)  
## }

**Now estimate indicator 1 :)**

indicator1<-estimate\_indicator1(ind1\_data = ind1\_data)

## Joining, by = "X\_uuid"

## # A tibble: 609 × 69  
## X\_uuid n\_pops n\_pops\_Ne\_data n\_pops\_more\_500 indicator1 country\_assessm…  
## <chr> <int> <int> <int> <dbl> <chr>   
## 1 010d85cd-5… 2 1 1 1 united\_states   
## 2 018d6a54-b… 47 46 0 0 united\_states   
## 3 019bd95f-b… 1 1 0 0 sweden   
## 4 01b10b29-9… 1 1 1 1 south\_africa   
## 5 0301e6b3-b… 3 3 3 1 france   
## 6 037d6c8f-7… 4 2 2 1 united\_states   
## 7 03f03179-1… 1 1 1 1 south\_africa   
## 8 0586b61e-7… 12 12 0 0 belgium   
## 9 065a53ba-0… 1 1 0 0 south\_africa   
## 10 06e6bb50-3… 1 1 0 0 belgium   
## # … with 599 more rows, and 63 more variables: taxonomic\_group <chr>,  
## # taxon <chr>, scientific\_authority <chr>, genus <chr>, year\_assesment <chr>,  
## # name\_assessor <chr>, email\_assessor <chr>, common\_name <chr>,  
## # kobo\_tabular <chr>, X\_validation\_status <chr>, GBIF\_taxonID <int>,  
## # NCBI\_taxonID <chr>, national\_taxonID <chr>, source\_national\_taxonID <chr>,  
## # other\_populations <chr>, time\_populations <chr>, defined\_populations <chr>,  
## # source\_definition\_populations <chr>, map\_populations <chr>, …

Check example data:

indicator1 %>% select(X\_uuid, taxon, country\_assessment, n\_pops, n\_pops\_Ne\_data, n\_pops\_more\_500, indicator1)

## # A tibble: 609 × 7  
## X\_uuid taxon country\_assessm… n\_pops n\_pops\_Ne\_data n\_pops\_more\_500  
## <chr> <chr> <chr> <int> <int> <int>  
## 1 010d85cd-51d6-4… Ethe… united\_states 2 1 1  
## 2 018d6a54-b069-4… Grap… united\_states 47 46 0  
## 3 019bd95f-b8e9-4… Cera… sweden 1 1 0  
## 4 01b10b29-9e13-4… Sphe… south\_africa 1 1 1  
## 5 0301e6b3-b4e3-4… Posi… france 3 3 3  
## 6 037d6c8f-7b29-4… Ethe… united\_states 4 2 2  
## 7 03f03179-14bb-4… Para… south\_africa 1 1 1  
## 8 0586b61e-7805-4… Bomb… belgium 12 12 0  
## 9 065a53ba-051b-4… Cara… south\_africa 1 1 0  
## 10 06e6bb50-3fa7-4… Myot… belgium 1 1 0  
## # … with 599 more rows, and 1 more variable: indicator1 <dbl>

### Indicator 2 or PM indicator: proportion of populations within species which are maintained.

Show most relevant columns of indicator 2 data:

ind2\_data %>% select(country\_assessment, taxon, n\_extant\_populations, n\_extint\_populations)

## country\_assessment  
## 1 sweden  
## 2 sweden  
## 3 sweden  
## 4 south\_africa  
## 5 south\_africa  
## 6 france  
## 7 france  
## 8 france  
## 9 france  
## 10 south\_africa  
## 11 france  
## 12 mexico  
## 13 south\_africa  
## 14 south\_africa  
## 15 south\_africa  
## 16 south\_africa  
## 17 south\_africa  
## 18 south\_africa  
## 19 france  
## 20 france  
## 21 france  
## 22 sweden  
## 23 sweden  
## 24 south\_africa  
## 25 south\_africa  
## 26 south\_africa  
## 27 south\_africa  
## 28 france  
## 29 australia  
## 30 south\_africa  
## 31 sweden  
## 32 south\_africa  
## 33 south\_africa  
## 34 sweden  
## 35 france  
## 36 sweden  
## 37 sweden  
## 38 sweden  
## 39 france  
## 40 south\_africa  
## 41 south\_africa  
## 42 south\_africa  
## 43 south\_africa  
## 44 south\_africa  
## 45 australia  
## 46 australia  
## 47 australia  
## 48 australia  
## 49 australia  
## 50 south\_africa  
## 51 south\_africa  
## 52 south\_africa  
## 53 south\_africa  
## 54 south\_africa  
## 55 south\_africa  
## 56 south\_africa  
## 57 australia  
## 58 sweden  
## 59 sweden  
## 60 sweden  
## 61 sweden  
## 62 france  
## 63 south\_africa  
## 64 south\_africa  
## 65 south\_africa  
## 66 south\_africa  
## 67 south\_africa  
## 68 south\_africa  
## 69 south\_africa  
## 70 south\_africa  
## 71 south\_africa  
## 72 south\_africa  
## 73 mexico  
## 74 mexico  
## 75 mexico  
## 76 mexico  
## 77 south\_africa  
## 78 south\_africa  
## 79 mexico  
## 80 mexico  
## 81 sweden  
## 82 sweden  
## 83 france  
## 84 mexico  
## 85 france  
## 86 france  
## 87 france  
## 88 australia  
## 89 australia  
## 90 australia  
## 91 france  
## 92 sweden  
## 93 france  
## 94 sweden  
## 95 sweden  
## 96 australia  
## 97 australia  
## 98 sweden  
## 99 australia  
## 100 australia  
## 101 sweden  
## 102 south\_africa  
## 103 south\_africa  
## 104 south\_africa  
## 105 south\_africa  
## 106 south\_africa  
## 107 south\_africa  
## 108 south\_africa  
## 109 south\_africa  
## 110 france  
## 111 france  
## 112 france  
## 113 mexico  
## 114 sweden  
## 115 south\_africa  
## 116 mexico  
## 117 south\_africa  
## 118 australia  
## 119 australia  
## 120 australia  
## 121 south\_africa  
## 122 australia  
## 123 australia  
## 124 australia  
## 125 australia  
## 126 australia  
## 127 australia  
## 128 australia  
## 129 australia  
## 130 australia  
## 131 australia  
## 132 australia  
## 133 mexico  
## 134 japan  
## 135 sweden  
## 136 australia  
## 137 australia  
## 138 australia  
## 139 australia  
## 140 mexico  
## 141 japan  
## 142 japan  
## 143 japan  
## 144 japan  
## 145 japan  
## 146 japan  
## 147 australia  
## 148 japan  
## 149 south\_africa  
## 150 south\_africa  
## 151 south\_africa  
## 152 south\_africa  
## 153 france  
## 154 south\_africa  
## 155 south\_africa  
## 156 australia  
## 157 south\_africa  
## 158 south\_africa  
## 159 united\_states  
## 160 united\_states  
## 161 south\_africa  
## 162 south\_africa  
## 163 south\_africa  
## 164 south\_africa  
## 165 south\_africa  
## 166 south\_africa  
## 167 south\_africa  
## 168 south\_africa  
## 169 united\_states  
## 170 united\_states  
## 171 united\_states  
## 172 south\_africa  
## 173 south\_africa  
## 174 south\_africa  
## 175 south\_africa  
## 176 south\_africa  
## 177 mexico  
## 178 south\_africa  
## 179 south\_africa  
## 180 south\_africa  
## 181 south\_africa  
## 182 united\_states  
## 183 united\_states  
## 184 united\_states  
## 185 united\_states  
## 186 united\_states  
## 187 united\_states  
## 188 south\_africa  
## 189 united\_states  
## 190 united\_states  
## 191 united\_states  
## 192 united\_states  
## 193 south\_africa  
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## 198 south\_africa  
## 199 south\_africa  
## 200 south\_africa  
## 201 south\_africa  
## 202 south\_africa  
## 203 south\_africa  
## 204 south\_africa  
## 205 south\_africa  
## 206 south\_africa  
## 207 south\_africa  
## 208 australia  
## 209 australia  
## 210 south\_africa  
## 211 south\_africa  
## 212 south\_africa  
## 213 united\_states  
## 214 united\_states  
## 215 united\_states  
## 216 united\_states  
## 217 united\_states  
## 218 mexico  
## 219 united\_states  
## 220 united\_states  
## 221 australia  
## 222 australia  
## 223 australia  
## 224 australia  
## 225 australia  
## 226 australia  
## 227 south\_africa  
## 228 south\_africa  
## 229 south\_africa  
## 230 united\_states  
## 231 united\_states  
## 232 united\_states  
## 233 united\_states  
## 234 south\_africa  
## 235 south\_africa  
## 236 united\_states  
## 237 united\_states  
## 238 australia  
## 239 united\_states  
## 240 united\_states  
## 241 united\_states  
## 242 south\_africa  
## 243 south\_africa  
## 244 south\_africa  
## 245 south\_africa  
## 246 south\_africa  
## 247 south\_africa  
## 248 south\_africa  
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## taxon  
## 1 Alces alces  
## 2 Siluris glanis  
## 3 Dendrocopos leucotos  
## 4 Encephalartos latrifrons  
## 5 Capensibufo rosei  
## 6 Galemys pyrenaicus  
## 7 Luscinia svecica  
## 8 Taxus baccata  
## 9 Angelica heterocarpa  
## 10 Syncerus caffer caffer  
## 11 Fagus sylvatica  
## 12 Juniperus monticola  
## 13 Hirundo atrocaerulea  
## 14 Bradypodion thamnobates  
## 15 Sclerophrys pantherina  
## 16 Aloe kniphofioides  
## 17 Bitis albanica  
## 18 Bitis armata  
## 19 Tetrao urogallus  
## 20 Miniopterus schreibersii  
## 21 Zingel asper  
## 22 Pelophylax lessonae  
## 23 Rana dalmatina  
## 24 Aloinopsis acuta  
## 25 Smaug giganteus  
## 26 Natalobatrachus bonebergi  
## 27 Heleophryne rosei  
## 28 Aquila fasciata  
## 29 Phyllurus kabikabi  
## 30 Carcharodon carcharias  
## 31 Lutra lutra  
## 32 Mimetes stokoei  
## 33 Stigmochelys pardalis  
## 34 Canis lupus  
## 35 Posidonia oceanica  
## 36 Coregonus albula morphotype trybomi  
## 37 Gymnadenia nigra  
## 38 Mertensia maritima  
## 39 Mauremys leprosa  
## 40 Mimetes saxatilis  
## 41 Microbatrachella capensis  
## 42 Arthroleptella rugosa  
## 43 Breviceps macrops  
## 44 Amblysomus hottentotus  
## 45 Acacia purpureopetala  
## 46 Macadamia integrifolia  
## 47 Wollemia nobilis  
## 48 Eidothea hardeniana  
## 49 Hoya australis oramicola  
## 50 Gypaetus barbatus  
## 51 Gyps coprotheres  
## 52 Hippocampus capensis  
## 53 Afrixalus knysnae  
## 54 Poicephalus robustus  
## 55 Hyperolius pickersgilli  
## 56 Damaliscus pygargus pygargus  
## 57 Dasyurus hallucatus  
## 58 Phengaris arion  
## 59 Lopinga achine  
## 60 Gulo gulo  
## 61 Vulpes lagopus  
## 62 Pinna nobilis  
## 63 Diceros bicornis  
## 64 Ceratotherium simum simum  
## 65 Equus zebra zebra  
## 66 Connochaetes taurinus  
## 67 Connochaetes gnou  
## 68 Giraffa giraffa Formally know as Giraffa camelopardalis giraffa (subspecies).  
## 69 Damaliscus pygargus phillipsi  
## 70 Halcyon senegalensis cyanoleuca  
## 71 Anthropoides paradiseus  
## 72 Mastomys natalensis  
## 73 Amazilia yucatanensis  
## 74 Selasphorus platycercus  
## 75 Alsophila firma  
## 76 Cyathea bicrenata  
## 77 Smutsia temminckii  
## 78 Antidorcas marsupialis  
## 79 Bombus ephippiatus  
## 80 Ctenosaura pectinata  
## 81 Phengaris alcon  
## 82 Gentiana pneumonanthe  
## 83 Macromia splendens  
## 84 Phonotimpus talquian  
## 85 Lutra Lutra  
## 86 Acipenser sturio  
## 87 Gypaetus barbatus  
## 88 Ctenotus lancelini  
## 89 Saltuarius eximius  
## 90 Carinascincus palfreymani  
## 91 Mustela lutreola  
## 92 Ursus arctos  
## 93 Rhinolophus euryale  
## 94 Barbastella barbastellus  
## 95 Emberiza calandra  
## 96 Pseudemydura umbrina  
## 97 Christinus guentheri  
## 98 Phocoena phocoena  
## 99 Myuchelys georgesi  
## 100 Myuchelys bellii  
## 101 Dysauxes ancilla  
## 102 Loxodonta africana  
## 103 Equus quagga  
## 104 Oryx gazella gazella  
## 105 Tragelaphus angasii  
## 106 Micaelamys namaquensis  
## 107 Micaelamys granti  
## 108 Graphiurus murinus  
## 109 Graphiurus ocularis  
## 110 Sitta whiteheadi  
## 111 Laminaria digitata  
## 112 Hieracium sandozianum  
## 113 Xenospiza baileyi  
## 114 Lytta vesicatoria  
## 115 Ptychadena uzungwensis  
## 116 Zea luxurians  
## 117 Spheniscus demersus  
## 118 Acacia auratiflora  
## 119 Hakea oldfieldii  
## 120 Senecio macrocarpus  
## 121 Acinonyx jubatus jubatus  
## 122 Tympanocryptis lineata  
## 123 Gymnobelideus leadbeateri  
## 124 Potorous gilbertii  
## 125 Macrotis lagotis  
## 126 Zyzomys pedunculatus  
## 127 Pteropus conspicillatus conspicillatus  
## 128 Pseudomys shortridgei  
## 129 Vombatus ursinus  
## 130 Hydromys chrysogaster  
## 131 Rhinonicteris aurantia  
## 132 Notechis scutatus  
## 133 Pinus strobiformis  
## 134 Illigera luzonensis  
## 135 Bufotes viridis  
## 136 Eucalyptus morrisbyi  
## 137 Actinotus schwarzii  
## 138 Pimelea spinescens subspecies spinescens  
## 139 Pimelea spinescens subspecies spinescens  
## 140 Pachycereus grandis  
## 141 Lagenophora lanata  
## 142 Aconitum jaluense subsp. jaluense  
## 143 Cerastium fischerianum var. molle  
## 144 Aconitum metajaponicum  
## 145 Primula reinii var. myogiensis  
## 146 Lonicera japonica var. miyagusukiana  
## 147 Nereia lophocladia  
## 148 Polygala tatarinowii  
## 149 Anhydrophryne rattrayi  
## 150 Anhydrophryne ngongoniensis  
## 151 Aloe pearsonii  
## 152 Diosma awilana  
## 153 Alca torda  
## 154 Neamblysomus julianae  
## 155 Bunolagus monticularis  
## 156 Phyllospora comosa  
## 157 Arthroleptis wahlbergii  
## 158 Cacosternum nanum  
## 159 Diplacus vandenbergensis  
## 160 Picoides borealis  
## 161 Psammobates geometricus  
## 162 Hippotragus equinus equinus  
## 163 Hippotragus niger niger  
## 164 Kinixys lobatsiana  
## 165 Ourebia ourebi ourebi  
## 166 Kinixys natalensis  
## 167 Kinixys spekii  
## 168 Chersina angulata  
## 169 Phacelia formosula  
## 170 Spiranthes delitescens  
## 171 Odocoileus virginianus clavium  
## 172 Clinus spatulatus  
## 173 Tylos granulatus  
## 174 Clinus cottoides  
## 175 Clinus superciliosus  
## 176 Poroderma africanum  
## 177 Ceiba aesculifolia  
## 178 Acroteriobatus annulatus  
## 179 Caffrogobius nudiceps  
## 180 Gilchristella aestuaria  
## 181 Merluccius capensis  
## 182 Tantilla oolitica  
## 183 Pleurobema rubrum  
## 184 Pleurobema rubrum  
## 185 Lagopus leucura rainierensis  
## 186 Artemisiospiza belli clementeae  
## 187 Etheostoma forbesi  
## 188 Donax serra  
## 189 Sclerocactus brevihamatus tobuschii  
## 190 Faxonius marchandi  
## 191 Drymarchon couperi  
## 192 Elliptio spinosa  
## 193 Bucorvus leadbeateri  
## 194 Felis nigripes  
## 195 Mungos mungo  
## 196 Helogale parvula  
## 197 Caracal caracal  
## 198 Parahyaena brunnea  
## 199 Suricata suricatta  
## 200 Canis mesomelas  
## 201 Proteles cristata cristata  
## 202 Felis silvestris lybica  
## 203 Otocyon megalotis megalotis  
## 204 Mellivora capensis  
## 205 Crocuta crocuta  
## 206 Heleophryne hewitti  
## 207 Cheilodactylus fasciatus  
## 208 Zieria ingramii  
## 209 Prosthanthera askania  
## 210 Cercopithecus albogularis labiatus  
## 211 Cercopithecus albogularis erythrarchus  
## 212 Cercopithecus albogularis schwarzi  
## 213 Chrysopsis floridana  
## 214 Obovaria subrotunda  
## 215 Obovaria subrotunda  
## 216 Eriogonum tiehmii  
## 217 Papaipema eryngii  
## 218 Juniperus blancoi  
## 219 Euphilotes enoptes smithi  
## 220 Stygobromus indentatus  
## 221 Acacia linifolia  
## 222 Caladenia gladiolata  
## 223 Caladenia intuta  
## 224 Banksia cuneata  
## 225 Caladenia woolcockiorum  
## 226 Pterostylis bryophila  
## 227 Heteromirafra ruddi  
## 228 Geronticus calvus  
## 229 Spizocorys fringillaris  
## 230 Cirsium scariosum loncholepis  
## 231 Astragalus schmolliae  
## 232 Sorex ornatus relictus  
## 233 Trichocentrum undulatum  
## 234 Calendulauda burra  
## 235 Hemimacronyx chloris  
## 236 Martes caurina  
## 237 Villosa fabalis  
## 238 Eucalyptus melliodora  
## 239 Toxolasma lividum  
## 240 Eriogonum gypsophilum  
## 241 Glyptemys muhlenbergii  
## 242 Austroglanis barnardi  
## 243 Austroglanis gilli  
## 244 Vandijkophrynus amatolicus  
## 245 Nesotragus moschatus zuluensis  
## 246 Pseudobarbus erubescens  
## 247 Promerops cafer  
## 248 Promerops gurneyi  
## 249 Percina antesella  
## 250 Graptopetalum bartramii  
## 251 Scirpus ancistrochaetus  
## 252 Lavinia exilicauda chi  
## 253 Moussonia deppeana  
## 254 Monadenia fidelis minor  
## 255 Layia carnosa  
## 256 Asclepias prostrata  
## 257 Synemon plana  
## 258 Bugeranus carunculatus  
## 259 Balearica regulorum regulorum  
## 260 Palicourea padifolia  
## 261 Leptoxis arkansensis  
## 262 Plethobasus cyphyus  
## 263 Etheostoma cinereum  
## 264 Cryptobranchus alleganiensis alleganiensis  
## 265 Cryptobranchus alleganiensis alleganiensis  
## 266 Ctenosaura macrolopha  
## 267 Centrocercus minimus  
## 268 Lasionectes exleyi  
## 269 Epioblasma triquetra  
## 270 Astragalus microcymbus  
## 271 Astragalus microcymbus  
## 272 Rhipsalis baccifera  
## 273 Psittacanthus schiedeanus  
## 274 Psittacanthus auriculatus  
## 275 Doricha eliza  
## 276 Lampornis amethystinus  
## 277 Campylopterus curvipennis  
## 278 Cynanthus sordidus  
## 279 Psittacanthus sonorae  
## 280 Psittacanthus mayanus  
## 281 Psittacanthus rhynchanthus  
## 282 Orconectes shoupi  
## 283 Macrochelys suwanniensis  
## 284 Boechera pusilla  
## 285 Ipomopsis polyantha  
## 286 Ctenosaura acanthura  
## 287 Chiranthodendron pentadactylon  
## 288 Psittacanthus calyculatus  
## 289 Liquidambar styraciflua  
## 290 Magnolia pedrazae  
## 291 Cyathea aristata  
## 292 Oncorhynchus apache  
## 293 Oncorhynchus apache  
## 294 Graptemys pearlensis  
## 295 Magnolia schiedeana  
## 296 Donrichardsia macroneuron  
## 297 Erimystax harryi  
## 298 Erimystax harryi  
## 299 Fundulus julisia  
## 300 Ptychocheilus lucius  
## 301 Leucorrhinia albifrons  
## 302 Phonotimpus talquian  
## 303 Ambystoma altamirani  
## 304 Ambystoma granulosum  
## 305 Podocarpus matudae  
## 306 Podocarpus guatemalensis  
## 307 Optioservus phaeus  
## 308 Acmispon dendroideus traskiae  
## 309 Hoplogonus bornemisszai  
## 310 Adclarkia dawsonensis  
## 311 Megascolides australis  
## 312 Austrocordulia leonardi  
## 313 Zephyrarchaea austini  
## 314 Bertmainius colonus  
## 315 Neopasiphae simplicior  
## 316 Leucopatus anophthalmus  
## 317 Anguis fragilis  
## 318 Pelophylax esculentus  
## 319 Icaricia icarioides fenderi  
## 320 Cambarus elkensis  
## 321 Cambarus elkensis  
## 322 Myotis septentrionalis  
## 323 Faxonius roberti  
## 324 Tephroseris palustris  
## 325 Juncus anceps  
## 326 Jacobaea erucifolia  
## 327 Lamprothamnium papulosom  
## 328 Emberiza hortulana  
## 329 Stenocereus quevedonis  
## 330 Crotalus catalinensis  
## 331 Saltator atriceps  
## 332 Icterus gularis  
## 333 Uma exsul  
## 334 Leavenworthia texana  
## 335 Cicindela theatina  
## 336 Bipes biporus  
## 337 Chilabothrus granti  
## 338 Pyrgulopsis morrisoni  
## 339 Eryngium sparganophyllum  
## 340 Melanerpes santacruzi  
## 341 Scutellaria ocmulgee  
## 342 Procyon pygmaeus  
## 343 Sideroxylon thornei  
## 344 Procambarus orcinus  
## 345 Alouatta palliata mexicana  
## 346 Campylorhynchus rufinucha  
## 347 Alouatta palliata mexicana  
## 348 Melanerpes aurifrons  
## 349 Parachondrostoma toxostoma  
## 350 Castilleja grisea  
## 351 Procambarus econfinae  
## 352 Ursus arctos arctos  
## 353 Castilleja tolucensis  
## 354 Aphelocoma coerulescens  
## 355 Aphelocoma coerulescens  
## 356 Aphelocoma coerulescens  
## 357 Lomatogonium carinthiacum  
## 358 Cetorhinus maximus  
## 359 Etheostoma trisella  
## 360 Cryptomastix devia  
## 361 Cryptomastix devia  
## 362 Solanum conocarpum  
## 363 Planorbella magnifica  
## 364 Pseudemys gorzugi  
## 365 Xyrauchen texanus  
## 366 Rhaphiomidas trochilus  
## 367 Plethodon hubrichti  
## 368 Notropis topeka  
## 369 Ochrosia iwasakiana  
## 370 Teucrium veronicoides var. veronicoides  
## 371 Speyeria callippe callippe  
## 372 Lespedeza leptostachya  
## 373 Perimyotis subflavus  
## 374 Carica papaya  
## 375 Elgaria panamintina  
## 376 Euphydryas anicia cloudcrofti  
## 377 Pedicularis furbishiae  
## 378 Streptanthus bracteatus  
## 379 Streptanthus bracteatus  
## 380 Bombus franklini  
## 381 Lynx lynx carpathicus  
## 382 Alouatta pigra  
## 383 Ammodramus maritimus macgillivraii  
## 384 Gopherus morafkai  
## 385 Euphilotes ancilla cryptica  
## 386 Zapus hudsonius luteus  
## 387 Euphilotes ancilla purpura  
## 388 Pinus albicaulis  
## 389 Sabia japonica  
## 390 Gambelia sila  
## 391 Enchinomastus erectocentrus acunensis  
## 392 Sedum minimum  
## 393 Colubrina asiatica  
## 394 Arenaria bryoides  
## 395 Cerastium purpusii  
## 396 Draba nivicola  
## 397 Plagiobothrys hirtus  
## 398 Ptychobranchus subtentum  
## 399 Notophthalmus perstriatus  
## 400 Notophthalmus perstriatus  
## 401 Notophthalmus perstriatus  
## 402 Notophthalmus perstriatus  
## 403 Drepanis coccinea  
## 404 Festuca livida  
## 405 Impatiens hypophylla var. microhypophylla  
## 406 Unio crassus  
## 407 Eresus sandaliatus  
## 408 Symplocos konishii  
## 409 Alosa fallax  
## 410 Saussurea yanagisawae  
## 411 Lonicera demissa var. borealis  
## 412 Prunus incisa var. bukosanensis  
## 413 Rhinolophus hipposideros  
## 414 Mimulus gemmiparus  
## 415 Pseudemys rubriventris  
## 416 Pseudemys rubriventris  
## 417 Alnus maritima  
## 418 Hydroprogne caspia  
## 419 Pelobates fuscus  
## 420 Alnus maritima maritima  
## 421 Alnus maritima georgiensis  
## 422 Alnus maritima oklahomensis  
## 423 Swertia pseudochinensis  
## 424 Primula sieboldii  
## 425 Maytenus diversifolia  
## 426 Asarum costatum  
## 427 Aster hispidus var. koidzumianus  
## 428 Isoetes asiatica  
## 429 Ornithorhynchus anatinus  
## 430 Rupicapra pyrenaica  
## 431 Turnix olivii  
## 432 Neophema chrysogaster  
## 433 Parnassius mnemosyne  
## 434 Litoria booroolongensis  
## 435 Glyphis glyphis  
## 436 Pulstilla patens  
## 437 Pulsatilla vulgaris gotlandica  
## 438 Stiphodon semoni  
## 439 Cottus petiti  
## 440 Euphydras maturna  
## 441 Tetrax tetrax tetrax  
## 442 Coenonympha hero  
## 443 Nicrophorus americanus  
## 444 Nicrophorus americanus  
## 445 Speyeria nokomis nokomis  
## 446 Delphinium variegatum kinkiense  
## 447 Rhynchospora crinipes  
## 448 Triturus cristatus  
## 449 Etheostoma chienense  
## 450 Corylopsis glabrescens  
## 451 Crepidiastrum chelidoniifolium  
## 452 Lonicera vidalii  
## 453 Chersobius boulengeri  
## 454 Chersobius signatus  
## 455 Bombina bombina  
## 456 Alisma wahlenbergii  
## 457 Bufo bufo  
## 458 Lacerta agilis  
## 459 Epidalea calamita  
## 460 Charina umbratica  
## 461 Zapus hudsonius luteus  
## 462 Lysimachia barystachys  
## 463 Hyla arborea  
## 464 Lissotriton vulgaris  
## 465 Petromyzon marinus  
## 466 Charadrius alexandrinus  
## 467 Geastrum flexuosum  
## 468 Homopus areolatus  
## 469 Homopus femoralis  
## 470 Cryptocarya chinensis  
## 471 Swertia swertopsis  
## 472 Primula hidakana var. hidakana  
## 473 Harpalus autumnalis  
## 474 Anthophora plagiata  
## 475 Anser erythropus  
## 476 Anthus campestris  
## 477 Bryoria nitidula  
## 478 Melitaea britomartis  
## 479 Dipodomys ingens  
## 480 Callicarpa shikokiana  
## 481 Acer miyabei var. miyabei  
## 482 Salix hukaoana  
## 483 Talpa aquitania  
## 484 Bryhnia scabrida  
## 485 Genista germanica  
## 486 Agonopterix bipunctosa  
## 487 Scolitantides Orion  
## 488 Harpalus flavescens  
## 489 Lonicera ramosissima var. kinkiensis  
## 490 Polystichum piceopaleaceum  
## 491 Carex aequialta  
## 492 Peperomia okinawensis  
## 493 Alectoris graeca  
## 494 Phocoena phocoena  
## 495 Puffinus puffinus  
## 496 Calotriton asper  
## 497 Luronium natans  
## 498 Chenopodium vulvaria  
## 499 Quercus glaucoides  
## 500 Quercus deserticola  
## 501 Quercus peduncularis  
## 502 Utricularia australis  
## 503 Oxytropis campestris subsp. rishiriensi  
## 504 Morus bassanus  
## 505 Phoenicopterus roseus  
## 506 Falco naumanni  
## 507 Plegadis falcinellus  
## 508 Zapornia pusilla  
## 509 Etheostoma chienense  
## 510 Hesperia dacotae  
## 511 Etheostoma maydeni  
## 512 Asplenium castaneoviride  
## 513 Phymatosorus nigrescens  
## 514 Pteris yamatensis  
## 515 Ophioglossum namegatae  
## 516 Asplenium ruta-muraria  
## 517 Pseudotsuga japonica  
## 518 Picea koyamae  
## 519 Sporobolus hancei  
## 520 Rhododendron pentaphyllum var. pentaphyllum  
## 521 Pimpinella thellungiana var. gustavohegiana  
## 522 Testudo hermanni  
## 523 Tyrrhenaria ceratina  
## 524 Anguilla anguilla  
## 525 Salmo salar  
## 526 Aeshna isoceles  
## 527 Calopteryx virgo  
## 528 Coenagrion hastulatum  
## 529 Coenagrion lunulatum  
## 530 Coenagrion pulchellum  
## 531 Gomphus flavipes  
## 532 Salix humboldtiana  
## 533 Leucorrhinia caudalis  
## 534 Leucorrhinia pectoralis  
## 535 Gomphus vulgatissimus  
## 536 Quercus hirtifolia  
## 537 Chionolaena lavandulifolia  
## 538 Rhynchospora crinipes  
## 539 Salix bonplandiana  
## 540 Heterelmis stephani  
## 541 Heterelmis stephani  
## 542 Quercus brandegeei  
## 543 Sterna dougallii  
## 544 Rana temporaria  
## 545 Rana arvalis  
## 546 Saxifraga osloënsis  
## 547 Calidris alpina schinzii  
## 548 Dicranum viride  
## 549 Myotis escalerai  
## 550 Leuciscus aspius  
## 551 Baptria tibiale  
## 552 Cerambyx cerdo  
## 553 Neophron percnopterus  
## 554 Glareola pratincola  
## 555 Pterocles alchata  
## 556 Dactylorhiza brennensis  
## 557 Dipodomys stephensi  
## 558 Popenaias popeii  
## 559 Pinus nigra salzmanii  
## 560 Senecio mairetianus  
## 561 Chalcophora mariana  
## 562 Depressaria nemolella  
## 563 Psophus stridulus  
## 564 Lepidium papilliferum  
## 565 Lepidium papilliferum  
## 566 Laterallus jamaicensis jamaicensis  
## 567 Procambarus pictus  
## 568 Clonophis kirtlandii  
## 569 Sisyrinchium sarmentosum  
## 570 Lomatium bradshawii  
## 571 Diomedea exulans  
## 572 Calocitta formosa  
## 573 Pseudophryne covacevichae  
## 574 Casuarius casuarius johnsonii  
## 575 Xiphorhynchus flavigaster  
## 576 Pedionomus torquatus  
## 577 Hypotaenidia sylvestris  
## 578 Myrmecobius fasciatus  
## 579 Carcharodon carcharias  
## 580 Neotamias minimus atristriatus  
## 581 Noturus munitus  
## 582 Pyrgulopsis thompsoni  
## 583 Pleurobema athearni  
## 584 Thalassarche cauta  
## 585 Alasmidonta varicosa  
## 586 Thalassarche chrysostoma  
## 587 Thalassarche melanophris  
## 588 Margaritifera margaritifera  
## 589 Leptogium rivulare  
## 590 Coronella austriaca  
## 591 Natrix natrix natrix  
## 592 Natrix natrix gotlandica  
## 593 Zootoca vivipara  
## 594 Vipera berus  
## 595 Ambuchanania leucobryoides  
## 596 Pyrgulopsis turbatrix  
## 597 Pherosphaera fitzgeraldii  
## 598 Leptotila verreauxi  
## 599 Cyathea exilis  
## 600 Xanthorrhoea bracteata  
## 601 Cyclarhys gujanensis  
## 602 Centaurea corymbosa  
## 603 Stenocereus pruinosus  
## 604 Styrax platanifolius texanus  
## 605 Ambystoma cingulatum  
## 606 Ambystoma cingulatum  
## 607 Etheostoma osburni  
## 608 Etheostoma osburni  
## 609 Alasmidonta varicosa  
## 610 Lepanthes eltoroensis  
## 611 Macronectes giganteus  
## 612 Macronectes halli  
## 613 Procellaria cinerea  
## 614 Phoebetria palpebrata  
## 615 Sylvilagus bachmani riparius  
## 616 Macrochelys temminckii  
## 617 Arabis georgiana  
## 618 Heterodon simus  
## 619 Eryngium proteiflorum  
## 620 Vireo atricapilla  
## 621 Bombus terricola  
## 622 Bombus terricola  
## 623 Malacothamnus clementinus  
## 624 Phacelia submutica  
## 625 Oncorhynchus clarkii virginalis  
## 626 Oncorhynchus clarkii virginalis  
## 627 Cirsium wrightii  
## 628 Notropis mekistocholas  
## 629 Notropis mekistocholas  
## 630 Eremophila alpestris strigata  
## 631 Percina rex  
## 632 Yermo xanthocephalus  
## 633 Hemphillia burringtoni  
## 634 Hemphillia burringtoni  
## 635 Castilleja levisecta  
## 636 Lupinus constancei  
## 637 Cambarus cracens  
## 638 Mustela nigripes  
## 639 Mustela nigripes  
## 640 Plestiodon egregius egregius  
## 641 Thoburnia atripinnis  
## 642 Strix occidentalis occidentalis  
## 643 Plestiodon egregius egregius  
## 644 Berberis alpina  
## 645 Cynomys leucurus  
## 646 Anaxyrus williamsi  
## 647 Texella reyesi  
## 648 Texella reyesi  
## 649 Sympetrum depressiusculum  
## 650 Apatura iris  
## 651 Cyaniris semiargus  
## 652 Erynnis tages  
## 653 Euphydryas aurinia  
## 654 Euplagia quadripunctaria  
## 655 Salmo salar  
## 656 Gadus morhua  
## 657 Hesperia comma  
## 658 Lasiommata megera  
## 659 Melitaea cinxia  
## 660 Proserpinus proserpina  
## 661 Pyronia tithonus  
## 662 Satyrium ilicis  
## 663 Barbastella barbastellus  
## 664 Myotis bechsteinii  
## 665 Myotis brandtii  
## 666 Myotis dasycneme  
## 667 Myotis daubentonii  
## 668 Myotis emarginatus  
## 669 Myotis myotis  
## 670 Myotis mystacinus  
## 671 Myotis nattereri  
## 672 Nyctalus leisleri  
## 673 Nyctalus noctula  
## 674 Pipistrellus nathusii  
## 675 Pipistrellus pipistrellus  
## 676 Pipistrellus pygmaeus  
## 677 Plecotus auritus  
## 678 Plecotus austriacus  
## 679 Rhinolophus ferrumequinum  
## 680 Eptesicus serotinus  
## 681 Pyrgus malvae  
## 682 Pinus ayacahuite  
## 683 Tapirus bairdii  
## 684 Lontra longicaudis  
## 685 Anacampsis fuscella  
## 686 Melitta tricincta  
## 687 Limosa limosa  
## 688 Euphrasia offficinalis officinalis  
## 689 Sabulina viscosa  
## 690 Eryngium maritimum  
## 691 Kinosternon vogti  
## 692 Pulsatilla vernalis  
## 693 Stauroderus scalaris  
## 694 Canthophorus impressus  
## 695 Pytho kolwensis  
## 696 Euphrasia stricta suecica  
## 697 Lycaena helle  
## 698 Egretta rufescens dickeyi  
## 699 Pseudorchis albida  
## 700 Euphydryas aurinia  
## 701 Circus pygargus  
## 702 Lampetra fluviatilis  
## 703 Ranunculus hederaceus  
## 704 Bryoria tenuis  
## 705 Myricaria germanica  
## 706 Ranunculus ophioglossifolius  
## 707 Heterodermia speciosa  
## 708 Botrychium simplex  
## 709 Pedostrangalia revestita  
## 710 Lobaria hallii  
## 711 Chirostoma estor  
## 712 Sistrurus catenatus  
## 713 Gossypium harknessii  
## 714 Gossypium trilobum  
## 715 Gossypium turneri  
## 716 Gossypium gossypioides  
## 717 Gossypium schwendimanii  
## 718 Gossypium thurberi  
## 719 Gossypium laxum  
## 720 Gossypium lobatum  
## 721 Gossypium davidsonii  
## 722 Gossypium aridum  
## 723 Castor fiber  
## 724 Cricetus cricetus  
## 725 Crocidura leucodon  
## 726 Lynx lynx  
## 727 Meles meles  
## 728 Muscardinus avellanarius  
## 729 Vespertilio murinus  
## 730 Stenobothrus stigmaticus  
## 731 Lutra lutra  
## 732 Lepus timidus  
## 733 Sorex isodon  
## 734 Sicista betulina  
## 735 Erinaceus europaeus  
## 736 Myotis bechsteinii  
## 737 Phoca vitulina  
## 738 Vulpes vulpes  
## 739 Aloe craibii  
## 740 Aloe peglerae  
## 741 Anhydrophryne hewitti  
## 742 Arthroleptella drewesii  
## 743 Arthroleptella subvoce  
## 744 Lyrurus tetrix  
## 745 Castor fiber  
## 746 Neotis ludwigii  
## 747 Xenopus gilli  
## 748 Myotis dasycneme  
## 749 Lessonia corrugata  
## 750 Ecklonia radiata  
## 751 Ecklonia radiata brevipes  
## 752 Durvillaea potatorum  
## 753 Durvillaea amatheiae  
## 754 Hormosira banksii  
## 755 Posidonia australis  
## 756 Sargassum fallax  
## 757 Scytothalia dorycarpa  
## 758 Apium repens  
## 759 Baldellia ranunculoides  
## 760 Bupleurum tenuissimum  
## 761 Carex diandra  
## 762 Carex trinervis  
## 763 Deschampsia setacea  
## 764 Eriophorum gracile  
## 765 Gentianella uliginosa  
## 766 Herminium monorchis  
## 767 Juncus capitatus  
## 768 Liparis loeselii  
## 769 Potamogeton acutifolius  
## 770 Potamogeton coloratus  
## 771 Potamogeton compressus  
## 772 Ranunculus ololeucos  
## 773 Schoenoplectus pungens  
## 774 Schoenoplectus triqueter  
## 775 Eresus sandaliatus  
## 776 Elater ferrugineus  
## 777 Cucujus cinnaberinus  
## 778 Dactylorhiza sphagnicola  
## 779 Orchis morio  
## 780 Orobanche rapum-genistae  
## 781 Platanthera bifolia  
## 782 Vertigo angustior  
## 783 Capreolus capreolus  
## 784 Conophytum regale  
## 785 Protea mucronifolia  
## 786 Protea odorata  
## 787 Cervus elaphus elaphus  
## 788 Halichoerus grypus  
## 789 Mentha pulegium  
## 790 Orchis purpurea  
## 791 Conophytum vanheerdei  
## 792 Conophytum antonii  
## 793 Scorzonera humilis  
## 794 Wahlenbergia hederacea  
## 795 Vertigo moulinsiana  
## 796 Anisus vorticulus  
## 797 Hamatocaulis vernicosus  
## 798 Unio crassus  
## 799 Lucanus cervus  
## 800 Thoburnia atripinnis  
## 801 Noturus munitus  
## 802 Toxolasma lividum  
## 803 Stratiotes aloides  
## 804 Lampetra fluviatilis  
## 805 Dolomedes fimbriatus  
## 806 Halimione pedunculata  
## 807 Cobitis taenia  
## 808 Notropis topeka  
## 809 Necturus lewisi  
## 810 Necturus lewisi  
## 811 Diphasiastrum tristachyum  
## 812 Luronium natans  
## 813 Somatochlora arctica  
## 814 Pilularia globulifera  
## 815 Lacerta agilis  
## 816 Osmoderma eremita  
## 817 Bufo calamita  
## 818 Kinosternon integrum  
## 819 Vipera berus  
## 820 Abronia deppii  
## 821 Populus nigra  
## 822 Rosalia alpina  
## 823 Iberolacerta bonnali  
## 824 Misgurnus fossilis  
## 825 Petromyzon marinus  
## 826 Phengaris alcon  
## 827 Ephippiger ephippiger  
## 828 Pelobates fuscus  
## 829 Tursiops aduncus  
## 830 Procambarus orcinus  
## 831 Thamnophis sirtalis tetrataenia  
## 832 Thamnophis sirtalis tetrataenia  
## 833 Triturus marmoratus  
## 834 Psammodromus algirus  
## 835 Hyla arborea  
## 836 Lampetra planeri  
## 837 Bombina variegata  
## 838 Lavinia exilicauda chi  
## 839 Pelophylax lessonae  
## 840 Dioon edule  
## 841 Triturus cristatus  
## 842 Salamandra salamandra  
## 843 Podarcis muralis  
## 844 Rana arvalis  
## 845 Coronella austriaca  
## 846 Halichoerus grypus  
## 847 Parnassius apollo  
## 848 Hydroprogne caspia  
## 849 Haematopus ostralegus ostralegus  
## 850 Phylloscopus ibericus  
## 851 Capra ibex  
## 852 Hipparchia semele  
## 853 Prionotropis rhodanica  
## 854 Nehalennia speciosa  
## 855 Natrix helvetica  
## 856 Oenanthe hispanica  
## 857 Rhodeus sericeus  
## 858 Cottus rhenanus  
## 859 Alytes obstetricans  
## 860 Dioon caputoi  
## 861 Hippocampus guttulatus  
## 862 Condylactis aurantiaca  
## 863 Boletus edulis  
## 864 Barbastella barbastellus  
## 865 Muscardinus avellanarius  
## 866 Rana dalmatina  
## 867 Anguis fragilis  
## 868 Coronella austriaca  
## 869 Gomphus clavatus  
## 870 Ficedula albicollis  
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## 872 Zea diploperennis  
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## 874 Zea mays mexicana  
## 875 Columba palumbus  
## 876 Penelope perspicax  
## 877 Crax alberti  
## 878 Hapalopsittaca fuertesi  
## 879 Oreothraupis arremonops  
## 880 Chlorochrysa nitidissima  
## 881 Ognorhynchus icterotis  
## 882 Tayassu pecari  
## 883 Myiothlypis basilica  
## 884 Hapalopsittaca amazonina  
## 885 Pauxi pauxi  
## 886 Pyrilia Pyrilia  
## 887 Bolborhynchus ferrugineifrons  
## 888 Coeligena prunellei  
## 889 Crypturellus kerriae  
## 890 Grallaria milleri  
## 891 Macroagelaius subalaris  
## 892 Pyrrhura calliptera  
## 893 Nystactes noanamae  
## 894 Penelope ortoni  
## 895 Rallus semiplumbeus  
## 896 Bangsia aureocincta  
## 897 Odontophorus atrifrons  
## 898 Colostethus thorntoni  
## 899 Dacnis hartlaubi  
## 900 Xenornis setifrons  
## 901 Atelopus famelicus  
## 902 Grallaria kaestneri  
## 903 Pyrrhura viridicata  
## 904 Arremon basilicus  
## 905 Odontophorus hyperythrus  
## 906 Oxypogon cyanolaemus  
## 907 Megascops gilesi  
## 908 Clibanornis rufipectus  
## 909 Thryophilus sernai  
## 910 Scytalopus alvarezlopezi  
## 911 Dubusia carrikeri  
## 912 Grallaria bangsi  
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## 914 Anthocephala berlepschi  
## 915 Pogonotriccus lanyoni  
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## 920 Drymophila hellmayri  
## 921 Synallaxis fuscorufa  
## 922 Eriocnemis isabellae  
## 923 Cucurbita argyrosperma sororia  
## 924 Trichomycterus sandovali  
## 925 Ageneiosus pardalis  
## 926 Espeletia paipana  
## 927 Espeletia jaramilloi  
## 928 Zamia obliqua  
## 929 Magnolia wolfii  
## 930 Libidibia ebano  
## 931 Podocnemis lewyana  
## 932 Anadia antioquensis  
## 933 Lepidochelys olivacea  
## 934 Euterpe precatoria  
## 935 Quercus humboldtii  
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## 937 Troglodytes monticola  
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## 939 1 NA  
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## 950 1 NA  
## 951 2 NA  
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## 957 1 NA  
## 958 2 1  
## 959 4 NA  
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## 963 1 NA  
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## 965 1 NA  
## 966 1 NA

Proportion of maintained populations (indicator) is the he proportion of populations within species which are maintained. This can be estimated based on the n\_extant\_populations and n\_extint\_populations, as follows:

ind2\_data$indicator2<- ind2\_data$n\_extant\_populations / (ind2\_data$n\_extant\_populations + ind2\_data$n\_extint\_populations)

Example output selecting the most relevant columns:

ind2\_data %>% select(country\_assessment, taxon, n\_extant\_populations, n\_extint\_populations, indicator2)

## country\_assessment  
## 1 sweden  
## 2 sweden  
## 3 sweden  
## 4 south\_africa  
## 5 south\_africa  
## 6 france  
## 7 france  
## 8 france  
## 9 france  
## 10 south\_africa  
## 11 france  
## 12 mexico  
## 13 south\_africa  
## 14 south\_africa  
## 15 south\_africa  
## 16 south\_africa  
## 17 south\_africa  
## 18 south\_africa  
## 19 france  
## 20 france  
## 21 france  
## 22 sweden  
## 23 sweden  
## 24 south\_africa  
## 25 south\_africa  
## 26 south\_africa  
## 27 south\_africa  
## 28 france  
## 29 australia  
## 30 south\_africa  
## 31 sweden  
## 32 south\_africa  
## 33 south\_africa  
## 34 sweden  
## 35 france  
## 36 sweden  
## 37 sweden  
## 38 sweden  
## 39 france  
## 40 south\_africa  
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## 56 south\_africa  
## 57 australia  
## 58 sweden  
## 59 sweden  
## 60 sweden  
## 61 sweden  
## 62 france  
## 63 south\_africa  
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## 76 mexico  
## 77 south\_africa  
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## 79 mexico  
## 80 mexico  
## 81 sweden  
## 82 sweden  
## 83 france  
## 84 mexico  
## 85 france  
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## 112 france  
## 113 mexico  
## 114 sweden  
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## 117 south\_africa  
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## 120 australia  
## 121 south\_africa  
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## 147 australia  
## 148 japan  
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## 965 colombia  
## 966 colombia  
## taxon  
## 1 Alces alces  
## 2 Siluris glanis  
## 3 Dendrocopos leucotos  
## 4 Encephalartos latrifrons  
## 5 Capensibufo rosei  
## 6 Galemys pyrenaicus  
## 7 Luscinia svecica  
## 8 Taxus baccata  
## 9 Angelica heterocarpa  
## 10 Syncerus caffer caffer  
## 11 Fagus sylvatica  
## 12 Juniperus monticola  
## 13 Hirundo atrocaerulea  
## 14 Bradypodion thamnobates  
## 15 Sclerophrys pantherina  
## 16 Aloe kniphofioides  
## 17 Bitis albanica  
## 18 Bitis armata  
## 19 Tetrao urogallus  
## 20 Miniopterus schreibersii  
## 21 Zingel asper  
## 22 Pelophylax lessonae  
## 23 Rana dalmatina  
## 24 Aloinopsis acuta  
## 25 Smaug giganteus  
## 26 Natalobatrachus bonebergi  
## 27 Heleophryne rosei  
## 28 Aquila fasciata  
## 29 Phyllurus kabikabi  
## 30 Carcharodon carcharias  
## 31 Lutra lutra  
## 32 Mimetes stokoei  
## 33 Stigmochelys pardalis  
## 34 Canis lupus  
## 35 Posidonia oceanica  
## 36 Coregonus albula morphotype trybomi  
## 37 Gymnadenia nigra  
## 38 Mertensia maritima  
## 39 Mauremys leprosa  
## 40 Mimetes saxatilis  
## 41 Microbatrachella capensis  
## 42 Arthroleptella rugosa  
## 43 Breviceps macrops  
## 44 Amblysomus hottentotus  
## 45 Acacia purpureopetala  
## 46 Macadamia integrifolia  
## 47 Wollemia nobilis  
## 48 Eidothea hardeniana  
## 49 Hoya australis oramicola  
## 50 Gypaetus barbatus  
## 51 Gyps coprotheres  
## 52 Hippocampus capensis  
## 53 Afrixalus knysnae  
## 54 Poicephalus robustus  
## 55 Hyperolius pickersgilli  
## 56 Damaliscus pygargus pygargus  
## 57 Dasyurus hallucatus  
## 58 Phengaris arion  
## 59 Lopinga achine  
## 60 Gulo gulo  
## 61 Vulpes lagopus  
## 62 Pinna nobilis  
## 63 Diceros bicornis  
## 64 Ceratotherium simum simum  
## 65 Equus zebra zebra  
## 66 Connochaetes taurinus  
## 67 Connochaetes gnou  
## 68 Giraffa giraffa Formally know as Giraffa camelopardalis giraffa (subspecies).  
## 69 Damaliscus pygargus phillipsi  
## 70 Halcyon senegalensis cyanoleuca  
## 71 Anthropoides paradiseus  
## 72 Mastomys natalensis  
## 73 Amazilia yucatanensis  
## 74 Selasphorus platycercus  
## 75 Alsophila firma  
## 76 Cyathea bicrenata  
## 77 Smutsia temminckii  
## 78 Antidorcas marsupialis  
## 79 Bombus ephippiatus  
## 80 Ctenosaura pectinata  
## 81 Phengaris alcon  
## 82 Gentiana pneumonanthe  
## 83 Macromia splendens  
## 84 Phonotimpus talquian  
## 85 Lutra Lutra  
## 86 Acipenser sturio  
## 87 Gypaetus barbatus  
## 88 Ctenotus lancelini  
## 89 Saltuarius eximius  
## 90 Carinascincus palfreymani  
## 91 Mustela lutreola  
## 92 Ursus arctos  
## 93 Rhinolophus euryale  
## 94 Barbastella barbastellus  
## 95 Emberiza calandra  
## 96 Pseudemydura umbrina  
## 97 Christinus guentheri  
## 98 Phocoena phocoena  
## 99 Myuchelys georgesi  
## 100 Myuchelys bellii  
## 101 Dysauxes ancilla  
## 102 Loxodonta africana  
## 103 Equus quagga  
## 104 Oryx gazella gazella  
## 105 Tragelaphus angasii  
## 106 Micaelamys namaquensis  
## 107 Micaelamys granti  
## 108 Graphiurus murinus  
## 109 Graphiurus ocularis  
## 110 Sitta whiteheadi  
## 111 Laminaria digitata  
## 112 Hieracium sandozianum  
## 113 Xenospiza baileyi  
## 114 Lytta vesicatoria  
## 115 Ptychadena uzungwensis  
## 116 Zea luxurians  
## 117 Spheniscus demersus  
## 118 Acacia auratiflora  
## 119 Hakea oldfieldii  
## 120 Senecio macrocarpus  
## 121 Acinonyx jubatus jubatus  
## 122 Tympanocryptis lineata  
## 123 Gymnobelideus leadbeateri  
## 124 Potorous gilbertii  
## 125 Macrotis lagotis  
## 126 Zyzomys pedunculatus  
## 127 Pteropus conspicillatus conspicillatus  
## 128 Pseudomys shortridgei  
## 129 Vombatus ursinus  
## 130 Hydromys chrysogaster  
## 131 Rhinonicteris aurantia  
## 132 Notechis scutatus  
## 133 Pinus strobiformis  
## 134 Illigera luzonensis  
## 135 Bufotes viridis  
## 136 Eucalyptus morrisbyi  
## 137 Actinotus schwarzii  
## 138 Pimelea spinescens subspecies spinescens  
## 139 Pimelea spinescens subspecies spinescens  
## 140 Pachycereus grandis  
## 141 Lagenophora lanata  
## 142 Aconitum jaluense subsp. jaluense  
## 143 Cerastium fischerianum var. molle  
## 144 Aconitum metajaponicum  
## 145 Primula reinii var. myogiensis  
## 146 Lonicera japonica var. miyagusukiana  
## 147 Nereia lophocladia  
## 148 Polygala tatarinowii  
## 149 Anhydrophryne rattrayi  
## 150 Anhydrophryne ngongoniensis  
## 151 Aloe pearsonii  
## 152 Diosma awilana  
## 153 Alca torda  
## 154 Neamblysomus julianae  
## 155 Bunolagus monticularis  
## 156 Phyllospora comosa  
## 157 Arthroleptis wahlbergii  
## 158 Cacosternum nanum  
## 159 Diplacus vandenbergensis  
## 160 Picoides borealis  
## 161 Psammobates geometricus  
## 162 Hippotragus equinus equinus  
## 163 Hippotragus niger niger  
## 164 Kinixys lobatsiana  
## 165 Ourebia ourebi ourebi  
## 166 Kinixys natalensis  
## 167 Kinixys spekii  
## 168 Chersina angulata  
## 169 Phacelia formosula  
## 170 Spiranthes delitescens  
## 171 Odocoileus virginianus clavium  
## 172 Clinus spatulatus  
## 173 Tylos granulatus  
## 174 Clinus cottoides  
## 175 Clinus superciliosus  
## 176 Poroderma africanum  
## 177 Ceiba aesculifolia  
## 178 Acroteriobatus annulatus  
## 179 Caffrogobius nudiceps  
## 180 Gilchristella aestuaria  
## 181 Merluccius capensis  
## 182 Tantilla oolitica  
## 183 Pleurobema rubrum  
## 184 Pleurobema rubrum  
## 185 Lagopus leucura rainierensis  
## 186 Artemisiospiza belli clementeae  
## 187 Etheostoma forbesi  
## 188 Donax serra  
## 189 Sclerocactus brevihamatus tobuschii  
## 190 Faxonius marchandi  
## 191 Drymarchon couperi  
## 192 Elliptio spinosa  
## 193 Bucorvus leadbeateri  
## 194 Felis nigripes  
## 195 Mungos mungo  
## 196 Helogale parvula  
## 197 Caracal caracal  
## 198 Parahyaena brunnea  
## 199 Suricata suricatta  
## 200 Canis mesomelas  
## 201 Proteles cristata cristata  
## 202 Felis silvestris lybica  
## 203 Otocyon megalotis megalotis  
## 204 Mellivora capensis  
## 205 Crocuta crocuta  
## 206 Heleophryne hewitti  
## 207 Cheilodactylus fasciatus  
## 208 Zieria ingramii  
## 209 Prosthanthera askania  
## 210 Cercopithecus albogularis labiatus  
## 211 Cercopithecus albogularis erythrarchus  
## 212 Cercopithecus albogularis schwarzi  
## 213 Chrysopsis floridana  
## 214 Obovaria subrotunda  
## 215 Obovaria subrotunda  
## 216 Eriogonum tiehmii  
## 217 Papaipema eryngii  
## 218 Juniperus blancoi  
## 219 Euphilotes enoptes smithi  
## 220 Stygobromus indentatus  
## 221 Acacia linifolia  
## 222 Caladenia gladiolata  
## 223 Caladenia intuta  
## 224 Banksia cuneata  
## 225 Caladenia woolcockiorum  
## 226 Pterostylis bryophila  
## 227 Heteromirafra ruddi  
## 228 Geronticus calvus  
## 229 Spizocorys fringillaris  
## 230 Cirsium scariosum loncholepis  
## 231 Astragalus schmolliae  
## 232 Sorex ornatus relictus  
## 233 Trichocentrum undulatum  
## 234 Calendulauda burra  
## 235 Hemimacronyx chloris  
## 236 Martes caurina  
## 237 Villosa fabalis  
## 238 Eucalyptus melliodora  
## 239 Toxolasma lividum  
## 240 Eriogonum gypsophilum  
## 241 Glyptemys muhlenbergii  
## 242 Austroglanis barnardi  
## 243 Austroglanis gilli  
## 244 Vandijkophrynus amatolicus  
## 245 Nesotragus moschatus zuluensis  
## 246 Pseudobarbus erubescens  
## 247 Promerops cafer  
## 248 Promerops gurneyi  
## 249 Percina antesella  
## 250 Graptopetalum bartramii  
## 251 Scirpus ancistrochaetus  
## 252 Lavinia exilicauda chi  
## 253 Moussonia deppeana  
## 254 Monadenia fidelis minor  
## 255 Layia carnosa  
## 256 Asclepias prostrata  
## 257 Synemon plana  
## 258 Bugeranus carunculatus  
## 259 Balearica regulorum regulorum  
## 260 Palicourea padifolia  
## 261 Leptoxis arkansensis  
## 262 Plethobasus cyphyus  
## 263 Etheostoma cinereum  
## 264 Cryptobranchus alleganiensis alleganiensis  
## 265 Cryptobranchus alleganiensis alleganiensis  
## 266 Ctenosaura macrolopha  
## 267 Centrocercus minimus  
## 268 Lasionectes exleyi  
## 269 Epioblasma triquetra  
## 270 Astragalus microcymbus  
## 271 Astragalus microcymbus  
## 272 Rhipsalis baccifera  
## 273 Psittacanthus schiedeanus  
## 274 Psittacanthus auriculatus  
## 275 Doricha eliza  
## 276 Lampornis amethystinus  
## 277 Campylopterus curvipennis  
## 278 Cynanthus sordidus  
## 279 Psittacanthus sonorae  
## 280 Psittacanthus mayanus  
## 281 Psittacanthus rhynchanthus  
## 282 Orconectes shoupi  
## 283 Macrochelys suwanniensis  
## 284 Boechera pusilla  
## 285 Ipomopsis polyantha  
## 286 Ctenosaura acanthura  
## 287 Chiranthodendron pentadactylon  
## 288 Psittacanthus calyculatus  
## 289 Liquidambar styraciflua  
## 290 Magnolia pedrazae  
## 291 Cyathea aristata  
## 292 Oncorhynchus apache  
## 293 Oncorhynchus apache  
## 294 Graptemys pearlensis  
## 295 Magnolia schiedeana  
## 296 Donrichardsia macroneuron  
## 297 Erimystax harryi  
## 298 Erimystax harryi  
## 299 Fundulus julisia  
## 300 Ptychocheilus lucius  
## 301 Leucorrhinia albifrons  
## 302 Phonotimpus talquian  
## 303 Ambystoma altamirani  
## 304 Ambystoma granulosum  
## 305 Podocarpus matudae  
## 306 Podocarpus guatemalensis  
## 307 Optioservus phaeus  
## 308 Acmispon dendroideus traskiae  
## 309 Hoplogonus bornemisszai  
## 310 Adclarkia dawsonensis  
## 311 Megascolides australis  
## 312 Austrocordulia leonardi  
## 313 Zephyrarchaea austini  
## 314 Bertmainius colonus  
## 315 Neopasiphae simplicior  
## 316 Leucopatus anophthalmus  
## 317 Anguis fragilis  
## 318 Pelophylax esculentus  
## 319 Icaricia icarioides fenderi  
## 320 Cambarus elkensis  
## 321 Cambarus elkensis  
## 322 Myotis septentrionalis  
## 323 Faxonius roberti  
## 324 Tephroseris palustris  
## 325 Juncus anceps  
## 326 Jacobaea erucifolia  
## 327 Lamprothamnium papulosom  
## 328 Emberiza hortulana  
## 329 Stenocereus quevedonis  
## 330 Crotalus catalinensis  
## 331 Saltator atriceps  
## 332 Icterus gularis  
## 333 Uma exsul  
## 334 Leavenworthia texana  
## 335 Cicindela theatina  
## 336 Bipes biporus  
## 337 Chilabothrus granti  
## 338 Pyrgulopsis morrisoni  
## 339 Eryngium sparganophyllum  
## 340 Melanerpes santacruzi  
## 341 Scutellaria ocmulgee  
## 342 Procyon pygmaeus  
## 343 Sideroxylon thornei  
## 344 Procambarus orcinus  
## 345 Alouatta palliata mexicana  
## 346 Campylorhynchus rufinucha  
## 347 Alouatta palliata mexicana  
## 348 Melanerpes aurifrons  
## 349 Parachondrostoma toxostoma  
## 350 Castilleja grisea  
## 351 Procambarus econfinae  
## 352 Ursus arctos arctos  
## 353 Castilleja tolucensis  
## 354 Aphelocoma coerulescens  
## 355 Aphelocoma coerulescens  
## 356 Aphelocoma coerulescens  
## 357 Lomatogonium carinthiacum  
## 358 Cetorhinus maximus  
## 359 Etheostoma trisella  
## 360 Cryptomastix devia  
## 361 Cryptomastix devia  
## 362 Solanum conocarpum  
## 363 Planorbella magnifica  
## 364 Pseudemys gorzugi  
## 365 Xyrauchen texanus  
## 366 Rhaphiomidas trochilus  
## 367 Plethodon hubrichti  
## 368 Notropis topeka  
## 369 Ochrosia iwasakiana  
## 370 Teucrium veronicoides var. veronicoides  
## 371 Speyeria callippe callippe  
## 372 Lespedeza leptostachya  
## 373 Perimyotis subflavus  
## 374 Carica papaya  
## 375 Elgaria panamintina  
## 376 Euphydryas anicia cloudcrofti  
## 377 Pedicularis furbishiae  
## 378 Streptanthus bracteatus  
## 379 Streptanthus bracteatus  
## 380 Bombus franklini  
## 381 Lynx lynx carpathicus  
## 382 Alouatta pigra  
## 383 Ammodramus maritimus macgillivraii  
## 384 Gopherus morafkai  
## 385 Euphilotes ancilla cryptica  
## 386 Zapus hudsonius luteus  
## 387 Euphilotes ancilla purpura  
## 388 Pinus albicaulis  
## 389 Sabia japonica  
## 390 Gambelia sila  
## 391 Enchinomastus erectocentrus acunensis  
## 392 Sedum minimum  
## 393 Colubrina asiatica  
## 394 Arenaria bryoides  
## 395 Cerastium purpusii  
## 396 Draba nivicola  
## 397 Plagiobothrys hirtus  
## 398 Ptychobranchus subtentum  
## 399 Notophthalmus perstriatus  
## 400 Notophthalmus perstriatus  
## 401 Notophthalmus perstriatus  
## 402 Notophthalmus perstriatus  
## 403 Drepanis coccinea  
## 404 Festuca livida  
## 405 Impatiens hypophylla var. microhypophylla  
## 406 Unio crassus  
## 407 Eresus sandaliatus  
## 408 Symplocos konishii  
## 409 Alosa fallax  
## 410 Saussurea yanagisawae  
## 411 Lonicera demissa var. borealis  
## 412 Prunus incisa var. bukosanensis  
## 413 Rhinolophus hipposideros  
## 414 Mimulus gemmiparus  
## 415 Pseudemys rubriventris  
## 416 Pseudemys rubriventris  
## 417 Alnus maritima  
## 418 Hydroprogne caspia  
## 419 Pelobates fuscus  
## 420 Alnus maritima maritima  
## 421 Alnus maritima georgiensis  
## 422 Alnus maritima oklahomensis  
## 423 Swertia pseudochinensis  
## 424 Primula sieboldii  
## 425 Maytenus diversifolia  
## 426 Asarum costatum  
## 427 Aster hispidus var. koidzumianus  
## 428 Isoetes asiatica  
## 429 Ornithorhynchus anatinus  
## 430 Rupicapra pyrenaica  
## 431 Turnix olivii  
## 432 Neophema chrysogaster  
## 433 Parnassius mnemosyne  
## 434 Litoria booroolongensis  
## 435 Glyphis glyphis  
## 436 Pulstilla patens  
## 437 Pulsatilla vulgaris gotlandica  
## 438 Stiphodon semoni  
## 439 Cottus petiti  
## 440 Euphydras maturna  
## 441 Tetrax tetrax tetrax  
## 442 Coenonympha hero  
## 443 Nicrophorus americanus  
## 444 Nicrophorus americanus  
## 445 Speyeria nokomis nokomis  
## 446 Delphinium variegatum kinkiense  
## 447 Rhynchospora crinipes  
## 448 Triturus cristatus  
## 449 Etheostoma chienense  
## 450 Corylopsis glabrescens  
## 451 Crepidiastrum chelidoniifolium  
## 452 Lonicera vidalii  
## 453 Chersobius boulengeri  
## 454 Chersobius signatus  
## 455 Bombina bombina  
## 456 Alisma wahlenbergii  
## 457 Bufo bufo  
## 458 Lacerta agilis  
## 459 Epidalea calamita  
## 460 Charina umbratica  
## 461 Zapus hudsonius luteus  
## 462 Lysimachia barystachys  
## 463 Hyla arborea  
## 464 Lissotriton vulgaris  
## 465 Petromyzon marinus  
## 466 Charadrius alexandrinus  
## 467 Geastrum flexuosum  
## 468 Homopus areolatus  
## 469 Homopus femoralis  
## 470 Cryptocarya chinensis  
## 471 Swertia swertopsis  
## 472 Primula hidakana var. hidakana  
## 473 Harpalus autumnalis  
## 474 Anthophora plagiata  
## 475 Anser erythropus  
## 476 Anthus campestris  
## 477 Bryoria nitidula  
## 478 Melitaea britomartis  
## 479 Dipodomys ingens  
## 480 Callicarpa shikokiana  
## 481 Acer miyabei var. miyabei  
## 482 Salix hukaoana  
## 483 Talpa aquitania  
## 484 Bryhnia scabrida  
## 485 Genista germanica  
## 486 Agonopterix bipunctosa  
## 487 Scolitantides Orion  
## 488 Harpalus flavescens  
## 489 Lonicera ramosissima var. kinkiensis  
## 490 Polystichum piceopaleaceum  
## 491 Carex aequialta  
## 492 Peperomia okinawensis  
## 493 Alectoris graeca  
## 494 Phocoena phocoena  
## 495 Puffinus puffinus  
## 496 Calotriton asper  
## 497 Luronium natans  
## 498 Chenopodium vulvaria  
## 499 Quercus glaucoides  
## 500 Quercus deserticola  
## 501 Quercus peduncularis  
## 502 Utricularia australis  
## 503 Oxytropis campestris subsp. rishiriensi  
## 504 Morus bassanus  
## 505 Phoenicopterus roseus  
## 506 Falco naumanni  
## 507 Plegadis falcinellus  
## 508 Zapornia pusilla  
## 509 Etheostoma chienense  
## 510 Hesperia dacotae  
## 511 Etheostoma maydeni  
## 512 Asplenium castaneoviride  
## 513 Phymatosorus nigrescens  
## 514 Pteris yamatensis  
## 515 Ophioglossum namegatae  
## 516 Asplenium ruta-muraria  
## 517 Pseudotsuga japonica  
## 518 Picea koyamae  
## 519 Sporobolus hancei  
## 520 Rhododendron pentaphyllum var. pentaphyllum  
## 521 Pimpinella thellungiana var. gustavohegiana  
## 522 Testudo hermanni  
## 523 Tyrrhenaria ceratina  
## 524 Anguilla anguilla  
## 525 Salmo salar  
## 526 Aeshna isoceles  
## 527 Calopteryx virgo  
## 528 Coenagrion hastulatum  
## 529 Coenagrion lunulatum  
## 530 Coenagrion pulchellum  
## 531 Gomphus flavipes  
## 532 Salix humboldtiana  
## 533 Leucorrhinia caudalis  
## 534 Leucorrhinia pectoralis  
## 535 Gomphus vulgatissimus  
## 536 Quercus hirtifolia  
## 537 Chionolaena lavandulifolia  
## 538 Rhynchospora crinipes  
## 539 Salix bonplandiana  
## 540 Heterelmis stephani  
## 541 Heterelmis stephani  
## 542 Quercus brandegeei  
## 543 Sterna dougallii  
## 544 Rana temporaria  
## 545 Rana arvalis  
## 546 Saxifraga osloënsis  
## 547 Calidris alpina schinzii  
## 548 Dicranum viride  
## 549 Myotis escalerai  
## 550 Leuciscus aspius  
## 551 Baptria tibiale  
## 552 Cerambyx cerdo  
## 553 Neophron percnopterus  
## 554 Glareola pratincola  
## 555 Pterocles alchata  
## 556 Dactylorhiza brennensis  
## 557 Dipodomys stephensi  
## 558 Popenaias popeii  
## 559 Pinus nigra salzmanii  
## 560 Senecio mairetianus  
## 561 Chalcophora mariana  
## 562 Depressaria nemolella  
## 563 Psophus stridulus  
## 564 Lepidium papilliferum  
## 565 Lepidium papilliferum  
## 566 Laterallus jamaicensis jamaicensis  
## 567 Procambarus pictus  
## 568 Clonophis kirtlandii  
## 569 Sisyrinchium sarmentosum  
## 570 Lomatium bradshawii  
## 571 Diomedea exulans  
## 572 Calocitta formosa  
## 573 Pseudophryne covacevichae  
## 574 Casuarius casuarius johnsonii  
## 575 Xiphorhynchus flavigaster  
## 576 Pedionomus torquatus  
## 577 Hypotaenidia sylvestris  
## 578 Myrmecobius fasciatus  
## 579 Carcharodon carcharias  
## 580 Neotamias minimus atristriatus  
## 581 Noturus munitus  
## 582 Pyrgulopsis thompsoni  
## 583 Pleurobema athearni  
## 584 Thalassarche cauta  
## 585 Alasmidonta varicosa  
## 586 Thalassarche chrysostoma  
## 587 Thalassarche melanophris  
## 588 Margaritifera margaritifera  
## 589 Leptogium rivulare  
## 590 Coronella austriaca  
## 591 Natrix natrix natrix  
## 592 Natrix natrix gotlandica  
## 593 Zootoca vivipara  
## 594 Vipera berus  
## 595 Ambuchanania leucobryoides  
## 596 Pyrgulopsis turbatrix  
## 597 Pherosphaera fitzgeraldii  
## 598 Leptotila verreauxi  
## 599 Cyathea exilis  
## 600 Xanthorrhoea bracteata  
## 601 Cyclarhys gujanensis  
## 602 Centaurea corymbosa  
## 603 Stenocereus pruinosus  
## 604 Styrax platanifolius texanus  
## 605 Ambystoma cingulatum  
## 606 Ambystoma cingulatum  
## 607 Etheostoma osburni  
## 608 Etheostoma osburni  
## 609 Alasmidonta varicosa  
## 610 Lepanthes eltoroensis  
## 611 Macronectes giganteus  
## 612 Macronectes halli  
## 613 Procellaria cinerea  
## 614 Phoebetria palpebrata  
## 615 Sylvilagus bachmani riparius  
## 616 Macrochelys temminckii  
## 617 Arabis georgiana  
## 618 Heterodon simus  
## 619 Eryngium proteiflorum  
## 620 Vireo atricapilla  
## 621 Bombus terricola  
## 622 Bombus terricola  
## 623 Malacothamnus clementinus  
## 624 Phacelia submutica  
## 625 Oncorhynchus clarkii virginalis  
## 626 Oncorhynchus clarkii virginalis  
## 627 Cirsium wrightii  
## 628 Notropis mekistocholas  
## 629 Notropis mekistocholas  
## 630 Eremophila alpestris strigata  
## 631 Percina rex  
## 632 Yermo xanthocephalus  
## 633 Hemphillia burringtoni  
## 634 Hemphillia burringtoni  
## 635 Castilleja levisecta  
## 636 Lupinus constancei  
## 637 Cambarus cracens  
## 638 Mustela nigripes  
## 639 Mustela nigripes  
## 640 Plestiodon egregius egregius  
## 641 Thoburnia atripinnis  
## 642 Strix occidentalis occidentalis  
## 643 Plestiodon egregius egregius  
## 644 Berberis alpina  
## 645 Cynomys leucurus  
## 646 Anaxyrus williamsi  
## 647 Texella reyesi  
## 648 Texella reyesi  
## 649 Sympetrum depressiusculum  
## 650 Apatura iris  
## 651 Cyaniris semiargus  
## 652 Erynnis tages  
## 653 Euphydryas aurinia  
## 654 Euplagia quadripunctaria  
## 655 Salmo salar  
## 656 Gadus morhua  
## 657 Hesperia comma  
## 658 Lasiommata megera  
## 659 Melitaea cinxia  
## 660 Proserpinus proserpina  
## 661 Pyronia tithonus  
## 662 Satyrium ilicis  
## 663 Barbastella barbastellus  
## 664 Myotis bechsteinii  
## 665 Myotis brandtii  
## 666 Myotis dasycneme  
## 667 Myotis daubentonii  
## 668 Myotis emarginatus  
## 669 Myotis myotis  
## 670 Myotis mystacinus  
## 671 Myotis nattereri  
## 672 Nyctalus leisleri  
## 673 Nyctalus noctula  
## 674 Pipistrellus nathusii  
## 675 Pipistrellus pipistrellus  
## 676 Pipistrellus pygmaeus  
## 677 Plecotus auritus  
## 678 Plecotus austriacus  
## 679 Rhinolophus ferrumequinum  
## 680 Eptesicus serotinus  
## 681 Pyrgus malvae  
## 682 Pinus ayacahuite  
## 683 Tapirus bairdii  
## 684 Lontra longicaudis  
## 685 Anacampsis fuscella  
## 686 Melitta tricincta  
## 687 Limosa limosa  
## 688 Euphrasia offficinalis officinalis  
## 689 Sabulina viscosa  
## 690 Eryngium maritimum  
## 691 Kinosternon vogti  
## 692 Pulsatilla vernalis  
## 693 Stauroderus scalaris  
## 694 Canthophorus impressus  
## 695 Pytho kolwensis  
## 696 Euphrasia stricta suecica  
## 697 Lycaena helle  
## 698 Egretta rufescens dickeyi  
## 699 Pseudorchis albida  
## 700 Euphydryas aurinia  
## 701 Circus pygargus  
## 702 Lampetra fluviatilis  
## 703 Ranunculus hederaceus  
## 704 Bryoria tenuis  
## 705 Myricaria germanica  
## 706 Ranunculus ophioglossifolius  
## 707 Heterodermia speciosa  
## 708 Botrychium simplex  
## 709 Pedostrangalia revestita  
## 710 Lobaria hallii  
## 711 Chirostoma estor  
## 712 Sistrurus catenatus  
## 713 Gossypium harknessii  
## 714 Gossypium trilobum  
## 715 Gossypium turneri  
## 716 Gossypium gossypioides  
## 717 Gossypium schwendimanii  
## 718 Gossypium thurberi  
## 719 Gossypium laxum  
## 720 Gossypium lobatum  
## 721 Gossypium davidsonii  
## 722 Gossypium aridum  
## 723 Castor fiber  
## 724 Cricetus cricetus  
## 725 Crocidura leucodon  
## 726 Lynx lynx  
## 727 Meles meles  
## 728 Muscardinus avellanarius  
## 729 Vespertilio murinus  
## 730 Stenobothrus stigmaticus  
## 731 Lutra lutra  
## 732 Lepus timidus  
## 733 Sorex isodon  
## 734 Sicista betulina  
## 735 Erinaceus europaeus  
## 736 Myotis bechsteinii  
## 737 Phoca vitulina  
## 738 Vulpes vulpes  
## 739 Aloe craibii  
## 740 Aloe peglerae  
## 741 Anhydrophryne hewitti  
## 742 Arthroleptella drewesii  
## 743 Arthroleptella subvoce  
## 744 Lyrurus tetrix  
## 745 Castor fiber  
## 746 Neotis ludwigii  
## 747 Xenopus gilli  
## 748 Myotis dasycneme  
## 749 Lessonia corrugata  
## 750 Ecklonia radiata  
## 751 Ecklonia radiata brevipes  
## 752 Durvillaea potatorum  
## 753 Durvillaea amatheiae  
## 754 Hormosira banksii  
## 755 Posidonia australis  
## 756 Sargassum fallax  
## 757 Scytothalia dorycarpa  
## 758 Apium repens  
## 759 Baldellia ranunculoides  
## 760 Bupleurum tenuissimum  
## 761 Carex diandra  
## 762 Carex trinervis  
## 763 Deschampsia setacea  
## 764 Eriophorum gracile  
## 765 Gentianella uliginosa  
## 766 Herminium monorchis  
## 767 Juncus capitatus  
## 768 Liparis loeselii  
## 769 Potamogeton acutifolius  
## 770 Potamogeton coloratus  
## 771 Potamogeton compressus  
## 772 Ranunculus ololeucos  
## 773 Schoenoplectus pungens  
## 774 Schoenoplectus triqueter  
## 775 Eresus sandaliatus  
## 776 Elater ferrugineus  
## 777 Cucujus cinnaberinus  
## 778 Dactylorhiza sphagnicola  
## 779 Orchis morio  
## 780 Orobanche rapum-genistae  
## 781 Platanthera bifolia  
## 782 Vertigo angustior  
## 783 Capreolus capreolus  
## 784 Conophytum regale  
## 785 Protea mucronifolia  
## 786 Protea odorata  
## 787 Cervus elaphus elaphus  
## 788 Halichoerus grypus  
## 789 Mentha pulegium  
## 790 Orchis purpurea  
## 791 Conophytum vanheerdei  
## 792 Conophytum antonii  
## 793 Scorzonera humilis  
## 794 Wahlenbergia hederacea  
## 795 Vertigo moulinsiana  
## 796 Anisus vorticulus  
## 797 Hamatocaulis vernicosus  
## 798 Unio crassus  
## 799 Lucanus cervus  
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## 806 Halimione pedunculata  
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## 808 Notropis topeka  
## 809 Necturus lewisi  
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## 811 Diphasiastrum tristachyum  
## 812 Luronium natans  
## 813 Somatochlora arctica  
## 814 Pilularia globulifera  
## 815 Lacerta agilis  
## 816 Osmoderma eremita  
## 817 Bufo calamita  
## 818 Kinosternon integrum  
## 819 Vipera berus  
## 820 Abronia deppii  
## 821 Populus nigra  
## 822 Rosalia alpina  
## 823 Iberolacerta bonnali  
## 824 Misgurnus fossilis  
## 825 Petromyzon marinus  
## 826 Phengaris alcon  
## 827 Ephippiger ephippiger  
## 828 Pelobates fuscus  
## 829 Tursiops aduncus  
## 830 Procambarus orcinus  
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## 834 Psammodromus algirus  
## 835 Hyla arborea  
## 836 Lampetra planeri  
## 837 Bombina variegata  
## 838 Lavinia exilicauda chi  
## 839 Pelophylax lessonae  
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## 841 Triturus cristatus  
## 842 Salamandra salamandra  
## 843 Podarcis muralis  
## 844 Rana arvalis  
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## 847 Parnassius apollo  
## 848 Hydroprogne caspia  
## 849 Haematopus ostralegus ostralegus  
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## 851 Capra ibex  
## 852 Hipparchia semele  
## 853 Prionotropis rhodanica  
## 854 Nehalennia speciosa  
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## 857 Rhodeus sericeus  
## 858 Cottus rhenanus  
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## 861 Hippocampus guttulatus  
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## 865 Muscardinus avellanarius  
## 866 Rana dalmatina  
## 867 Anguis fragilis  
## 868 Coronella austriaca  
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## 870 Ficedula albicollis  
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## 873 Zea mays parviglumis  
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## 877 Crax alberti  
## 878 Hapalopsittaca fuertesi  
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## 880 Chlorochrysa nitidissima  
## 881 Ognorhynchus icterotis  
## 882 Tayassu pecari  
## 883 Myiothlypis basilica  
## 884 Hapalopsittaca amazonina  
## 885 Pauxi pauxi  
## 886 Pyrilia Pyrilia  
## 887 Bolborhynchus ferrugineifrons  
## 888 Coeligena prunellei  
## 889 Crypturellus kerriae  
## 890 Grallaria milleri  
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## 892 Pyrrhura calliptera  
## 893 Nystactes noanamae  
## 894 Penelope ortoni  
## 895 Rallus semiplumbeus  
## 896 Bangsia aureocincta  
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## 898 Colostethus thorntoni  
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## 900 Xenornis setifrons  
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## 902 Grallaria kaestneri  
## 903 Pyrrhura viridicata  
## 904 Arremon basilicus  
## 905 Odontophorus hyperythrus  
## 906 Oxypogon cyanolaemus  
## 907 Megascops gilesi  
## 908 Clibanornis rufipectus  
## 909 Thryophilus sernai  
## 910 Scytalopus alvarezlopezi  
## 911 Dubusia carrikeri  
## 912 Grallaria bangsi  
## 913 Oxypogon stuebelii  
## 914 Anthocephala berlepschi  
## 915 Pogonotriccus lanyoni  
## 916 Scytalopus stilesi  
## 917 Grallaria fenwickorum  
## 918 Myiotheretes pernix  
## 919 Scytalopus sanctaemartae  
## 920 Drymophila hellmayri  
## 921 Synallaxis fuscorufa  
## 922 Eriocnemis isabellae  
## 923 Cucurbita argyrosperma sororia  
## 924 Trichomycterus sandovali  
## 925 Ageneiosus pardalis  
## 926 Espeletia paipana  
## 927 Espeletia jaramilloi  
## 928 Zamia obliqua  
## 929 Magnolia wolfii  
## 930 Libidibia ebano  
## 931 Podocnemis lewyana  
## 932 Anadia antioquensis  
## 933 Lepidochelys olivacea  
## 934 Euterpe precatoria  
## 935 Quercus humboldtii  
## 936 Magnolia polyhypsophylla  
## 937 Troglodytes monticola  
## 938 Scytalopus rodriguezi  
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## 940 Atlapetes blancae  
## 941 Odontophorus strophium  
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## 944 Psarocolius cassini  
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## 946 Diglossa gloriosissima  
## 947 Ara ambiguus  
## 948 Sula granti  
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## 951 Sula leucogaster  
## 952 Dacnis berlepschi  
## 953 Glaucidium nubicola  
## 954 Basileuterus ignotus  
## 955 Tangara fucosa  
## 956 Micrastur plumbeus  
## 957 Anas bahamensis bahamensis  
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## 959 Spizaetus isidori  
## 960 Vultur gryphus  
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## 962 Buteogallus solitarius  
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## 459 69 6 0.92000000  
## 460 2 0 1.00000000  
## 461 77 NA NA  
## 462 24 3 0.88888889  
## 463 2 1 0.66666667  
## 464 57 1 0.98275862  
## 465 14 5 0.73684211  
## 466 0 3 0.00000000  
## 467 1 0 1.00000000  
## 468 2 NA NA  
## 469 2 NA NA  
## 470 2 0 1.00000000  
## 471 21 0 1.00000000  
## 472 7 0 1.00000000  
## 473 1 0 1.00000000  
## 474 2 5 0.28571429  
## 475 1 1 0.50000000  
## 476 1 4 0.20000000  
## 477 6 4 0.60000000  
## 478 2 8 0.20000000  
## 479 6 NA NA  
## 480 3 0 1.00000000  
## 481 11 0 1.00000000  
## 482 4 1 0.80000000  
## 483 1 0 1.00000000  
## 484 20 3 0.86956522  
## 485 1 12 0.07692308  
## 486 6 3 0.66666667  
## 487 5 3 0.62500000  
## 488 2 1 0.66666667  
## 489 3 0 1.00000000  
## 490 1 0 1.00000000  
## 491 3 0 1.00000000  
## 492 3 0 1.00000000  
## 493 1 NA NA  
## 494 1 0 1.00000000  
## 495 2 NA NA  
## 496 176 NA NA  
## 497 4 2 0.66666667  
## 498 3 2 0.60000000  
## 499 1 NA NA  
## 500 3 NA NA  
## 501 2 NA NA  
## 502 3 0 1.00000000  
## 503 1 0 1.00000000  
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## 505 1 NA NA  
## 506 3 NA NA  
## 507 2 NA NA  
## 508 1 NA NA  
## 509 1 0 1.00000000  
## 510 4 1 0.80000000  
## 511 4 3 0.57142857  
## 512 3 4 0.42857143  
## 513 1 1 0.50000000  
## 514 1 0 1.00000000  
## 515 3 0 1.00000000  
## 516 3 0 1.00000000  
## 517 2 0 1.00000000  
## 518 1 0 1.00000000  
## 519 2 1 0.66666667  
## 520 3 0 1.00000000  
## 521 6 0 1.00000000  
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## 525 1 1 0.50000000  
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## 527 1 NA NA  
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## 529 3 9 0.25000000  
## 530 4 NA NA  
## 531 1 2 0.33333333  
## 532 13 NA NA  
## 533 8 4 0.66666667  
## 534 1 NA NA  
## 535 2 10 0.16666667  
## 536 3 NA NA  
## 537 15 NA NA  
## 538 37 2 0.94871795  
## 539 5 NA NA  
## 540 0 2 0.00000000  
## 541 1 1 0.50000000  
## 542 5 NA NA  
## 543 3 0 1.00000000  
## 544 11 0 1.00000000  
## 545 11 0 1.00000000  
## 546 7 4 0.63636364  
## 547 8 0 1.00000000  
## 548 30 2 0.93750000  
## 549 1 NA NA  
## 550 15 0 1.00000000  
## 551 3 2 0.60000000  
## 552 1 2 0.33333333  
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## 554 1 NA NA  
## 555 1 NA NA  
## 556 2 NA NA  
## 557 17 3 0.85000000  
## 558 6 4 0.60000000  
## 559 4 0 1.00000000  
## 560 19 NA NA  
## 561 2 6 0.25000000  
## 562 2 0 1.00000000  
## 563 80 0 1.00000000  
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## 565 105 10 0.91304348  
## 566 4 3 0.57142857  
## 567 19 2 0.90476190  
## 568 NA NA NA  
## 569 18 NA NA  
## 570 24 1 0.96000000  
## 571 1 0 1.00000000  
## 572 3 NA NA  
## 573 36 NA NA  
## 574 3 NA NA  
## 575 4 NA NA  
## 576 1 NA NA  
## 577 1 0 1.00000000  
## 578 10 NA NA  
## 579 1 0 1.00000000  
## 580 2 0 1.00000000  
## 581 12 4 0.75000000  
## 582 23 NA NA  
## 583 2 0 1.00000000  
## 584 3 0 1.00000000  
## 585 241 NA NA  
## 586 1 0 1.00000000  
## 587 4 0 1.00000000  
## 588 286 421 0.40452617  
## 589 18 6 0.75000000  
## 590 11 0 1.00000000  
## 591 8 0 1.00000000  
## 592 2 0 1.00000000  
## 593 13 0 1.00000000  
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## 596 36 2 0.94736842  
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## 598 4 NA NA  
## 599 2 NA NA  
## 600 18 NA NA  
## 601 3 NA NA  
## 602 6 NA NA  
## 603 25 NA NA  
## 604 3 NA NA  
## 605 9 16 0.36000000  
## 606 4 0 1.00000000  
## 607 18 17 0.51428571  
## 608 5 2 0.71428571  
## 609 4 NA NA  
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## 611 6 0 1.00000000  
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## 614 3 0 1.00000000  
## 615 4 0 1.00000000  
## 616 7 NA NA  
## 617 19 7 0.73076923  
## 618 89 133 0.40090090  
## 619 19 NA NA  
## 620 40 NA NA  
## 621 15 3 0.83333333  
## 622 47364 7908 0.85692575  
## 623 1 0 1.00000000  
## 624 5 0 1.00000000  
## 625 4 1 0.80000000  
## 626 122 6 0.95312500  
## 627 8 5 0.61538462  
## 628 1 0 1.00000000  
## 629 8 0 1.00000000  
## 630 3 3 0.50000000  
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## 632 2 0 1.00000000  
## 633 16 NA NA  
## 634 95 NA NA  
## 635 45 25 0.64285714  
## 636 4 0 1.00000000  
## 637 2 0 1.00000000  
## 638 14 15 0.48275862  
## 639 1 NA NA  
## 640 15 8 0.65217391  
## 641 24 0 1.00000000  
## 642 2 0 1.00000000  
## 643 19 4 0.82608696  
## 644 9 NA NA  
## 645 3 0 1.00000000  
## 646 1 0 1.00000000  
## 647 77 NA NA  
## 648 6 NA NA  
## 649 2 8 0.20000000  
## 650 1 NA NA  
## 651 2 NA NA  
## 652 8 NA NA  
## 653 5 5 0.50000000  
## 654 1 NA NA  
## 655 36 17 0.67924528  
## 656 3 0 1.00000000  
## 657 6 NA NA  
## 658 1 NA NA  
## 659 4 NA NA  
## 660 1 NA NA  
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## 662 5 NA NA  
## 663 2 NA NA  
## 664 1 NA NA  
## 665 NA NA NA  
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## 675 1 NA NA  
## 676 NA NA NA  
## 677 1 NA NA  
## 678 6 NA NA  
## 679 4 2 0.66666667  
## 680 1 NA NA  
## 681 6 NA NA  
## 682 NA NA NA  
## 683 6 4 0.60000000  
## 684 19 NA NA  
## 685 13 0 1.00000000  
## 686 7 2 0.77777778  
## 687 7 0 1.00000000  
## 688 30 20 0.60000000  
## 689 1 49 0.02000000  
## 690 4 1 0.80000000  
## 691 1 NA NA  
## 692 840 285 0.74666667  
## 693 10 6 0.62500000  
## 694 100 0 1.00000000  
## 695 14 4 0.77777778  
## 696 10 20 0.33333333  
## 697 5 9 0.35714286  
## 698 NA NA NA  
## 699 60 35 0.63157895  
## 700 45 11 0.80357143  
## 701 1 0 1.00000000  
## 702 127 0 1.00000000  
## 703 4 1 0.80000000  
## 704 38 5 0.88372093  
## 705 13 7 0.65000000  
## 706 2 3 0.40000000  
## 707 10 5 0.66666667  
## 708 8 4 0.66666667  
## 709 25 16 0.60975610  
## 710 9 1 0.90000000  
## 711 11 NA NA  
## 712 347 211 0.62186380  
## 713 4 0 1.00000000  
## 714 1 0 1.00000000  
## 715 1 0 1.00000000  
## 716 2 0 1.00000000  
## 717 1 0 1.00000000  
## 718 1 0 1.00000000  
## 719 2 0 1.00000000  
## 720 1 0 1.00000000  
## 721 3 0 1.00000000  
## 722 8 0 1.00000000  
## 723 1 NA NA  
## 724 1 2 0.33333333  
## 725 NA NA NA  
## 726 1 NA NA  
## 727 1 NA NA  
## 728 2 4 0.33333333  
## 729 NA NA NA  
## 730 6 4 0.60000000  
## 731 1 NA NA  
## 732 6 0 1.00000000  
## 733 2 0 1.00000000  
## 734 3 0 1.00000000  
## 735 18 0 1.00000000  
## 736 2 0 1.00000000  
## 737 5 0 1.00000000  
## 738 2 0 1.00000000  
## 739 6 0 1.00000000  
## 740 4 1 0.80000000  
## 741 1 0 1.00000000  
## 742 2 0 1.00000000  
## 743 3 0 1.00000000  
## 744 1 0 1.00000000  
## 745 1 0 1.00000000  
## 746 1 0 1.00000000  
## 747 2 1 0.66666667  
## 748 1 1 0.50000000  
## 749 2 0 1.00000000  
## 750 14 1 0.93333333  
## 751 2 0 1.00000000  
## 752 2 NA NA  
## 753 3 NA NA  
## 754 5 NA NA  
## 755 5 0 1.00000000  
## 756 5 1 0.83333333  
## 757 2 1 0.66666667  
## 758 4 NA NA  
## 759 20 NA NA  
## 760 1 NA NA  
## 761 11 NA NA  
## 762 3 NA NA  
## 763 1 NA NA  
## 764 2 4 0.33333333  
## 765 3 NA NA  
## 766 1 2 0.33333333  
## 767 1 2 0.33333333  
## 768 2 5 0.28571429  
## 769 13 NA NA  
## 770 9 NA NA  
## 771 2 NA NA  
## 772 22 NA NA  
## 773 2 NA NA  
## 774 5 NA NA  
## 775 4 NA NA  
## 776 2 NA NA  
## 777 1 NA NA  
## 778 26 NA NA  
## 779 5 NA NA  
## 780 15 NA NA  
## 781 18 NA NA  
## 782 18 NA NA  
## 783 3 0 1.00000000  
## 784 1 0 1.00000000  
## 785 2 0 1.00000000  
## 786 1 4 0.20000000  
## 787 2 0 1.00000000  
## 788 30 0 1.00000000  
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## 790 21 NA NA  
## 791 1 0 1.00000000  
## 792 1 0 1.00000000  
## 793 68 NA NA  
## 794 54 NA NA  
## 795 26 NA NA  
## 796 3 NA NA  
## 797 4 5 0.44444444  
## 798 5 6 0.45454545  
## 799 30 NA NA  
## 800 9 0 1.00000000  
## 801 5 1 0.83333333  
## 802 65 67 0.49242424  
## 803 48 NA NA  
## 804 4 NA NA  
## 805 72 NA NA  
## 806 2 NA NA  
## 807 7 10 0.41176471  
## 808 13 NA NA  
## 809 9 0 1.00000000  
## 810 3 0 1.00000000  
## 811 4 NA NA  
## 812 17 1 0.94444444  
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## 814 6 NA NA  
## 815 9 NA NA  
## 816 NA NA NA  
## 817 13 NA NA  
## 818 NA NA NA  
## 819 16 NA NA  
## 820 NA NA NA  
## 821 5 NA NA  
## 822 13 NA NA  
## 823 15 0 1.00000000  
## 824 7 4 0.63636364  
## 825 1 NA NA  
## 826 4 NA NA  
## 827 1 NA NA  
## 828 4 4 0.50000000  
## 829 2 0 1.00000000  
## 830 1 NA NA  
## 831 12 1 0.92307692  
## 832 12 1 0.92307692  
## 833 1 0 1.00000000  
## 834 3 NA NA  
## 835 8 23 0.25806452  
## 836 10 NA NA  
## 837 12 58 0.17142857  
## 838 3 1 0.75000000  
## 839 91 NA NA  
## 840 12 NA NA  
## 841 242 NA NA  
## 842 311 NA NA  
## 843 1 NA NA  
## 844 42 NA NA  
## 845 79 NA NA  
## 846 1 0 1.00000000  
## 847 6 NA NA  
## 848 7 6 0.53846154  
## 849 2 0 1.00000000  
## 850 1 0 1.00000000  
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## 852 2 NA NA  
## 853 1 NA NA  
## 854 1 1 0.50000000  
## 855 30 NA NA  
## 856 1 NA NA  
## 857 37 9 0.80434783  
## 858 10 NA NA  
## 859 186 NA NA  
## 860 2 NA NA  
## 861 4 NA NA  
## 862 2 NA NA  
## 863 1 0 1.00000000  
## 864 6 0 1.00000000  
## 865 12 1 0.92307692  
## 866 4 0 1.00000000  
## 867 10 0 1.00000000  
## 868 11 0 1.00000000  
## 869 284 116 0.71000000  
## 870 1 0 1.00000000  
## 871 2 0 1.00000000  
## 872 2 0 1.00000000  
## 873 13 0 1.00000000  
## 874 6 0 1.00000000  
## 875 1 0 1.00000000  
## 876 6 5 0.54545455  
## 877 4 6 0.40000000  
## 878 2 4 0.33333333  
## 879 2 1 0.66666667  
## 880 3 1 0.75000000  
## 881 10 12 0.45454545  
## 882 5 5 0.50000000  
## 883 1 NA NA  
## 884 8 NA NA  
## 885 2 1 0.66666667  
## 886 2 3 0.40000000  
## 887 3 NA NA  
## 888 3 NA NA  
## 889 1 0 1.00000000  
## 890 1 1 0.50000000  
## 891 3 2 0.60000000  
## 892 5 5 0.50000000  
## 893 4 NA NA  
## 894 1 1 0.50000000  
## 895 7 2 0.77777778  
## 896 4 1 0.80000000  
## 897 2 2 0.50000000  
## 898 3 1 0.75000000  
## 899 11 1 0.91666667  
## 900 1 1 0.50000000  
## 901 1 1 0.50000000  
## 902 2 NA NA  
## 903 1 NA NA  
## 904 1 NA NA  
## 905 1 NA NA  
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## 932 1 NA NA  
## 933 2 NA NA  
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## 953 1 NA NA  
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## 956 1 NA NA  
## 957 1 NA NA  
## 958 2 1 0.66666667  
## 959 4 NA NA  
## 960 4 NA NA  
## 961 4 NA NA  
## 962 4 NA NA  
## 963 1 NA NA  
## 964 4 NA NA  
## 965 1 NA NA  
## 966 1 NA NA

### Indicator 3 or genetic monitoring indicator: number of species with genetic diversity monitoring

Example of indicator 3 data selecting the most relevant columns:

ind3\_data %>% select(country\_assessment, taxon, multiassessment, temp\_gen\_monitoring, gen\_studies, gen\_monitoring\_years, source\_genetic\_studies)

## country\_assessment  
## 1 sweden  
## 2 sweden  
## 3 sweden  
## 4 south\_africa  
## 5 south\_africa  
## 6 france  
## 7 france  
## 8 france  
## 9 france  
## 10 south\_africa  
## 11 france  
## 12 mexico  
## 13 south\_africa  
## 14 south\_africa  
## 15 south\_africa  
## 16 south\_africa  
## 17 south\_africa  
## 18 south\_africa  
## 19 france  
## 20 france  
## 21 france  
## 22 sweden  
## 23 sweden  
## 24 south\_africa  
## 25 south\_africa  
## 26 south\_africa  
## 27 south\_africa  
## 28 france  
## 29 australia  
## 30 south\_africa  
## 31 sweden  
## 32 south\_africa  
## 33 south\_africa  
## 34 sweden  
## 35 france  
## 36 sweden  
## 37 sweden  
## 38 sweden  
## 39 france  
## 40 south\_africa  
## 41 south\_africa  
## 42 south\_africa  
## 43 south\_africa  
## 44 south\_africa  
## 45 australia  
## 46 australia  
## 47 australia  
## 48 australia  
## 49 australia  
## 50 south\_africa  
## 51 south\_africa  
## 52 south\_africa  
## 53 south\_africa  
## 54 south\_africa  
## 55 south\_africa  
## 56 south\_africa  
## 57 australia  
## 58 sweden  
## 59 sweden  
## 60 sweden  
## 61 sweden  
## 62 france  
## 63 south\_africa  
## 64 south\_africa  
## 65 south\_africa  
## 66 south\_africa  
## 67 south\_africa  
## 68 south\_africa  
## 69 south\_africa  
## 70 south\_africa  
## 71 south\_africa  
## 72 south\_africa  
## 73 mexico  
## 74 mexico  
## 75 mexico  
## 76 mexico  
## 77 south\_africa  
## 78 south\_africa  
## 79 mexico  
## 80 mexico  
## 81 sweden  
## 82 sweden  
## 83 france  
## 84 mexico  
## 85 france  
## 86 france  
## 87 france  
## 88 australia  
## 89 australia  
## 90 australia  
## 91 france  
## 92 sweden  
## 93 france  
## 94 sweden  
## 95 sweden  
## 96 australia  
## 97 australia  
## 98 sweden  
## 99 australia  
## 100 australia  
## 101 sweden  
## 102 south\_africa  
## 103 south\_africa  
## 104 south\_africa  
## 105 south\_africa  
## 106 south\_africa  
## 107 south\_africa  
## 108 south\_africa  
## 109 south\_africa  
## 110 france  
## 111 france  
## 112 france  
## 113 mexico  
## 114 sweden  
## 115 south\_africa  
## 116 mexico  
## 117 south\_africa  
## 118 australia  
## 119 australia  
## 120 australia  
## 121 south\_africa  
## 122 australia  
## 123 australia  
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## 132 australia  
## 133 mexico  
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## 135 sweden  
## 136 australia  
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## 139 australia  
## 140 mexico  
## 141 japan  
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## 146 japan  
## 147 australia  
## 148 japan  
## 149 south\_africa  
## 150 south\_africa  
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## 152 south\_africa  
## 153 france  
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## 156 australia  
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## 159 united\_states  
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## 177 mexico  
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## 237 united\_states  
## 238 australia  
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## 241 united\_states  
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## taxon  
## 1 Alces alces  
## 2 Siluris glanis  
## 3 Dendrocopos leucotos  
## 4 Encephalartos latrifrons  
## 5 Capensibufo rosei  
## 6 Galemys pyrenaicus  
## 7 Luscinia svecica  
## 8 Taxus baccata  
## 9 Angelica heterocarpa  
## 10 Syncerus caffer caffer  
## 11 Fagus sylvatica  
## 12 Juniperus monticola  
## 13 Hirundo atrocaerulea  
## 14 Bradypodion thamnobates  
## 15 Sclerophrys pantherina  
## 16 Aloe kniphofioides  
## 17 Bitis albanica  
## 18 Bitis armata  
## 19 Tetrao urogallus  
## 20 Miniopterus schreibersii  
## 21 Zingel asper  
## 22 Pelophylax lessonae  
## 23 Rana dalmatina  
## 24 Aloinopsis acuta  
## 25 Smaug giganteus  
## 26 Natalobatrachus bonebergi  
## 27 Heleophryne rosei  
## 28 Aquila fasciata  
## 29 Phyllurus kabikabi  
## 30 Carcharodon carcharias  
## 31 Lutra lutra  
## 32 Mimetes stokoei  
## 33 Stigmochelys pardalis  
## 34 Canis lupus  
## 35 Posidonia oceanica  
## 36 Coregonus albula morphotype trybomi  
## 37 Gymnadenia nigra  
## 38 Mertensia maritima  
## 39 Mauremys leprosa  
## 40 Mimetes saxatilis  
## 41 Microbatrachella capensis  
## 42 Arthroleptella rugosa  
## 43 Breviceps macrops  
## 44 Amblysomus hottentotus  
## 45 Acacia purpureopetala  
## 46 Macadamia integrifolia  
## 47 Wollemia nobilis  
## 48 Eidothea hardeniana  
## 49 Hoya australis oramicola  
## 50 Gypaetus barbatus  
## 51 Gyps coprotheres  
## 52 Hippocampus capensis  
## 53 Afrixalus knysnae  
## 54 Poicephalus robustus  
## 55 Hyperolius pickersgilli  
## 56 Damaliscus pygargus pygargus  
## 57 Dasyurus hallucatus  
## 58 Phengaris arion  
## 59 Lopinga achine  
## 60 Gulo gulo  
## 61 Vulpes lagopus  
## 62 Pinna nobilis  
## 63 Diceros bicornis  
## 64 Ceratotherium simum simum  
## 65 Equus zebra zebra  
## 66 Connochaetes taurinus  
## 67 Connochaetes gnou  
## 68 Giraffa giraffa Formally know as Giraffa camelopardalis giraffa (subspecies).  
## 69 Damaliscus pygargus phillipsi  
## 70 Halcyon senegalensis cyanoleuca  
## 71 Anthropoides paradiseus  
## 72 Mastomys natalensis  
## 73 Amazilia yucatanensis  
## 74 Selasphorus platycercus  
## 75 Alsophila firma  
## 76 Cyathea bicrenata  
## 77 Smutsia temminckii  
## 78 Antidorcas marsupialis  
## 79 Bombus ephippiatus  
## 80 Ctenosaura pectinata  
## 81 Phengaris alcon  
## 82 Gentiana pneumonanthe  
## 83 Macromia splendens  
## 84 Phonotimpus talquian  
## 85 Lutra Lutra  
## 86 Acipenser sturio  
## 87 Gypaetus barbatus  
## 88 Ctenotus lancelini  
## 89 Saltuarius eximius  
## 90 Carinascincus palfreymani  
## 91 Mustela lutreola  
## 92 Ursus arctos  
## 93 Rhinolophus euryale  
## 94 Barbastella barbastellus  
## 95 Emberiza calandra  
## 96 Pseudemydura umbrina  
## 97 Christinus guentheri  
## 98 Phocoena phocoena  
## 99 Myuchelys georgesi  
## 100 Myuchelys bellii  
## 101 Dysauxes ancilla  
## 102 Loxodonta africana  
## 103 Equus quagga  
## 104 Oryx gazella gazella  
## 105 Tragelaphus angasii  
## 106 Micaelamys namaquensis  
## 107 Micaelamys granti  
## 108 Graphiurus murinus  
## 109 Graphiurus ocularis  
## 110 Sitta whiteheadi  
## 111 Laminaria digitata  
## 112 Hieracium sandozianum  
## 113 Xenospiza baileyi  
## 114 Lytta vesicatoria  
## 115 Ptychadena uzungwensis  
## 116 Zea luxurians  
## 117 Spheniscus demersus  
## 118 Acacia auratiflora  
## 119 Hakea oldfieldii  
## 120 Senecio macrocarpus  
## 121 Acinonyx jubatus jubatus  
## 122 Tympanocryptis lineata  
## 123 Gymnobelideus leadbeateri  
## 124 Potorous gilbertii  
## 125 Macrotis lagotis  
## 126 Zyzomys pedunculatus  
## 127 Pteropus conspicillatus conspicillatus  
## 128 Pseudomys shortridgei  
## 129 Vombatus ursinus  
## 130 Hydromys chrysogaster  
## 131 Rhinonicteris aurantia  
## 132 Notechis scutatus  
## 133 Pinus strobiformis  
## 134 Illigera luzonensis  
## 135 Bufotes viridis  
## 136 Eucalyptus morrisbyi  
## 137 Actinotus schwarzii  
## 138 Pimelea spinescens subspecies spinescens  
## 139 Pimelea spinescens subspecies spinescens  
## 140 Pachycereus grandis  
## 141 Lagenophora lanata  
## 142 Aconitum jaluense subsp. jaluense  
## 143 Cerastium fischerianum var. molle  
## 144 Aconitum metajaponicum  
## 145 Primula reinii var. myogiensis  
## 146 Lonicera japonica var. miyagusukiana  
## 147 Nereia lophocladia  
## 148 Polygala tatarinowii  
## 149 Anhydrophryne rattrayi  
## 150 Anhydrophryne ngongoniensis  
## 151 Aloe pearsonii  
## 152 Diosma awilana  
## 153 Alca torda  
## 154 Neamblysomus julianae  
## 155 Bunolagus monticularis  
## 156 Phyllospora comosa  
## 157 Arthroleptis wahlbergii  
## 158 Cacosternum nanum  
## 159 Diplacus vandenbergensis  
## 160 Picoides borealis  
## 161 Psammobates geometricus  
## 162 Hippotragus equinus equinus  
## 163 Hippotragus niger niger  
## 164 Kinixys lobatsiana  
## 165 Ourebia ourebi ourebi  
## 166 Kinixys natalensis  
## 167 Kinixys spekii  
## 168 Chersina angulata  
## 169 Phacelia formosula  
## 170 Spiranthes delitescens  
## 171 Odocoileus virginianus clavium  
## 172 Clinus spatulatus  
## 173 Tylos granulatus  
## 174 Clinus cottoides  
## 175 Clinus superciliosus  
## 176 Poroderma africanum  
## 177 Ceiba aesculifolia  
## 178 Acroteriobatus annulatus  
## 179 Caffrogobius nudiceps  
## 180 Gilchristella aestuaria  
## 181 Merluccius capensis  
## 182 Tantilla oolitica  
## 183 Pleurobema rubrum  
## 184 Pleurobema rubrum  
## 185 Lagopus leucura rainierensis  
## 186 Artemisiospiza belli clementeae  
## 187 Etheostoma forbesi  
## 188 Donax serra  
## 189 Sclerocactus brevihamatus tobuschii  
## 190 Faxonius marchandi  
## 191 Drymarchon couperi  
## 192 Elliptio spinosa  
## 193 Bucorvus leadbeateri  
## 194 Felis nigripes  
## 195 Mungos mungo  
## 196 Helogale parvula  
## 197 Caracal caracal  
## 198 Parahyaena brunnea  
## 199 Suricata suricatta  
## 200 Canis mesomelas  
## 201 Proteles cristata cristata  
## 202 Felis silvestris lybica  
## 203 Otocyon megalotis megalotis  
## 204 Mellivora capensis  
## 205 Crocuta crocuta  
## 206 Heleophryne hewitti  
## 207 Cheilodactylus fasciatus  
## 208 Zieria ingramii  
## 209 Prosthanthera askania  
## 210 Cercopithecus albogularis labiatus  
## 211 Cercopithecus albogularis erythrarchus  
## 212 Cercopithecus albogularis schwarzi  
## 213 Chrysopsis floridana  
## 214 Obovaria subrotunda  
## 215 Obovaria subrotunda  
## 216 Eriogonum tiehmii  
## 217 Papaipema eryngii  
## 218 Juniperus blancoi  
## 219 Euphilotes enoptes smithi  
## 220 Stygobromus indentatus  
## 221 Acacia linifolia  
## 222 Caladenia gladiolata  
## 223 Caladenia intuta  
## 224 Banksia cuneata  
## 225 Caladenia woolcockiorum  
## 226 Pterostylis bryophila  
## 227 Heteromirafra ruddi  
## 228 Geronticus calvus  
## 229 Spizocorys fringillaris  
## 230 Cirsium scariosum loncholepis  
## 231 Astragalus schmolliae  
## 232 Sorex ornatus relictus  
## 233 Trichocentrum undulatum  
## 234 Calendulauda burra  
## 235 Hemimacronyx chloris  
## 236 Martes caurina  
## 237 Villosa fabalis  
## 238 Eucalyptus melliodora  
## 239 Toxolasma lividum  
## 240 Eriogonum gypsophilum  
## 241 Glyptemys muhlenbergii  
## 242 Austroglanis barnardi  
## 243 Austroglanis gilli  
## 244 Vandijkophrynus amatolicus  
## 245 Nesotragus moschatus zuluensis  
## 246 Pseudobarbus erubescens  
## 247 Promerops cafer  
## 248 Promerops gurneyi  
## 249 Percina antesella  
## 250 Graptopetalum bartramii  
## 251 Scirpus ancistrochaetus  
## 252 Lavinia exilicauda chi  
## 253 Moussonia deppeana  
## 254 Monadenia fidelis minor  
## 255 Layia carnosa  
## 256 Asclepias prostrata  
## 257 Synemon plana  
## 258 Bugeranus carunculatus  
## 259 Balearica regulorum regulorum  
## 260 Palicourea padifolia  
## 261 Leptoxis arkansensis  
## 262 Plethobasus cyphyus  
## 263 Etheostoma cinereum  
## 264 Cryptobranchus alleganiensis alleganiensis  
## 265 Cryptobranchus alleganiensis alleganiensis  
## 266 Ctenosaura macrolopha  
## 267 Centrocercus minimus  
## 268 Lasionectes exleyi  
## 269 Epioblasma triquetra  
## 270 Astragalus microcymbus  
## 271 Astragalus microcymbus  
## 272 Rhipsalis baccifera  
## 273 Psittacanthus schiedeanus  
## 274 Psittacanthus auriculatus  
## 275 Doricha eliza  
## 276 Lampornis amethystinus  
## 277 Campylopterus curvipennis  
## 278 Cynanthus sordidus  
## 279 Psittacanthus sonorae  
## 280 Psittacanthus mayanus  
## 281 Psittacanthus rhynchanthus  
## 282 Orconectes shoupi  
## 283 Macrochelys suwanniensis  
## 284 Boechera pusilla  
## 285 Ipomopsis polyantha  
## 286 Ctenosaura acanthura  
## 287 Chiranthodendron pentadactylon  
## 288 Psittacanthus calyculatus  
## 289 Liquidambar styraciflua  
## 290 Magnolia pedrazae  
## 291 Cyathea aristata  
## 292 Oncorhynchus apache  
## 293 Oncorhynchus apache  
## 294 Graptemys pearlensis  
## 295 Magnolia schiedeana  
## 296 Donrichardsia macroneuron  
## 297 Erimystax harryi  
## 298 Erimystax harryi  
## 299 Fundulus julisia  
## 300 Ptychocheilus lucius  
## 301 Leucorrhinia albifrons  
## 302 Phonotimpus talquian  
## 303 Ambystoma altamirani  
## 304 Ambystoma granulosum  
## 305 Podocarpus matudae  
## 306 Podocarpus guatemalensis  
## 307 Optioservus phaeus  
## 308 Acmispon dendroideus traskiae  
## 309 Hoplogonus bornemisszai  
## 310 Adclarkia dawsonensis  
## 311 Megascolides australis  
## 312 Austrocordulia leonardi  
## 313 Zephyrarchaea austini  
## 314 Bertmainius colonus  
## 315 Neopasiphae simplicior  
## 316 Leucopatus anophthalmus  
## 317 Anguis fragilis  
## 318 Pelophylax esculentus  
## 319 Icaricia icarioides fenderi  
## 320 Cambarus elkensis  
## 321 Cambarus elkensis  
## 322 Myotis septentrionalis  
## 323 Faxonius roberti  
## 324 Tephroseris palustris  
## 325 Juncus anceps  
## 326 Jacobaea erucifolia  
## 327 Lamprothamnium papulosom  
## 328 Emberiza hortulana  
## 329 Stenocereus quevedonis  
## 330 Crotalus catalinensis  
## 331 Saltator atriceps  
## 332 Icterus gularis  
## 333 Uma exsul  
## 334 Leavenworthia texana  
## 335 Cicindela theatina  
## 336 Bipes biporus  
## 337 Chilabothrus granti  
## 338 Pyrgulopsis morrisoni  
## 339 Eryngium sparganophyllum  
## 340 Melanerpes santacruzi  
## 341 Scutellaria ocmulgee  
## 342 Procyon pygmaeus  
## 343 Sideroxylon thornei  
## 344 Procambarus orcinus  
## 345 Alouatta palliata mexicana  
## 346 Campylorhynchus rufinucha  
## 347 Alouatta palliata mexicana  
## 348 Melanerpes aurifrons  
## 349 Parachondrostoma toxostoma  
## 350 Castilleja grisea  
## 351 Procambarus econfinae  
## 352 Ursus arctos arctos  
## 353 Castilleja tolucensis  
## 354 Aphelocoma coerulescens  
## 355 Aphelocoma coerulescens  
## 356 Aphelocoma coerulescens  
## 357 Lomatogonium carinthiacum  
## 358 Cetorhinus maximus  
## 359 Etheostoma trisella  
## 360 Cryptomastix devia  
## 361 Cryptomastix devia  
## 362 Solanum conocarpum  
## 363 Planorbella magnifica  
## 364 Pseudemys gorzugi  
## 365 Xyrauchen texanus  
## 366 Rhaphiomidas trochilus  
## 367 Plethodon hubrichti  
## 368 Notropis topeka  
## 369 Ochrosia iwasakiana  
## 370 Teucrium veronicoides var. veronicoides  
## 371 Speyeria callippe callippe  
## 372 Lespedeza leptostachya  
## 373 Perimyotis subflavus  
## 374 Carica papaya  
## 375 Elgaria panamintina  
## 376 Euphydryas anicia cloudcrofti  
## 377 Pedicularis furbishiae  
## 378 Streptanthus bracteatus  
## 379 Streptanthus bracteatus  
## 380 Bombus franklini  
## 381 Lynx lynx carpathicus  
## 382 Alouatta pigra  
## 383 Ammodramus maritimus macgillivraii  
## 384 Gopherus morafkai  
## 385 Euphilotes ancilla cryptica  
## 386 Zapus hudsonius luteus  
## 387 Euphilotes ancilla purpura  
## 388 Pinus albicaulis  
## 389 Sabia japonica  
## 390 Gambelia sila  
## 391 Enchinomastus erectocentrus acunensis  
## 392 Sedum minimum  
## 393 Colubrina asiatica  
## 394 Arenaria bryoides  
## 395 Cerastium purpusii  
## 396 Draba nivicola  
## 397 Plagiobothrys hirtus  
## 398 Ptychobranchus subtentum  
## 399 Notophthalmus perstriatus  
## 400 Notophthalmus perstriatus  
## 401 Notophthalmus perstriatus  
## 402 Notophthalmus perstriatus  
## 403 Drepanis coccinea  
## 404 Festuca livida  
## 405 Impatiens hypophylla var. microhypophylla  
## 406 Unio crassus  
## 407 Eresus sandaliatus  
## 408 Symplocos konishii  
## 409 Alosa fallax  
## 410 Saussurea yanagisawae  
## 411 Lonicera demissa var. borealis  
## 412 Prunus incisa var. bukosanensis  
## 413 Rhinolophus hipposideros  
## 414 Mimulus gemmiparus  
## 415 Pseudemys rubriventris  
## 416 Pseudemys rubriventris  
## 417 Alnus maritima  
## 418 Hydroprogne caspia  
## 419 Pelobates fuscus  
## 420 Alnus maritima maritima  
## 421 Alnus maritima georgiensis  
## 422 Alnus maritima oklahomensis  
## 423 Swertia pseudochinensis  
## 424 Primula sieboldii  
## 425 Maytenus diversifolia  
## 426 Asarum costatum  
## 427 Aster hispidus var. koidzumianus  
## 428 Isoetes asiatica  
## 429 Ornithorhynchus anatinus  
## 430 Rupicapra pyrenaica  
## 431 Turnix olivii  
## 432 Neophema chrysogaster  
## 433 Parnassius mnemosyne  
## 434 Litoria booroolongensis  
## 435 Glyphis glyphis  
## 436 Pulstilla patens  
## 437 Pulsatilla vulgaris gotlandica  
## 438 Stiphodon semoni  
## 439 Cottus petiti  
## 440 Euphydras maturna  
## 441 Tetrax tetrax tetrax  
## 442 Coenonympha hero  
## 443 Nicrophorus americanus  
## 444 Nicrophorus americanus  
## 445 Speyeria nokomis nokomis  
## 446 Delphinium variegatum kinkiense  
## 447 Rhynchospora crinipes  
## 448 Triturus cristatus  
## 449 Etheostoma chienense  
## 450 Corylopsis glabrescens  
## 451 Crepidiastrum chelidoniifolium  
## 452 Lonicera vidalii  
## 453 Chersobius boulengeri  
## 454 Chersobius signatus  
## 455 Bombina bombina  
## 456 Alisma wahlenbergii  
## 457 Bufo bufo  
## 458 Lacerta agilis  
## 459 Epidalea calamita  
## 460 Charina umbratica  
## 461 Zapus hudsonius luteus  
## 462 Lysimachia barystachys  
## 463 Hyla arborea  
## 464 Lissotriton vulgaris  
## 465 Petromyzon marinus  
## 466 Charadrius alexandrinus  
## 467 Geastrum flexuosum  
## 468 Homopus areolatus  
## 469 Homopus femoralis  
## 470 Cryptocarya chinensis  
## 471 Swertia swertopsis  
## 472 Primula hidakana var. hidakana  
## 473 Harpalus autumnalis  
## 474 Anthophora plagiata  
## 475 Anser erythropus  
## 476 Anthus campestris  
## 477 Bryoria nitidula  
## 478 Melitaea britomartis  
## 479 Dipodomys ingens  
## 480 Callicarpa shikokiana  
## 481 Acer miyabei var. miyabei  
## 482 Salix hukaoana  
## 483 Talpa aquitania  
## 484 Bryhnia scabrida  
## 485 Genista germanica  
## 486 Agonopterix bipunctosa  
## 487 Scolitantides Orion  
## 488 Harpalus flavescens  
## 489 Lonicera ramosissima var. kinkiensis  
## 490 Polystichum piceopaleaceum  
## 491 Carex aequialta  
## 492 Peperomia okinawensis  
## 493 Alectoris graeca  
## 494 Phocoena phocoena  
## 495 Puffinus puffinus  
## 496 Calotriton asper  
## 497 Luronium natans  
## 498 Chenopodium vulvaria  
## 499 Quercus glaucoides  
## 500 Quercus deserticola  
## 501 Quercus peduncularis  
## 502 Utricularia australis  
## 503 Oxytropis campestris subsp. rishiriensi  
## 504 Morus bassanus  
## 505 Phoenicopterus roseus  
## 506 Falco naumanni  
## 507 Plegadis falcinellus  
## 508 Zapornia pusilla  
## 509 Etheostoma chienense  
## 510 Hesperia dacotae  
## 511 Etheostoma maydeni  
## 512 Asplenium castaneoviride  
## 513 Phymatosorus nigrescens  
## 514 Pteris yamatensis  
## 515 Ophioglossum namegatae  
## 516 Asplenium ruta-muraria  
## 517 Pseudotsuga japonica  
## 518 Picea koyamae  
## 519 Sporobolus hancei  
## 520 Rhododendron pentaphyllum var. pentaphyllum  
## 521 Pimpinella thellungiana var. gustavohegiana  
## 522 Testudo hermanni  
## 523 Tyrrhenaria ceratina  
## 524 Anguilla anguilla  
## 525 Salmo salar  
## 526 Aeshna isoceles  
## 527 Calopteryx virgo  
## 528 Coenagrion hastulatum  
## 529 Coenagrion lunulatum  
## 530 Coenagrion pulchellum  
## 531 Gomphus flavipes  
## 532 Salix humboldtiana  
## 533 Leucorrhinia caudalis  
## 534 Leucorrhinia pectoralis  
## 535 Gomphus vulgatissimus  
## 536 Quercus hirtifolia  
## 537 Chionolaena lavandulifolia  
## 538 Rhynchospora crinipes  
## 539 Salix bonplandiana  
## 540 Heterelmis stephani  
## 541 Heterelmis stephani  
## 542 Quercus brandegeei  
## 543 Sterna dougallii  
## 544 Rana temporaria  
## 545 Rana arvalis  
## 546 Saxifraga osloënsis  
## 547 Calidris alpina schinzii  
## 548 Dicranum viride  
## 549 Myotis escalerai  
## 550 Leuciscus aspius  
## 551 Baptria tibiale  
## 552 Cerambyx cerdo  
## 553 Neophron percnopterus  
## 554 Glareola pratincola  
## 555 Pterocles alchata  
## 556 Dactylorhiza brennensis  
## 557 Dipodomys stephensi  
## 558 Popenaias popeii  
## 559 Pinus nigra salzmanii  
## 560 Senecio mairetianus  
## 561 Chalcophora mariana  
## 562 Depressaria nemolella  
## 563 Psophus stridulus  
## 564 Lepidium papilliferum  
## 565 Lepidium papilliferum  
## 566 Laterallus jamaicensis jamaicensis  
## 567 Procambarus pictus  
## 568 Clonophis kirtlandii  
## 569 Sisyrinchium sarmentosum  
## 570 Lomatium bradshawii  
## 571 Diomedea exulans  
## 572 Calocitta formosa  
## 573 Pseudophryne covacevichae  
## 574 Casuarius casuarius johnsonii  
## 575 Xiphorhynchus flavigaster  
## 576 Pedionomus torquatus  
## 577 Hypotaenidia sylvestris  
## 578 Myrmecobius fasciatus  
## 579 Carcharodon carcharias  
## 580 Neotamias minimus atristriatus  
## 581 Noturus munitus  
## 582 Pyrgulopsis thompsoni  
## 583 Pleurobema athearni  
## 584 Thalassarche cauta  
## 585 Alasmidonta varicosa  
## 586 Thalassarche chrysostoma  
## 587 Thalassarche melanophris  
## 588 Margaritifera margaritifera  
## 589 Leptogium rivulare  
## 590 Coronella austriaca  
## 591 Natrix natrix natrix  
## 592 Natrix natrix gotlandica  
## 593 Zootoca vivipara  
## 594 Vipera berus  
## 595 Ambuchanania leucobryoides  
## 596 Pyrgulopsis turbatrix  
## 597 Pherosphaera fitzgeraldii  
## 598 Leptotila verreauxi  
## 599 Cyathea exilis  
## 600 Xanthorrhoea bracteata  
## 601 Cyclarhys gujanensis  
## 602 Centaurea corymbosa  
## 603 Stenocereus pruinosus  
## 604 Styrax platanifolius texanus  
## 605 Ambystoma cingulatum  
## 606 Ambystoma cingulatum  
## 607 Etheostoma osburni  
## 608 Etheostoma osburni  
## 609 Alasmidonta varicosa  
## 610 Lepanthes eltoroensis  
## 611 Macronectes giganteus  
## 612 Macronectes halli  
## 613 Procellaria cinerea  
## 614 Phoebetria palpebrata  
## 615 Sylvilagus bachmani riparius  
## 616 Macrochelys temminckii  
## 617 Arabis georgiana  
## 618 Heterodon simus  
## 619 Eryngium proteiflorum  
## 620 Vireo atricapilla  
## 621 Bombus terricola  
## 622 Bombus terricola  
## 623 Malacothamnus clementinus  
## 624 Phacelia submutica  
## 625 Oncorhynchus clarkii virginalis  
## 626 Oncorhynchus clarkii virginalis  
## 627 Cirsium wrightii  
## 628 Notropis mekistocholas  
## 629 Notropis mekistocholas  
## 630 Eremophila alpestris strigata  
## 631 Percina rex  
## 632 Yermo xanthocephalus  
## 633 Hemphillia burringtoni  
## 634 Hemphillia burringtoni  
## 635 Castilleja levisecta  
## 636 Lupinus constancei  
## 637 Cambarus cracens  
## 638 Mustela nigripes  
## 639 Mustela nigripes  
## 640 Plestiodon egregius egregius  
## 641 Thoburnia atripinnis  
## 642 Strix occidentalis occidentalis  
## 643 Plestiodon egregius egregius  
## 644 Berberis alpina  
## 645 Cynomys leucurus  
## 646 Anaxyrus williamsi  
## 647 Texella reyesi  
## 648 Texella reyesi  
## 649 Sympetrum depressiusculum  
## 650 Apatura iris  
## 651 Cyaniris semiargus  
## 652 Erynnis tages  
## 653 Euphydryas aurinia  
## 654 Euplagia quadripunctaria  
## 655 Salmo salar  
## 656 Gadus morhua  
## 657 Hesperia comma  
## 658 Lasiommata megera  
## 659 Melitaea cinxia  
## 660 Proserpinus proserpina  
## 661 Pyronia tithonus  
## 662 Satyrium ilicis  
## 663 Barbastella barbastellus  
## 664 Myotis bechsteinii  
## 665 Myotis brandtii  
## 666 Myotis dasycneme  
## 667 Myotis daubentonii  
## 668 Myotis emarginatus  
## 669 Myotis myotis  
## 670 Myotis mystacinus  
## 671 Myotis nattereri  
## 672 Nyctalus leisleri  
## 673 Nyctalus noctula  
## 674 Pipistrellus nathusii  
## 675 Pipistrellus pipistrellus  
## 676 Pipistrellus pygmaeus  
## 677 Plecotus auritus  
## 678 Plecotus austriacus  
## 679 Rhinolophus ferrumequinum  
## 680 Eptesicus serotinus  
## 681 Pyrgus malvae  
## 682 Pinus ayacahuite  
## 683 Tapirus bairdii  
## 684 Lontra longicaudis  
## 685 Anacampsis fuscella  
## 686 Melitta tricincta  
## 687 Limosa limosa  
## 688 Euphrasia offficinalis officinalis  
## 689 Sabulina viscosa  
## 690 Eryngium maritimum  
## 691 Kinosternon vogti  
## 692 Pulsatilla vernalis  
## 693 Stauroderus scalaris  
## 694 Canthophorus impressus  
## 695 Pytho kolwensis  
## 696 Euphrasia stricta suecica  
## 697 Lycaena helle  
## 698 Egretta rufescens dickeyi  
## 699 Pseudorchis albida  
## 700 Euphydryas aurinia  
## 701 Circus pygargus  
## 702 Lampetra fluviatilis  
## 703 Ranunculus hederaceus  
## 704 Bryoria tenuis  
## 705 Myricaria germanica  
## 706 Ranunculus ophioglossifolius  
## 707 Heterodermia speciosa  
## 708 Botrychium simplex  
## 709 Pedostrangalia revestita  
## 710 Lobaria hallii  
## 711 Chirostoma estor  
## 712 Sistrurus catenatus  
## 713 Gossypium harknessii  
## 714 Gossypium trilobum  
## 715 Gossypium turneri  
## 716 Gossypium gossypioides  
## 717 Gossypium schwendimanii  
## 718 Gossypium thurberi  
## 719 Gossypium laxum  
## 720 Gossypium lobatum  
## 721 Gossypium davidsonii  
## 722 Gossypium aridum  
## 723 Castor fiber  
## 724 Cricetus cricetus  
## 725 Crocidura leucodon  
## 726 Lynx lynx  
## 727 Meles meles  
## 728 Muscardinus avellanarius  
## 729 Vespertilio murinus  
## 730 Stenobothrus stigmaticus  
## 731 Lutra lutra  
## 732 Lepus timidus  
## 733 Sorex isodon  
## 734 Sicista betulina  
## 735 Erinaceus europaeus  
## 736 Myotis bechsteinii  
## 737 Phoca vitulina  
## 738 Vulpes vulpes  
## 739 Aloe craibii  
## 740 Aloe peglerae  
## 741 Anhydrophryne hewitti  
## 742 Arthroleptella drewesii  
## 743 Arthroleptella subvoce  
## 744 Lyrurus tetrix  
## 745 Castor fiber  
## 746 Neotis ludwigii  
## 747 Xenopus gilli  
## 748 Myotis dasycneme  
## 749 Lessonia corrugata  
## 750 Ecklonia radiata  
## 751 Ecklonia radiata brevipes  
## 752 Durvillaea potatorum  
## 753 Durvillaea amatheiae  
## 754 Hormosira banksii  
## 755 Posidonia australis  
## 756 Sargassum fallax  
## 757 Scytothalia dorycarpa  
## 758 Apium repens  
## 759 Baldellia ranunculoides  
## 760 Bupleurum tenuissimum  
## 761 Carex diandra  
## 762 Carex trinervis  
## 763 Deschampsia setacea  
## 764 Eriophorum gracile  
## 765 Gentianella uliginosa  
## 766 Herminium monorchis  
## 767 Juncus capitatus  
## 768 Liparis loeselii  
## 769 Potamogeton acutifolius  
## 770 Potamogeton coloratus  
## 771 Potamogeton compressus  
## 772 Ranunculus ololeucos  
## 773 Schoenoplectus pungens  
## 774 Schoenoplectus triqueter  
## 775 Eresus sandaliatus  
## 776 Elater ferrugineus  
## 777 Cucujus cinnaberinus  
## 778 Dactylorhiza sphagnicola  
## 779 Orchis morio  
## 780 Orobanche rapum-genistae  
## 781 Platanthera bifolia  
## 782 Vertigo angustior  
## 783 Capreolus capreolus  
## 784 Conophytum regale  
## 785 Protea mucronifolia  
## 786 Protea odorata  
## 787 Cervus elaphus elaphus  
## 788 Halichoerus grypus  
## 789 Mentha pulegium  
## 790 Orchis purpurea  
## 791 Conophytum vanheerdei  
## 792 Conophytum antonii  
## 793 Scorzonera humilis  
## 794 Wahlenbergia hederacea  
## 795 Vertigo moulinsiana  
## 796 Anisus vorticulus  
## 797 Hamatocaulis vernicosus  
## 798 Unio crassus  
## 799 Lucanus cervus  
## 800 Thoburnia atripinnis  
## 801 Noturus munitus  
## 802 Toxolasma lividum  
## 803 Stratiotes aloides  
## 804 Lampetra fluviatilis  
## 805 Dolomedes fimbriatus  
## 806 Halimione pedunculata  
## 807 Cobitis taenia  
## 808 Notropis topeka  
## 809 Necturus lewisi  
## 810 Necturus lewisi  
## 811 Diphasiastrum tristachyum  
## 812 Luronium natans  
## 813 Somatochlora arctica  
## 814 Pilularia globulifera  
## 815 Lacerta agilis  
## 816 Osmoderma eremita  
## 817 Bufo calamita  
## 818 Kinosternon integrum  
## 819 Vipera berus  
## 820 Abronia deppii  
## 821 Populus nigra  
## 822 Rosalia alpina  
## 823 Iberolacerta bonnali  
## 824 Misgurnus fossilis  
## 825 Petromyzon marinus  
## 826 Phengaris alcon  
## 827 Ephippiger ephippiger  
## 828 Pelobates fuscus  
## 829 Tursiops aduncus  
## 830 Procambarus orcinus  
## 831 Thamnophis sirtalis tetrataenia  
## 832 Thamnophis sirtalis tetrataenia  
## 833 Triturus marmoratus  
## 834 Psammodromus algirus  
## 835 Hyla arborea  
## 836 Lampetra planeri  
## 837 Bombina variegata  
## 838 Lavinia exilicauda chi  
## 839 Pelophylax lessonae  
## 840 Dioon edule  
## 841 Triturus cristatus  
## 842 Salamandra salamandra  
## 843 Podarcis muralis  
## 844 Rana arvalis  
## 845 Coronella austriaca  
## 846 Halichoerus grypus  
## 847 Parnassius apollo  
## 848 Hydroprogne caspia  
## 849 Haematopus ostralegus ostralegus  
## 850 Phylloscopus ibericus  
## 851 Capra ibex  
## 852 Hipparchia semele  
## 853 Prionotropis rhodanica  
## 854 Nehalennia speciosa  
## 855 Natrix helvetica  
## 856 Oenanthe hispanica  
## 857 Rhodeus sericeus  
## 858 Cottus rhenanus  
## 859 Alytes obstetricans  
## 860 Dioon caputoi  
## 861 Hippocampus guttulatus  
## 862 Condylactis aurantiaca  
## 863 Boletus edulis  
## 864 Barbastella barbastellus  
## 865 Muscardinus avellanarius  
## 866 Rana dalmatina  
## 867 Anguis fragilis  
## 868 Coronella austriaca  
## 869 Gomphus clavatus  
## 870 Ficedula albicollis  
## 871 Zea perennis  
## 872 Zea diploperennis  
## 873 Zea mays parviglumis  
## 874 Zea mays mexicana  
## 875 Columba palumbus  
## 876 Penelope perspicax  
## 877 Crax alberti  
## 878 Hapalopsittaca fuertesi  
## 879 Oreothraupis arremonops  
## 880 Chlorochrysa nitidissima  
## 881 Ognorhynchus icterotis  
## 882 Tayassu pecari  
## 883 Myiothlypis basilica  
## 884 Hapalopsittaca amazonina  
## 885 Pauxi pauxi  
## 886 Pyrilia Pyrilia  
## 887 Bolborhynchus ferrugineifrons  
## 888 Coeligena prunellei  
## 889 Crypturellus kerriae  
## 890 Grallaria milleri  
## 891 Macroagelaius subalaris  
## 892 Pyrrhura calliptera  
## 893 Nystactes noanamae  
## 894 Penelope ortoni  
## 895 Rallus semiplumbeus  
## 896 Bangsia aureocincta  
## 897 Odontophorus atrifrons  
## 898 Colostethus thorntoni  
## 899 Dacnis hartlaubi  
## 900 Xenornis setifrons  
## 901 Atelopus famelicus  
## 902 Grallaria kaestneri  
## 903 Pyrrhura viridicata  
## 904 Arremon basilicus  
## 905 Odontophorus hyperythrus  
## 906 Oxypogon cyanolaemus  
## 907 Megascops gilesi  
## 908 Clibanornis rufipectus  
## 909 Thryophilus sernai  
## 910 Scytalopus alvarezlopezi  
## 911 Dubusia carrikeri  
## 912 Grallaria bangsi  
## 913 Oxypogon stuebelii  
## 914 Anthocephala berlepschi  
## 915 Pogonotriccus lanyoni  
## 916 Scytalopus stilesi  
## 917 Grallaria fenwickorum  
## 918 Myiotheretes pernix  
## 919 Scytalopus sanctaemartae  
## 920 Drymophila hellmayri  
## 921 Synallaxis fuscorufa  
## 922 Eriocnemis isabellae  
## 923 Cucurbita argyrosperma sororia  
## 924 Trichomycterus sandovali  
## 925 Ageneiosus pardalis  
## 926 Espeletia paipana  
## 927 Espeletia jaramilloi  
## 928 Zamia obliqua  
## 929 Magnolia wolfii  
## 930 Libidibia ebano  
## 931 Podocnemis lewyana  
## 932 Anadia antioquensis  
## 933 Lepidochelys olivacea  
## 934 Euterpe precatoria  
## 935 Quercus humboldtii  
## 936 Magnolia polyhypsophylla  
## 937 Troglodytes monticola  
## 938 Scytalopus rodriguezi  
## 939 Scytalopus canus  
## 940 Atlapetes blancae  
## 941 Odontophorus strophium  
## 942 Odontophorus dialeucos  
## 943 Eriocnemis mirabilis  
## 944 Psarocolius cassini  
## 945 Molothrus armenti  
## 946 Diglossa gloriosissima  
## 947 Ara ambiguus  
## 948 Sula granti  
## 949 Phoenicopterus ruber  
## 950 Egretta rufescens  
## 951 Sula leucogaster  
## 952 Dacnis berlepschi  
## 953 Glaucidium nubicola  
## 954 Basileuterus ignotus  
## 955 Tangara fucosa  
## 956 Micrastur plumbeus  
## 957 Anas bahamensis bahamensis  
## 958 Anas georgica  
## 959 Spizaetus isidori  
## 960 Vultur gryphus  
## 961 Crax globulosa  
## 962 Buteogallus solitarius  
## 963 Doliornis remseni  
## 964 Netta erythrophthalma  
## 965 Cephalopterus penduliger  
## 966 Cryptoleucopteryx plumbea  
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## 6 2011-2013  
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## 31 1883-2013  
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## 34 1829-2020  
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## 36 1995-2003  
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## 54 Historical (samples collected between 1870–1946) and contemporary (samples collected between1951–2014) were compared  
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## 57 Early-mid 2000s to 2016-2019.  
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## 60 1978-1998  
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## 63 1775-2008  
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## 92 1985-2002  
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## 113 2012 and 2020, Genetic structure using mtDNA  
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## 799 Cox, K., McKeown, N., Vanden Broeck, A., Van Breusegem, A., Cammaerts, R., & Thomaes, A. (2020). Genetic structure of recently fragmented suburban populations of European stag beetle. Ecology and Evolution, 10(21), 12290-12306.  
## 800 <NA>  
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## 803 <NA>  
## 804 <NA>  
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## 818 <NA>  
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## 823 <NA>  
## 824 Brys, R, Halfmaerten, D, Neyrinck, S, et al. Reliable eDNA detection and quantification of the European weather loach (Misgurnus fossilis). J Fish Biol. 2021; 98: 399– 414. https://doi.org/10.1111/jfb.14315; Brys R., Halfmaerten D., Neyrinck S., Mergeay J. & Belpaire C. 2019. Environmental DNA based monitoring of the near-extinct European Weather Loach in Flanders. Natuur.focus 18(2): 51-59; Genetic information: Mergeay et al. unpublished data  
## 825 <NA>  
## 826 Vanden Broeck A, Maes D, Kelager A, Wynhoff I, WallisDeVries MF, Nash DR, Oostermeijer JGB, Van Dyck H & Mergeay J (2017) Gene flow and effective population sizes of the butterfly Maculinea alcon inahighlyfragmented, anthropogeniclandscape.BiologicalConservation209:89-97. https://doi.org/10.1016/j.biocon.2017.02.001  
## 827 <NA>  
## 828 <NA>  
## 829 <NA>  
## 830 <NA>  
## 831 <NA>  
## 832 <NA>  
## 833 Jehle, R., Arntzen, J. W., Burke, T., Krupa, A. P., & Hödl, W. (2001). The annual number of breeding adults and the effective population size of syntopic newts (Triturus cristatus, T. marmoratus). Molecular Ecology, 10(4), 839-850. ; Jehle, R., Wilson, G. A., Arntzen, J. W., & Burke, T. (2005). Contemporary gene flow and the spatio‐temporal genetic structure of subdivided newt populations (Triturus cristatus, T. marmoratus). Journal of Evolutionary Biology, 18(3), 619-628.;  
## 834 <NA>  
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## 838 <NA>  
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## 852 De Ro A., Vanden Broeck A., Verschaeve L., Jacobs I., T’Jollyn F., Van Dyck H., Maes D. (2022). Genetische diversiteit en populatiestructuur van de heivlinder in Vlaanderen. Richtlijnen voor translocaties, genetische monitoring en een duurzaam soortbehoud. Rapporten van het Instituut voor Natuur- en Bosonderzoek jaar (4). Instituut voor Natuur- en Bosonderzoek, Brussel.\nDOI: doi.org/10.21436/inbor.71086387  
## 853 <NA>  
## 854 <NA>  
## 855 <NA>  
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## 857 <NA>  
## 858 <NA>  
## 859 Auwerx J, De Corte Z, Mergeay J, Picavet B, Speybroeck J, van Doorn L, Wagemaker N (2021). Ex situ kweek van de vroedmeesterpad (Alytes obstetricans) in Vlaanderen. Rapporten van het Instituut voor Natuur- en Bosonderzoek 2021 (32). Instituut voor Natuur- en Bosonderzoek, Brussel. DOI: doi.org/10.21436/inbor.39518999; https://purews.inbo.be/ws/portalfiles/portal/19486785/AArk\_newsletter\_50.pdf  
## 860 <NA>  
## 861 Riquet et al. 2019, https://link.springer.com/article/10.1007/s10592-019-01210-3; López et al. 2015, https://doi.org/10.1371/journal.pone.0117538; Woodall et al. 2017, doi: 10.1007/s00227-017-3274-y; Riquet et al. 2019; DOI: 10.1111/evo.13696  
## 862 <NA>  
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## 865 <NA>  
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## 869 <NA>  
## 870 Nadachowska-Brzyska, K., Dutoit, L., Smeds, L., Kardos, M., Gustafsson, L., & Ellegren, H. (2021). Genomic inference of contemporary effective population size in a large island population of collared flycatchers (Ficedula albicollis). Molecular Ecology, 30, 3965– 3973. https://doi.org/10.1111/mec.16025  
## 871 Diana María Rivera-Rodríguez, Alicia Mastretta-Yanes, Lino De la Cruz Larios, Fernando Santacruz-Ruvalcaba, José Ariel Ruiz Corral, Ana Wegier, Benjamin Hernandez, José de Jesús Sánchez González (under review) Genomic diversity and population structure of teosintes (Zea spp.) and its conservation implications; expert José de Jesús Sánchez González; expert Diana María Rivera-Rodríguez  
## 872 Diana María Rivera-Rodríguez, Alicia Mastretta-Yanes, Lino De la Cruz Larios, Fernando Santacruz-Ruvalcaba, José Ariel Ruiz Corral, Ana Wegier, Benjamin Hernandez, José de Jesús Sánchez González (under review) Genomic diversity and population structure of teosintes (Zea spp.) and its conservation implications; expert José de Jesús Sánchez González; expert Diana María Rivera-Rodríguez  
## 873 Diana María Rivera-Rodríguez, Alicia Mastretta-Yanes, Lino De la Cruz Larios, Fernando Santacruz-Ruvalcaba, José Ariel Ruiz Corral, Ana Wegier, Benjamin Hernandez, José de Jesús Sánchez González (under review) Genomic diversity and population structure of teosintes (Zea spp.) and its conservation implications; Sánchez González JdJ, Ruiz Corral JA, García GM, Ojeda GR, Larios LDlC, Holland JB, et al. (2018) Ecogeography of teosinte. PLoS ONE 13(2): e0192676. https://doi.org/10.1371/journal.pone.0192676; expert José de Jesús Sánchez González; expert Diana María Rivera-Rodríguez; expert Flavio Aragón  
## 874 Diana María Rivera-Rodríguez, Alicia Mastretta-Yanes, Lino De la Cruz Larios, Fernando Santacruz-Ruvalcaba, José Ariel Ruiz Corral, Ana Wegier, Benjamin Hernandez, José de Jesús Sánchez González (under review) Genomic diversity and population structure of teosintes (Zea spp.) and its conservation implications; Sánchez González JdJ, Ruiz Corral JA, García GM, Ojeda GR, Larios LDlC, Holland JB, et al. (2018) Ecogeography of teosinte. PLoS ONE 13(2): e0192676. https://doi.org/10.1371/journal.pone.0192676; expert José de Jesús Sánchez González; expert Diana María Rivera-Rodríguez; expert Flavio Aragón  
## 875 <NA>  
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## 900 <NA>  
## 901 <NA>  
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## 914 <NA>  
## 915 <NA>  
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## 926 <NA>  
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## 934 <NA>  
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## 946 <NA>  
## 947 <NA>  
## 948 <NA>  
## 949 <NA>  
## 950 <NA>  
## 951 <NA>  
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## 953 <NA>  
## 954 <NA>  
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## 956 <NA>  
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## 958 <NA>  
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## 960 <NA>  
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## 963 <NA>  
## 964 <NA>  
## 965 <NA>  
## 966 <NA>

Indicator 3 refers to the number (count) of taxa by country in which genetic monitoring is occurring. This is stored in the variable temp\_gen\_monitoring as a “yes/no” answer for each taxon, so to estimate the indicator, we only need to count how many said “yes”, keeping only one of the records when the taxon was multiassessed.

indicator3<-ind3\_data %>%  
 # keep only one record if the taxon was assessed more than once within the country  
 select(country\_assessment, taxon, temp\_gen\_monitoring) %>%  
 filter(!duplicated(.)) %>%  
  
 # count "yes" in tem\_gen\_monitoring by country  
 filter(temp\_gen\_monitoring=="yes") %>%  
 group\_by(country\_assessment) %>%  
 summarise(n\_taxon\_gen\_monitoring= n())

Example output:

indicator3

## # A tibble: 7 × 2  
## country\_assessment n\_taxon\_gen\_monitoring  
## <chr> <int>  
## 1 australia 10  
## 2 belgium 10  
## 3 france 7  
## 4 mexico 7  
## 5 south\_africa 5  
## 6 sweden 20  
## 7 united\_states 6

### Join indicators and metadata in a single table

It could be useful to have the estimated indicator and the metadata in a single large table.

indicators\_full<-left\_join(metadata, indicator1) %>%   
 left\_join(ind2\_data) %>%   
 left\_join(ind3\_data)

## Joining, by = c("country\_assessment", "taxonomic\_group", "taxon",  
## "scientific\_authority", "genus", "year\_assesment", "name\_assessor",  
## "email\_assessor", "common\_name", "kobo\_tabular", "X\_validation\_status",  
## "X\_uuid", "GBIF\_taxonID", "NCBI\_taxonID", "national\_taxonID",  
## "source\_national\_taxonID", "other\_populations", "time\_populations",  
## "defined\_populations", "source\_definition\_populations", "map\_populations",  
## "map\_populations\_URL", "habitat\_decline\_area", "source\_populations",  
## "popsize\_data", "ne\_pops\_exists", "nc\_pops\_exists", "ratio\_exists",  
## "species\_related", "ratio\_species\_related", "ratio\_year",  
## "source\_popsize\_ratios", "species\_comments", "realm", "IUCN\_habitat",  
## "other\_habitat", "national\_endemic", "transboundary\_type", "other\_explain",  
## "country\_proportion", "species\_range", "rarity", "occurrence\_extent",  
## "occurrence\_area", "pop\_fragmentation\_level", "species\_range\_comments",  
## "global\_IUCN", "regional\_redlist", "other\_assessment\_status",  
## "other\_assessment\_name", "source\_status\_distribution", "fecundity",  
## "semelparous\_offpring", "reproductive\_strategy", "reproductive\_strategy\_other",  
## "adult\_age\_data", "other\_reproductive\_strategy", "longevity\_max",  
## "longevity\_median", "longevity\_maturity", "longevity\_age",  
## "life\_history\_based\_on", "life\_history\_sp\_basedon", "sources\_life\_history",  
## "multiassessment")  
## Joining, by = c("country\_assessment", "taxonomic\_group", "taxon",  
## "scientific\_authority", "genus", "year\_assesment", "name\_assessor",  
## "email\_assessor", "X\_validation\_status", "X\_uuid", "other\_populations",  
## "time\_populations", "defined\_populations", "source\_definition\_populations",  
## "map\_populations", "map\_populations\_URL", "habitat\_decline\_area",  
## "source\_populations", "multiassessment")  
## Joining, by = c("country\_assessment", "taxonomic\_group", "taxon",  
## "scientific\_authority", "genus", "year\_assesment", "name\_assessor",  
## "email\_assessor", "X\_validation\_status", "X\_uuid", "multiassessment")

### Save indicators data

Save indicators data and metadata to csv files, useful for analyses outside R.

# save processed data  
write.csv(ind1\_data, "ind1\_data.csv", row.names = FALSE)  
write.csv(indicators\_full, "indicators\_full.csv", row.names = FALSE)  
write.csv(ind2\_data, "ind2\_data.csv", row.names = FALSE)  
write.csv(ind3\_data, "ind3\_data.csv", row.names = FALSE)  
write.csv(metadata, "metadata.csv", row.names = FALSE)

## Change country name to nicer labels

To have nice levels in the plots we will change the way country names are written:

# make factor  
metadata$country\_assessment<-as.factor(metadata$country\_assessment)  
indicators\_full$country\_assessment<-as.factor(indicators\_full$country\_assessment)  
ind2\_data$country\_assessment<-as.factor(ind2\_data$country\_assessment)  
ind1\_data$country\_assessment<-as.factor(ind1\_data$country\_assessment)  
indicator1$country\_assessment<-as.factor(indicator1$country\_assessment)  
  
# original levels  
levels(metadata$country\_assessment)

## [1] "australia" "belgium" "colombia" "france"   
## [5] "japan" "mexico" "south\_africa" "sweden"   
## [9] "united\_states"

# change  
levels(metadata$country\_assessment)<-c("Australia", "Belgium", "Colombia", "France", "Japan", "Mexico", "South Africa", "Sweden", "USA")  
levels(indicators\_full$country\_assessment)<-c("Australia", "Belgium", "Colombia", "France", "Japan", "Mexico", "South Africa", "Sweden", "USA")  
levels(ind1\_data$country\_assessment)<-c("Australia", "Belgium", "Colombia", "France", "Japan", "Mexico", "South Africa", "Sweden", "USA")  
levels(ind2\_data$country\_assessment)<-c("Australia", "Belgium", "Colombia", "France", "Japan", "Mexico", "South Africa", "Sweden", "USA")  
levels(indicator1$country\_assessment)<-c("Australia", "Belgium", "Colombia", "France", "Japan", "Mexico", "South Africa", "Sweden", "USA")

## Simplify combinations of methods to define populations

The methods used to define populations come from a check box question were one or more of the following categories can be selected: genetic\_clusters, geographic\_boundaries, eco\_biogeo\_proxies, adaptive\_traits, management\_units, other. As a consequence any combination of the former can be possible. Leading to the following frequency table:

table(indicators\_full$defined\_populations)

##   
## adaptive\_traits   
## 5   
## adaptive\_traits management\_units   
## 1   
## dispersal\_buffer   
## 159   
## dispersal\_buffer adaptive\_traits   
## 2   
## dispersal\_buffer eco\_biogeo\_proxies   
## 1   
## dispersal\_buffer other   
## 1   
## eco\_biogeo\_proxies   
## 44   
## eco\_biogeo\_proxies adaptive\_traits   
## 3   
## eco\_biogeo\_proxies dispersal\_buffer   
## 7   
## eco\_biogeo\_proxies management\_units   
## 3   
## eco\_biogeo\_proxies other   
## 2   
## genetic\_clusters   
## 108   
## genetic\_clusters adaptive\_traits   
## 7   
## genetic\_clusters dispersal\_buffer   
## 11   
## genetic\_clusters eco\_biogeo\_proxies   
## 26   
## genetic\_clusters eco\_biogeo\_proxies adaptive\_traits   
## 3   
## genetic\_clusters eco\_biogeo\_proxies adaptive\_traits management\_units   
## 2   
## genetic\_clusters eco\_biogeo\_proxies management\_units   
## 1   
## genetic\_clusters geographic\_boundaries   
## 70   
## genetic\_clusters geographic\_boundaries adaptive\_traits   
## 5   
## genetic\_clusters geographic\_boundaries eco\_biogeo\_proxies   
## 8   
## genetic\_clusters geographic\_boundaries eco\_biogeo\_proxies adaptive\_traits   
## 1   
## genetic\_clusters geographic\_boundaries eco\_biogeo\_proxies adaptive\_traits management\_units   
## 1   
## genetic\_clusters geographic\_boundaries eco\_biogeo\_proxies management\_units   
## 1   
## genetic\_clusters geographic\_boundaries management\_units   
## 8   
## genetic\_clusters management\_units   
## 5   
## genetic\_clusters other   
## 2   
## geographic\_boundaries   
## 274   
## geographic\_boundaries adaptive\_traits   
## 12   
## geographic\_boundaries adaptive\_traits management\_units other   
## 1   
## geographic\_boundaries dispersal\_buffer   
## 1   
## geographic\_boundaries eco\_biogeo\_proxies   
## 114   
## geographic\_boundaries eco\_biogeo\_proxies adaptive\_traits   
## 3   
## geographic\_boundaries eco\_biogeo\_proxies management\_units   
## 3   
## geographic\_boundaries eco\_biogeo\_proxies other   
## 2   
## geographic\_boundaries management\_units   
## 24   
## geographic\_boundaries other   
## 12   
## management\_units   
## 29   
## management\_units other   
## 1   
## other   
## 19

It is hard to group the above methods, so we will keep the original groups with n >=19 in the above list, and tag the combinations that appear few times as as “other\_combinations”.

Which groups have n>=19?

x<-as.data.frame(table(indicators\_full$defined\_populations)[table(indicators\_full$defined\_populations) >= 19])  
colnames(x)[1]<-"method"  
  
x

## method Freq  
## 1 dispersal\_buffer 159  
## 2 eco\_biogeo\_proxies 44  
## 3 genetic\_clusters 108  
## 4 genetic\_clusters eco\_biogeo\_proxies 26  
## 5 genetic\_clusters geographic\_boundaries 70  
## 6 geographic\_boundaries 274  
## 7 geographic\_boundaries eco\_biogeo\_proxies 114  
## 8 geographic\_boundaries management\_units 24  
## 9 management\_units 29  
## 10 other 19

We can add this new column to the metadata and indicator data:

### for indicators   
indicators\_full<- indicators\_full %>%   
 mutate(defined\_populations\_simplified = case\_when(  
 # if the method is in the list of methods n>=19 then keep it  
 defined\_populations %in% x$method ~ defined\_populations,  
 TRUE ~ "other\_combinations"))  
  
  
### for meta  
metadata<- metadata %>%   
 mutate(defined\_populations\_simplified = case\_when(  
 # if the method is in the list of methods n>=19 then keep it  
 defined\_populations %in% x$method ~ defined\_populations,  
 TRUE ~ "other\_combinations"))  
  
### for ind1 raw data  
ind1\_data<- ind1\_data %>%   
 mutate(defined\_populations\_simplified = case\_when(  
 # if the method is in the list of methods n>=19 then keep it  
 defined\_populations %in% x$method ~ defined\_populations,  
 TRUE ~ "other\_combinations"))

Check n for simplified methods:

table(indicators\_full$defined\_populations\_simplified)

##   
## dispersal\_buffer   
## 159   
## eco\_biogeo\_proxies   
## 44   
## genetic\_clusters   
## 108   
## genetic\_clusters eco\_biogeo\_proxies   
## 26   
## genetic\_clusters geographic\_boundaries   
## 70   
## geographic\_boundaries   
## 274   
## geographic\_boundaries eco\_biogeo\_proxies   
## 114   
## geographic\_boundaries management\_units   
## 24   
## management\_units   
## 29   
## other   
## 19   
## other\_combinations   
## 115

Table of equivalences:

indicators\_full %>%   
 select(defined\_populations, defined\_populations\_simplified) %>%   
 filter(!duplicated(defined\_populations))

## defined\_populations  
## 1 genetic\_clusters  
## 2 genetic\_clusters geographic\_boundaries  
## 3 geographic\_boundaries  
## 4 genetic\_clusters eco\_biogeo\_proxies  
## 5 geographic\_boundaries management\_units  
## 6 genetic\_clusters geographic\_boundaries management\_units  
## 7 genetic\_clusters other  
## 8 genetic\_clusters geographic\_boundaries eco\_biogeo\_proxies management\_units  
## 9 eco\_biogeo\_proxies  
## 10 geographic\_boundaries other  
## 11 genetic\_clusters geographic\_boundaries eco\_biogeo\_proxies  
## 12 dispersal\_buffer  
## 13 management\_units  
## 14 geographic\_boundaries eco\_biogeo\_proxies  
## 15 genetic\_clusters adaptive\_traits  
## 16 other  
## 17 geographic\_boundaries eco\_biogeo\_proxies adaptive\_traits  
## 18 genetic\_clusters geographic\_boundaries adaptive\_traits  
## 19 adaptive\_traits  
## 20 genetic\_clusters eco\_biogeo\_proxies adaptive\_traits  
## 21 genetic\_clusters geographic\_boundaries eco\_biogeo\_proxies adaptive\_traits management\_units  
## 22 genetic\_clusters management\_units  
## 23 geographic\_boundaries eco\_biogeo\_proxies other  
## 24 genetic\_clusters dispersal\_buffer  
## 25 eco\_biogeo\_proxies other  
## 26 eco\_biogeo\_proxies management\_units  
## 27 genetic\_clusters geographic\_boundaries eco\_biogeo\_proxies adaptive\_traits  
## 28 geographic\_boundaries eco\_biogeo\_proxies management\_units  
## 29 eco\_biogeo\_proxies adaptive\_traits  
## 30 geographic\_boundaries adaptive\_traits  
## 31 genetic\_clusters eco\_biogeo\_proxies adaptive\_traits management\_units  
## 32 genetic\_clusters eco\_biogeo\_proxies management\_units  
## 33 management\_units other  
## 34 geographic\_boundaries adaptive\_traits management\_units other  
## 35 dispersal\_buffer other  
## 36 dispersal\_buffer adaptive\_traits  
## 37 adaptive\_traits management\_units  
## 38 dispersal\_buffer eco\_biogeo\_proxies  
## 39 eco\_biogeo\_proxies dispersal\_buffer  
## 40 geographic\_boundaries dispersal\_buffer  
## defined\_populations\_simplified  
## 1 genetic\_clusters  
## 2 genetic\_clusters geographic\_boundaries  
## 3 geographic\_boundaries  
## 4 genetic\_clusters eco\_biogeo\_proxies  
## 5 geographic\_boundaries management\_units  
## 6 other\_combinations  
## 7 other\_combinations  
## 8 other\_combinations  
## 9 eco\_biogeo\_proxies  
## 10 other\_combinations  
## 11 other\_combinations  
## 12 dispersal\_buffer  
## 13 management\_units  
## 14 geographic\_boundaries eco\_biogeo\_proxies  
## 15 other\_combinations  
## 16 other  
## 17 other\_combinations  
## 18 other\_combinations  
## 19 other\_combinations  
## 20 other\_combinations  
## 21 other\_combinations  
## 22 other\_combinations  
## 23 other\_combinations  
## 24 other\_combinations  
## 25 other\_combinations  
## 26 other\_combinations  
## 27 other\_combinations  
## 28 other\_combinations  
## 29 other\_combinations  
## 30 other\_combinations  
## 31 other\_combinations  
## 32 other\_combinations  
## 33 other\_combinations  
## 34 other\_combinations  
## 35 other\_combinations  
## 36 other\_combinations  
## 37 other\_combinations  
## 38 other\_combinations  
## 39 other\_combinations  
## 40 other\_combinations

Create nicer names for ploting

# original method names  
levels(as.factor(indicators\_full$defined\_populations\_simplified))

## [1] "dispersal\_buffer"   
## [2] "eco\_biogeo\_proxies"   
## [3] "genetic\_clusters"   
## [4] "genetic\_clusters eco\_biogeo\_proxies"   
## [5] "genetic\_clusters geographic\_boundaries"   
## [6] "geographic\_boundaries"   
## [7] "geographic\_boundaries eco\_biogeo\_proxies"  
## [8] "geographic\_boundaries management\_units"   
## [9] "management\_units"   
## [10] "other"   
## [11] "other\_combinations"

# nicer names  
nice\_names <- c("dispersal buffer",  
 "eco- biogeographic proxies",  
 "genetic clusters",  
 "genetic clusters & eco- biogeographic proxies",  
 "genetic clusters & geographic boundaries",  
 "geographic boundaries",  
 "geographic boundaries & eco- biogeographic proxies",  
 "geographic boundaries & management units",  
 "management units",  
 "other",   
 "other combinations")  
  
  
### add them  
indicators\_full$defined\_populations\_nicenames <- factor(  
 indicators\_full$defined\_populations\_simplified,  
 levels = levels(as.factor(indicators\_full$defined\_populations\_simplified)),  
 labels = nice\_names)  
  
# metadata  
metadata$defined\_populations\_nicenames <- factor(  
 metadata$defined\_populations\_simplified,  
 levels = levels(as.factor(metadata$defined\_populations\_simplified)),  
 labels = nice\_names)  
  
#check names match  
select(metadata, defined\_populations\_nicenames, defined\_populations\_simplified)

## defined\_populations\_nicenames  
## 1 genetic clusters  
## 2 genetic clusters & geographic boundaries  
## 3 geographic boundaries  
## 4 genetic clusters  
## 5 genetic clusters  
## 6 genetic clusters & eco- biogeographic proxies  
## 7 geographic boundaries & management units  
## 8 other combinations  
## 9 other combinations  
## 10 other combinations  
## 11 other combinations  
## 12 genetic clusters & geographic boundaries  
## 13 geographic boundaries  
## 14 genetic clusters  
## 15 genetic clusters & geographic boundaries  
## 16 geographic boundaries  
## 17 eco- biogeographic proxies  
## 18 eco- biogeographic proxies  
## 19 other combinations  
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## 783 genetic\_clusters geographic\_boundaries  
## 784 geographic\_boundaries  
## 785 geographic\_boundaries  
## 786 geographic\_boundaries  
## 787 other\_combinations  
## 788 eco\_biogeo\_proxies  
## 789 dispersal\_buffer  
## 790 dispersal\_buffer  
## 791 geographic\_boundaries  
## 792 geographic\_boundaries  
## 793 dispersal\_buffer  
## 794 dispersal\_buffer  
## 795 dispersal\_buffer  
## 796 dispersal\_buffer  
## 797 dispersal\_buffer  
## 798 other\_combinations  
## 799 other\_combinations  
## 800 geographic\_boundaries management\_units  
## 801 genetic\_clusters eco\_biogeo\_proxies  
## 802 management\_units  
## 803 dispersal\_buffer  
## 804 other\_combinations  
## 805 dispersal\_buffer  
## 806 dispersal\_buffer  
## 807 other\_combinations  
## 808 geographic\_boundaries eco\_biogeo\_proxies  
## 809 management\_units  
## 810 geographic\_boundaries  
## 811 dispersal\_buffer  
## 812 dispersal\_buffer  
## 813 dispersal\_buffer  
## 814 dispersal\_buffer  
## 815 dispersal\_buffer  
## 816 dispersal\_buffer  
## 817 other\_combinations  
## 818 geographic\_boundaries  
## 819 other\_combinations  
## 820 geographic\_boundaries eco\_biogeo\_proxies  
## 821 genetic\_clusters geographic\_boundaries  
## 822 geographic\_boundaries  
## 823 genetic\_clusters geographic\_boundaries  
## 824 genetic\_clusters  
## 825 dispersal\_buffer  
## 826 other\_combinations  
## 827 dispersal\_buffer  
## 828 dispersal\_buffer  
## 829 genetic\_clusters eco\_biogeo\_proxies  
## 830 genetic\_clusters  
## 831 geographic\_boundaries eco\_biogeo\_proxies  
## 832 geographic\_boundaries eco\_biogeo\_proxies  
## 833 other\_combinations  
## 834 geographic\_boundaries  
## 835 other\_combinations  
## 836 other\_combinations  
## 837 dispersal\_buffer  
## 838 eco\_biogeo\_proxies  
## 839 dispersal\_buffer  
## 840 other\_combinations  
## 841 other\_combinations  
## 842 dispersal\_buffer  
## 843 dispersal\_buffer  
## 844 other\_combinations  
## 845 dispersal\_buffer  
## 846 geographic\_boundaries eco\_biogeo\_proxies  
## 847 geographic\_boundaries  
## 848 management\_units  
## 849 geographic\_boundaries  
## 850 other\_combinations  
## 851 geographic\_boundaries management\_units  
## 852 other\_combinations  
## 853 geographic\_boundaries  
## 854 geographic\_boundaries  
## 855 dispersal\_buffer  
## 856 geographic\_boundaries  
## 857 other\_combinations  
## 858 other\_combinations  
## 859 dispersal\_buffer  
## 860 genetic\_clusters  
## 861 genetic\_clusters geographic\_boundaries  
## 862 other\_combinations  
## 863 other\_combinations  
## 864 eco\_biogeo\_proxies  
## 865 dispersal\_buffer  
## 866 dispersal\_buffer  
## 867 other  
## 868 dispersal\_buffer  
## 869 geographic\_boundaries  
## 870 geographic\_boundaries  
## 871 genetic\_clusters  
## 872 genetic\_clusters  
## 873 genetic\_clusters geographic\_boundaries  
## 874 other\_combinations  
## 875 genetic\_clusters eco\_biogeo\_proxies  
## 876 geographic\_boundaries eco\_biogeo\_proxies  
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## 911 geographic\_boundaries eco\_biogeo\_proxies  
## 912 geographic\_boundaries eco\_biogeo\_proxies  
## 913 geographic\_boundaries eco\_biogeo\_proxies  
## 914 geographic\_boundaries eco\_biogeo\_proxies  
## 915 geographic\_boundaries eco\_biogeo\_proxies  
## 916 other\_combinations  
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## 923 geographic\_boundaries  
## 924 geographic\_boundaries eco\_biogeo\_proxies  
## 925 geographic\_boundaries eco\_biogeo\_proxies  
## 926 geographic\_boundaries eco\_biogeo\_proxies  
## 927 geographic\_boundaries eco\_biogeo\_proxies  
## 928 geographic\_boundaries eco\_biogeo\_proxies  
## 929 geographic\_boundaries eco\_biogeo\_proxies  
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## 931 geographic\_boundaries eco\_biogeo\_proxies  
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## 941 geographic\_boundaries eco\_biogeo\_proxies  
## 942 other\_combinations  
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## 944 geographic\_boundaries eco\_biogeo\_proxies  
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## 946 geographic\_boundaries eco\_biogeo\_proxies  
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## 950 geographic\_boundaries eco\_biogeo\_proxies  
## 951 geographic\_boundaries eco\_biogeo\_proxies  
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## 962 geographic\_boundaries eco\_biogeo\_proxies  
## 963 geographic\_boundaries eco\_biogeo\_proxies  
## 964 geographic\_boundaries eco\_biogeo\_proxies  
## 965 genetic\_clusters geographic\_boundaries  
## 966 geographic\_boundaries eco\_biogeo\_proxies

levels(indicators\_full$defined\_populations\_nicenames)

## [1] "dispersal buffer"   
## [2] "eco- biogeographic proxies"   
## [3] "genetic clusters"   
## [4] "genetic clusters & eco- biogeographic proxies"   
## [5] "genetic clusters & geographic boundaries"   
## [6] "geographic boundaries"   
## [7] "geographic boundaries & eco- biogeographic proxies"  
## [8] "geographic boundaries & management units"   
## [9] "management units"   
## [10] "other"   
## [11] "other combinations"

## Averaging multiassessments (alternative assessments)

Some taxa were assessed twice or more times, for example to account for uncertainty on how to divide populations. This information is stored in variable multiassessment of the metadata (created by get\_metadata()). An example of taxa with multiple assessments:

metadata %>%  
filter(multiassessment=="multiassessment") %>%  
 select(taxonomic\_group, taxon, country\_assessment, multiassessment) %>%  
 arrange(taxon, country\_assessment) %>%  
 head()

## taxonomic\_group taxon country\_assessment multiassessment  
## 1 invertebrate Alasmidonta varicosa USA multiassessment  
## 2 invertebrate Alasmidonta varicosa USA multiassessment  
## 3 mammal Alouatta palliata mexicana Mexico multiassessment  
## 4 mammal Alouatta palliata mexicana Mexico multiassessment  
## 5 amphibian Ambystoma cingulatum USA multiassessment  
## 6 amphibian Ambystoma cingulatum USA multiassessment

Alternative assessments allow to account for uncertainty in the number of populations or the size of them. We can examine how the indicators value species by species as done elsewhere in these analyses (see below “Values for indicator 1 and 2 for multiassessed species), but to examine global trends, some of the figures below use the average. **The averages are stored in a different column, labeled indicator[1 or 2]\_mean.**

indicators\_averaged<-indicators\_full %>%  
 # group desired multiassessments  
 group\_by(country\_assessment, multiassessment, taxon) %>%  
 # estimate means  
 mutate(indicator1\_mean=mean(indicator1, na.rm=TRUE)) %>%  
 mutate(indicator2\_mean=mean(indicator2, na.rm=TRUE)) %>%  
 # change NaN for NA (needed due to the NAs and 0s in the dataset)  
 mutate\_all(~ifelse(is.nan(.), NA, .))

## `mutate\_all()` ignored the following grouping variables:  
## • Columns `country\_assessment`, `multiassessment`, `taxon`  
## ℹ Use `mutate\_at(df, vars(-group\_cols()), myoperation)` to silence the message.

Examples of how this looks to check it was done properly. For indicator 1:

indicators\_averaged %>%  
 filter(taxon == "Barbastella barbastellus") %>%  
 select(taxon, country\_assessment, multiassessment, indicator1, indicator1\_mean)

## # A tibble: 3 × 5  
## # Groups: country\_assessment, multiassessment, taxon [2]  
## taxon country\_assessm… multiassessment indicator1 indicator1\_mean  
## <chr> <fct> <chr> <dbl> <dbl>  
## 1 Barbastella barba… Sweden multiassessment NA 0.167  
## 2 Barbastella barba… Belgium single\_assessm… 0 0   
## 3 Barbastella barba… Sweden multiassessment 0.167 0.167

indicators\_averaged %>%  
 filter(taxon == "Rana dalmatina") %>%  
 select(taxon, country\_assessment, multiassessment, indicator1, indicator1\_mean)

## # A tibble: 2 × 5  
## # Groups: country\_assessment, multiassessment, taxon [1]  
## taxon country\_assessment multiassessment indicator1 indicator1\_mean  
## <chr> <fct> <chr> <dbl> <dbl>  
## 1 Rana dalmatina Sweden multiassessment 0.375 0.562  
## 2 Rana dalmatina Sweden multiassessment 0.75 0.562

indicators\_averaged %>%  
 filter(taxon == "Ambystoma cingulatum") %>%  
 select(taxon, country\_assessment, multiassessment, indicator1, indicator1\_mean)

## # A tibble: 4 × 5  
## # Groups: country\_assessment, multiassessment, taxon [1]  
## taxon country\_assessm… multiassessment indicator1 indicator1\_mean  
## <chr> <fct> <chr> <dbl> <dbl>  
## 1 Ambystoma cingula… USA multiassessment NA NA  
## 2 Ambystoma cingula… USA multiassessment NA NA  
## 3 Ambystoma cingula… USA multiassessment NA NA  
## 4 Ambystoma cingula… USA multiassessment NA NA

For Proportion of maintained populations (indicator):

indicators\_averaged %>%  
 filter(taxon == "Ambystoma cingulatum") %>%  
 select(taxon, country\_assessment, multiassessment, indicator2, indicator2\_mean)

## # A tibble: 4 × 5  
## # Groups: country\_assessment, multiassessment, taxon [1]  
## taxon country\_assessm… multiassessment indicator2 indicator2\_mean  
## <chr> <fct> <chr> <dbl> <dbl>  
## 1 Ambystoma cingula… USA multiassessment 0.36 0.68  
## 2 Ambystoma cingula… USA multiassessment 0.36 0.68  
## 3 Ambystoma cingula… USA multiassessment 1 0.68  
## 4 Ambystoma cingula… USA multiassessment 1 0.68

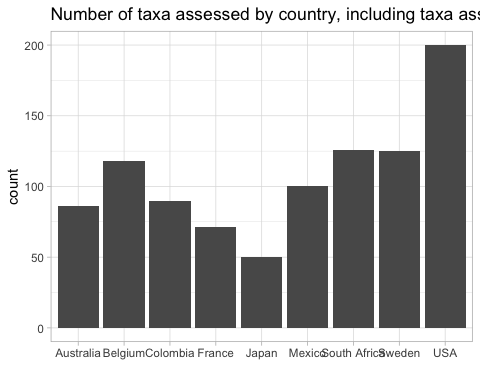
Because we will use the averages to show a single value for multiasssessed taxa, we can keep only the first record for multiassessed taxa.

indicators\_averaged\_one<-indicators\_averaged[!duplicated(cbind(indicators\_averaged$taxon, indicators\_averaged$country\_assessment)), ]

## General description of records and taxa assessed by country

Records by country, including taxa assessed more than once (see below for details on this)

ggplot(metadata, aes(x=country\_assessment)) +   
 geom\_bar(stat = "count") +  
 xlab("") +  
 ggtitle("Number of taxa assessed by country, including taxa assed more than once") +  
 theme\_light()



To explore what kind of taxa countries assessed regardless of if they assessed them once or more, we are going to use the subset indicators\_averaged\_one, were we averaged the indicators and kept only 1 record per assessment.

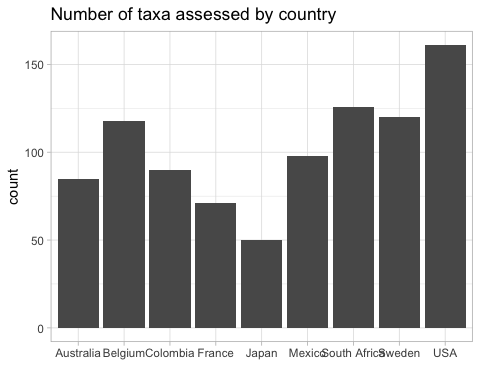
How many taxa were assessed (i.e. counting only once taxa that were assessed multiple times)?

# how many?  
nrow(indicators\_averaged\_one)

## [1] 919

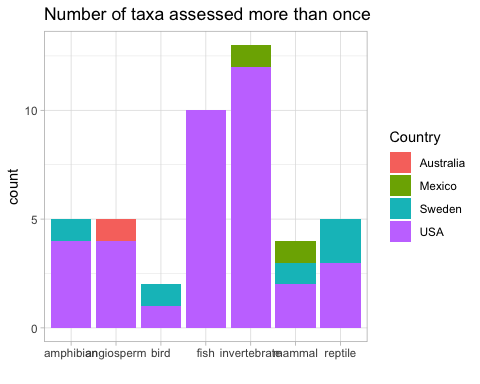
Plot taxa assessed excluding duplicates, i.e. the real number of taxa assessed:

p1<-ggplot(indicators\_averaged\_one, aes(x=country\_assessment)) +   
 geom\_bar(stat = "count") +  
 xlab("") +  
 ggtitle("Number of taxa assessed by country") +  
 theme\_light()  
p1



Of which countries and taxonomic groups are the taxa that were assessed more than once?

p2<- indicators\_averaged\_one %>% # we use the \_unique dataset so that multiassesed records are counted only once  
 filter(multiassessment=="multiassessment") %>%  
  
ggplot(aes(x=taxonomic\_group, fill=country\_assessment)) +   
 geom\_bar(stat = "count") +  
 theme(axis.text.x = element\_text(angle = 45)) +  
 labs(fill="Country") +  
 xlab("") +  
 ggtitle("Number of taxa assessed more than once") +  
 theme\_light()  
  
p2



### Heatmap of the taxa assessed by country (counting multiassessments only once)

We aimed to represent different taxonomic groups within animals (amphibians, birds, fishes, invertebrates, mammals and reptiles), plants (angiosperms, bryophytes, gymnosperms and pteridophytes), fungi and others (e.g. lichens). Order levels to represent those categories:

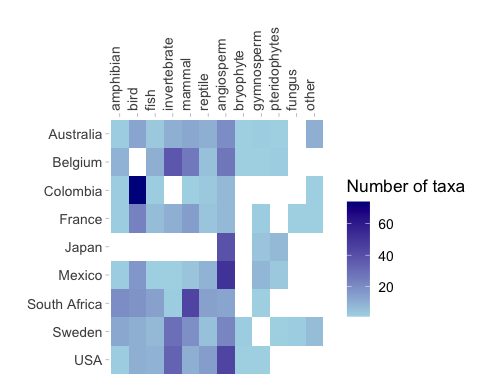
indicators\_averaged\_one$taxonomic\_group<- factor(indicators\_averaged\_one$taxonomic\_group,  
 levels = c("amphibian", "bird", "fish", "invertebrate", "mammal", "reptile", "angiosperm", "bryophyte", "gymnosperm", "pteridophytes", "fungus", "other"))

Make a heatmap

## Agregate data to get counts   
  
agg\_data <- indicators\_averaged\_one %>% # we use the \_unique dataset so that multiassesed records are counted only once  
 filter(multiassessment!="multiassessment") %>%  
 group\_by(country\_assessment, taxonomic\_group) %>%  
 summarize(count = n())

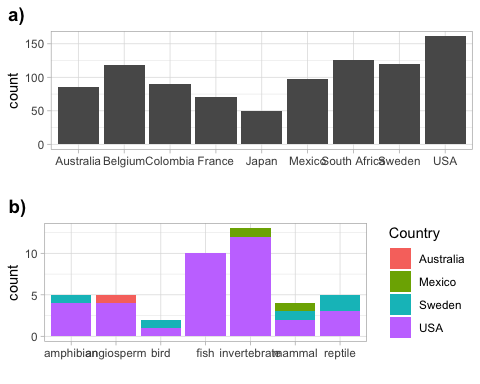
## `summarise()` has grouped output by 'country\_assessment'. You can override  
## using the `.groups` argument.

# country names in desired order  
agg\_data$country\_assessment <- factor(agg\_data$country\_assessment,   
 levels = rev(levels(agg\_data$country\_assessment)))  
   
   
## Create a heat map  
p\_heat<- ggplot(agg\_data, aes(x = taxonomic\_group, y = country\_assessment, fill = count)) +   
 geom\_tile() +   
 scale\_fill\_gradient(low = "lightblue", high = "darkblue") + # Adjust color scale as needed  
 labs(x = "",  
 y = "",  
 fill = "Number of taxa"  
 ) +   
 scale\_x\_discrete(position = "top") +  
 theme\_light() +   
 theme(panel.border = element\_blank(), axis.text.x = element\_text(angle = 90, hjust = 0),  
 legend.position = "right", text = element\_text(size = 13),  
 panel.grid.major = element\_blank(), panel.grid.minor = element\_blank(), # remove background  
 )  
p\_heat



### Supplementary Figure: Number of species and multiassessed species per country

plot\_grid(p1 + ggtitle(""),  
 p2 + ggtitle(""), ncol = 1, labels = c("a)", "b)"))



## Population size data (Has Nc or Ne? what type of Nc?)

Transform NAs to insuff\_data\_species, since effectively they are the same:

# check NAs  
summary(as.factor(metadata$popsize\_data))

## data\_for\_species insuff\_data\_species yes NA's   
## 130 216 613 7

# Replace NA to insuff\_data\_species  
metadata <-metadata %>%   
 mutate(popsize\_data=replace\_na(popsize\_data, "insuff\_data\_species"))  
  
# check  
summary(as.factor(metadata$popsize\_data))

## data\_for\_species insuff\_data\_species yes   
## 130 223 613

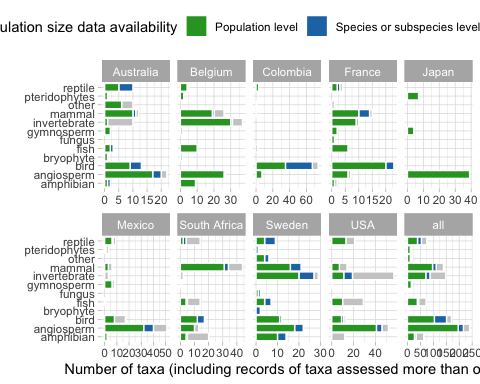
Re-order popsize\_data to have inssuficient data at the end in the plots

metadata$popsize\_data<-factor(metadata$popsize\_data,   
 levels= c("insuff\_data\_species", "data\_for\_species","yes"))

### Supplementary Figure: Population size data availability by country

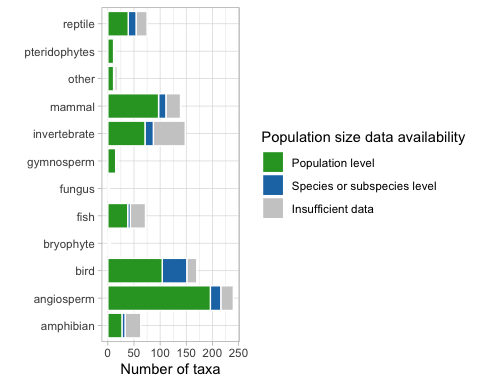
Countries have population size data (Nc or Ne) regardless of the taxonomic group. The last panel includes the entire dataset:

## Duplicate data with an additional column "facet"  
  
df<-CreateAllFacet(metadata, "country\_assessment")  
  
# order with "all" as last  
df$facet <- factor(df$facet, levels=c("Australia", "Belgium", "Colombia", "France", "Japan", "Mexico", "South Africa", "Sweden", "USA", "all"))  
  
# Plot  
ggplot(df, aes(x=taxonomic\_group, fill=popsize\_data)) +   
 geom\_bar(stat = "count", color="white") +  
 coord\_flip() +  
 facet\_wrap(~facet, ncol = 5, scales="free\_x") +  
 scale\_fill\_manual(values=c("#2ca02c", "#1f77b4", "grey80"),  
 breaks=c("yes", "data\_for\_species", "insuff\_data\_species"),  
 labels=c("Population level", "Species or subspecies level", "Insufficient data")) +   
 labs(fill="Population size data availability",  
 x="",  
 y="Number of taxa (including records of taxa assessed more than once)") +  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="top")



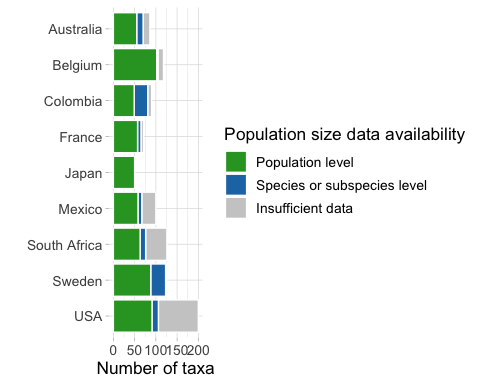
Population size data availability in the entire dataset, by taxon group:

ggplot(metadata, aes(x=taxonomic\_group, fill=popsize\_data)) +   
 geom\_bar(stat = "count", color="white") +  
 coord\_flip() +  
 scale\_fill\_manual(values=c("#2ca02c", "#1f77b4", "grey80"),  
 breaks=c("yes", "data\_for\_species", "insuff\_data\_species"),  
 labels=c("Population level", "Species or subspecies level", "Insufficient data")) +   
 labs(fill="Population size data availability",  
 x="",  
 y="Number of taxa") +  
 theme\_light() +  
 theme(legend.position="right")



Population size data availability in the entire dataset, by taxon country:

p.popsize<-ggplot(metadata, aes(x=country\_assessment, fill=popsize\_data)) +   
 geom\_bar(stat = "count", color="white") +  
 coord\_flip() +   
 scale\_x\_discrete(limits=rev) +  
 scale\_fill\_manual(values=c("#2ca02c", "#1f77b4", "grey80"),  
 breaks=c("yes", "data\_for\_species", "insuff\_data\_species"),  
 labels=c("Population level", "Species or subspecies level", "Insufficient data")) +   
 labs(fill="Population size data availability",  
 x="",  
 y="Number of taxa") +  
 theme\_light() +  
 theme(text = element\_text(size = 13), panel.border = element\_blank(), legend.position="right")  
p.popsize



Species level yes/no table with percentages

#total n  
nrow(indicators\_full)

## [1] 982

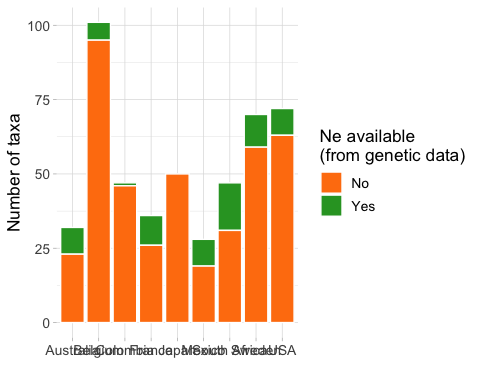
# table  
df<- indicators\_full %>%  
 group\_by(popsize\_data) %>%  
 summarise(n=n(),  
 percentage = (n / nrow(metadata)) \* 100)  
   
kable(df, digits = 0)

| popsize\_data | n | percentage |
| --- | --- | --- |
| data\_for\_species | 131 | 14 |
| insuff\_data\_species | 230 | 24 |
| yes | 614 | 64 |
| NA | 7 | 1 |

### Ne data yes or not? & Type of Nc data

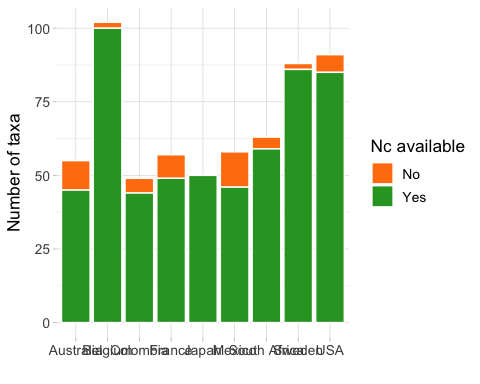
Ne available by taxa? (species level)

p1<- metadata %>%   
 filter(!is.na(ne\_pops\_exists)) %>%   
 filter(ne\_pops\_exists!="other\_genetic\_info") %>%  
 ggplot(aes(x=country\_assessment, fill=ne\_pops\_exists)) +   
 geom\_bar(color="white") +  
scale\_fill\_manual(labels=c("No", "Yes"),  
 breaks=c("no\_genetic\_data", "ne\_available"),  
 values=c("#ff7f0e", "#2ca02c")) +  
xlab("") +  
ylab("Number of taxa") +  
labs(fill="Ne available \n(from genetic data)") +  
theme\_light() +  
theme(text = element\_text(size = 13), legend.position = "right", panel.border = element\_blank())  
  
p1



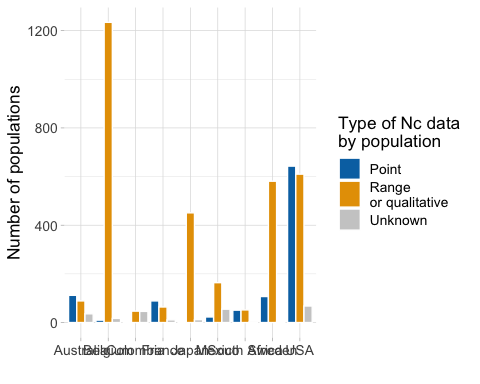
Nc data available by taxa? (species level)

p2<-metadata %>%  
 filter(!is.na(nc\_pops\_exists)) %>%  
 ggplot(aes(x=country\_assessment, fill=nc\_pops\_exists)) +  
 geom\_bar(color="white") +  
scale\_fill\_manual(labels=c("No", "Yes"),  
 breaks=c("no", "yes"),  
 values=c("#ff7f0e", "#2ca02c")) +  
 labs(fill="Nc available") +  
 xlab("") +  
 ylab("Number of taxa") +  
 theme\_light() +  
 theme(text = element\_text(size = 13), legend.position = "right", panel.border = element\_blank())  
p2



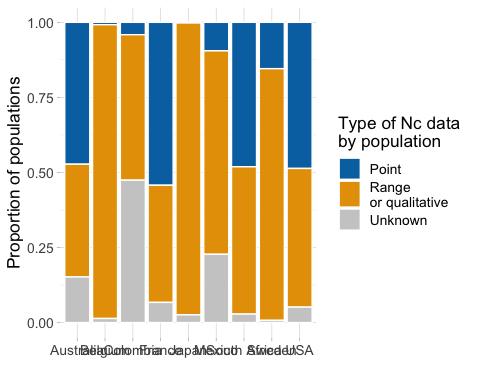
What kind of Nc data? (dodge bars) This is at population level.

ind1\_data %>%  
 filter(!is.na(NcType)) %>%  
 ggplot(aes(x=country\_assessment, fill=NcType))+  
 geom\_bar(position = "dodge", color="white") +  
 scale\_fill\_manual(labels=c("Point", "Range \nor qualitative", "Unknown"),  
 breaks=c("Nc\_point", "Nc\_range", "unknown"),  
 values=c("#0072B2", "#E69F00", "grey80")) +  
 xlab("") +  
 ylab("Number of populations") +  
 labs(fill="Type of Nc data \nby population") +  
 theme\_light() +  
 theme(text = element\_text(size = 13), legend.position = "right", panel.border = element\_blank())



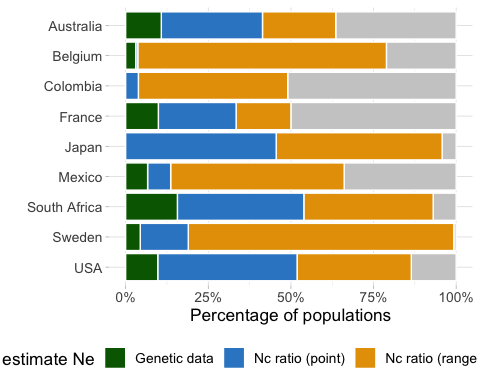
What kind of Nc data? (fill bars). This is at population level.

p3<-ind1\_data %>%  
 filter(!is.na(NcType)) %>%  
 ggplot(aes(x=country\_assessment, fill=NcType))+  
 geom\_bar(position = "fill", color="white") +  
 scale\_fill\_manual(labels=c("Point", "Range \nor qualitative", "Unknown"),  
 breaks=c("Nc\_point", "Nc\_range", "unknown"),  
 values=c("#0072B2", "#E69F00", "grey80")) +  
 xlab("") +  
 ylab("Proportion of populations") +  
 labs(fill="Type of Nc data \nby population") +  
 theme\_light() +  
 theme(text = element\_text(size = 13), legend.position = "right", panel.border = element\_blank())  
p3



Data availability at the population level cosidering Ne and Nc combined. This plot shows where data came from for the Ne value used for estimating the indicator.

p4<-ind1\_data %>%  
 # NA as a category  
 mutate(Ne\_calculated\_from = replace\_na(Ne\_calculated\_from, "NA")) %>%  
 # reorder to have NA at the end (here at the start because we will use coord\_flip below)  
 mutate(Ne\_calculated\_from = factor(Ne\_calculated\_from, levels=c("NA", "NcRange ratio", "NcPoint ratio", "genetic data"))) %>%  
 ggplot(aes(x=country\_assessment, fill=Ne\_calculated\_from))+  
 geom\_bar(position = "fill", color="white") +  
 scale\_fill\_manual(labels=c("Genetic data", "Nc ratio (point)", "Nc ratio (range or qualitative)", "Missing data"),  
 breaks=c("genetic data", "NcPoint ratio", "NcRange ratio", "NA"),  
 values=c("darkgreen", "#3388CC", "#E69F00", "grey80")) +  
 xlab("") +  
 scale\_x\_discrete(limits=rev) +   
 ylab("Percentage of populations") +  
 scale\_y\_continuous(labels = scales::percent) + # show axis in % instead of decimal  
 labs(fill="Data used to estimate Ne") +  
 theme\_light() +  
 coord\_flip() +  
 theme(text = element\_text(size = 13), legend.position = "bottom", panel.border = element\_blank())  
p4



### Supplementary Figure: Ne and Nc data availabiltiy by taxa

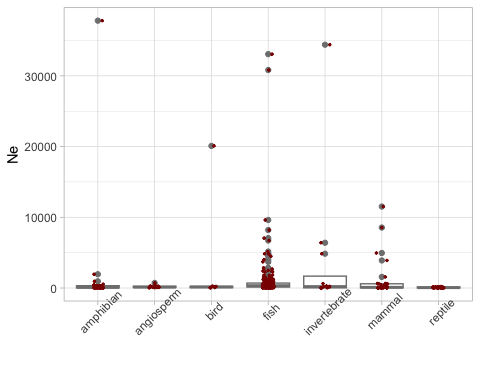
plot\_grid(p1 + theme(legend.justification = c(0,.5)), # legend.justification is used to aling legends  
 p2 + theme(legend.justification = c(0,.5)),  
 ncol=1, rel\_widths = c(1,1,1,1), align = "v", labels=c("a)", "b)"), vjust = .7)



## Range of values for Ne and Nc data

Range of Ne values by taxonomic group, without possible outliers (Ne > 100000)

ind1\_data %>%  
 filter(Ne < 100000) %>%  
 filter(!is.na(Ne)) %>%  
   
 ggplot(aes(x=taxonomic\_group, y=Ne)) +  
 geom\_boxplot(color="grey50") +  
 geom\_jitter(size=.5, width = 0.1, color="darkred") +  
 xlab("") +  
 theme\_light() +  
 theme(axis.text.x = element\_text(angle = 45))



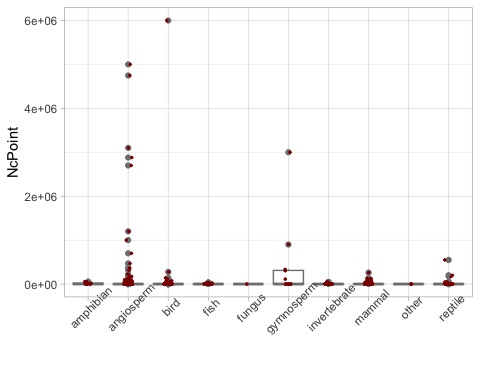
Check outliers

ind1\_data %>%   
 filter(Ne > 100000) %>%  
 select(country\_assessment, name\_assessor, taxon, taxonomic\_group, Ne, NeLower, NeUpper, multiassessment, population)

## # A tibble: 2 × 9  
## country\_assessment name\_assessor taxon taxonomic\_group Ne NeLower NeUpper  
## <fct> <chr> <chr> <chr> <dbl> <dbl> <dbl>  
## 1 Mexico Alexander Lla… Icte… bird 125500 122000 128000  
## 2 Mexico Alexander Lla… Icte… bird 331400 324000 338000  
## # … with 2 more variables: multiassessment <chr>, population <chr>

Range of Nc values (actual data point provided) by taxonomic group. Without possible outliers.

ind1\_data %>%  
 filter(!is.na(NcPoint)) %>%  
 filter(NcPoint < 10000000) %>%  
   
 ggplot(aes(x=taxonomic\_group, y=NcPoint)) +  
 geom\_boxplot(color="grey50") +  
 geom\_jitter(size=.5, width = 0.1, color="darkred") +  
 xlab("") +  
 theme\_light() +  
 theme(axis.text.x = element\_text(angle = 45))



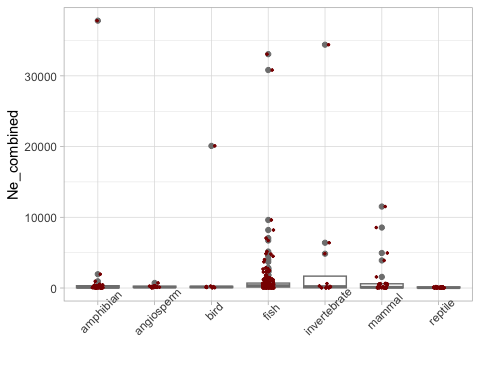
Check outliers

ind1\_data %>%   
 filter(NcPoint > 10000000) %>%   
 select(country\_assessment, name\_assessor, taxon, taxonomic\_group, population, NcPoint, NcLower, NcUpper, multiassessment, population)

## # A tibble: 5 × 9  
## country\_assessment name\_assessor taxon taxonomic\_group population NcPoint  
## <fct> <chr> <chr> <chr> <chr> <dbl>  
## 1 France Myriam Heuertz Fagus sy… angiosperm pop1 3.82e8  
## 2 France Myriam Heuertz Fagus sy… angiosperm pop2 3.82e8  
## 3 France Myriam Heuertz Fagus sy… angiosperm pop3 3.38e7  
## 4 USA Austin Koontz Layia ca… angiosperm pop4 1.22e7  
## 5 USA Caitlin Miller Lomatium… angiosperm pop1 1.08e7  
## # … with 3 more variables: NcLower <int>, NcUpper <int>, multiassessment <chr>

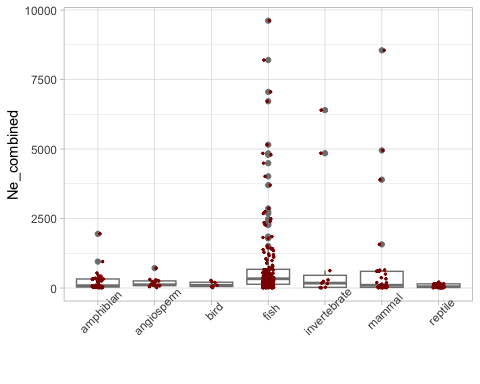
Range of Ne values by taxonomic group from different sources. Without possible outliers.

ind1\_data %>%  
 filter(!is.na(Ne\_combined)) %>%  
 filter(Ne < 100000) %>%  
   
 ggplot(aes(x=taxonomic\_group, y=Ne\_combined)) +  
 geom\_boxplot(color="grey50") +  
 geom\_jitter(size=.5, width = 0.1, color="darkred") +  
 xlab("") +  
 theme\_light() +  
 theme(axis.text.x = element\_text(angle = 45))



Range of Ne values by taxonomic group from different sources. Zoom to Ne < 10,000

ind1\_data %>%  
 filter(!is.na(Ne\_combined)) %>%  
 filter(Ne < 10000) %>%  
   
 ggplot(aes(x=taxonomic\_group, y=Ne\_combined)) +  
 geom\_boxplot(color="grey50") +  
 geom\_jitter(size=.5, width = 0.1, color="darkred") +  
 xlab("") +  
 theme\_light() +  
 theme(axis.text.x = element\_text(angle = 45))



## Missing data on extant and extinct populations

We have NA in Proportion of maintained populations (indicator) because in some cases the number of extinct populations is unknown, therefore the operation cannot be computed.

### Counts

Total records with NA in extant populations:

sum(is.na(indicators\_full$n\_extant\_populations))

## [1] 19

Taxa with NA in extant populations:

indicators\_full %>%  
 filter(is.na(n\_extant\_populations)) %>%  
 select(country\_assessment, taxonomic\_group, taxon, n\_extant\_populations, n\_extint\_populations)

## country\_assessment taxonomic\_group taxon  
## 1 South Africa angiosperm Diosma awilana  
## 2 South Africa reptile Kinixys lobatsiana  
## 3 South Africa reptile Kinixys natalensis  
## 4 South Africa fish Cheilodactylus fasciatus  
## 5 Australia angiosperm Eucalyptus melliodora  
## 6 Mexico reptile Ctenosaura macrolopha  
## 7 USA invertebrate Bombus franklini  
## 8 South Africa reptile Chersobius boulengeri  
## 9 South Africa reptile Chersobius signatus  
## 10 USA reptile Clonophis kirtlandii  
## 11 Belgium mammal Myotis brandtii  
## 12 Belgium mammal Pipistrellus pygmaeus  
## 13 Mexico gymnosperm Pinus ayacahuite  
## 14 Mexico bird Egretta rufescens dickeyi  
## 15 Belgium mammal Crocidura leucodon  
## 16 Belgium mammal Vespertilio murinus  
## 17 Belgium invertebrate Osmoderma eremita  
## 18 Mexico reptile Kinosternon integrum  
## 19 Mexico reptile Abronia deppii  
## n\_extant\_populations n\_extint\_populations  
## 1 NA NA  
## 2 NA NA  
## 3 NA NA  
## 4 NA NA  
## 5 NA NA  
## 6 NA NA  
## 7 NA NA  
## 8 NA NA  
## 9 NA NA  
## 10 NA NA  
## 11 NA NA  
## 12 NA NA  
## 13 NA NA  
## 14 NA NA  
## 15 NA NA  
## 16 NA NA  
## 17 NA NA  
## 18 NA NA  
## 19 NA NA

Total taxa with NA in **extinct** populations:

sum(is.na(indicators\_full$n\_extint\_populations))

## [1] 417

Do taxa with NA for extant also have NA for extinct?

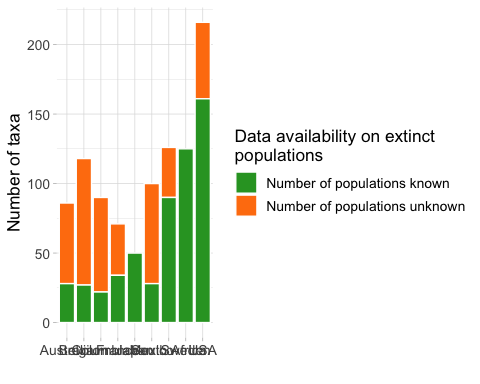
indicators\_full$taxon[is.na(indicators\_full$n\_extant\_populations)] %in% indicators\_full$taxon[is.na(indicators\_full$n\_extint\_populations)]

## [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE  
## [16] TRUE TRUE TRUE TRUE

So out of the 982, we have **417 records with NA in n\_extinct** and **19 records with NA in n\_extant**. Of them, 19 have NA in both n\_extant and n\_extinct.

### Plot missing data extinct populations

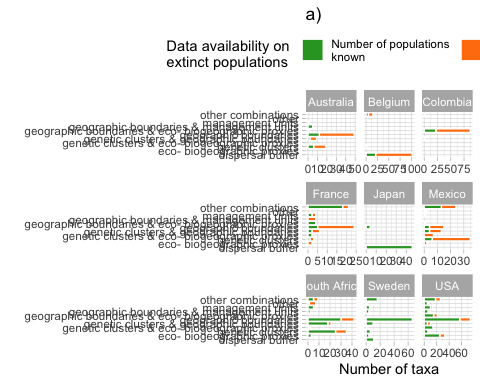
p5<-indicators\_full %>%  
 ggplot(aes(x=country\_assessment, fill=!is.na(n\_extint\_populations))) + # Notice this shows which taxa DO NOT have NA, ie exctint pops are KNOWN  
 geom\_bar(color="white") +  
 scale\_fill\_manual(labels=c("Number of populations known", "Number of populations unknown"),  
 breaks =c("TRUE", "FALSE"),  
 values=c("#2ca02c", "#ff7f0e")) +   
 labs(fill="Data availability on extinct \npopulations") +  
 xlab("") + ylab("Number of taxa") +  
 theme\_light() +  
 theme(text = element\_text(size = 13), legend.position = "right", panel.border = element\_blank())  
p5



### Supplementary Figure: Missing data in extinct populations by country and method and by taxonomic group

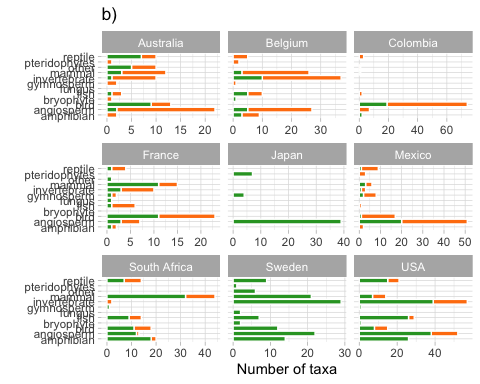
Missing data in number of extinct populations by method to define populations:

pa<-indicators\_full %>%  
 ggplot(aes(x=defined\_populations\_nicenames, fill=!is.na(n\_extint\_populations))) +  
 geom\_bar(color="white") +  
 coord\_flip()+   
 scale\_fill\_manual(labels=c("Number of populations \nknown", "Number of populations \nunknown"),  
 breaks =c("TRUE", "FALSE"),  
 values=c("#2ca02c", "#ff7f0e")) +   
 labs(fill="Data availability on \nextinct populations") +  
 xlab("") + ylab("Number of taxa") +  
 facet\_wrap(country\_assessment ~., nrow = 3, scales="free\_x") +  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="top") + ggtitle("a)")  
 pa



Missing data in number of extinct populations by method to define populations:

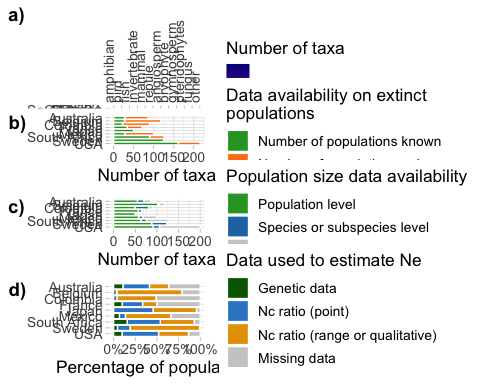
pb<-indicators\_full %>%  
 ggplot(aes(x=taxonomic\_group, fill=!is.na(n\_extint\_populations)))+  
 geom\_bar(color="white") +  
 coord\_flip()+   
 scale\_fill\_manual(labels=c("Number of populations \nknown", "Number of populations \nunknown"),  
 breaks =c("TRUE", "FALSE"),  
 values=c("#2ca02c", "#ff7f0e")) +   
 labs(fill="Data availability on \nextinct populations") +  
 xlab("") + ylab("Number of taxa") +  
 facet\_wrap(country\_assessment ~., nrow = 3, scales="free\_x") +  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="none") + ggtitle("b)")  
pb



## Main Figure: Taxa by country and data availability to estimate Ne indciator (origion of data to estimate Ne) and PM indicator (missing data on pop extinction):

Distribution of Nc, Ne and types of Ne in a single figure with 4 panels, using count for a, b & c, and proportions for d:

# plot  
  
plot\_grid(p\_heat + theme(legend.position = "right", legend.justification = c(0,.5)), # legend.justification aligns legends  
   
 p5 + coord\_flip() +   
 scale\_x\_discrete(limits=rev) +  
 theme(legend.position = "right", legend.justification = c(0,.5)),  
   
 p.popsize + theme(legend.position = "right", legend.justification = c(0,.5)),  
   
 p4 + theme(legend.position = "right", legend.justification = c(0,.5)),   
   
 ncol = 1, labels = c("a)", "b)", "c)", "d)"), align = "v",  
 rel\_heights = c(1.3, 1, 1))



## Main Figure: Method to define populations used by country and taxa (alluvial)

Reformat data

# reformat data  
foralluvial<-metadata %>% group\_by(country\_assessment, defined\_populations\_nicenames, taxonomic\_group) %>%  
 summarise(n=n())

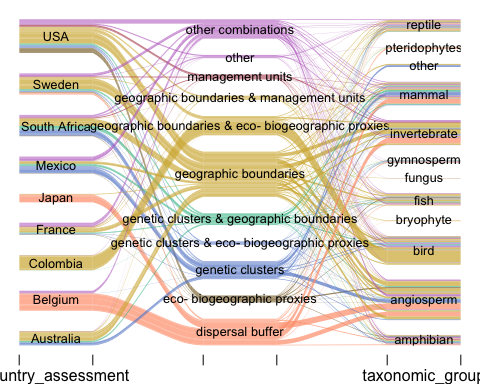
## `summarise()` has grouped output by 'country\_assessment',  
## 'defined\_populations\_nicenames'. You can override using the `.groups` argument.

# define colors  
my\_cols<- simplifiedmethods\_colors  
  
# we need a vector of colors by country for each row of the dataset, so:  
methodspop<-as.factor(foralluvial$defined\_populations\_nicenames)  
levels(methodspop)<-my\_cols  
methodspop<-as.vector(methodspop)  
head(methodspop)

## [1] "#668cd1" "#668cd1" "#668cd1" "#668cd1" "#668cd1" "#45c097"

Plot

# plot  
alluvial(foralluvial[,1:3], freq = foralluvial$n,  
 col=methodspop,   
 blocks=FALSE,  
 gap.width = 0.5,  
 cex=.8,   
 xw = 0.1,  
 cw = 0.2,  
 border = NA,  
 alpha = .7)



Get count to add numbers outside R:

# n for country  
metadata %>% group\_by(country\_assessment) %>%  
 summarise(n=n())

## # A tibble: 9 × 2  
## country\_assessment n  
## <fct> <int>  
## 1 Australia 86  
## 2 Belgium 118  
## 3 Colombia 90  
## 4 France 71  
## 5 Japan 50  
## 6 Mexico 100  
## 7 South Africa 126  
## 8 Sweden 125  
## 9 USA 200

# n for taxonomic group  
metadata %>% group\_by(taxonomic\_group) %>%  
 summarise(n=n())

## # A tibble: 12 × 2  
## taxonomic\_group n  
## <chr> <int>  
## 1 amphibian 63  
## 2 angiosperm 240  
## 3 bird 170  
## 4 bryophyte 5  
## 5 fish 72  
## 6 fungus 3  
## 7 gymnosperm 19  
## 8 invertebrate 148  
## 9 mammal 139  
## 10 other 18  
## 11 pteridophytes 14  
## 12 reptile 75

## Exploratory plots for the association of distribution range (restricted vs wide) on the indicators

All the following plots and analyses consider the average of multiassessed species (variable \_mean), so that they are shown only once.

To have nicer looking plots, change “wide\_ranging” for “wide ranging”:

indicators\_averaged\_one$species\_range<-gsub("wide\_ranging", "wide ranging", indicators\_averaged\_one$species\_range)

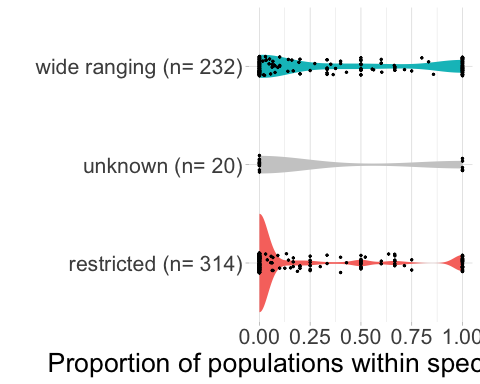
### Indicator 1 (Ne>5000)

Plot Indicator 1 by type of range in the entire dataset. Filtering NA in species range:

# get sample size by desired category  
sample\_size <- indicators\_averaged\_one %>%  
 filter(!is.na(indicator1\_mean)) %>%   
 filter(!is.na(species\_range)) %>%   
 group\_by(species\_range) %>% summarize(num=n())  
  
# plot  
p1<-indicators\_averaged\_one %>%   
 filter(!is.na(indicator1\_mean)) %>%   
 filter(!is.na(species\_range)) %>%   
 # add sampling size   
 left\_join(sample\_size) %>%   
 mutate(myaxis = paste0(species\_range, " (n= ", num, ")")) %>%  
  
 # plot  
 ggplot(aes(x=myaxis, y=indicator1\_mean , fill=species\_range)) +  
 geom\_violin(width=1, linewidth = 0) +  
 geom\_jitter(size=.5, width = 0.1) +  
 xlab("") + ylab("Proportion of populations within species with Ne>500") +  
 coord\_flip() +  
 scale\_fill\_manual(breaks=c("wide ranging", "restricted", "unknown"),  
 labels=c("wide ranging", "restricted", "unknown"),  
 values=c("#00BFC4", "#F8766D", "grey80")) +  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="none", text= element\_text(size=20))

## Joining, by = "species\_range"

p1

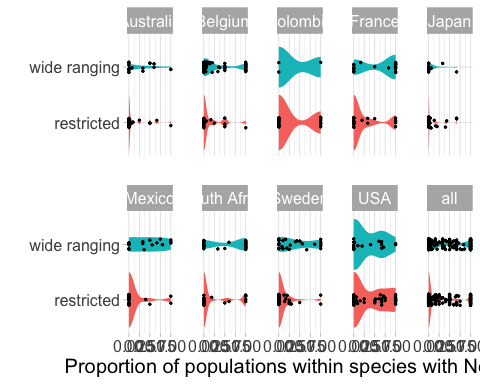


### Supplementary Figure: Plot Ne Indicator by country and type of range. Remove “unknown” and NA for better visualization.

### Duplicate dataframe to have a column with "all data" for faceting  
df<-CreateAllFacet(indicators\_averaged\_one, "country\_assessment")  
  
# order with "all" as last  
df$facet <- factor(df$facet, levels=c("Australia", "Belgium", "Colombia", "France", "Japan", "Mexico", "South Africa", "Sweden", "USA", "all"))  
  
## plot  
df %>%   
 # filter out "unknown" range  
 filter(species\_range !="unknown") %>%   
   
# plot  
ggplot(aes(x=species\_range, y=indicator1\_mean , fill=species\_range)) +  
 geom\_violin(width=1, linewidth = 0) +  
 geom\_jitter(size=.5, width = 0.1) +  
 xlab("") + ylab("Proportion of populations within species with Ne>500") +  
 coord\_flip() +  
 scale\_x\_discrete(breaks=c("wide ranging", "restricted"),  
 labels=c("wide ranging", "restricted")) +  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="none", text= element\_text(size=15)) +  
 facet\_wrap(~facet, ncol = 5) +  
 theme(panel.spacing = unit(1.5, "lines"))

## Warning: Removed 658 rows containing non-finite values (`stat\_ydensity()`).

## Warning: Removed 658 rows containing missing values (`geom\_point()`).



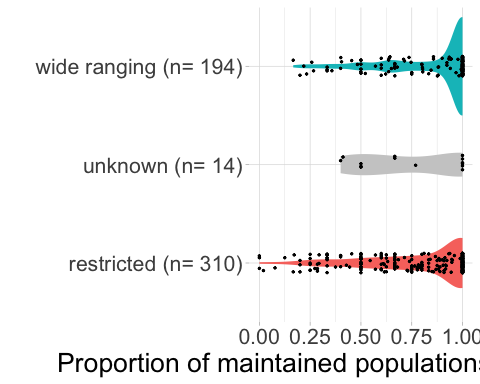
### Indicator 2 (mantained populations)

Plot Indicator 2 by type of range in the entire dataset. Filtering NA in species range:

# get sample size by desired category  
sample\_size <- indicators\_averaged\_one %>%  
 filter(!is.na(indicator2\_mean)) %>%   
 filter(!is.na(species\_range)) %>%   
 group\_by(species\_range) %>% summarize(num=n())  
  
# plot  
p2<-indicators\_averaged\_one %>%   
 filter(!is.na(indicator2\_mean)) %>%   
 filter(!is.na(species\_range)) %>%   
 # add sampling size   
 left\_join(sample\_size) %>%   
 mutate(myaxis = paste0(species\_range, " (n= ", num, ")")) %>%  
  
 # plot  
 ggplot(aes(x=myaxis, y=indicator2\_mean , fill=species\_range)) +  
 geom\_violin(width=1, linewidth = 0) +  
 geom\_jitter(size=.5, width = 0.1) +  
 xlab("") + ylab("Proportion of maintained populations within species") +  
 coord\_flip() +  
 scale\_fill\_manual(breaks=c("wide ranging", "restricted", "unknown"),  
 labels=c("wide ranging", "restricted", "unknown"),  
 values=c("#00BFC4", "#F8766D", "grey80")) +  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="none", text= element\_text(size=20))

## Joining, by = "species\_range"

p2



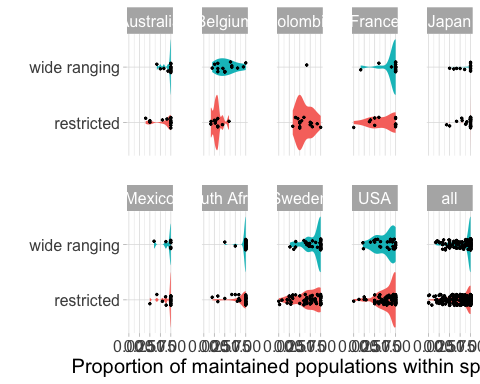
Plot Indicator 2 by country and type of range. We remove NA and unknown for better visualization.

### Duplicate dataframe to have a column with "all data" for faceting  
df<-CreateAllFacet(indicators\_averaged\_one, "country\_assessment")  
  
# order with "all" as last  
df$facet <- factor(df$facet, levels=c("Australia", "Belgium", "Colombia", "France", "Japan", "Mexico", "South Africa", "Sweden", "USA", "all"))  
  
## plot  
df %>%   
 # filter out "unknown" range  
 filter(species\_range !="unknown") %>%   
   
# plot  
ggplot(aes(x=species\_range, y=indicator2\_mean , fill=species\_range)) +  
 geom\_violin(width=1, linewidth = 0) +  
 geom\_jitter(size=.5, width = 0.1) +  
 xlab("") + ylab("Proportion of maintained populations within species") +  
 coord\_flip() +  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="none", text= element\_text(size=15)) +  
 facet\_wrap(~facet, ncol = 5) +  
 theme(panel.spacing = unit(1.5, "lines"))

## Warning: Removed 742 rows containing non-finite values (`stat\_ydensity()`).

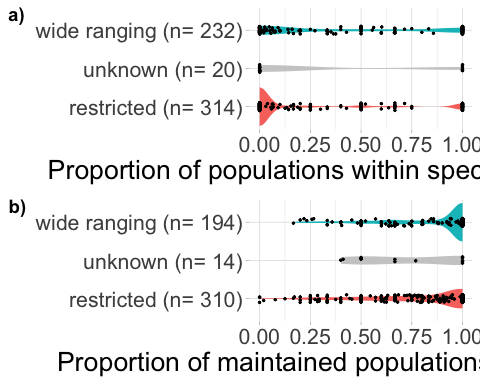
## Warning: Groups with fewer than two data points have been dropped.

## Warning: Removed 742 rows containing missing values (`geom\_point()`).



### Single plot PM and Ne indicators by range type

plot\_grid(p1, p2, ncol=1, align = "v", labels=c("a)", "b)"))



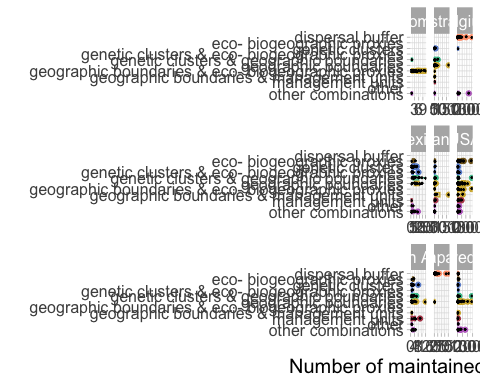
## Sampling size of different variables useful to interpret the statistical models run below

The plots and tables below are meant to visualize the sampling size and data distribution of some of the variables used in the models below. Data is a subset filtering outliers (>500 populations) and using the simplified methods (see above). Multiassessed species are considered independently (each assessment is a data point).

### Supplementary Figure: Number of maintained populations by country and method

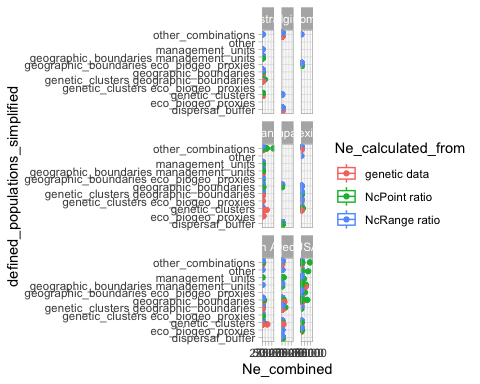
Number of maintained populations by country and method is useful to interpret the models that would be run below.

indicators\_full %>%   
 filter(n\_extant\_populations<500) %>% # filter outliers  
 # order countries vertically by similar number of pops  
 mutate(country\_assessment = factor(country\_assessment,   
 levels=c("Colombia", "Australia", "Belgium",  
 "Mexico", "France", "USA",   
 "South Africa", "Japan", "Sweden"))) %>%  
 ggplot(aes(x=defined\_populations\_nicenames, y=n\_extant\_populations,   
 fill=defined\_populations\_nicenames, color=defined\_populations\_nicenames)) +  
 geom\_boxplot() +  
 geom\_jitter(size=.3, width = 0.1, color="black") +  
 coord\_flip() +  
 facet\_wrap(country\_assessment ~ ., nrow=3, scales="free\_x") +  
 xlab("") +  
 ylab("Number of maintained populations") +  
 scale\_fill\_manual(values=alpha(simplifiedmethods\_colors, .3),  
 breaks=levels(as.factor(indicators\_full$defined\_populations\_nicenames))) +  
 scale\_color\_manual(values=simplifiedmethods\_colors,  
 breaks=levels(as.factor(indicators\_full$defined\_populations\_nicenames))) +  
 scale\_x\_discrete(limits=rev) +  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="none",  
 text = element\_text(size = 15))



### Ne values

ind1\_data %>%   
 filter(Ne\_combined < 100000) %>% # filter outliers  
  
 ggplot(aes(x=defined\_populations\_simplified, y=Ne\_combined,   
 color=Ne\_calculated\_from)) +  
 geom\_boxplot(position = "dodge") +  
 geom\_jitter(position = position\_dodge(width = 0.75)) +   
 facet\_wrap(country\_assessment ~ ., nrow=3) +  
 coord\_flip() +  
 theme\_light()

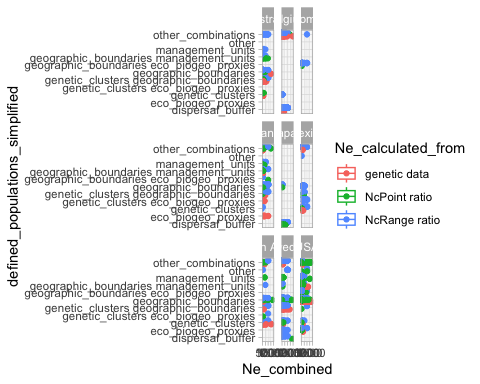


Zoom to Ne 500

ind1\_data %>%   
 filter(Ne\_combined < 100000) %>% # filter outliers  
  
 ggplot(aes(x=defined\_populations\_simplified, y=Ne\_combined,   
 color=Ne\_calculated\_from)) +  
 ylim(0,2000)+  
 geom\_boxplot(position = "dodge") +  
 geom\_jitter(position = position\_dodge(width = 0.75)) +   
 facet\_wrap(country\_assessment ~ ., nrow=3) +  
 coord\_flip() +  
 theme\_light()

## Warning: Removed 104 rows containing non-finite values (`stat\_boxplot()`).

## Warning: Removed 104 rows containing missing values (`geom\_point()`).



Summary table for sampling size by method and source of Ne:

x<- ind1\_data %>%   
 filter(!is.na(Ne\_calculated\_from)) %>%   
 group\_by(defined\_populations\_simplified, Ne\_calculated\_from) %>%  
 summarise(n=n())

## `summarise()` has grouped output by 'defined\_populations\_simplified'. You can  
## override using the `.groups` argument.

kable(x)

| defined\_populations\_simplified | Ne\_calculated\_from | n |
| --- | --- | --- |
| dispersal\_buffer | genetic data | 10 |
| dispersal\_buffer | NcPoint ratio | 226 |
| dispersal\_buffer | NcRange ratio | 1114 |
| eco\_biogeo\_proxies | genetic data | 8 |
| eco\_biogeo\_proxies | NcPoint ratio | 55 |
| eco\_biogeo\_proxies | NcRange ratio | 82 |
| genetic\_clusters | genetic data | 43 |
| genetic\_clusters | NcPoint ratio | 32 |
| genetic\_clusters | NcRange ratio | 59 |
| genetic\_clusters eco\_biogeo\_proxies | genetic data | 4 |
| genetic\_clusters eco\_biogeo\_proxies | NcPoint ratio | 3 |
| genetic\_clusters eco\_biogeo\_proxies | NcRange ratio | 18 |
| genetic\_clusters geographic\_boundaries | genetic data | 44 |
| genetic\_clusters geographic\_boundaries | NcPoint ratio | 34 |
| genetic\_clusters geographic\_boundaries | NcRange ratio | 83 |
| geographic\_boundaries | genetic data | 142 |
| geographic\_boundaries | NcPoint ratio | 478 |
| geographic\_boundaries | NcRange ratio | 594 |
| geographic\_boundaries eco\_biogeo\_proxies | genetic data | 8 |
| geographic\_boundaries eco\_biogeo\_proxies | NcPoint ratio | 68 |
| geographic\_boundaries eco\_biogeo\_proxies | NcRange ratio | 200 |
| geographic\_boundaries management\_units | genetic data | 29 |
| geographic\_boundaries management\_units | NcPoint ratio | 189 |
| geographic\_boundaries management\_units | NcRange ratio | 22 |
| management\_units | NcPoint ratio | 48 |
| management\_units | NcRange ratio | 76 |
| other | NcPoint ratio | 3 |
| other | NcRange ratio | 14 |
| other\_combinations | genetic data | 61 |
| other\_combinations | NcPoint ratio | 130 |
| other\_combinations | NcRange ratio | 712 |

Same as above but adding country:

x<- ind1\_data %>%   
 filter(!is.na(Ne\_calculated\_from)) %>%   
 group\_by(country\_assessment, defined\_populations\_simplified, Ne\_calculated\_from) %>%  
 summarise(n=n())

## `summarise()` has grouped output by 'country\_assessment',  
## 'defined\_populations\_simplified'. You can override using the `.groups`  
## argument.

kable(x)

| country\_assessment | defined\_populations\_simplified | Ne\_calculated\_from | n |
| --- | --- | --- | --- |
| Australia | genetic\_clusters | genetic data | 7 |
| Australia | genetic\_clusters | NcPoint ratio | 8 |
| Australia | genetic\_clusters geographic\_boundaries | genetic data | 15 |
| Australia | genetic\_clusters geographic\_boundaries | NcPoint ratio | 13 |
| Australia | genetic\_clusters geographic\_boundaries | NcRange ratio | 7 |
| Australia | geographic\_boundaries | genetic data | 15 |
| Australia | geographic\_boundaries | NcPoint ratio | 76 |
| Australia | geographic\_boundaries | NcRange ratio | 59 |
| Australia | geographic\_boundaries management\_units | NcPoint ratio | 8 |
| Australia | geographic\_boundaries management\_units | NcRange ratio | 3 |
| Australia | management\_units | NcRange ratio | 3 |
| Australia | other\_combinations | NcRange ratio | 4 |
| Belgium | dispersal\_buffer | genetic data | 10 |
| Belgium | dispersal\_buffer | NcPoint ratio | 8 |
| Belgium | dispersal\_buffer | NcRange ratio | 844 |
| Belgium | genetic\_clusters | NcRange ratio | 7 |
| Belgium | other\_combinations | genetic data | 40 |
| Belgium | other\_combinations | NcPoint ratio | 2 |
| Belgium | other\_combinations | NcRange ratio | 379 |
| Colombia | geographic\_boundaries eco\_biogeo\_proxies | NcPoint ratio | 4 |
| Colombia | geographic\_boundaries eco\_biogeo\_proxies | NcRange ratio | 46 |
| Colombia | other\_combinations | NcRange ratio | 1 |
| France | eco\_biogeo\_proxies | genetic data | 7 |
| France | genetic\_clusters | genetic data | 3 |
| France | genetic\_clusters | NcRange ratio | 1 |
| France | genetic\_clusters eco\_biogeo\_proxies | genetic data | 3 |
| France | genetic\_clusters eco\_biogeo\_proxies | NcPoint ratio | 1 |
| France | genetic\_clusters geographic\_boundaries | genetic data | 6 |
| France | genetic\_clusters geographic\_boundaries | NcPoint ratio | 6 |
| France | genetic\_clusters geographic\_boundaries | NcRange ratio | 7 |
| France | geographic\_boundaries | NcPoint ratio | 12 |
| France | geographic\_boundaries | NcRange ratio | 22 |
| France | geographic\_boundaries eco\_biogeo\_proxies | NcPoint ratio | 1 |
| France | geographic\_boundaries eco\_biogeo\_proxies | NcRange ratio | 2 |
| France | geographic\_boundaries management\_units | genetic data | 15 |
| France | geographic\_boundaries management\_units | NcPoint ratio | 38 |
| France | geographic\_boundaries management\_units | NcRange ratio | 12 |
| France | management\_units | NcPoint ratio | 10 |
| France | management\_units | NcRange ratio | 8 |
| France | other\_combinations | genetic data | 3 |
| France | other\_combinations | NcPoint ratio | 20 |
| France | other\_combinations | NcRange ratio | 10 |
| Japan | dispersal\_buffer | NcPoint ratio | 214 |
| Japan | dispersal\_buffer | NcRange ratio | 232 |
| Japan | geographic\_boundaries | NcPoint ratio | 1 |
| Japan | geographic\_boundaries | NcRange ratio | 5 |
| Mexico | genetic\_clusters | genetic data | 13 |
| Mexico | genetic\_clusters | NcPoint ratio | 15 |
| Mexico | genetic\_clusters | NcRange ratio | 24 |
| Mexico | genetic\_clusters eco\_biogeo\_proxies | genetic data | 1 |
| Mexico | genetic\_clusters eco\_biogeo\_proxies | NcRange ratio | 17 |
| Mexico | genetic\_clusters geographic\_boundaries | genetic data | 2 |
| Mexico | genetic\_clusters geographic\_boundaries | NcPoint ratio | 6 |
| Mexico | genetic\_clusters geographic\_boundaries | NcRange ratio | 15 |
| Mexico | geographic\_boundaries | NcRange ratio | 75 |
| Mexico | other | NcRange ratio | 1 |
| Mexico | other\_combinations | genetic data | 4 |
| Mexico | other\_combinations | NcRange ratio | 26 |
| South Africa | genetic\_clusters | genetic data | 12 |
| South Africa | genetic\_clusters | NcPoint ratio | 3 |
| South Africa | genetic\_clusters | NcRange ratio | 6 |
| South Africa | genetic\_clusters eco\_biogeo\_proxies | NcPoint ratio | 2 |
| South Africa | genetic\_clusters eco\_biogeo\_proxies | NcRange ratio | 1 |
| South Africa | genetic\_clusters geographic\_boundaries | genetic data | 2 |
| South Africa | genetic\_clusters geographic\_boundaries | NcPoint ratio | 2 |
| South Africa | genetic\_clusters geographic\_boundaries | NcRange ratio | 11 |
| South Africa | geographic\_boundaries | genetic data | 2 |
| South Africa | geographic\_boundaries | NcPoint ratio | 28 |
| South Africa | geographic\_boundaries | NcRange ratio | 21 |
| South Africa | geographic\_boundaries management\_units | NcRange ratio | 1 |
| South Africa | management\_units | NcPoint ratio | 1 |
| South Africa | other | NcRange ratio | 1 |
| South Africa | other\_combinations | genetic data | 2 |
| South Africa | other\_combinations | NcPoint ratio | 8 |
| South Africa | other\_combinations | NcRange ratio | 4 |
| Sweden | dispersal\_buffer | NcPoint ratio | 4 |
| Sweden | dispersal\_buffer | NcRange ratio | 38 |
| Sweden | eco\_biogeo\_proxies | NcRange ratio | 26 |
| Sweden | genetic\_clusters | genetic data | 7 |
| Sweden | genetic\_clusters | NcPoint ratio | 3 |
| Sweden | genetic\_clusters | NcRange ratio | 11 |
| Sweden | genetic\_clusters geographic\_boundaries | genetic data | 19 |
| Sweden | genetic\_clusters geographic\_boundaries | NcPoint ratio | 6 |
| Sweden | genetic\_clusters geographic\_boundaries | NcRange ratio | 41 |
| Sweden | geographic\_boundaries | genetic data | 2 |
| Sweden | geographic\_boundaries | NcPoint ratio | 67 |
| Sweden | geographic\_boundaries | NcRange ratio | 168 |
| Sweden | geographic\_boundaries management\_units | NcPoint ratio | 3 |
| Sweden | geographic\_boundaries management\_units | NcRange ratio | 5 |
| Sweden | management\_units | NcPoint ratio | 12 |
| Sweden | other | NcRange ratio | 10 |
| Sweden | other\_combinations | genetic data | 3 |
| Sweden | other\_combinations | NcPoint ratio | 7 |
| Sweden | other\_combinations | NcRange ratio | 265 |
| USA | eco\_biogeo\_proxies | genetic data | 1 |
| USA | eco\_biogeo\_proxies | NcPoint ratio | 55 |
| USA | eco\_biogeo\_proxies | NcRange ratio | 56 |
| USA | genetic\_clusters | genetic data | 1 |
| USA | genetic\_clusters | NcPoint ratio | 3 |
| USA | genetic\_clusters | NcRange ratio | 10 |
| USA | genetic\_clusters geographic\_boundaries | NcPoint ratio | 1 |
| USA | genetic\_clusters geographic\_boundaries | NcRange ratio | 2 |
| USA | geographic\_boundaries | genetic data | 123 |
| USA | geographic\_boundaries | NcPoint ratio | 294 |
| USA | geographic\_boundaries | NcRange ratio | 244 |
| USA | geographic\_boundaries eco\_biogeo\_proxies | genetic data | 8 |
| USA | geographic\_boundaries eco\_biogeo\_proxies | NcPoint ratio | 63 |
| USA | geographic\_boundaries eco\_biogeo\_proxies | NcRange ratio | 152 |
| USA | geographic\_boundaries management\_units | genetic data | 14 |
| USA | geographic\_boundaries management\_units | NcPoint ratio | 140 |
| USA | geographic\_boundaries management\_units | NcRange ratio | 1 |
| USA | management\_units | NcPoint ratio | 25 |
| USA | management\_units | NcRange ratio | 65 |
| USA | other | NcPoint ratio | 3 |
| USA | other | NcRange ratio | 2 |
| USA | other\_combinations | genetic data | 9 |
| USA | other\_combinations | NcPoint ratio | 93 |
| USA | other\_combinations | NcRange ratio | 23 |

### Distribution type (wide / restricted)

x<-indicators\_full %>% filter(species\_range !="unknown") %>%  
 group\_by(defined\_populations\_nicenames, species\_range) %>%   
 summarise(n=n())

## `summarise()` has grouped output by 'defined\_populations\_nicenames'. You can  
## override using the `.groups` argument.

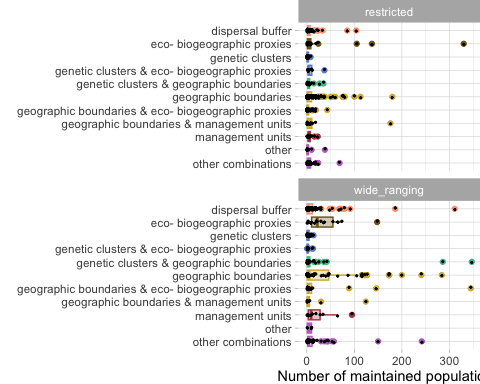
kable(x)

| defined\_populations\_nicenames | species\_range | n |
| --- | --- | --- |
| dispersal buffer | restricted | 54 |
| dispersal buffer | wide\_ranging | 99 |
| eco- biogeographic proxies | restricted | 26 |
| eco- biogeographic proxies | wide\_ranging | 17 |
| genetic clusters | restricted | 46 |
| genetic clusters | wide\_ranging | 60 |
| genetic clusters & eco- biogeographic proxies | restricted | 8 |
| genetic clusters & eco- biogeographic proxies | wide\_ranging | 18 |
| genetic clusters & geographic boundaries | restricted | 34 |
| genetic clusters & geographic boundaries | wide\_ranging | 34 |
| geographic boundaries | restricted | 202 |
| geographic boundaries | wide\_ranging | 71 |
| geographic boundaries & eco- biogeographic proxies | restricted | 74 |
| geographic boundaries & eco- biogeographic proxies | wide\_ranging | 17 |
| geographic boundaries & management units | restricted | 14 |
| geographic boundaries & management units | wide\_ranging | 10 |
| management units | restricted | 14 |
| management units | wide\_ranging | 13 |
| other | restricted | 13 |
| other | wide\_ranging | 4 |
| other combinations | restricted | 45 |
| other combinations | wide\_ranging | 64 |

### Supplementary Figure: number of mantained populations by method to define populations and range type

Facet by range type:

p<-indicators\_full %>%   
 filter(!is.na(n\_extant\_populations)) %>%   
 filter(n\_extant\_populations<500) %>%  
 filter(species\_range !="unknown") %>%  
 filter(!is.na(species\_range)) %>%  
   
 ggplot(aes(x=defined\_populations\_nicenames, y=n\_extant\_populations)) +  
 geom\_boxplot(aes(color=defined\_populations\_nicenames,  
 fill=defined\_populations\_nicenames)) +   
 xlab("") + ylab("Number of maintained populations") +  
 coord\_flip() +  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="none",  
 plot.margin = unit(c(0, 0, 0, 0), "cm")) + # this is used to decrease the space between plots  
 scale\_color\_manual(values=simplifiedmethods\_colors,  
 breaks=levels(as.factor(indicators\_full$defined\_populations\_nicenames))) +  
 scale\_fill\_manual(values=alpha(simplifiedmethods\_colors, 0.3),  
 breaks=levels(as.factor(indicators\_full$defined\_populations\_nicenames))) +  
 facet\_wrap("species\_range", ncol=1) +   
 geom\_jitter(size=.4, width = 0.1, color="black") +  
 scale\_x\_discrete(limits=rev)  
  
p



## Statistical models: test for associations between method used to define populations / range type on the number of populations and the indicator values

The analyses and plots below us a subset of data filtering outliers (>500 populations) and using the simplified methods (see above). Multiassessed species are considered independently (each assessment is a data point).

### (a) Does the number of maintained pops vary with method used?

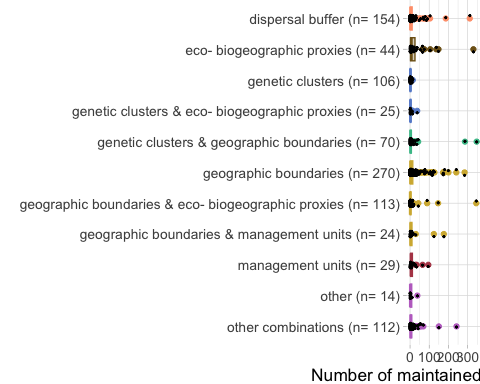
First we tested whether the different methods reported in this study were associated with varying numbers of populations obtained. For this analysis, we also controlled for range type, as we expect species with wider ranges to plausibly have more populations than species with narrower ranges.

Plot number of populations by method.

# Prepare data for plot with nice labels:  
# sample size of TOTAL populations  
sample\_size <- indicators\_full %>%  
 filter(!is.na(n\_extant\_populations)) %>%   
 filter(n\_extant\_populations<500) %>%  
 group\_by(defined\_populations\_nicenames) %>% summarize(num=n())  
  
# custom axis  
## new dataframe  
df<-indicators\_full %>%   
 filter(!is.na(n\_extant\_populations)) %>%   
 filter(n\_extant\_populations<500) %>%  
 # add sampling size   
 left\_join(sample\_size) %>%  
 mutate(myaxis = paste0(defined\_populations\_nicenames, " (n= ", num, ")")) %>%  
#myaxis needs levels in the same order than defined\_populations\_nicenames  
 mutate(myaxis = factor(myaxis,   
 levels=levels(as.factor(myaxis))[c(1,12,2:11,13)])) # reorders levels

## Joining, by = "defined\_populations\_nicenames"

# plot for number of pops  
 pa<- df %>%  
 ggplot(aes(x=myaxis, y=n\_extant\_populations, color=defined\_populations\_nicenames,  
 fill=defined\_populations\_nicenames)) +  
 geom\_boxplot() + xlab("") + ylab("Number of maintained populations") +  
 geom\_jitter(size=.4, width = 0.1, color="black") +  
 coord\_flip() +  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="none",  
 plot.margin = unit(c(0, 0, 0, 0), "cm")) + # this is used to decrease the space between plots  
 scale\_color\_manual(values=simplifiedmethods\_colors,  
 breaks=levels(as.factor(indicators\_full$defined\_populations\_nicenames))) +  
 scale\_fill\_manual(values=alpha(simplifiedmethods\_colors, 0.3),  
 breaks=levels(as.factor(indicators\_full$defined\_populations\_nicenames))) +  
 scale\_x\_discrete(limits=rev) +   
 theme(text = element\_text(size = 13))  
pa



Prepare data for model (remove outliers, “unknown” category and NA in desired variable) and check n:

# remove missing data   
data\_for\_model<-indicators\_full %>%   
 filter(!is.na(n\_extant\_populations)) %>%  
 filter(species\_range !="unknown") %>% # we remove "unknonw" because its n is too low, thus unbalancing the model  
 filter(n\_extant\_populations<500) # doesn't make a difference in the test below, but useful for plots  
  
# check n per method  
table(data\_for\_model$defined\_populations\_simplified)

##   
## dispersal\_buffer   
## 149   
## eco\_biogeo\_proxies   
## 43   
## genetic\_clusters   
## 104   
## genetic\_clusters eco\_biogeo\_proxies   
## 25   
## genetic\_clusters geographic\_boundaries   
## 68   
## geographic\_boundaries   
## 269   
## geographic\_boundaries eco\_biogeo\_proxies   
## 90   
## geographic\_boundaries management\_units   
## 24   
## management\_units   
## 27   
## other   
## 14   
## other\_combinations   
## 106

# total n  
nrow(data\_for\_model)

## [1] 919

# re-level to use geographic boundaries as reference category for the analysis  
data\_for\_model$defined\_populations\_simplified<-relevel(as.factor(data\_for\_model$defined\_populations\_simplified),  
 ref="geographic\_boundaries")  
  
# make sure specis range is a factor  
data\_for\_model$species\_range<-as.factor(data\_for\_model$species\_range)

Run model asking: Does the number of maintained pops vary with method and range?

m.a1<-glmer(data\_for\_model$n\_extant\_populations ~ data\_for\_model$defined\_populations\_simplified + data\_for\_model$species\_range + (1|data\_for\_model$country\_assessment), family ="poisson")  
  
summary(m.a1)

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: poisson ( log )  
## Formula:   
## data\_for\_model$n\_extant\_populations ~ data\_for\_model$defined\_populations\_simplified +   
## data\_for\_model$species\_range + (1 | data\_for\_model$country\_assessment)  
##   
## AIC BIC logLik deviance df.resid   
## 25019.5 25082.2 -12496.8 24993.5 906   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -8.057 -2.887 -1.133 0.695 89.652   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## data\_for\_model$country\_assessment (Intercept) 0.9191 0.9587   
## Number of obs: 919, groups: data\_for\_model$country\_assessment, 9  
##   
## Fixed effects:  
## Estimate  
## (Intercept) 1.97560  
## data\_for\_model$defined\_populations\_simplifieddispersal\_buffer -1.26073  
## data\_for\_model$defined\_populations\_simplifiedeco\_biogeo\_proxies -0.13462  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters -1.55617  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies -1.97499  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.04942  
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies -0.19851  
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries management\_units -0.13256  
## data\_for\_model$defined\_populations\_simplifiedmanagement\_units -0.84557  
## data\_for\_model$defined\_populations\_simplifiedother -1.30402  
## data\_for\_model$defined\_populations\_simplifiedother\_combinations -0.77247  
## data\_for\_model$species\_rangewide\_ranging 1.09745  
## Std. Error  
## (Intercept) 0.32026  
## data\_for\_model$defined\_populations\_simplifieddispersal\_buffer 0.05067  
## data\_for\_model$defined\_populations\_simplifiedeco\_biogeo\_proxies 0.03225  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters 0.06222  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.08953  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.03548  
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.03936  
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.05084  
## data\_for\_model$defined\_populations\_simplifiedmanagement\_units 0.05480  
## data\_for\_model$defined\_populations\_simplifiedother 0.11140  
## data\_for\_model$defined\_populations\_simplifiedother\_combinations 0.03493  
## data\_for\_model$species\_rangewide\_ranging 0.01957  
## z value  
## (Intercept) 6.169  
## data\_for\_model$defined\_populations\_simplifieddispersal\_buffer -24.879  
## data\_for\_model$defined\_populations\_simplifiedeco\_biogeo\_proxies -4.174  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters -25.009  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies -22.060  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 1.393  
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies -5.044  
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries management\_units -2.607  
## data\_for\_model$defined\_populations\_simplifiedmanagement\_units -15.431  
## data\_for\_model$defined\_populations\_simplifiedother -11.705  
## data\_for\_model$defined\_populations\_simplifiedother\_combinations -22.114  
## data\_for\_model$species\_rangewide\_ranging 56.074  
## Pr(>|z|)  
## (Intercept) 6.88e-10  
## data\_for\_model$defined\_populations\_simplifieddispersal\_buffer < 2e-16  
## data\_for\_model$defined\_populations\_simplifiedeco\_biogeo\_proxies 2.99e-05  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters < 2e-16  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies < 2e-16  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.16363  
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 4.56e-07  
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.00913  
## data\_for\_model$defined\_populations\_simplifiedmanagement\_units < 2e-16  
## data\_for\_model$defined\_populations\_simplifiedother < 2e-16  
## data\_for\_model$defined\_populations\_simplifiedother\_combinations < 2e-16  
## data\_for\_model$species\_rangewide\_ranging < 2e-16  
##   
## (Intercept) \*\*\*  
## data\_for\_model$defined\_populations\_simplifieddispersal\_buffer \*\*\*  
## data\_for\_model$defined\_populations\_simplifiedeco\_biogeo\_proxies \*\*\*  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters \*\*\*  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies \*\*\*  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries   
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies \*\*\*  
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries management\_units \*\*   
## data\_for\_model$defined\_populations\_simplifiedmanagement\_units \*\*\*  
## data\_for\_model$defined\_populations\_simplifiedother \*\*\*  
## data\_for\_model$defined\_populations\_simplifiedother\_combinations \*\*\*  
## data\_for\_model$species\_rangewide\_ranging \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) dt\_fr\_mdl$dfnd\_ppltns\_smplfdd\_  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdd\_ -0.034   
## dt\_fr\_$\_\_\_\_ -0.012 0.093   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdg\_ -0.014 0.096   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgn\_e\_\_ -0.004 0.039   
## dt\_f\_$\_\_\_g\_ -0.022 0.117   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgg\_e\_\_ -0.020 0.073   
## dt\_f\_$\_\_\_m\_ -0.012 0.056   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdm\_ -0.006 0.063   
## dt\_fr\_mdl$d\_\_ -0.005 0.031   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdt\_ -0.027 0.419   
## dt\_fr\_mdl$s\_\_ -0.029 -0.090   
## d\_\_$\_\_\_\_ dt\_fr\_mdl$dfnd\_ppltns\_smplfdg\_  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdd\_   
## dt\_fr\_$\_\_\_\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdg\_ 0.096   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgn\_e\_\_ 0.099 0.045   
## dt\_f\_$\_\_\_g\_ 0.158 0.152   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgg\_e\_\_ 0.223 0.077   
## dt\_f\_$\_\_\_m\_ 0.131 0.067   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdm\_ 0.152 0.064   
## dt\_fr\_mdl$d\_\_ 0.062 0.030   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdt\_ 0.178 0.131   
## dt\_fr\_mdl$s\_\_ -0.102 -0.082   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgn\_e\_\_ d\_\_$\_g  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdd\_   
## dt\_fr\_$\_\_\_\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdg\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgn\_e\_\_   
## dt\_f\_$\_\_\_g\_ 0.068   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgg\_e\_\_ 0.085 0.130  
## dt\_f\_$\_\_\_m\_ 0.047 0.109  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdm\_ 0.060 0.103  
## dt\_fr\_mdl$d\_\_ 0.023 0.053  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdt\_ 0.073 0.196  
## dt\_fr\_mdl$s\_\_ -0.085 -0.077  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgg\_e\_\_ d\_\_$\_m  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdd\_   
## dt\_fr\_$\_\_\_\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdg\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgn\_e\_\_   
## dt\_f\_$\_\_\_g\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgg\_e\_\_   
## dt\_f\_$\_\_\_m\_ 0.113   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdm\_ 0.130 0.077  
## dt\_fr\_mdl$d\_\_ 0.050 0.034  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdt\_ 0.148 0.106  
## dt\_fr\_mdl$s\_\_ -0.101 -0.005  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdm\_ dt\_fr\_mdl$d\_\_  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdd\_   
## dt\_fr\_$\_\_\_\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdg\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgn\_e\_\_   
## dt\_f\_$\_\_\_g\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgg\_e\_\_   
## dt\_f\_$\_\_\_m\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdm\_   
## dt\_fr\_mdl$d\_\_ 0.036   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdt\_ 0.114 0.053   
## dt\_fr\_mdl$s\_\_ -0.118 -0.010   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdt\_  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdd\_   
## dt\_fr\_$\_\_\_\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdg\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgn\_e\_\_   
## dt\_f\_$\_\_\_g\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgg\_e\_\_   
## dt\_f\_$\_\_\_m\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdm\_   
## dt\_fr\_mdl$d\_\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdt\_   
## dt\_fr\_mdl$s\_\_ -0.110

Considering the role of method was so important for determining the number of populations, we also tested whether this effect remained after removing “wide-ranging” from the model. The objective here was to test whether method alone would also produce varying numbers of populations, for example if species rangedness were unknown.

Does the number of maintained pops vary with method used? (does method still influence number of populations if we exclude range type from the model):

m.a2<-glmer(data\_for\_model$n\_extant\_populations ~ data\_for\_model$defined\_populations\_simplified +   
 (1|data\_for\_model$country\_assessment), family ="poisson")

See results:

summary(m.a2)

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: poisson ( log )  
## Formula:   
## data\_for\_model$n\_extant\_populations ~ data\_for\_model$defined\_populations\_simplified +   
## (1 | data\_for\_model$country\_assessment)  
##   
## AIC BIC logLik deviance df.resid   
## 28258.3 28316.2 -14117.1 28234.3 907   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -6.326 -2.953 -1.239 0.283 74.519   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## data\_for\_model$country\_assessment (Intercept) 1.041 1.02   
## Number of obs: 919, groups: data\_for\_model$country\_assessment, 9  
##   
## Fixed effects:  
## Estimate  
## (Intercept) 2.37273  
## data\_for\_model$defined\_populations\_simplifieddispersal\_buffer -0.98301  
## data\_for\_model$defined\_populations\_simplifiedeco\_biogeo\_proxies 0.05544  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters -1.25178  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies -1.48212  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.20082  
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.03979  
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries management\_units -0.11256  
## data\_for\_model$defined\_populations\_simplifiedmanagement\_units -0.44813  
## data\_for\_model$defined\_populations\_simplifiedother -1.24179  
## data\_for\_model$defined\_populations\_simplifiedother\_combinations -0.54510  
## Std. Error  
## (Intercept) 0.34082  
## data\_for\_model$defined\_populations\_simplifieddispersal\_buffer 0.05291  
## data\_for\_model$defined\_populations\_simplifiedeco\_biogeo\_proxies 0.03232  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters 0.06198  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.08929  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.03468  
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.03952  
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.05066  
## data\_for\_model$defined\_populations\_simplifiedmanagement\_units 0.05449  
## data\_for\_model$defined\_populations\_simplifiedother 0.11149  
## data\_for\_model$defined\_populations\_simplifiedother\_combinations 0.03467  
## z value  
## (Intercept) 6.962  
## data\_for\_model$defined\_populations\_simplifieddispersal\_buffer -18.578  
## data\_for\_model$defined\_populations\_simplifiedeco\_biogeo\_proxies 1.715  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters -20.197  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies -16.599  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 5.790  
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 1.007  
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries management\_units -2.222  
## data\_for\_model$defined\_populations\_simplifiedmanagement\_units -8.223  
## data\_for\_model$defined\_populations\_simplifiedother -11.138  
## data\_for\_model$defined\_populations\_simplifiedother\_combinations -15.722  
## Pr(>|z|)  
## (Intercept) 3.36e-12  
## data\_for\_model$defined\_populations\_simplifieddispersal\_buffer < 2e-16  
## data\_for\_model$defined\_populations\_simplifiedeco\_biogeo\_proxies 0.0863  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters < 2e-16  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies < 2e-16  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 7.02e-09  
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.3141  
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.0263  
## data\_for\_model$defined\_populations\_simplifiedmanagement\_units < 2e-16  
## data\_for\_model$defined\_populations\_simplifiedother < 2e-16  
## data\_for\_model$defined\_populations\_simplifiedother\_combinations < 2e-16  
##   
## (Intercept) \*\*\*  
## data\_for\_model$defined\_populations\_simplifieddispersal\_buffer \*\*\*  
## data\_for\_model$defined\_populations\_simplifiedeco\_biogeo\_proxies .   
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters \*\*\*  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies \*\*\*  
## data\_for\_model$defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries \*\*\*  
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies   
## data\_for\_model$defined\_populations\_simplifiedgeographic\_boundaries management\_units \*   
## data\_for\_model$defined\_populations\_simplifiedmanagement\_units \*\*\*  
## data\_for\_model$defined\_populations\_simplifiedother \*\*\*  
## data\_for\_model$defined\_populations\_simplifiedother\_combinations \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) dt\_fr\_mdl$dfnd\_ppltns\_smplfdd\_  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdd\_ -0.036   
## dt\_fr\_$\_\_\_\_ -0.015 0.088   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdg\_ -0.015 0.083   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgn\_e\_\_ -0.006 0.034   
## dt\_f\_$\_\_\_g\_ -0.021 0.096   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgg\_e\_\_ -0.023 0.069   
## dt\_f\_$\_\_\_m\_ -0.011 0.058   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdm\_ -0.010 0.054   
## dt\_fr\_md$\_\_ -0.005 0.028   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdt\_ -0.028 0.414   
## d\_\_$\_\_\_\_ dt\_fr\_mdl$dfnd\_ppltns\_smplfdg\_  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdd\_   
## dt\_fr\_$\_\_\_\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdg\_ 0.092   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgn\_e\_\_ 0.094 0.042   
## dt\_f\_$\_\_\_g\_ 0.173 0.131   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgg\_e\_\_ 0.224 0.073   
## dt\_f\_$\_\_\_m\_ 0.140 0.060   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdm\_ 0.145 0.057   
## dt\_fr\_md$\_\_ 0.069 0.031   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdt\_ 0.185 0.120   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgn\_e\_\_ d\_\_$\_g  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdd\_   
## dt\_fr\_$\_\_\_\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdg\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgn\_e\_\_   
## dt\_f\_$\_\_\_g\_ 0.069   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgg\_e\_\_ 0.080 0.141  
## dt\_f\_$\_\_\_m\_ 0.050 0.113  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdm\_ 0.052 0.106  
## dt\_fr\_md$\_\_ 0.026 0.054  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdt\_ 0.072 0.179  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgg\_e\_\_ d\_\_$\_m  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdd\_   
## dt\_fr\_$\_\_\_\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdg\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgn\_e\_\_   
## dt\_f\_$\_\_\_g\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgg\_e\_\_   
## dt\_f\_$\_\_\_m\_ 0.118   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdm\_ 0.123 0.081  
## dt\_fr\_md$\_\_ 0.058 0.038  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdt\_ 0.153 0.113  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdm\_ dt\_\_$\_\_  
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdd\_   
## dt\_fr\_$\_\_\_\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdg\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgn\_e\_\_   
## dt\_f\_$\_\_\_g\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdgg\_e\_\_   
## dt\_f\_$\_\_\_m\_   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdm\_   
## dt\_fr\_md$\_\_ 0.039   
## dt\_fr\_mdl$dfnd\_ppltns\_smplfdt\_ 0.111 0.055

Extending from this result, we also tested whether species range alone is an important predictor of the number of extant populations, as species range is determined by the geographic spread of the species, but not necessarily fragmentation

Does the number of maintained pops vary with range?

m.a3<-glmer(n\_extant\_populations ~ species\_range + (1|country\_assessment), family = "poisson", data = data\_for\_model)  
  
summary(m.a3)

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: poisson ( log )  
## Formula: n\_extant\_populations ~ species\_range + (1 | country\_assessment)  
## Data: data\_for\_model  
##   
## AIC BIC logLik deviance df.resid   
## 27562.5 27576.9 -13778.2 27556.5 916   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -6.726 -2.937 -1.259 -0.054 93.983   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## country\_assessment (Intercept) 0.713 0.8444   
## Number of obs: 919, groups: country\_assessment, 9  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 1.55158 0.28212 5.50 3.81e-08 \*\*\*  
## species\_rangewide\_ranging 0.90544 0.01912 47.35 < 2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr)  
## spcs\_rngwd\_ -0.041

### (b) Does the proportion of maintained populations (indicator2) vary with method used to define populations?

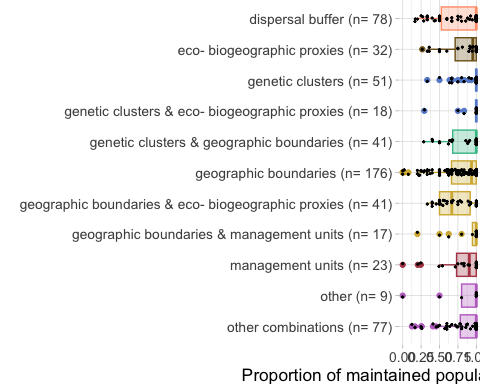
Our next goal was to determine whether study design (i.e. clustering method to define populations) and/or species-level variables (number of populations, range type) appropriately were associated with the measurement of the genetic indicators.

Plot PM indicator by method to define populations:

# Prepare data for plot with nice labels:  
# sample size of TOTAL populations  
sample\_size <- indicators\_full %>%  
 filter(!is.na(indicator2)) %>%   
 filter(n\_extant\_populations<500) %>%   
 group\_by(defined\_populations\_nicenames) %>% summarize(num=n())  
  
# custom axis  
## new dataframe  
df<-indicators\_full %>%   
 filter(n\_extant\_populations<500) %>%  
 filter(!is.na(indicator2)) %>%   
 # add sampling size   
 left\_join(sample\_size) %>%  
 mutate(myaxis = paste0(defined\_populations\_nicenames, " (n= ", num, ")")) %>%  
#myaxis needs levels in the same order than defined\_populations\_nicenames  
 mutate(myaxis = factor(myaxis,   
 levels=levels(as.factor(myaxis))[c(1,12,2:11,13)])) # reorders levels

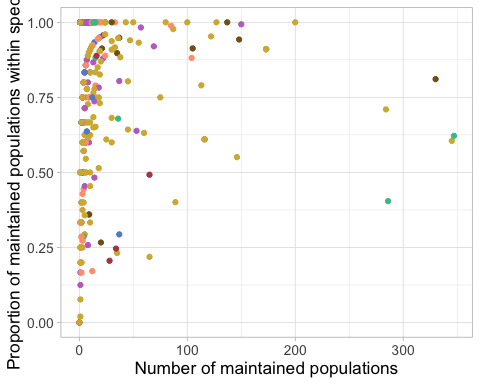
## Joining, by = "defined\_populations\_nicenames"

## plot for Proportion of maintained populations (indicator)  
pb<- df %>%  
 filter(n\_extant\_populations<500) %>%  
 ggplot(aes(x=myaxis, y=indicator2, color=defined\_populations\_nicenames,   
 fill=defined\_populations\_nicenames)) +  
 geom\_boxplot() + xlab("") + ylab("Proportion of maintained populations within species") +  
 geom\_jitter(size=.4, width = 0.1, color="black") +  
 coord\_flip() +  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="none",  
 plot.margin = unit(c(0, 0, 0, 0), "cm")) + # this is used to decrease the space between plots)   
 scale\_fill\_manual(values=alpha(simplifiedmethods\_colors, 0.3),  
 breaks=levels(as.factor(indicators\_full$defined\_populations\_nicenames))) +  
 scale\_color\_manual(values=simplifiedmethods\_colors,  
 breaks=levels(as.factor(indicators\_full$defined\_populations\_nicenames))) +  
 scale\_x\_discrete(limits=rev) +  
 theme(text = element\_text(size = 13))  
pb

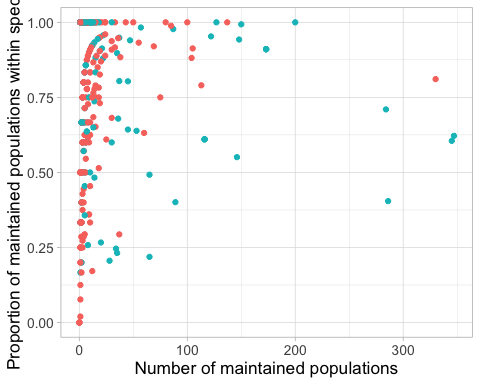


Plot Scatter plot of indicator2 vs extant pops

psupA<- indicators\_full %>%  
 # filter outliers with too many pops and missing data  
 filter(n\_extant\_populations<500) %>%  
 filter(!is.na(indicator2)) %>%  
 filter(!is.na(n\_extant\_populations)) %>%  
 filter(species\_range !="unknown") %>%  
   
 # plot  
 ggplot(aes(x=n\_extant\_populations, y=indicator2, color=defined\_populations\_nicenames)) +  
 geom\_point() +  
 theme\_light() +  
 scale\_color\_manual(values=simplifiedmethods\_colors,  
 breaks=levels(as.factor(indicators\_full$defined\_populations\_nicenames))) +  
 theme(legend.position = "none") +  
 ylab("Proportion of maintained populations within species") +  
 xlab("Number of maintained populations") +  
 theme(text = element\_text(size = 13))  
psupA



psupA.1<- indicators\_full %>%  
 # filter outliers with too many pops and missing data  
 filter(n\_extant\_populations<500) %>%  
 filter(!is.na(indicator2)) %>%  
 filter(!is.na(n\_extant\_populations)) %>%  
 filter(species\_range !="unknown") %>%  
   
 # plot  
 ggplot(aes(x=n\_extant\_populations, y=indicator2, color=species\_range)) +  
 geom\_point() +  
 theme\_light() +  
 theme(legend.position = "none") +  
 ylab("Proportion of maintained populations within species") +  
 xlab("Number of maintained populations") +  
 theme(text = element\_text(size = 13))  
psupA.1



First we want to test if the Proportion of maintained populations (indicator 2) vary with method used.

Prepare data for model (remove outliers and NA in desired variable) and check n:

# remove missing data   
data\_for\_model<-indicators\_full %>%   
 filter(!is.na(indicator2)) %>%  
 filter(n\_extant\_populations<500) # doesn't make a difference in the test below, but useful for plots  
  
# check n per method  
table(data\_for\_model$defined\_populations\_simplified)

##   
## dispersal\_buffer   
## 78   
## eco\_biogeo\_proxies   
## 32   
## genetic\_clusters   
## 51   
## genetic\_clusters eco\_biogeo\_proxies   
## 18   
## genetic\_clusters geographic\_boundaries   
## 41   
## geographic\_boundaries   
## 176   
## geographic\_boundaries eco\_biogeo\_proxies   
## 41   
## geographic\_boundaries management\_units   
## 17   
## management\_units   
## 23   
## other   
## 9   
## other\_combinations   
## 77

# total n  
nrow(data\_for\_model)

## [1] 563

# re-level to use geographic boundaries as reference category for the analysis  
data\_for\_model$defined\_populations\_simplified<-relevel(as.factor(data\_for\_model$defined\_populations\_simplified),  
 ref="geographic\_boundaries")

Run model asking: Does Proportion of maintained populations (indicator 2) vary with method used? Controlling for variation in indicator2 among countries:

m.b1<-glmmTMB(indicator2 ~ defined\_populations\_simplified + (1|country\_assessment), family = "ordbeta", data = data\_for\_model)

See results:

summary(m.b1)

## Family: ordbeta ( logit )  
## Formula:   
## indicator2 ~ defined\_populations\_simplified + (1 | country\_assessment)  
## Data: data\_for\_model  
##   
## AIC BIC logLik deviance df.resid   
## 681.1 746.1 -325.5 651.1 548   
##   
## Random effects:  
##   
## Conditional model:  
## Groups Name Variance Std.Dev.  
## country\_assessment (Intercept) 0.3346 0.5784   
## Number of obs: 563, groups: country\_assessment, 9  
##   
## Dispersion parameter for ordbeta family (): 4.01   
##   
## Conditional model:  
## Estimate  
## (Intercept) 0.58841  
## defined\_populations\_simplifieddispersal\_buffer 0.25985  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.07072  
## defined\_populations\_simplifiedgenetic\_clusters 0.53440  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.84496  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries -0.02910  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies -0.08488  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.34632  
## defined\_populations\_simplifiedmanagement\_units -0.17010  
## defined\_populations\_simplifiedother 0.07577  
## defined\_populations\_simplifiedother\_combinations 0.44042  
## Std. Error  
## (Intercept) 0.22695  
## defined\_populations\_simplifieddispersal\_buffer 0.24779  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.21201  
## defined\_populations\_simplifiedgenetic\_clusters 0.25882  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.44301  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.21721  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.23326  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.33767  
## defined\_populations\_simplifiedmanagement\_units 0.24776  
## defined\_populations\_simplifiedother 0.51341  
## defined\_populations\_simplifiedother\_combinations 0.16779  
## z value  
## (Intercept) 2.593  
## defined\_populations\_simplifieddispersal\_buffer 1.049  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.334  
## defined\_populations\_simplifiedgenetic\_clusters 2.065  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 1.907  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries -0.134  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies -0.364  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 1.026  
## defined\_populations\_simplifiedmanagement\_units -0.686  
## defined\_populations\_simplifiedother 0.148  
## defined\_populations\_simplifiedother\_combinations 2.625  
## Pr(>|z|)  
## (Intercept) 0.00952  
## defined\_populations\_simplifieddispersal\_buffer 0.29432  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.73869  
## defined\_populations\_simplifiedgenetic\_clusters 0.03895  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.05648  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.89343  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.71593  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.30506  
## defined\_populations\_simplifiedmanagement\_units 0.49237  
## defined\_populations\_simplifiedother 0.88267  
## defined\_populations\_simplifiedother\_combinations 0.00867  
##   
## (Intercept) \*\*  
## defined\_populations\_simplifieddispersal\_buffer   
## defined\_populations\_simplifiedeco\_biogeo\_proxies   
## defined\_populations\_simplifiedgenetic\_clusters \*   
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies .   
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries   
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies   
## defined\_populations\_simplifiedgeographic\_boundaries management\_units   
## defined\_populations\_simplifiedmanagement\_units   
## defined\_populations\_simplifiedother   
## defined\_populations\_simplifiedother\_combinations \*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Given the preceding relationships detected between method, number of populations, and species’ range, we investigated associations between these variables and our indicator values in more detail, to aid in understanding the underlying mechanisms that were driving the association between method (especially genetic clusters) and indicator 2. That is, we hypothesised that the relationship between method and indicator 2 may be an indirect result of the association between method and number of populations and species range.

First we added number of populations to our model testing the relationship between method and indicator 2

m.b2<-glmmTMB(indicator2 ~ defined\_populations\_simplified + n\_extant\_populations + (1|country\_assessment), family = "ordbeta", data = data\_for\_model)  
  
summary(m.b2)

## Family: ordbeta ( logit )  
## Formula:   
## indicator2 ~ defined\_populations\_simplified + n\_extant\_populations +   
## (1 | country\_assessment)  
## Data: data\_for\_model  
##   
## AIC BIC logLik deviance df.resid   
## 681.7 751.1 -324.9 649.7 547   
##   
## Random effects:  
##   
## Conditional model:  
## Groups Name Variance Std.Dev.  
## country\_assessment (Intercept) 0.3337 0.5776   
## Number of obs: 563, groups: country\_assessment, 9  
##   
## Dispersion parameter for ordbeta family (): 4.07   
##   
## Conditional model:  
## Estimate  
## (Intercept) 0.567903  
## defined\_populations\_simplifieddispersal\_buffer 0.270059  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.062122  
## defined\_populations\_simplifiedgenetic\_clusters 0.544212  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.873104  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries -0.050636  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies -0.088213  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.373182  
## defined\_populations\_simplifiedmanagement\_units -0.150412  
## defined\_populations\_simplifiedother 0.098218  
## defined\_populations\_simplifiedother\_combinations 0.445949  
## n\_extant\_populations 0.001158  
## Std. Error  
## (Intercept) 0.227117  
## defined\_populations\_simplifieddispersal\_buffer 0.246619  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.210763  
## defined\_populations\_simplifiedgenetic\_clusters 0.258211  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.442994  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.217858  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.233333  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.336928  
## defined\_populations\_simplifiedmanagement\_units 0.247638  
## defined\_populations\_simplifiedother 0.511800  
## defined\_populations\_simplifiedother\_combinations 0.166517  
## n\_extant\_populations 0.001020  
## z value  
## (Intercept) 2.501  
## defined\_populations\_simplifieddispersal\_buffer 1.095  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.295  
## defined\_populations\_simplifiedgenetic\_clusters 2.108  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 1.971  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries -0.232  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies -0.378  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 1.108  
## defined\_populations\_simplifiedmanagement\_units -0.607  
## defined\_populations\_simplifiedother 0.192  
## defined\_populations\_simplifiedother\_combinations 2.678  
## n\_extant\_populations 1.135  
## Pr(>|z|)  
## (Intercept) 0.0124  
## defined\_populations\_simplifieddispersal\_buffer 0.2735  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.7682  
## defined\_populations\_simplifiedgenetic\_clusters 0.0351  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.0487  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.8162  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.7054  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.2680  
## defined\_populations\_simplifiedmanagement\_units 0.5436  
## defined\_populations\_simplifiedother 0.8478  
## defined\_populations\_simplifiedother\_combinations 0.0074  
## n\_extant\_populations 0.2563  
##   
## (Intercept) \*   
## defined\_populations\_simplifieddispersal\_buffer   
## defined\_populations\_simplifiedeco\_biogeo\_proxies   
## defined\_populations\_simplifiedgenetic\_clusters \*   
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies \*   
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries   
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies   
## defined\_populations\_simplifiedgeographic\_boundaries management\_units   
## defined\_populations\_simplifiedmanagement\_units   
## defined\_populations\_simplifiedother   
## defined\_populations\_simplifiedother\_combinations \*\*  
## n\_extant\_populations   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Then we tested (see plot psupA) if there is a relationship between number of maintained populations and the PM indicator, overall, and/or with some methods?

Prepare data for model (remove outliers and NA in desired variable) and check n:

# remove missing data   
data\_for\_model<-indicators\_full %>%   
 filter(!is.na(indicator2)) %>%  
 filter(!is.na(n\_extant\_populations)) %>%  
 filter(n\_extant\_populations<500) # doesn't make a difference in the test below, but useful for plots  
  
# check number of methods  
length(unique(data\_for\_model$defined\_populations\_simplified))

## [1] 11

# check n per method  
table(data\_for\_model$defined\_populations\_simplified)

##   
## dispersal\_buffer   
## 78   
## eco\_biogeo\_proxies   
## 32   
## genetic\_clusters   
## 51   
## genetic\_clusters eco\_biogeo\_proxies   
## 18   
## genetic\_clusters geographic\_boundaries   
## 41   
## geographic\_boundaries   
## 176   
## geographic\_boundaries eco\_biogeo\_proxies   
## 41   
## geographic\_boundaries management\_units   
## 17   
## management\_units   
## 23   
## other   
## 9   
## other\_combinations   
## 77

# total n  
nrow(data\_for\_model)

## [1] 563

# re-level to use geographic boundaries as reference category for the analysis  
data\_for\_model$defined\_populations\_simplified<-relevel(as.factor(data\_for\_model$defined\_populations\_simplified),  
 ref="geographic\_boundaries")

We tested for a relationship between number of populations alone with indicator 2 in our dataset (i.e. when not controlling for method).

Does number of populations alone affect indicator2 (i.e. not controlling for method)?:

msupA1 <- glmmTMB(indicator2 ~ n\_extant\_populations + (1|country\_assessment), family = "ordbeta", data= data\_for\_model)

Summary:

summary(msupA1)

## Family: ordbeta ( logit )  
## Formula: indicator2 ~ n\_extant\_populations + (1 | country\_assessment)  
## Data: data\_for\_model  
##   
## AIC BIC logLik deviance df.resid   
## 679.6 705.6 -333.8 667.6 557   
##   
## Random effects:  
##   
## Conditional model:  
## Groups Name Variance Std.Dev.  
## country\_assessment (Intercept) 0.3213 0.5669   
## Number of obs: 563, groups: country\_assessment, 9  
##   
## Dispersion parameter for ordbeta family (): 4.01   
##   
## Conditional model:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.7078135 0.2053016 3.448 0.000565 \*\*\*  
## n\_extant\_populations 0.0007304 0.0010130 0.721 0.470923   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

But, there were statistically significant interactions between number of populations and some of the methods used, on indicator 2.

Does the effect of method on indicator2 depend on number of maintained pops?

# run model  
msupA2 <- glmmTMB(indicator2 ~ defined\_populations\_simplified + n\_extant\_populations + defined\_populations\_simplified\*n\_extant\_populations + (1|country\_assessment), family = "ordbeta", data = data\_for\_model)

## Warning in (function (start, objective, gradient = NULL, hessian = NULL, : NA/  
## NaN function evaluation

Summary:

summary(msupA2)

## Family: ordbeta ( logit )  
## Formula:   
## indicator2 ~ defined\_populations\_simplified + n\_extant\_populations +   
## defined\_populations\_simplified \* n\_extant\_populations + (1 |   
## country\_assessment)  
## Data: data\_for\_model  
##   
## AIC BIC logLik deviance df.resid   
## 667.8 780.5 -307.9 615.8 537   
##   
## Random effects:  
##   
## Conditional model:  
## Groups Name Variance Std.Dev.  
## country\_assessment (Intercept) 0.3125 0.5591   
## Number of obs: 563, groups: country\_assessment, 9  
##   
## Dispersion parameter for ordbeta family (): 4.64   
##   
## Conditional model:  
## Estimate  
## (Intercept) 0.4925006  
## defined\_populations\_simplifieddispersal\_buffer 0.2460489  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.0188120  
## defined\_populations\_simplifiedgenetic\_clusters 0.5377349  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 2.0994080  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.1492989  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.1119634  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.1085245  
## defined\_populations\_simplifiedmanagement\_units 0.3590284  
## defined\_populations\_simplifiedother -1.4970103  
## defined\_populations\_simplifiedother\_combinations 0.3071256  
## n\_extant\_populations 0.0032484  
## defined\_populations\_simplifieddispersal\_buffer:n\_extant\_populations 0.0054877  
## defined\_populations\_simplifiedeco\_biogeo\_proxies:n\_extant\_populations -0.0003051  
## defined\_populations\_simplifiedgenetic\_clusters:n\_extant\_populations 0.0143372  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:n\_extant\_populations -0.1030565  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:n\_extant\_populations -0.0053672  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:n\_extant\_populations -0.0056177  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:n\_extant\_populations 0.0484225  
## defined\_populations\_simplifiedmanagement\_units:n\_extant\_populations -0.0309641  
## defined\_populations\_simplifiedother:n\_extant\_populations 0.4660849  
## defined\_populations\_simplifiedother\_combinations:n\_extant\_populations 0.0074657  
## Std. Error  
## (Intercept) 0.2237159  
## defined\_populations\_simplifieddispersal\_buffer 0.2488836  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.2386934  
## defined\_populations\_simplifiedgenetic\_clusters 0.3856654  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.6606466  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.2328456  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.2574985  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.4294699  
## defined\_populations\_simplifiedmanagement\_units 0.3349141  
## defined\_populations\_simplifiedother 0.9685209  
## defined\_populations\_simplifiedother\_combinations 0.1918873  
## n\_extant\_populations 0.0016599  
## defined\_populations\_simplifieddispersal\_buffer:n\_extant\_populations 0.0073093  
## defined\_populations\_simplifiedeco\_biogeo\_proxies:n\_extant\_populations 0.0030605  
## defined\_populations\_simplifiedgenetic\_clusters:n\_extant\_populations 0.0617807  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:n\_extant\_populations 0.0330792  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:n\_extant\_populations 0.0025023  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:n\_extant\_populations 0.0028528  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:n\_extant\_populations 0.0531971  
## defined\_populations\_simplifiedmanagement\_units:n\_extant\_populations 0.0149745  
## defined\_populations\_simplifiedother:n\_extant\_populations 0.2848729  
## defined\_populations\_simplifiedother\_combinations:n\_extant\_populations 0.0050503  
## z value  
## (Intercept) 2.201  
## defined\_populations\_simplifieddispersal\_buffer 0.989  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.079  
## defined\_populations\_simplifiedgenetic\_clusters 1.394  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 3.178  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.641  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.435  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.253  
## defined\_populations\_simplifiedmanagement\_units 1.072  
## defined\_populations\_simplifiedother -1.546  
## defined\_populations\_simplifiedother\_combinations 1.601  
## n\_extant\_populations 1.957  
## defined\_populations\_simplifieddispersal\_buffer:n\_extant\_populations 0.751  
## defined\_populations\_simplifiedeco\_biogeo\_proxies:n\_extant\_populations -0.100  
## defined\_populations\_simplifiedgenetic\_clusters:n\_extant\_populations 0.232  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:n\_extant\_populations -3.115  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:n\_extant\_populations -2.145  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:n\_extant\_populations -1.969  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:n\_extant\_populations 0.910  
## defined\_populations\_simplifiedmanagement\_units:n\_extant\_populations -2.068  
## defined\_populations\_simplifiedother:n\_extant\_populations 1.636  
## defined\_populations\_simplifiedother\_combinations:n\_extant\_populations 1.478  
## Pr(>|z|)  
## (Intercept) 0.02770  
## defined\_populations\_simplifieddispersal\_buffer 0.32285  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.93718  
## defined\_populations\_simplifiedgenetic\_clusters 0.16323  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.00148  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.52140  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.66370  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.80050  
## defined\_populations\_simplifiedmanagement\_units 0.28372  
## defined\_populations\_simplifiedother 0.12219  
## defined\_populations\_simplifiedother\_combinations 0.10948  
## n\_extant\_populations 0.05035  
## defined\_populations\_simplifieddispersal\_buffer:n\_extant\_populations 0.45278  
## defined\_populations\_simplifiedeco\_biogeo\_proxies:n\_extant\_populations 0.92060  
## defined\_populations\_simplifiedgenetic\_clusters:n\_extant\_populations 0.81649  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:n\_extant\_populations 0.00184  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:n\_extant\_populations 0.03196  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:n\_extant\_populations 0.04893  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:n\_extant\_populations 0.36269  
## defined\_populations\_simplifiedmanagement\_units:n\_extant\_populations 0.03866  
## defined\_populations\_simplifiedother:n\_extant\_populations 0.10182  
## defined\_populations\_simplifiedother\_combinations:n\_extant\_populations 0.13934  
##   
## (Intercept) \*   
## defined\_populations\_simplifieddispersal\_buffer   
## defined\_populations\_simplifiedeco\_biogeo\_proxies   
## defined\_populations\_simplifiedgenetic\_clusters   
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies \*\*  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries   
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies   
## defined\_populations\_simplifiedgeographic\_boundaries management\_units   
## defined\_populations\_simplifiedmanagement\_units   
## defined\_populations\_simplifiedother   
## defined\_populations\_simplifiedother\_combinations   
## n\_extant\_populations .   
## defined\_populations\_simplifieddispersal\_buffer:n\_extant\_populations   
## defined\_populations\_simplifiedeco\_biogeo\_proxies:n\_extant\_populations   
## defined\_populations\_simplifiedgenetic\_clusters:n\_extant\_populations   
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:n\_extant\_populations \*\*  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:n\_extant\_populations \*   
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:n\_extant\_populations \*   
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:n\_extant\_populations   
## defined\_populations\_simplifiedmanagement\_units:n\_extant\_populations \*   
## defined\_populations\_simplifiedother:n\_extant\_populations   
## defined\_populations\_simplifiedother\_combinations:n\_extant\_populations   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Because the method used to define a population appears to be important for these relationships, we conducted an additional analysis to simplify our analysis to only those species for which a single method was used to determine population clusters, and repeated the model presented above (evaluating a possible interaction between method and number of populations on indicator 2).

First, subset the data to only those taxa where a single method was used:

ind2\_single\_methods<-indicators\_full %>%   
 filter(!is.na(indicator2)) %>%   
 filter(n\_extant\_populations<500) %>% # doesn't make a difference in the test below, but useful for   
 filter(defined\_populations\_simplified=="genetic\_clusters" |   
 defined\_populations\_simplified=="geographic\_boundaries" |  
 defined\_populations\_simplified=="eco\_biogeo\_proxies" |   
 defined\_populations\_simplified=="management\_units" |  
 defined\_populations\_simplified=="dispersal\_buffer")  
  
  
# check number of methods  
length(unique(ind2\_single\_methods$defined\_populations\_simplified))

## [1] 5

# check n by method  
table(ind2\_single\_methods$defined\_populations\_simplified)

##   
## dispersal\_buffer eco\_biogeo\_proxies genetic\_clusters   
## 78 32 51   
## geographic\_boundaries management\_units   
## 176 23

# check n total  
nrow(ind2\_single\_methods)

## [1] 360

# re-level to use geographic boundaries as reference category for the analysis  
ind2\_single\_methods$defined\_populations\_simplified<-relevel(as.factor(ind2\_single\_methods$defined\_populations\_simplified),  
 ref="geographic\_boundaries")

Does the effect of “single” method on indicator2 depend on number of maintained pops?

msupA3<-glmmTMB(indicator2 ~ n\_extant\_populations + defined\_populations\_simplified + n\_extant\_populations\*defined\_populations\_simplified + (1|country\_assessment), family = "ordbeta", data = ind2\_single\_methods)  
  
# summary  
summary(msupA3)

## Family: ordbeta ( logit )  
## Formula:   
## indicator2 ~ n\_extant\_populations + defined\_populations\_simplified +   
## n\_extant\_populations \* defined\_populations\_simplified + (1 |   
## country\_assessment)  
## Data: ind2\_single\_methods  
##   
## AIC BIC logLik deviance df.resid   
## 449.4 503.8 -210.7 421.4 346   
##   
## Random effects:  
##   
## Conditional model:  
## Groups Name Variance Std.Dev.  
## country\_assessment (Intercept) 0.2512 0.5012   
## Number of obs: 360, groups: country\_assessment, 8  
##   
## Dispersion parameter for ordbeta family (): 4.29   
##   
## Conditional model:  
## Estimate  
## (Intercept) 0.4640580  
## n\_extant\_populations 0.0022418  
## defined\_populations\_simplifieddispersal\_buffer 0.2080042  
## defined\_populations\_simplifiedeco\_biogeo\_proxies -0.0533983  
## defined\_populations\_simplifiedgenetic\_clusters 0.7560365  
## defined\_populations\_simplifiedmanagement\_units 0.4187629  
## n\_extant\_populations:defined\_populations\_simplifieddispersal\_buffer 0.0060574  
## n\_extant\_populations:defined\_populations\_simplifiedeco\_biogeo\_proxies 0.0002143  
## n\_extant\_populations:defined\_populations\_simplifiedgenetic\_clusters -0.0009572  
## n\_extant\_populations:defined\_populations\_simplifiedmanagement\_units -0.0345958  
## Std. Error  
## (Intercept) 0.2262534  
## n\_extant\_populations 0.0016874  
## defined\_populations\_simplifieddispersal\_buffer 0.2911548  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.2434107  
## defined\_populations\_simplifiedgenetic\_clusters 0.3879537  
## defined\_populations\_simplifiedmanagement\_units 0.3409384  
## n\_extant\_populations:defined\_populations\_simplifieddispersal\_buffer 0.0073889  
## n\_extant\_populations:defined\_populations\_simplifiedeco\_biogeo\_proxies 0.0030383  
## n\_extant\_populations:defined\_populations\_simplifiedgenetic\_clusters 0.0624312  
## n\_extant\_populations:defined\_populations\_simplifiedmanagement\_units 0.0158856  
## z value  
## (Intercept) 2.051  
## n\_extant\_populations 1.329  
## defined\_populations\_simplifieddispersal\_buffer 0.714  
## defined\_populations\_simplifiedeco\_biogeo\_proxies -0.219  
## defined\_populations\_simplifiedgenetic\_clusters 1.949  
## defined\_populations\_simplifiedmanagement\_units 1.228  
## n\_extant\_populations:defined\_populations\_simplifieddispersal\_buffer 0.820  
## n\_extant\_populations:defined\_populations\_simplifiedeco\_biogeo\_proxies 0.070  
## n\_extant\_populations:defined\_populations\_simplifiedgenetic\_clusters -0.015  
## n\_extant\_populations:defined\_populations\_simplifiedmanagement\_units -2.178  
## Pr(>|z|)  
## (Intercept) 0.0403  
## n\_extant\_populations 0.1840  
## defined\_populations\_simplifieddispersal\_buffer 0.4750  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.8264  
## defined\_populations\_simplifiedgenetic\_clusters 0.0513  
## defined\_populations\_simplifiedmanagement\_units 0.2193  
## n\_extant\_populations:defined\_populations\_simplifieddispersal\_buffer 0.4123  
## n\_extant\_populations:defined\_populations\_simplifiedeco\_biogeo\_proxies 0.9438  
## n\_extant\_populations:defined\_populations\_simplifiedgenetic\_clusters 0.9878  
## n\_extant\_populations:defined\_populations\_simplifiedmanagement\_units 0.0294  
##   
## (Intercept) \*  
## n\_extant\_populations   
## defined\_populations\_simplifieddispersal\_buffer   
## defined\_populations\_simplifiedeco\_biogeo\_proxies   
## defined\_populations\_simplifiedgenetic\_clusters .  
## defined\_populations\_simplifiedmanagement\_units   
## n\_extant\_populations:defined\_populations\_simplifieddispersal\_buffer   
## n\_extant\_populations:defined\_populations\_simplifiedeco\_biogeo\_proxies   
## n\_extant\_populations:defined\_populations\_simplifiedgenetic\_clusters   
## n\_extant\_populations:defined\_populations\_simplifiedmanagement\_units \*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Because we found a relationship between method and number of populations on indicator PM, and a relationship between species range and number of populations, we further tested whether the effect of method on indicator PM is moderated by species range.

First filter data to consider only wide ranging and restricted categories (ie remove unknown due to small sampling size)

## Remove unknown  
data<- indicators\_averaged\_one %>%  
 filter(!is.na(indicator2\_mean)) %>%   
 filter(species\_range !="unknown")  
  
# summary of indicator  
summary(data$indicator2\_mean)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 0.0000 0.6667 1.0000 0.8264 1.0000 1.0000

# re-level to use geographic boundaries as reference category for the analysis  
data$defined\_populations\_simplified<-relevel(as.factor(data$defined\_populations\_simplified),  
 ref="geographic\_boundaries")  
  
# make sure species range is a factor  
data$species\_range<-as.factor(data$species\_range)

Run model: Does method still impact indicator2 if we control for species range?

## + country  
m.b3 <- glmmTMB(indicator2\_mean ~ defined\_populations\_simplified + species\_range + (1|country\_assessment), family = "ordbeta", data = data)  
  
  
# summary results  
summary(m.b3)

## Family: ordbeta ( logit )  
## Formula:   
## indicator2\_mean ~ defined\_populations\_simplified + species\_range +   
## (1 | country\_assessment)  
## Data: data  
##   
## AIC BIC logLik deviance df.resid   
## 604.5 672.1 -286.3 572.5 488   
##   
## Random effects:  
##   
## Conditional model:  
## Groups Name Variance Std.Dev.  
## country\_assessment (Intercept) 0.3345 0.5784   
## Number of obs: 504, groups: country\_assessment, 9  
##   
## Dispersion parameter for ordbeta family (): 4.04   
##   
## Conditional model:  
## Estimate  
## (Intercept) 0.60804  
## defined\_populations\_simplifieddispersal\_buffer 0.08659  
## defined\_populations\_simplifiedeco\_biogeo\_proxies -0.09268  
## defined\_populations\_simplifiedgenetic\_clusters 0.24434  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.17471  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries -0.17172  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies -0.29551  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.25322  
## defined\_populations\_simplifiedmanagement\_units -0.40567  
## defined\_populations\_simplifiedother -0.11961  
## defined\_populations\_simplifiedother\_combinations 0.25855  
## species\_rangewide ranging 0.37873  
## Std. Error  
## (Intercept) 0.23038  
## defined\_populations\_simplifieddispersal\_buffer 0.25664  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.24320  
## defined\_populations\_simplifiedgenetic\_clusters 0.26630  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.52553  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.22064  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.25083  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.33743  
## defined\_populations\_simplifiedmanagement\_units 0.29794  
## defined\_populations\_simplifiedother 0.51439  
## defined\_populations\_simplifiedother\_combinations 0.17706  
## species\_rangewide ranging 0.11803  
## z value  
## (Intercept) 2.639  
## defined\_populations\_simplifieddispersal\_buffer 0.337  
## defined\_populations\_simplifiedeco\_biogeo\_proxies -0.381  
## defined\_populations\_simplifiedgenetic\_clusters 0.918  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.332  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries -0.778  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies -1.178  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.750  
## defined\_populations\_simplifiedmanagement\_units -1.362  
## defined\_populations\_simplifiedother -0.233  
## defined\_populations\_simplifiedother\_combinations 1.460  
## species\_rangewide ranging 3.209  
## Pr(>|z|)  
## (Intercept) 0.00831  
## defined\_populations\_simplifieddispersal\_buffer 0.73581  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.70315  
## defined\_populations\_simplifiedgenetic\_clusters 0.35885  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.73955  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.43640  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.23876  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.45299  
## defined\_populations\_simplifiedmanagement\_units 0.17333  
## defined\_populations\_simplifiedother 0.81613  
## defined\_populations\_simplifiedother\_combinations 0.14422  
## species\_rangewide ranging 0.00133  
##   
## (Intercept) \*\*  
## defined\_populations\_simplifieddispersal\_buffer   
## defined\_populations\_simplifiedeco\_biogeo\_proxies   
## defined\_populations\_simplifiedgenetic\_clusters   
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies   
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries   
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies   
## defined\_populations\_simplifiedgeographic\_boundaries management\_units   
## defined\_populations\_simplifiedmanagement\_units   
## defined\_populations\_simplifiedother   
## defined\_populations\_simplifiedother\_combinations   
## species\_rangewide ranging \*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Similarly to the effect of number of populations on indicator 2, we further tested whether there was an interaction between method and species range, i.e. to determine whether species range was only associated with indicator 2 for some methods.

## run model   
m.b4 <- glmmTMB(indicator2\_mean ~ defined\_populations\_simplified + species\_range + defined\_populations\_simplified\*species\_range + (1|country\_assessment), family = "ordbeta", data = data)  
  
  
# summary results  
summary(m.b4)

## Family: ordbeta ( logit )  
## Formula:   
## indicator2\_mean ~ defined\_populations\_simplified + species\_range +   
## defined\_populations\_simplified \* species\_range + (1 | country\_assessment)  
## Data: data  
##   
## AIC BIC logLik deviance df.resid   
## 610.0 719.8 -279.0 558.0 478   
##   
## Random effects:  
##   
## Conditional model:  
## Groups Name Variance Std.Dev.  
## country\_assessment (Intercept) 0.3401 0.5831   
## Number of obs: 504, groups: country\_assessment, 9  
##   
## Dispersion parameter for ordbeta family (): 4.23   
##   
## Conditional model:  
## Estimate  
## (Intercept) 5.606e-01  
## defined\_populations\_simplifieddispersal\_buffer 2.209e-01  
## defined\_populations\_simplifiedeco\_biogeo\_proxies -1.726e-01  
## defined\_populations\_simplifiedgenetic\_clusters 1.575e-01  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies -2.853e-01  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries -2.155e-01  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies -4.549e-02  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 6.932e-02  
## defined\_populations\_simplifiedmanagement\_units 2.216e-02  
## defined\_populations\_simplifiedother -3.876e-01  
## defined\_populations\_simplifiedother\_combinations 2.774e-01  
## species\_rangewide ranging 5.126e-01  
## defined\_populations\_simplifieddispersal\_buffer:species\_rangewide ranging -3.300e-01  
## defined\_populations\_simplifiedeco\_biogeo\_proxies:species\_rangewide ranging 4.776e-02  
## defined\_populations\_simplifiedgenetic\_clusters:species\_rangewide ranging 6.842e-02  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:species\_rangewide ranging 1.977e+01  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:species\_rangewide ranging 5.824e-02  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:species\_rangewide ranging -7.361e-01  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:species\_rangewide ranging 6.680e-01  
## defined\_populations\_simplifiedmanagement\_units:species\_rangewide ranging -9.713e-01  
## defined\_populations\_simplifiedother:species\_rangewide ranging 1.859e+01  
## defined\_populations\_simplifiedother\_combinations:species\_rangewide ranging -1.222e-01  
## Std. Error  
## (Intercept) 2.342e-01  
## defined\_populations\_simplifieddispersal\_buffer 2.883e-01  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 3.146e-01  
## defined\_populations\_simplifiedgenetic\_clusters 4.044e-01  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 5.450e-01  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 2.648e-01  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 2.938e-01  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 3.766e-01  
## defined\_populations\_simplifiedmanagement\_units 4.014e-01  
## defined\_populations\_simplifiedother 5.286e-01  
## defined\_populations\_simplifiedother\_combinations 2.308e-01  
## species\_rangewide ranging 2.258e-01  
## defined\_populations\_simplifieddispersal\_buffer:species\_rangewide ranging 3.497e-01  
## defined\_populations\_simplifiedeco\_biogeo\_proxies:species\_rangewide ranging 4.812e-01  
## defined\_populations\_simplifiedgenetic\_clusters:species\_rangewide ranging 5.398e-01  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:species\_rangewide ranging 1.042e+04  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:species\_rangewide ranging 4.622e-01  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:species\_rangewide ranging 4.543e-01  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:species\_rangewide ranging 8.601e-01  
## defined\_populations\_simplifiedmanagement\_units:species\_rangewide ranging 5.937e-01  
## defined\_populations\_simplifiedother:species\_rangewide ranging 7.096e+03  
## defined\_populations\_simplifiedother\_combinations:species\_rangewide ranging 3.750e-01  
## z value  
## (Intercept) 2.394  
## defined\_populations\_simplifieddispersal\_buffer 0.766  
## defined\_populations\_simplifiedeco\_biogeo\_proxies -0.549  
## defined\_populations\_simplifiedgenetic\_clusters 0.390  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies -0.523  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries -0.814  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies -0.155  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.184  
## defined\_populations\_simplifiedmanagement\_units 0.055  
## defined\_populations\_simplifiedother -0.733  
## defined\_populations\_simplifiedother\_combinations 1.202  
## species\_rangewide ranging 2.270  
## defined\_populations\_simplifieddispersal\_buffer:species\_rangewide ranging -0.944  
## defined\_populations\_simplifiedeco\_biogeo\_proxies:species\_rangewide ranging 0.099  
## defined\_populations\_simplifiedgenetic\_clusters:species\_rangewide ranging 0.127  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:species\_rangewide ranging 0.002  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:species\_rangewide ranging 0.126  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:species\_rangewide ranging -1.620  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:species\_rangewide ranging 0.777  
## defined\_populations\_simplifiedmanagement\_units:species\_rangewide ranging -1.636  
## defined\_populations\_simplifiedother:species\_rangewide ranging 0.003  
## defined\_populations\_simplifiedother\_combinations:species\_rangewide ranging -0.326  
## Pr(>|z|)  
## (Intercept) 0.0167  
## defined\_populations\_simplifieddispersal\_buffer 0.4434  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.5833  
## defined\_populations\_simplifiedgenetic\_clusters 0.6969  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.6006  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.4159  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.8770  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.8540  
## defined\_populations\_simplifiedmanagement\_units 0.9560  
## defined\_populations\_simplifiedother 0.4634  
## defined\_populations\_simplifiedother\_combinations 0.2293  
## species\_rangewide ranging 0.0232  
## defined\_populations\_simplifieddispersal\_buffer:species\_rangewide ranging 0.3454  
## defined\_populations\_simplifiedeco\_biogeo\_proxies:species\_rangewide ranging 0.9209  
## defined\_populations\_simplifiedgenetic\_clusters:species\_rangewide ranging 0.8991  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:species\_rangewide ranging 0.9985  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:species\_rangewide ranging 0.8997  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:species\_rangewide ranging 0.1052  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:species\_rangewide ranging 0.4374  
## defined\_populations\_simplifiedmanagement\_units:species\_rangewide ranging 0.1018  
## defined\_populations\_simplifiedother:species\_rangewide ranging 0.9979  
## defined\_populations\_simplifiedother\_combinations:species\_rangewide ranging 0.7445  
##   
## (Intercept) \*  
## defined\_populations\_simplifieddispersal\_buffer   
## defined\_populations\_simplifiedeco\_biogeo\_proxies   
## defined\_populations\_simplifiedgenetic\_clusters   
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies   
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries   
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies   
## defined\_populations\_simplifiedgeographic\_boundaries management\_units   
## defined\_populations\_simplifiedmanagement\_units   
## defined\_populations\_simplifiedother   
## defined\_populations\_simplifiedother\_combinations   
## species\_rangewide ranging \*  
## defined\_populations\_simplifieddispersal\_buffer:species\_rangewide ranging   
## defined\_populations\_simplifiedeco\_biogeo\_proxies:species\_rangewide ranging   
## defined\_populations\_simplifiedgenetic\_clusters:species\_rangewide ranging   
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:species\_rangewide ranging   
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:species\_rangewide ranging   
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:species\_rangewide ranging   
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:species\_rangewide ranging   
## defined\_populations\_simplifiedmanagement\_units:species\_rangewide ranging   
## defined\_populations\_simplifiedother:species\_rangewide ranging   
## defined\_populations\_simplifiedother\_combinations:species\_rangewide ranging   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

### (c) Proportion of populations with Ne>500 (indicator1)

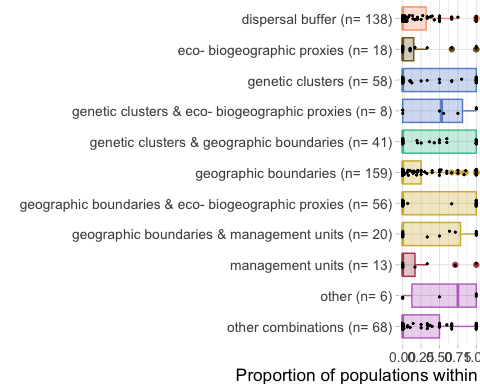
Our analysis of Ne indicator followed a parallel structure to our analysis of PM indicator.

Plot Ne indicator by method to define pops.

# Prepare data for plot with nice labels:  
# sample size of TOTAL populations  
sample\_size <- indicators\_full %>%  
 filter(!is.na(indicator1)) %>%   
 filter(n\_extant\_populations<500) %>%   
 group\_by(defined\_populations\_nicenames) %>% summarize(num=n())  
  
# custom axis  
## new dataframe  
df<-indicators\_full %>%   
 filter(n\_extant\_populations<500) %>%  
 filter(!is.na(indicator1)) %>%   
 # add sampling size   
 left\_join(sample\_size) %>%  
 mutate(myaxis = paste0(defined\_populations\_nicenames, " (n= ", num, ")")) %>%  
#myaxis needs levels in the same order than defined\_populations\_nicenames  
 mutate(myaxis = factor(myaxis,   
 levels=levels(as.factor(myaxis))[c(1,12,2:11,13)])) # reorders levels

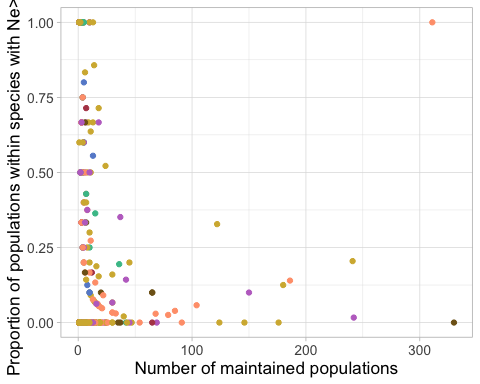
## Joining, by = "defined\_populations\_nicenames"

## plot   
pc<- df %>%  
 ggplot(aes(x=myaxis, y=indicator1, color=defined\_populations\_nicenames,   
 fill=defined\_populations\_nicenames)) +  
 geom\_boxplot() + xlab("") + ylab("Proportion of populations within species with Ne>500") +  
 geom\_jitter(size=.4, width = 0.1, color="black") +  
 coord\_flip() +  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="none",  
 plot.margin = unit(c(0, 0, 0, 0), "cm")) + # this is used to decrease the space between plots)   
 scale\_fill\_manual(values=alpha(simplifiedmethods\_colors, 0.3),  
 breaks=levels(as.factor(indicators\_full$defined\_populations\_nicenames))) +  
 scale\_color\_manual(values=simplifiedmethods\_colors,  
 breaks=levels(as.factor(indicators\_full$defined\_populations\_nicenames))) +  
 scale\_x\_discrete(limits=rev) +  
 theme(text = element\_text(size = 13))  
pc

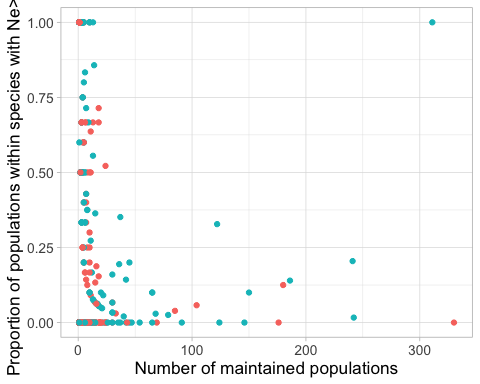


Scatter plot of indicator1 vs extant pops

psupB<- indicators\_full %>%  
 # filter outliers with too many pops and missing data  
 filter(n\_extant\_populations<500) %>%  
 filter(!is.na(indicator1)) %>%  
 filter(!is.na(n\_extant\_populations)) %>%  
 filter(species\_range !="unknown") %>%  
   
   
 # plot  
 ggplot(aes(x=n\_extant\_populations, y=indicator1, color=defined\_populations\_nicenames)) +  
 geom\_point() +  
 theme\_light() +  
 scale\_color\_manual(values=simplifiedmethods\_colors,  
 breaks=levels(as.factor(indicators\_full$defined\_populations\_nicenames))) +  
 theme(legend.position = "none") +  
 ylab("Proportion of populations within species with Ne>500") +  
 xlab("Number of maintained populations") +  
 theme(text = element\_text(size = 13))  
psupB



## Coloring by range   
psupB.1<- indicators\_full %>%  
 # filter outliers with too many pops and missing data  
 filter(n\_extant\_populations<500) %>%  
 filter(!is.na(indicator1)) %>%  
 filter(!is.na(n\_extant\_populations)) %>%  
 filter(species\_range !="unknown") %>%  
   
   
 # plot  
 ggplot(aes(x=n\_extant\_populations, y=indicator1, color=species\_range)) +  
 geom\_point() +  
 theme\_light() +  
 theme(legend.position = "none") +  
 ylab("Proportion of populations within species with Ne>500") +  
 xlab("Number of maintained populations") +  
 theme(text = element\_text(size = 13))  
psupB.1



First we tested whether method used was associated with variation in indicator (figure c)

Prepare data for model (remove outliers and NA in desired variable) and check n:

# remove missing data   
data\_for\_model<-indicators\_full %>%   
 filter(!is.na(indicator1)) %>%  
 filter(n\_extant\_populations<500) # doesn't make a difference in the test below, but useful for plots  
  
# check n per method  
table(data\_for\_model$defined\_populations\_simplified)

##   
## dispersal\_buffer   
## 138   
## eco\_biogeo\_proxies   
## 18   
## genetic\_clusters   
## 58   
## genetic\_clusters eco\_biogeo\_proxies   
## 8   
## genetic\_clusters geographic\_boundaries   
## 41   
## geographic\_boundaries   
## 159   
## geographic\_boundaries eco\_biogeo\_proxies   
## 56   
## geographic\_boundaries management\_units   
## 20   
## management\_units   
## 13   
## other   
## 6   
## other\_combinations   
## 68

# total n  
nrow(data\_for\_model)

## [1] 585

# re-level to use geographic boundaries as reference category for the analysis  
data\_for\_model$defined\_populations\_simplified<-relevel(as.factor(data\_for\_model$defined\_populations\_simplified),  
 ref="geographic\_boundaries")

Run model asking: Does Ne indicator vary with method used? Controlling for variation in indicator among countries:

m.c1<-glmmTMB(indicator1 ~ defined\_populations\_simplified + (1|country\_assessment), family = "ordbeta", data = data\_for\_model)

See results:

summary(m.c1)

## Family: ordbeta ( logit )  
## Formula:   
## indicator1 ~ defined\_populations\_simplified + (1 | country\_assessment)  
## Data: data\_for\_model  
##   
## AIC BIC logLik deviance df.resid   
## 1082.2 1147.8 -526.1 1052.2 570   
##   
## Random effects:  
##   
## Conditional model:  
## Groups Name Variance Std.Dev.  
## country\_assessment (Intercept) 0.08216 0.2866   
## Number of obs: 585, groups: country\_assessment, 9  
##   
## Dispersion parameter for ordbeta family (): 3.88   
##   
## Conditional model:  
## Estimate  
## (Intercept) -0.87277  
## defined\_populations\_simplifieddispersal\_buffer 0.29210  
## defined\_populations\_simplifiedeco\_biogeo\_proxies -0.17477  
## defined\_populations\_simplifiedgenetic\_clusters 0.51445  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 1.03077  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.52363  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies -0.09502  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.62861  
## defined\_populations\_simplifiedmanagement\_units -0.04810  
## defined\_populations\_simplifiedother 1.05279  
## defined\_populations\_simplifiedother\_combinations 0.35747  
## Std. Error  
## (Intercept) 0.17691  
## defined\_populations\_simplifieddispersal\_buffer 0.30559  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.31388  
## defined\_populations\_simplifiedgenetic\_clusters 0.23409  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.43867  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.24584  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.33583  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.33280  
## defined\_populations\_simplifiedmanagement\_units 0.41720  
## defined\_populations\_simplifiedother 0.62077  
## defined\_populations\_simplifiedother\_combinations 0.20335  
## z value  
## (Intercept) -4.934  
## defined\_populations\_simplifieddispersal\_buffer 0.956  
## defined\_populations\_simplifiedeco\_biogeo\_proxies -0.557  
## defined\_populations\_simplifiedgenetic\_clusters 2.198  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 2.350  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 2.130  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies -0.283  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 1.889  
## defined\_populations\_simplifiedmanagement\_units -0.115  
## defined\_populations\_simplifiedother 1.696  
## defined\_populations\_simplifiedother\_combinations 1.758  
## Pr(>|z|)  
## (Intercept) 8.07e-07  
## defined\_populations\_simplifieddispersal\_buffer 0.3391  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.5777  
## defined\_populations\_simplifiedgenetic\_clusters 0.0280  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.0188  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.0332  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.7772  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.0589  
## defined\_populations\_simplifiedmanagement\_units 0.9082  
## defined\_populations\_simplifiedother 0.0899  
## defined\_populations\_simplifiedother\_combinations 0.0788  
##   
## (Intercept) \*\*\*  
## defined\_populations\_simplifieddispersal\_buffer   
## defined\_populations\_simplifiedeco\_biogeo\_proxies   
## defined\_populations\_simplifiedgenetic\_clusters \*   
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies \*   
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries \*   
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies   
## defined\_populations\_simplifiedgeographic\_boundaries management\_units .   
## defined\_populations\_simplifiedmanagement\_units   
## defined\_populations\_simplifiedother .   
## defined\_populations\_simplifiedother\_combinations .   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

we next investigated whether the relationships between methods and the indicator were moderated by the role of number of populations and species range. Ie:

Does method still influence indicator1 if we control for number of populations?

m.c2 <- glmmTMB(indicator1 ~ defined\_populations\_simplified + n\_extant\_populations + (1|country\_assessment), family = "ordbeta", data = data\_for\_model)  
  
summary(m.c2)

## Family: ordbeta ( logit )  
## Formula:   
## indicator1 ~ defined\_populations\_simplified + n\_extant\_populations +   
## (1 | country\_assessment)  
## Data: data\_for\_model  
##   
## AIC BIC logLik deviance df.resid   
## 1076.2 1146.2 -522.1 1044.2 569   
##   
## Random effects:  
##   
## Conditional model:  
## Groups Name Variance Std.Dev.  
## country\_assessment (Intercept) 0.05326 0.2308   
## Number of obs: 585, groups: country\_assessment, 9  
##   
## Dispersion parameter for ordbeta family (): 4.28   
##   
## Conditional model:  
## Estimate  
## (Intercept) -0.747106  
## defined\_populations\_simplifieddispersal\_buffer 0.168023  
## defined\_populations\_simplifiedeco\_biogeo\_proxies -0.130620  
## defined\_populations\_simplifiedgenetic\_clusters 0.434933  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.979502  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.471630  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies -0.124338  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.616210  
## defined\_populations\_simplifiedmanagement\_units -0.065216  
## defined\_populations\_simplifiedother 0.961420  
## defined\_populations\_simplifiedother\_combinations 0.356210  
## n\_extant\_populations -0.004787  
## Std. Error  
## (Intercept) 0.167921  
## defined\_populations\_simplifieddispersal\_buffer 0.284721  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.306985  
## defined\_populations\_simplifiedgenetic\_clusters 0.229850  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.425920  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.241430  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.320972  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.325202  
## defined\_populations\_simplifiedmanagement\_units 0.405594  
## defined\_populations\_simplifiedother 0.613489  
## defined\_populations\_simplifiedother\_combinations 0.196025  
## n\_extant\_populations 0.001795  
## z value  
## (Intercept) -4.449  
## defined\_populations\_simplifieddispersal\_buffer 0.590  
## defined\_populations\_simplifiedeco\_biogeo\_proxies -0.425  
## defined\_populations\_simplifiedgenetic\_clusters 1.892  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 2.300  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 1.953  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies -0.387  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 1.895  
## defined\_populations\_simplifiedmanagement\_units -0.161  
## defined\_populations\_simplifiedother 1.567  
## defined\_populations\_simplifiedother\_combinations 1.817  
## n\_extant\_populations -2.667  
## Pr(>|z|)  
## (Intercept) 8.62e-06  
## defined\_populations\_simplifieddispersal\_buffer 0.55510  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.67048  
## defined\_populations\_simplifiedgenetic\_clusters 0.05846  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.02146  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.05076  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.69848  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.05811  
## defined\_populations\_simplifiedmanagement\_units 0.87226  
## defined\_populations\_simplifiedother 0.11708  
## defined\_populations\_simplifiedother\_combinations 0.06919  
## n\_extant\_populations 0.00765  
##   
## (Intercept) \*\*\*  
## defined\_populations\_simplifieddispersal\_buffer   
## defined\_populations\_simplifiedeco\_biogeo\_proxies   
## defined\_populations\_simplifiedgenetic\_clusters .   
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies \*   
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries .   
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies   
## defined\_populations\_simplifiedgeographic\_boundaries management\_units .   
## defined\_populations\_simplifiedmanagement\_units   
## defined\_populations\_simplifiedother   
## defined\_populations\_simplifiedother\_combinations .   
## n\_extant\_populations \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

We then tested if there a relationship between number of maintained populations and indicator1, overall, and/or with some methods? (model associated to plot psupB)

Prepare data for model (remove outliers and NA in desired variable) and check n:

# remove missing data   
data\_for\_model<-indicators\_full %>%   
 filter(!is.na(indicator1)) %>%  
 filter(!is.na(n\_extant\_populations)) %>%  
 filter(n\_extant\_populations<500) # doesn't make a difference in the test below, but useful for plots  
  
# check number of methods  
length(unique(data\_for\_model$defined\_populations\_simplified))

## [1] 11

# check n per method  
table(data\_for\_model$defined\_populations\_simplified)

##   
## dispersal\_buffer   
## 138   
## eco\_biogeo\_proxies   
## 18   
## genetic\_clusters   
## 58   
## genetic\_clusters eco\_biogeo\_proxies   
## 8   
## genetic\_clusters geographic\_boundaries   
## 41   
## geographic\_boundaries   
## 159   
## geographic\_boundaries eco\_biogeo\_proxies   
## 56   
## geographic\_boundaries management\_units   
## 20   
## management\_units   
## 13   
## other   
## 6   
## other\_combinations   
## 68

# total n  
nrow(data\_for\_model)

## [1] 585

# re-level to use geographic boundaries as reference category for the analysis  
data\_for\_model$defined\_populations\_simplified<-relevel(as.factor(data\_for\_model$defined\_populations\_simplified),  
 ref="geographic\_boundaries")

Does the number of maintained pops alone affect the Ne indicator? (i.e. not controlling for method)

msupB1<-glmmTMB(indicator1 ~ n\_extant\_populations + (1|country\_assessment), family = "ordbeta", data= data\_for\_model)

Summary:

summary(msupB1)

## Family: ordbeta ( logit )  
## Formula: indicator1 ~ n\_extant\_populations + (1 | country\_assessment)  
## Data: data\_for\_model  
##   
## AIC BIC logLik deviance df.resid   
## 1073.1 1099.4 -530.6 1061.1 579   
##   
## Random effects:  
##   
## Conditional model:  
## Groups Name Variance Std.Dev.  
## country\_assessment (Intercept) 0.05368 0.2317   
## Number of obs: 585, groups: country\_assessment, 9  
##   
## Dispersion parameter for ordbeta family (): 4.08   
##   
## Conditional model:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -0.523723 0.119543 -4.381 1.18e-05 \*\*\*  
## n\_extant\_populations -0.005059 0.001786 -2.832 0.00462 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Does the effect of method depend on the number of populations? Or put another way, does the importance of number of populations also depend on method?

# run model  
msupB2 <- glmmTMB(indicator1 ~ defined\_populations\_simplified + n\_extant\_populations + defined\_populations\_simplified\*n\_extant\_populations + (1|country\_assessment), family = "ordbeta", data = data\_for\_model)

## Warning in (function (start, objective, gradient = NULL, hessian = NULL, : NA/  
## NaN function evaluation

Summary:

summary(msupB2)

## Family: ordbeta ( logit )  
## Formula:   
## indicator1 ~ defined\_populations\_simplified + n\_extant\_populations +   
## defined\_populations\_simplified \* n\_extant\_populations + (1 |   
## country\_assessment)  
## Data: data\_for\_model  
##   
## AIC BIC logLik deviance df.resid   
## 1073.3 1187.0 -510.7 1021.3 559   
##   
## Random effects:  
##   
## Conditional model:  
## Groups Name Variance Std.Dev.  
## country\_assessment (Intercept) 0.08117 0.2849   
## Number of obs: 585, groups: country\_assessment, 9  
##   
## Dispersion parameter for ordbeta family (): 4.61   
##   
## Conditional model:  
## Estimate  
## (Intercept) -0.852589  
## defined\_populations\_simplifieddispersal\_buffer 0.334354  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.153242  
## defined\_populations\_simplifiedgenetic\_clusters 1.245572  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 1.039658  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.679947  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.657931  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.977634  
## defined\_populations\_simplifiedmanagement\_units 0.393156  
## defined\_populations\_simplifiedother -0.833994  
## defined\_populations\_simplifiedother\_combinations 0.453543  
## n\_extant\_populations -0.001760  
## defined\_populations\_simplifieddispersal\_buffer:n\_extant\_populations -0.003768  
## defined\_populations\_simplifiedeco\_biogeo\_proxies:n\_extant\_populations -0.013816  
## defined\_populations\_simplifiedgenetic\_clusters:n\_extant\_populations -0.173984  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:n\_extant\_populations 0.010480  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:n\_extant\_populations -0.015563  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:n\_extant\_populations -0.111981  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:n\_extant\_populations -0.029675  
## defined\_populations\_simplifiedmanagement\_units:n\_extant\_populations -0.054893  
## defined\_populations\_simplifiedother:n\_extant\_populations 0.726473  
## defined\_populations\_simplifiedother\_combinations:n\_extant\_populations -0.003624  
## Std. Error  
## (Intercept) 0.184087  
## defined\_populations\_simplifieddispersal\_buffer 0.281372  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.405021  
## defined\_populations\_simplifiedgenetic\_clusters 0.359940  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.628292  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.305385  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.492350  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.412312  
## defined\_populations\_simplifiedmanagement\_units 0.606730  
## defined\_populations\_simplifiedother 1.578475  
## defined\_populations\_simplifiedother\_combinations 0.205909  
## n\_extant\_populations 0.002589  
## defined\_populations\_simplifieddispersal\_buffer:n\_extant\_populations 0.004387  
## defined\_populations\_simplifiedeco\_biogeo\_proxies:n\_extant\_populations 0.011100  
## defined\_populations\_simplifiedgenetic\_clusters:n\_extant\_populations 0.064272  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:n\_extant\_populations 0.084200  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:n\_extant\_populations 0.022474  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:n\_extant\_populations 0.058478  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:n\_extant\_populations 0.028637  
## defined\_populations\_simplifiedmanagement\_units:n\_extant\_populations 0.067364  
## defined\_populations\_simplifiedother:n\_extant\_populations 0.792738  
## defined\_populations\_simplifiedother\_combinations:n\_extant\_populations 0.003936  
## z value  
## (Intercept) -4.631  
## defined\_populations\_simplifieddispersal\_buffer 1.188  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.378  
## defined\_populations\_simplifiedgenetic\_clusters 3.460  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 1.655  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 2.227  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 1.336  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 2.371  
## defined\_populations\_simplifiedmanagement\_units 0.648  
## defined\_populations\_simplifiedother -0.528  
## defined\_populations\_simplifiedother\_combinations 2.203  
## n\_extant\_populations -0.680  
## defined\_populations\_simplifieddispersal\_buffer:n\_extant\_populations -0.859  
## defined\_populations\_simplifiedeco\_biogeo\_proxies:n\_extant\_populations -1.245  
## defined\_populations\_simplifiedgenetic\_clusters:n\_extant\_populations -2.707  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:n\_extant\_populations 0.124  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:n\_extant\_populations -0.693  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:n\_extant\_populations -1.915  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:n\_extant\_populations -1.036  
## defined\_populations\_simplifiedmanagement\_units:n\_extant\_populations -0.815  
## defined\_populations\_simplifiedother:n\_extant\_populations 0.916  
## defined\_populations\_simplifiedother\_combinations:n\_extant\_populations -0.921  
## Pr(>|z|)  
## (Intercept) 3.63e-06  
## defined\_populations\_simplifieddispersal\_buffer 0.234716  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.705167  
## defined\_populations\_simplifiedgenetic\_clusters 0.000539  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.097978  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.025979  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.181449  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.017735  
## defined\_populations\_simplifiedmanagement\_units 0.516991  
## defined\_populations\_simplifiedother 0.597254  
## defined\_populations\_simplifiedother\_combinations 0.027620  
## n\_extant\_populations 0.496614  
## defined\_populations\_simplifieddispersal\_buffer:n\_extant\_populations 0.390425  
## defined\_populations\_simplifiedeco\_biogeo\_proxies:n\_extant\_populations 0.213261  
## defined\_populations\_simplifiedgenetic\_clusters:n\_extant\_populations 0.006790  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:n\_extant\_populations 0.900943  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:n\_extant\_populations 0.488612  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:n\_extant\_populations 0.055503  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:n\_extant\_populations 0.300085  
## defined\_populations\_simplifiedmanagement\_units:n\_extant\_populations 0.415149  
## defined\_populations\_simplifiedother:n\_extant\_populations 0.359452  
## defined\_populations\_simplifiedother\_combinations:n\_extant\_populations 0.357200  
##   
## (Intercept) \*\*\*  
## defined\_populations\_simplifieddispersal\_buffer   
## defined\_populations\_simplifiedeco\_biogeo\_proxies   
## defined\_populations\_simplifiedgenetic\_clusters \*\*\*  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies .   
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries \*   
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies   
## defined\_populations\_simplifiedgeographic\_boundaries management\_units \*   
## defined\_populations\_simplifiedmanagement\_units   
## defined\_populations\_simplifiedother   
## defined\_populations\_simplifiedother\_combinations \*   
## n\_extant\_populations   
## defined\_populations\_simplifieddispersal\_buffer:n\_extant\_populations   
## defined\_populations\_simplifiedeco\_biogeo\_proxies:n\_extant\_populations   
## defined\_populations\_simplifiedgenetic\_clusters:n\_extant\_populations \*\*   
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:n\_extant\_populations   
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:n\_extant\_populations   
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:n\_extant\_populations .   
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:n\_extant\_populations   
## defined\_populations\_simplifiedmanagement\_units:n\_extant\_populations   
## defined\_populations\_simplifiedother:n\_extant\_populations   
## defined\_populations\_simplifiedother\_combinations:n\_extant\_populations   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Because “what’s a population and how do you define them?” is such an important question, we can also test the effect of methods alone. First, subset the data to only those taxa where a single method was used:

ind1\_single\_methods<-indicators\_full %>%   
 filter(!is.na(indicator1)) %>%   
 filter(n\_extant\_populations<500) %>% # doesn't make a difference in the test below, but useful for   
 filter(defined\_populations\_simplified=="genetic\_clusters" |   
 defined\_populations\_simplified=="geographic\_boundaries" |  
 defined\_populations\_simplified=="eco\_biogeo\_proxies" |   
 defined\_populations\_simplified=="management\_units" |  
 defined\_populations\_simplified=="dispersal\_buffer")  
  
  
# check number of methods  
length(unique(ind1\_single\_methods$defined\_populations\_simplified))

## [1] 5

# check n by method  
table(ind1\_single\_methods$defined\_populations\_simplified)

##   
## dispersal\_buffer eco\_biogeo\_proxies genetic\_clusters   
## 138 18 58   
## geographic\_boundaries management\_units   
## 159 13

# check n total  
nrow(ind1\_single\_methods)

## [1] 386

# re-level to use geographic boundaries as reference category for the analysis  
ind1\_single\_methods$defined\_populations\_simplified<-relevel(as.factor(ind1\_single\_methods$defined\_populations\_simplified),  
 ref="geographic\_boundaries")

Run model:

# run model  
msupB3 <- glmmTMB(indicator1 ~ n\_extant\_populations + defined\_populations\_simplified + n\_extant\_populations\*defined\_populations\_simplified + (1|country\_assessment), family = "ordbeta", data = ind1\_single\_methods)

## Warning in (function (start, objective, gradient = NULL, hessian = NULL, : NA/  
## NaN function evaluation

Summary:

summary(msupB3)

## Family: ordbeta ( logit )  
## Formula:   
## indicator1 ~ n\_extant\_populations + defined\_populations\_simplified +   
## n\_extant\_populations \* defined\_populations\_simplified + (1 |   
## country\_assessment)  
## Data: ind1\_single\_methods  
##   
## AIC BIC logLik deviance df.resid   
## 696.5 751.9 -334.3 668.5 372   
##   
## Random effects:  
##   
## Conditional model:  
## Groups Name Variance Std.Dev.  
## country\_assessment (Intercept) 0.06442 0.2538   
## Number of obs: 386, groups: country\_assessment, 8  
##   
## Dispersion parameter for ordbeta family (): 3.82   
##   
## Conditional model:  
## Estimate  
## (Intercept) -0.8202422  
## n\_extant\_populations -0.0004588  
## defined\_populations\_simplifieddispersal\_buffer 0.2073110  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.1552506  
## defined\_populations\_simplifiedgenetic\_clusters 1.1421148  
## defined\_populations\_simplifiedmanagement\_units 0.3522263  
## n\_extant\_populations:defined\_populations\_simplifieddispersal\_buffer -0.0035240  
## n\_extant\_populations:defined\_populations\_simplifiedeco\_biogeo\_proxies -0.0119132  
## n\_extant\_populations:defined\_populations\_simplifiedgenetic\_clusters -0.1530545  
## n\_extant\_populations:defined\_populations\_simplifiedmanagement\_units -0.0501060  
## Std. Error  
## (Intercept) 0.2069251  
## n\_extant\_populations 0.0026755  
## defined\_populations\_simplifieddispersal\_buffer 0.4011019  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.4211192  
## defined\_populations\_simplifiedgenetic\_clusters 0.3761327  
## defined\_populations\_simplifiedmanagement\_units 0.6106084  
## n\_extant\_populations:defined\_populations\_simplifieddispersal\_buffer 0.0043892  
## n\_extant\_populations:defined\_populations\_simplifiedeco\_biogeo\_proxies 0.0110470  
## n\_extant\_populations:defined\_populations\_simplifiedgenetic\_clusters 0.0678790  
## n\_extant\_populations:defined\_populations\_simplifiedmanagement\_units 0.0661245  
## z value  
## (Intercept) -3.964  
## n\_extant\_populations -0.171  
## defined\_populations\_simplifieddispersal\_buffer 0.517  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.369  
## defined\_populations\_simplifiedgenetic\_clusters 3.036  
## defined\_populations\_simplifiedmanagement\_units 0.577  
## n\_extant\_populations:defined\_populations\_simplifieddispersal\_buffer -0.803  
## n\_extant\_populations:defined\_populations\_simplifiedeco\_biogeo\_proxies -1.078  
## n\_extant\_populations:defined\_populations\_simplifiedgenetic\_clusters -2.255  
## n\_extant\_populations:defined\_populations\_simplifiedmanagement\_units -0.758  
## Pr(>|z|)  
## (Intercept) 7.37e-05  
## n\_extant\_populations 0.86384  
## defined\_populations\_simplifieddispersal\_buffer 0.60526  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.71238  
## defined\_populations\_simplifiedgenetic\_clusters 0.00239  
## defined\_populations\_simplifiedmanagement\_units 0.56404  
## n\_extant\_populations:defined\_populations\_simplifieddispersal\_buffer 0.42205  
## n\_extant\_populations:defined\_populations\_simplifiedeco\_biogeo\_proxies 0.28085  
## n\_extant\_populations:defined\_populations\_simplifiedgenetic\_clusters 0.02415  
## n\_extant\_populations:defined\_populations\_simplifiedmanagement\_units 0.44860  
##   
## (Intercept) \*\*\*  
## n\_extant\_populations   
## defined\_populations\_simplifieddispersal\_buffer   
## defined\_populations\_simplifiedeco\_biogeo\_proxies   
## defined\_populations\_simplifiedgenetic\_clusters \*\*   
## defined\_populations\_simplifiedmanagement\_units   
## n\_extant\_populations:defined\_populations\_simplifieddispersal\_buffer   
## n\_extant\_populations:defined\_populations\_simplifiedeco\_biogeo\_proxies   
## n\_extant\_populations:defined\_populations\_simplifiedgenetic\_clusters \*   
## n\_extant\_populations:defined\_populations\_simplifiedmanagement\_units   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Finally, we tested for associations between range type on Ne>500 indicator.

First filter data to consider only wide ranging and restricted categories (ie remove unknown due to small sampling size)

## Remove unknown  
data<- indicators\_averaged\_one %>%  
 filter(!is.na(indicator1\_mean)) %>%   
 filter(species\_range !="unknown")  
  
# summary of indicator  
summary(data$indicator1\_mean)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 0.0000 0.0000 0.0000 0.2698 0.5000 1.0000

# re-level to use geographic boundaries as reference category for the analysis  
data$defined\_populations\_simplified<-relevel(as.factor(data$defined\_populations\_simplified),  
 ref="geographic\_boundaries")  
  
# make sure specis range is a factor  
data$species\_range<-as.factor(data$species\_range)

Is there still an effect of method on indicator1 if we control for species range?

## run model + country  
m.c3 <- glmmTMB(indicator1\_mean ~ defined\_populations\_simplified + species\_range + (1|country\_assessment), family = "ordbeta", data = data)  
  
  
# summary results  
summary(m.c3)

## Family: ordbeta ( logit )  
## Formula:   
## indicator1\_mean ~ defined\_populations\_simplified + species\_range +   
## (1 | country\_assessment)  
## Data: data  
##   
## AIC BIC logLik deviance df.resid   
## 996.1 1065.0 -482.1 964.1 530   
##   
## Random effects:  
##   
## Conditional model:  
## Groups Name Variance Std.Dev.  
## country\_assessment (Intercept) 0.1099 0.3316   
## Number of obs: 546, groups: country\_assessment, 9  
##   
## Dispersion parameter for ordbeta family (): 3.86   
##   
## Conditional model:  
## Estimate  
## (Intercept) -1.0882  
## defined\_populations\_simplifieddispersal\_buffer 0.1366  
## defined\_populations\_simplifiedeco\_biogeo\_proxies -0.2520  
## defined\_populations\_simplifiedgenetic\_clusters 0.6945  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.8027  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.3713  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies -0.2095  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.3842  
## defined\_populations\_simplifiedmanagement\_units -0.1487  
## defined\_populations\_simplifiedother 1.0211  
## defined\_populations\_simplifiedother\_combinations 0.2036  
## species\_rangewide ranging 0.5804  
## Std. Error  
## (Intercept) 0.1954  
## defined\_populations\_simplifieddispersal\_buffer 0.2835  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.3498  
## defined\_populations\_simplifiedgenetic\_clusters 0.2596  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.4535  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.2513  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.3640  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.3077  
## defined\_populations\_simplifiedmanagement\_units 0.4332  
## defined\_populations\_simplifiedother 0.6165  
## defined\_populations\_simplifiedother\_combinations 0.2106  
## species\_rangewide ranging 0.1359  
## z value  
## (Intercept) -5.569  
## defined\_populations\_simplifieddispersal\_buffer 0.482  
## defined\_populations\_simplifiedeco\_biogeo\_proxies -0.720  
## defined\_populations\_simplifiedgenetic\_clusters 2.676  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 1.770  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 1.478  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies -0.576  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 1.248  
## defined\_populations\_simplifiedmanagement\_units -0.343  
## defined\_populations\_simplifiedother 1.656  
## defined\_populations\_simplifiedother\_combinations 0.967  
## species\_rangewide ranging 4.270  
## Pr(>|z|)  
## (Intercept) 2.56e-08  
## defined\_populations\_simplifieddispersal\_buffer 0.62996  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.47126  
## defined\_populations\_simplifiedgenetic\_clusters 0.00746  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.07673  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.13950  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.56493  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.21187  
## defined\_populations\_simplifiedmanagement\_units 0.73148  
## defined\_populations\_simplifiedother 0.09768  
## defined\_populations\_simplifiedother\_combinations 0.33362  
## species\_rangewide ranging 1.96e-05  
##   
## (Intercept) \*\*\*  
## defined\_populations\_simplifieddispersal\_buffer   
## defined\_populations\_simplifiedeco\_biogeo\_proxies   
## defined\_populations\_simplifiedgenetic\_clusters \*\*   
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies .   
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries   
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies   
## defined\_populations\_simplifiedgeographic\_boundaries management\_units   
## defined\_populations\_simplifiedmanagement\_units   
## defined\_populations\_simplifiedother .   
## defined\_populations\_simplifiedother\_combinations   
## species\_rangewide ranging \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Finally, we tested interactions between method and species range, to determine whether the effect of species range only applies when some methods are used.

Is the effect of method on Ne indicator moderated by species range?

## run model   
m.c4 <- glmmTMB(indicator1\_mean ~ defined\_populations\_simplified + species\_range + defined\_populations\_simplified\*species\_range + (1|country\_assessment), family = "ordbeta", data = data)  
  
  
# summary results  
summary(m.c4)

## Family: ordbeta ( logit )  
## Formula:   
## indicator1\_mean ~ defined\_populations\_simplified + species\_range +   
## defined\_populations\_simplified \* species\_range + (1 | country\_assessment)  
## Data: data  
##   
## AIC BIC logLik deviance df.resid   
## 986.3 1098.2 -467.2 934.3 520   
##   
## Random effects:  
##   
## Conditional model:  
## Groups Name Variance Std.Dev.  
## country\_assessment (Intercept) 0.1448 0.3806   
## Number of obs: 546, groups: country\_assessment, 9  
##   
## Dispersion parameter for ordbeta family (): 4.28   
##   
## Conditional model:  
## Estimate  
## (Intercept) -1.132e+00  
## defined\_populations\_simplifieddispersal\_buffer 3.897e-01  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 1.159e-01  
## defined\_populations\_simplifiedgenetic\_clusters 2.089e-01  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies -1.694e+01  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries -6.287e-02  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies -4.092e-01  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 5.794e-01  
## defined\_populations\_simplifiedmanagement\_units -2.115e+01  
## defined\_populations\_simplifiedother 5.774e-01  
## defined\_populations\_simplifiedother\_combinations 7.044e-01  
## species\_rangewide ranging 6.077e-01  
## defined\_populations\_simplifieddispersal\_buffer:species\_rangewide ranging -3.304e-01  
## defined\_populations\_simplifiedeco\_biogeo\_proxies:species\_rangewide ranging -9.104e-01  
## defined\_populations\_simplifiedgenetic\_clusters:species\_rangewide ranging 9.516e-01  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:species\_rangewide ranging 1.800e+01  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:species\_rangewide ranging 7.208e-01  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:species\_rangewide ranging 4.872e-01  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:species\_rangewide ranging -3.476e-01  
## defined\_populations\_simplifiedmanagement\_units:species\_rangewide ranging 2.125e+01  
## defined\_populations\_simplifiedother:species\_rangewide ranging 2.562e+01  
## defined\_populations\_simplifiedother\_combinations:species\_rangewide ranging -8.039e-01  
## Std. Error  
## (Intercept) 2.139e-01  
## defined\_populations\_simplifieddispersal\_buffer 3.600e-01  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 4.208e-01  
## defined\_populations\_simplifiedgenetic\_clusters 3.562e-01  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 4.435e+03  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 3.843e-01  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 4.536e-01  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 4.105e-01  
## defined\_populations\_simplifiedmanagement\_units 2.239e+04  
## defined\_populations\_simplifiedother 6.554e-01  
## defined\_populations\_simplifiedother\_combinations 2.766e-01  
## species\_rangewide ranging 2.563e-01  
## defined\_populations\_simplifieddispersal\_buffer:species\_rangewide ranging 3.722e-01  
## defined\_populations\_simplifiedeco\_biogeo\_proxies:species\_rangewide ranging 6.851e-01  
## defined\_populations\_simplifiedgenetic\_clusters:species\_rangewide ranging 5.013e-01  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:species\_rangewide ranging 4.435e+03  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:species\_rangewide ranging 5.237e-01  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:species\_rangewide ranging 7.121e-01  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:species\_rangewide ranging 6.100e-01  
## defined\_populations\_simplifiedmanagement\_units:species\_rangewide ranging 2.239e+04  
## defined\_populations\_simplifiedother:species\_rangewide ranging 1.821e+05  
## defined\_populations\_simplifiedother\_combinations:species\_rangewide ranging 3.930e-01  
## z value  
## (Intercept) -5.294  
## defined\_populations\_simplifieddispersal\_buffer 1.082  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.275  
## defined\_populations\_simplifiedgenetic\_clusters 0.586  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies -0.004  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries -0.164  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies -0.902  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 1.411  
## defined\_populations\_simplifiedmanagement\_units -0.001  
## defined\_populations\_simplifiedother 0.881  
## defined\_populations\_simplifiedother\_combinations 2.547  
## species\_rangewide ranging 2.371  
## defined\_populations\_simplifieddispersal\_buffer:species\_rangewide ranging -0.888  
## defined\_populations\_simplifiedeco\_biogeo\_proxies:species\_rangewide ranging -1.329  
## defined\_populations\_simplifiedgenetic\_clusters:species\_rangewide ranging 1.898  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:species\_rangewide ranging 0.004  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:species\_rangewide ranging 1.376  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:species\_rangewide ranging 0.684  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:species\_rangewide ranging -0.570  
## defined\_populations\_simplifiedmanagement\_units:species\_rangewide ranging 0.001  
## defined\_populations\_simplifiedother:species\_rangewide ranging 0.000  
## defined\_populations\_simplifiedother\_combinations:species\_rangewide ranging -2.046  
## Pr(>|z|)  
## (Intercept) 1.2e-07  
## defined\_populations\_simplifieddispersal\_buffer 0.2791  
## defined\_populations\_simplifiedeco\_biogeo\_proxies 0.7830  
## defined\_populations\_simplifiedgenetic\_clusters 0.5576  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies 0.9970  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries 0.8701  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies 0.3670  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units 0.1581  
## defined\_populations\_simplifiedmanagement\_units 0.9992  
## defined\_populations\_simplifiedother 0.3783  
## defined\_populations\_simplifiedother\_combinations 0.0109  
## species\_rangewide ranging 0.0178  
## defined\_populations\_simplifieddispersal\_buffer:species\_rangewide ranging 0.3747  
## defined\_populations\_simplifiedeco\_biogeo\_proxies:species\_rangewide ranging 0.1839  
## defined\_populations\_simplifiedgenetic\_clusters:species\_rangewide ranging 0.0577  
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:species\_rangewide ranging 0.9968  
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:species\_rangewide ranging 0.1687  
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:species\_rangewide ranging 0.4939  
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:species\_rangewide ranging 0.5688  
## defined\_populations\_simplifiedmanagement\_units:species\_rangewide ranging 0.9992  
## defined\_populations\_simplifiedother:species\_rangewide ranging 0.9999  
## defined\_populations\_simplifiedother\_combinations:species\_rangewide ranging 0.0408  
##   
## (Intercept) \*\*\*  
## defined\_populations\_simplifieddispersal\_buffer   
## defined\_populations\_simplifiedeco\_biogeo\_proxies   
## defined\_populations\_simplifiedgenetic\_clusters   
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies   
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries   
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies   
## defined\_populations\_simplifiedgeographic\_boundaries management\_units   
## defined\_populations\_simplifiedmanagement\_units   
## defined\_populations\_simplifiedother   
## defined\_populations\_simplifiedother\_combinations \*   
## species\_rangewide ranging \*   
## defined\_populations\_simplifieddispersal\_buffer:species\_rangewide ranging   
## defined\_populations\_simplifiedeco\_biogeo\_proxies:species\_rangewide ranging   
## defined\_populations\_simplifiedgenetic\_clusters:species\_rangewide ranging .   
## defined\_populations\_simplifiedgenetic\_clusters eco\_biogeo\_proxies:species\_rangewide ranging   
## defined\_populations\_simplifiedgenetic\_clusters geographic\_boundaries:species\_rangewide ranging   
## defined\_populations\_simplifiedgeographic\_boundaries eco\_biogeo\_proxies:species\_rangewide ranging   
## defined\_populations\_simplifiedgeographic\_boundaries management\_units:species\_rangewide ranging   
## defined\_populations\_simplifiedmanagement\_units:species\_rangewide ranging   
## defined\_populations\_simplifiedother:species\_rangewide ranging   
## defined\_populations\_simplifiedother\_combinations:species\_rangewide ranging \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

### Main Figure (representing the models above): Single plot 5 panels. Boxplots plots for the effect of method on: number of populations, proportion of maintained populations (indicator 2) and Proportion of populations with Ne>500 (indicator 1), AND Violin plots for the distribution of the indicator values by range type.

Top a,b,c panel boxplots:

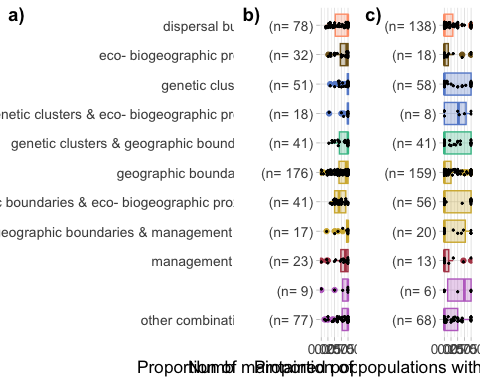
##### plot for Proportion of maintained populations (indicator 2) only with n in axis labels  
  
# sample size   
sample\_size <- indicators\_full %>%  
 filter(!is.na(indicator2)) %>%   
 filter(n\_extant\_populations<500) %>%   
 group\_by(defined\_populations\_nicenames) %>% summarize(num=n())  
  
# custom axis  
## new dataframe  
df<-indicators\_full %>%   
 filter(n\_extant\_populations<500) %>%  
 filter(!is.na(indicator2)) %>%   
 # add sampling size   
 left\_join(sample\_size) %>%  
 mutate(myaxis = as.factor(paste0(defined\_populations\_nicenames, " (n= ", num, ")")))

## Joining, by = "defined\_populations\_nicenames"

pb.1<- df %>%  
 filter(n\_extant\_populations<500) %>%  
 ggplot(aes(x=myaxis, y=indicator2, color=defined\_populations\_nicenames,   
 fill=defined\_populations\_nicenames)) +  
 geom\_boxplot() + xlab("") + ylab("Proportion of maintained populations within species") +  
 geom\_jitter(size=.4, width = 0.1, color="black") +  
 coord\_flip() +  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="none",  
 plot.margin = unit(c(0.2, 0.2, 0.2, 0.2), "cm")) + # this is used to decrease the space between plots)   
 scale\_fill\_manual(values=alpha(simplifiedmethods\_colors, 0.3),  
 breaks=levels(as.factor(indicators\_full$defined\_populations\_nicenames))) +  
 scale\_color\_manual(values=simplifiedmethods\_colors,  
 breaks=levels(as.factor(indicators\_full$defined\_populations\_nicenames))) +  
   
 scale\_x\_discrete(limits=rev,   
 labels= rev(sub(".\*(\\(n= \\d+\\))", "\\1", levels(df$myaxis)))) + # extract "(n = number)") and show them in reverse order  
 theme(text = element\_text(size = 13))  
  
  
##### plot for Proportion populations Ne>500 (indicator 1) only with n in axis labels  
# Prepare data for plot with nice labels:  
# sample size of TOTAL populations  
sample\_size <- indicators\_full %>%  
 filter(!is.na(indicator1)) %>%   
 filter(n\_extant\_populations<500) %>%   
 group\_by(defined\_populations\_nicenames) %>% summarize(num=n())  
  
# custom axis  
## new dataframe  
df<-indicators\_full %>%   
 filter(n\_extant\_populations<500) %>%  
 filter(!is.na(indicator1)) %>%   
 # add sampling size   
 left\_join(sample\_size) %>%  
 mutate(myaxis = as.factor(paste0(defined\_populations\_nicenames, " (n= ", num, ")")))

## Joining, by = "defined\_populations\_nicenames"

## plot   
pc.1<- df %>%  
 ggplot(aes(x=myaxis, y=indicator1, color=defined\_populations\_nicenames,   
 fill=defined\_populations\_nicenames)) +  
 geom\_boxplot() + xlab("") + ylab("Proportion of populations within species with Ne>500") +  
 geom\_jitter(size=.4, width = 0.1, color="black") +  
 coord\_flip() +  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="none",  
 plot.margin = unit(c(0.2, 0.2, 0.2, 0.2), "cm")) + # this is used to decrease the space between plots)   
 scale\_fill\_manual(values=alpha(simplifiedmethods\_colors, 0.3),  
 breaks=levels(as.factor(indicators\_full$defined\_populations\_nicenames))) +  
 scale\_color\_manual(values=simplifiedmethods\_colors,  
 breaks=levels(as.factor(indicators\_full$defined\_populations\_nicenames))) +  
 scale\_x\_discrete(limits=rev,   
 labels= rev(sub(".\*(\\(n= \\d+\\))", "\\1", levels(df$myaxis)))) + # extract "(n = number)") and show them in reverse order  
 theme(text = element\_text(size = 13))  
  
  
## Plot 3 panels  
plot\_grid(pa, pb.1, pc.1, ncol=3, rel\_widths = c(1.9,1,1), align = "h", labels=c("a)", "b)", "c)"))



Bottom d, e violin plots. Indicators by of range type coloring points to show genetic clusters

For PM indicator:

# add variable stating if genetic methods are used  
indicators\_averaged\_one<- indicators\_averaged\_one %>%  
mutate(genetic\_to\_define\_pops = ifelse(grepl("genetic", defined\_populations\_simplified), 'genetic method', 'non genetic'))  
  
  
# get sample size by desired category  
sample\_size <- indicators\_averaged\_one %>%  
 filter(!is.na(indicator2\_mean)) %>%   
 filter(!is.na(species\_range)) %>%   
 group\_by(species\_range) %>% summarize(num=n())  
  
# plot  
pd<-indicators\_averaged\_one %>%   
 filter(!is.na(indicator2\_mean)) %>%   
 filter(!is.na(species\_range)) %>%   
   
 # add sampling size   
 left\_join(sample\_size) %>%   
 mutate(myaxis = paste0(species\_range, " (n= ", num, ")")) %>%  
  
 # plot  
 ggplot(aes(x=myaxis, y=indicator2\_mean)) +  
 geom\_violin(width=1, linewidth = 0, fill="grey70") +  
 xlab("") + ylab("Proportion of maintained populations within species") +  
 coord\_flip() +  
 new\_scale\_color() + # to color points without confuisng ggplot  
 geom\_jitter(size=1.2, width = 0.1, aes(color = genetic\_to\_define\_pops)) +  
 scale\_color\_manual(values=c("red", "black")) +  
 labs(color=NULL) + # hide legend title  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="none", text= element\_text(size=20))

## Joining, by = "species\_range"

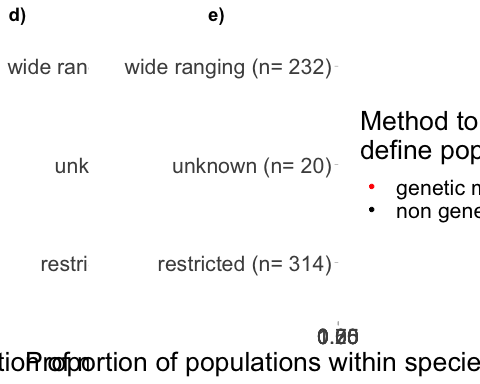
For Ne indicator:

# add variable stating if genetic methods are used  
indicators\_averaged\_one<- indicators\_averaged\_one %>%  
mutate(genetic\_to\_define\_pops = ifelse(grepl("genetic", defined\_populations\_simplified), 'genetic method', 'non genetic'))  
  
  
# get sample size by desired category  
sample\_size <- indicators\_averaged\_one %>%  
 filter(!is.na(indicator1\_mean)) %>%   
 filter(!is.na(species\_range)) %>%   
 group\_by(species\_range) %>% summarize(num=n())  
  
# plot  
pe <- indicators\_averaged\_one %>%   
 filter(!is.na(indicator1\_mean)) %>%   
 filter(!is.na(species\_range)) %>%   
   
 # add sampling size   
 left\_join(sample\_size) %>%   
 mutate(myaxis = paste0(species\_range, " (n= ", num, ")")) %>%  
  
 # plot  
 ggplot(aes(x=myaxis, y=indicator1\_mean)) +  
 geom\_violin(width=1, linewidth = 0, fill="grey70") +  
 xlab("") + ylab("Proportion of populations within species with Ne>500") +  
 coord\_flip() +  
 new\_scale\_color() + # to color the points without confusing ggplot  
 geom\_jitter(size=1.2, width = 0.1, aes(color = genetic\_to\_define\_pops)) +  
 scale\_color\_manual(values=c("red", "black")) +   
 theme\_light() +  
 labs(color="Method to \ndefine populations") + # nicer legend title  
 theme(panel.border = element\_blank(), legend.position="right", text= element\_text(size=20))

## Joining, by = "species\_range"

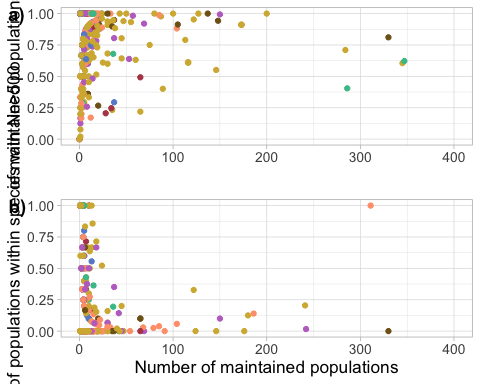
Two panel figure:

plot\_grid(pd + theme(legend.position = "non2"), # legend can be shown only below both plots   
 pe,  
 ncol = 2,  
 rel\_widths = c(1,1.4), align = "h", labels=c("d)", "e)"))



### Supplementary Figure: Single figure 2 panels scatter plots number of populations vs indicators

# plot  
plot\_grid(psupA + xlim(0,400) + xlab(""), # remove xlab from top plot and match x axis size  
 psupB+ xlim(0,400),   
 ncol=1, align = "v", labels=c("a)", "b)"))



## Indicatros by threat status (IUCN Red List)

All the following plots and analyses consider the average of multiassessed species (variable \_mean), so that they are shown only once.

### (a) Ne > 500 indicator and red list status

Plot indicator 1 by global IUCN in the entire dataset:

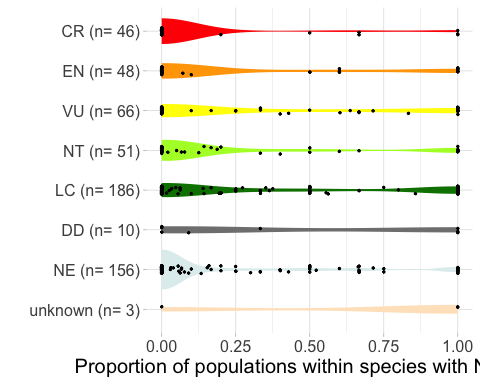
## Global IUCN  
  
# Capitalize abbreviations   
indicators\_averaged\_one$global\_IUCN<-as.factor(indicators\_averaged\_one$global\_IUCN)  
levels(indicators\_averaged\_one$global\_IUCN)

## [1] "cr" "dd" "en" "lc" "not\_assessed"  
## [6] "nt" "unknown" "vu"

indicators\_averaged\_one$global\_IUCN<-factor(indicators\_averaged\_one$global\_IUCN,   
 levels=c("cr", "en", "vu", "nt", "lc", "dd", "not\_assessed","unknown"))  
levels(indicators\_averaged\_one$global\_IUCN) <- c("CR", "EN", "VU", "NT", "LC", "DD", "NE", "unknown")  
  
## prepare data  
# add sampling size  
sample\_size <- indicators\_averaged\_one %>%  
 filter(!is.na(indicator1\_mean)) %>%   
 filter(!is.na(global\_IUCN)) %>%   
 group\_by(global\_IUCN) %>% summarize(num=n())  
  
# new df   
df<- indicators\_averaged\_one %>%   
 filter(!is.na(indicator1\_mean)) %>%   
 filter(!is.na(global\_IUCN)) %>%   
 # add sampling size   
 left\_join(sample\_size) %>%  
 mutate(myaxis = paste0(global\_IUCN, " (n= ", num, ")"))

## Joining, by = "global\_IUCN"

# change order of levels so that they are in the desired order  
df$myaxis<-factor(df$myaxis,   
 #grep is used below to get the sample size, which may change depending on the data  
 levels=c(grep("CR", unique(df$myaxis), value = TRUE),  
 grep("EN", unique(df$myaxis), value = TRUE),  
 grep("VU", unique(df$myaxis), value = TRUE),  
 grep("NT", unique(df$myaxis), value = TRUE),  
 grep("LC", unique(df$myaxis), value = TRUE),  
 grep("DD", unique(df$myaxis), value = TRUE),  
 grep("NE", unique(df$myaxis), value = TRUE),  
 grep("unknown", unique(df$myaxis), value = TRUE)))  
   
# plot  
p1<-df %>%  
 ggplot(aes(x=myaxis, y=indicator1\_mean , fill=global\_IUCN)) +  
 geom\_violin(width=1, linewidth = 0) +  
 geom\_jitter(size=.5, width = 0.1) +  
 xlab("") + ylab("Proportion of populations within species with Ne>500") +  
 coord\_flip() +  
 scale\_fill\_manual(values= IUCNcolors, # iucn color codes  
 breaks=c(levels(df$global\_IUCN))) +  
 scale\_x\_discrete(limits=rev) +  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="none",   
 plot.title = element\_text(hjust = 0.5), # center title  
 text= element\_text(size=15))  
p1



Summary table:

x <- indicators\_averaged\_one %>%  
 filter(!is.na(indicator1\_mean)) %>%   
 filter(!is.na(global\_IUCN)) %>%   
 group\_by(global\_IUCN) %>%   
 summarize(n=n(),  
 mean=mean(indicator1\_mean),  
 median=median(indicator1\_mean),  
 per.0=sum(indicator1\_mean==0) / n \*100,  
 per.below.25=sum(indicator1\_mean<0.25) / n \*100,  
 per.below.90=sum(indicator1\_mean<0.90) / n \*100,  
 per.above.75=sum(indicator1\_mean>0.75)/ n \*100,  
 per1=sum(indicator1\_mean==1) / n \*100)  
  
  
kable(x, digits=2)

| global\_IUCN | n | mean | median | per.0 | per.below.25 | per.below.90 | per.above.75 | per1 |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| CR | 46 | 0.11 | 0.00 | 84.78 | 86.96 | 93.48 | 6.52 | 6.52 |
| EN | 48 | 0.25 | 0.00 | 66.67 | 70.83 | 81.25 | 18.75 | 18.75 |
| VU | 66 | 0.32 | 0.00 | 56.06 | 59.09 | 78.79 | 22.73 | 21.21 |
| NT | 51 | 0.24 | 0.00 | 54.90 | 72.55 | 84.31 | 15.69 | 15.69 |
| LC | 186 | 0.37 | 0.05 | 47.31 | 55.91 | 72.04 | 29.03 | 27.96 |
| DD | 10 | 0.44 | 0.21 | 40.00 | 50.00 | 60.00 | 40.00 | 40.00 |
| NE | 156 | 0.19 | 0.00 | 63.46 | 74.36 | 91.03 | 8.97 | 8.97 |
| unknown | 3 | 0.67 | 1.00 | 33.33 | 33.33 | 33.33 | 66.67 | 66.67 |

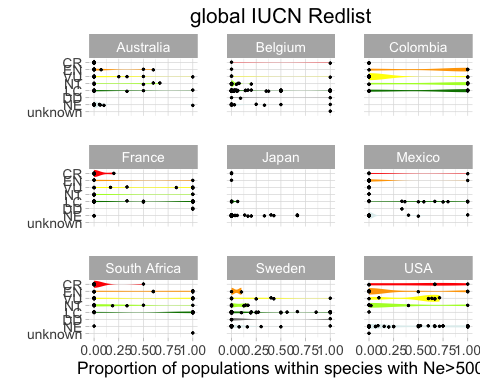
Indicator 1 by country and global IUCN

# plot  
indicators\_averaged\_one %>%   
 filter(!is.na(regional\_redlist)) %>%  
 # plot  
 ggplot(aes(x=global\_IUCN, y=indicator1\_mean, fill=global\_IUCN)) +  
 geom\_violin(width=1, linewidth = 0) +  
 geom\_jitter(size=.5, width = 0.1) +  
 xlab("") + ylab("Proportion of populations within species with Ne>500") +  
 coord\_flip() +  
 scale\_fill\_manual(values= IUCNcolors, # iucn color codes  
 breaks=c(levels(indicators\_averaged\_one$global\_IUCN))) +  
 scale\_x\_discrete(limits=rev) +  
 theme\_light() +  
 ggtitle("global IUCN Redlist") +  
 theme(panel.border = element\_blank(), legend.position="none",   
 plot.title = element\_text(hjust = 0.5), # center title  
 text= element\_text(size=13)) +  
 facet\_wrap(~country\_assessment, ncol = 3) +  
 theme(panel.spacing = unit(1.5, "lines"))

## Warning: Removed 342 rows containing non-finite values (`stat\_ydensity()`).

## Warning: Groups with fewer than two data points have been dropped.  
## Groups with fewer than two data points have been dropped.  
## Groups with fewer than two data points have been dropped.  
## Groups with fewer than two data points have been dropped.  
## Groups with fewer than two data points have been dropped.  
## Groups with fewer than two data points have been dropped.  
## Groups with fewer than two data points have been dropped.  
## Groups with fewer than two data points have been dropped.

## Warning: Removed 342 rows containing missing values (`geom\_point()`).



### (b) Proportion of Maintained Populations and red list status?

Plot indicator 2 by global IUCN in the entire dataset:

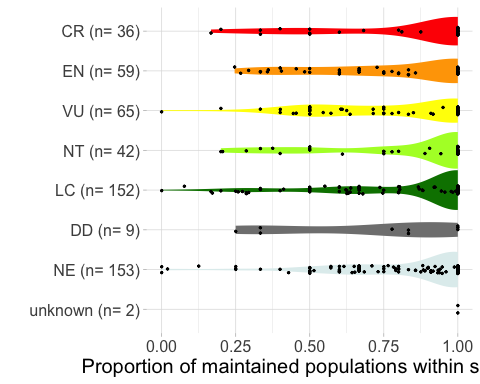
## Global IUCN  
## prepare data  
# add sampling size  
sample\_size <- indicators\_averaged\_one %>%  
 filter(!is.na(indicator2\_mean)) %>%   
 filter(!is.na(global\_IUCN)) %>%   
 group\_by(global\_IUCN) %>% summarize(num=n())  
  
# new df   
df<- indicators\_averaged\_one %>%   
 filter(!is.na(indicator2\_mean)) %>%   
 filter(!is.na(global\_IUCN)) %>%   
 # add sampling size   
 left\_join(sample\_size) %>%  
 mutate(myaxis = paste0(global\_IUCN, " (n= ", num, ")"))

## Joining, by = "global\_IUCN"

# change order of levels so that they are in the desired order  
df$myaxis<-factor(df$myaxis,   
 #grep is used below to get the sample size, which may change depending on the data  
 levels=c(grep("CR", unique(df$myaxis), value = TRUE),  
 grep("EN", unique(df$myaxis), value = TRUE),  
 grep("VU", unique(df$myaxis), value = TRUE),  
 grep("NT", unique(df$myaxis), value = TRUE),  
 grep("LC", unique(df$myaxis), value = TRUE),  
 grep("DD", unique(df$myaxis), value = TRUE),  
 grep("NE", unique(df$myaxis), value = TRUE),  
 grep("unknown", unique(df$myaxis), value = TRUE)))  
  
   
# plot  
p2<-df %>%  
 ggplot(aes(x=myaxis, y=indicator2 , fill=global\_IUCN)) +  
 geom\_violin(width=1, linewidth = 0) +  
 geom\_jitter(size=.5, width = 0.1) +  
 xlab("") + ylab("Proportion of maintained populations within species") +  
 coord\_flip() +  
 scale\_fill\_manual(values= IUCNcolors, # iucn color codes  
 breaks=c(levels(df$global\_IUCN))) +  
 scale\_x\_discrete(limits=rev) +  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="none",   
 plot.title = element\_text(hjust = 0.5), # center title  
 text= element\_text(size=15))  
p2

## Warning: Removed 2 rows containing non-finite values (`stat\_ydensity()`).

## Warning: Removed 2 rows containing missing values (`geom\_point()`).



Summary table:

x <- indicators\_averaged\_one %>%  
 filter(!is.na(indicator2\_mean)) %>%   
 filter(!is.na(global\_IUCN)) %>%   
 group\_by(global\_IUCN) %>%   
 summarize(n=n(),  
 mean=mean(indicator2\_mean),  
 median=median(indicator2\_mean),  
 per.0=sum(indicator2\_mean==0) / n \*100,  
 per.below.25=sum(indicator2\_mean<0.25) / n \*100,  
 per.below.90=sum(indicator2\_mean<0.90) / n \*100,  
 per.above.75=sum(indicator2\_mean>0.75)/ n \*100,  
 per1=sum(indicator2\_mean==1) / n \*100)  
  
  
kable(x, digits=2)

| global\_IUCN | n | mean | median | per.0 | per.below.25 | per.below.90 | per.above.75 | per1 |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| CR | 36 | 0.83 | 1.00 | 0.00 | 5.56 | 36.11 | 75.00 | 63.89 |
| EN | 59 | 0.79 | 0.86 | 0.00 | 1.69 | 50.85 | 61.02 | 49.15 |
| VU | 65 | 0.78 | 0.91 | 1.54 | 3.08 | 49.23 | 60.00 | 44.62 |
| NT | 42 | 0.83 | 1.00 | 0.00 | 4.76 | 38.10 | 71.43 | 57.14 |
| LC | 152 | 0.84 | 1.00 | 0.66 | 3.29 | 34.21 | 72.37 | 61.18 |
| DD | 9 | 0.71 | 0.83 | 0.00 | 0.00 | 66.67 | 66.67 | 33.33 |
| NE | 153 | 0.84 | 0.95 | 0.65 | 1.96 | 40.52 | 69.93 | 48.37 |
| unknown | 2 | 1.00 | 1.00 | 0.00 | 0.00 | 0.00 | 100.00 | 100.00 |

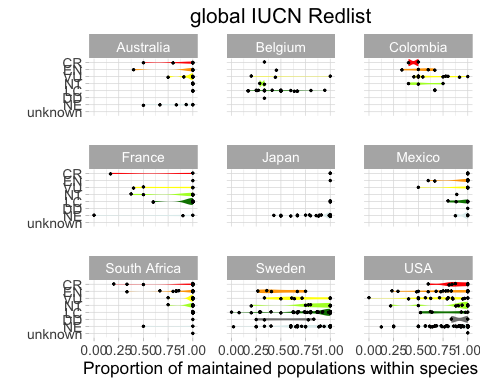
Indicator 2 by country and global IUCN

# plot  
indicators\_averaged\_one %>%   
 filter(!is.na(regional\_redlist)) %>%  
 # plot  
 ggplot(aes(x=global\_IUCN, y=indicator2\_mean, fill=global\_IUCN)) +  
 geom\_violin(width=1, linewidth = 0) +  
 geom\_jitter(size=.5, width = 0.1) +  
 xlab("") + ylab("Proportion of maintained populations within species") +  
 coord\_flip() +  
 scale\_fill\_manual(values= IUCNcolors, # iucn color codes  
 breaks=c(levels(indicators\_averaged\_one$global\_IUCN))) +  
 scale\_x\_discrete(limits=rev) +  
 theme\_light() +  
 ggtitle("global IUCN Redlist") +  
 theme(panel.border = element\_blank(), legend.position="none",   
 plot.title = element\_text(hjust = 0.5), # center title  
 text= element\_text(size=13)) +  
 facet\_wrap(~country\_assessment, ncol = 3) +  
 theme(panel.spacing = unit(1.5, "lines"))

## Warning: Removed 390 rows containing non-finite values (`stat\_ydensity()`).

## Warning: Groups with fewer than two data points have been dropped.  
## Groups with fewer than two data points have been dropped.  
## Groups with fewer than two data points have been dropped.  
## Groups with fewer than two data points have been dropped.  
## Groups with fewer than two data points have been dropped.  
## Groups with fewer than two data points have been dropped.  
## Groups with fewer than two data points have been dropped.  
## Groups with fewer than two data points have been dropped.  
## Groups with fewer than two data points have been dropped.  
## Groups with fewer than two data points have been dropped.

## Warning: Removed 390 rows containing missing values (`geom\_point()`).

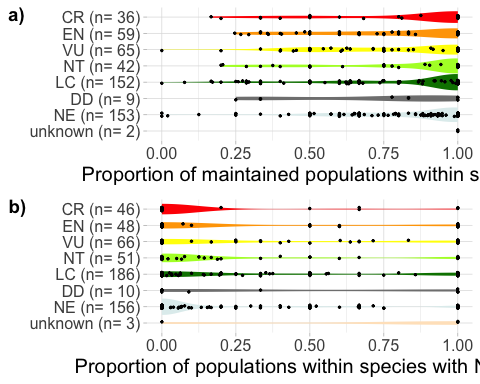


### Main Figure: Single plot 2 pannels IUCN redlist and indicator range values

plot\_grid(p2,  
 p1,  
 ncol=1, align = "v", labels=c("a)", "b)"))

## Warning: Removed 2 rows containing non-finite values (`stat\_ydensity()`).

## Warning: Removed 2 rows containing missing values (`geom\_point()`).



## Indicator values by taxonomic group

All the following plots and analyses consider the average of multiassessed species (variable \_mean), so that they are shown only once.

We also grouped taxa with small n (<5) into “others”, according to the following table:

table(indicators\_averaged\_one$taxonomic\_group)

##   
## amphibian bird fish invertebrate mammal   
## 56 167 62 135 135   
## reptile angiosperm bryophyte gymnosperm pteridophytes   
## 70 235 5 19 14   
## fungus other   
## 3 18

They are grouped along with “other” in a new category “others” in the new variable taxonomic\_group\_simplified:

indicators\_averaged\_one <- indicators\_averaged\_one %>%   
 ungroup() %>%   
 mutate(taxonomic\_group\_simplified = case\_when(  
 # if the taxon group is in the list of groups with small n change to "others"  
 as.character(taxonomic\_group) %!in% c("bryophyte", "fungus", "other") ~ as.character(taxonomic\_group),  
 TRUE ~ "others"))  
  
# check:  
table(indicators\_averaged\_one$taxonomic\_group\_simplified)

##   
## amphibian angiosperm bird fish gymnosperm   
## 56 235 167 62 19   
## invertebrate mammal others pteridophytes reptile   
## 135 135 26 14 70

We also create a group of only 3 categories for animals, plants and others:

# Define the grouping map  
grouping\_map <- c(  
 "amphibian", "bird", "fish", "invertebrate", "mammal",  
 "angiosperm", "gymnosperm", "reptile", "pteridophytes", "others"  
)  
  
# Create a new variable taxonomic\_group\_3  
indicators\_averaged\_one <- indicators\_averaged\_one %>%  
 mutate(  
 taxonomic\_group\_3 = case\_when(  
 taxonomic\_group\_simplified %in% grouping\_map[1:5] ~ "animals",  
 taxonomic\_group\_simplified %in% grouping\_map[6:9] ~ "plants",  
 taxonomic\_group\_simplified %in% grouping\_map[10] ~ "others",  
 TRUE ~ NA\_character\_  
 )  
 )  
  
# reorder levels  
indicators\_averaged\_one$taxonomic\_group\_3<- factor(indicators\_averaged\_one$taxonomic\_group\_3,   
 levels=c("animals", "plants", "others"))

### Violin plots, histograms and summary tables for each indicator by taxonomic group

**Indicator Ne > 500**

## prepare data  
# add sampling size  
sample\_size <- indicators\_averaged\_one %>%  
 filter(!is.na(indicator1\_mean)) %>%   
 group\_by(taxonomic\_group\_simplified) %>% summarize(num=n())  
  
# new df   
df<- indicators\_averaged\_one %>%   
 filter(!is.na(indicator1\_mean)) %>%   
 # add sampling size   
 left\_join(sample\_size) %>%  
 mutate(myaxis = paste0(taxonomic\_group\_simplified, " (n= ", num, ")"))

## Joining, by = "taxonomic\_group\_simplified"

# change order of levels so that they are in the desired order  
df$myaxis<-factor(df$myaxis,   
 #grep is used below to get the sample size, which may change depending on the data  
 levels=c(grep("amphibian", unique(df$myaxis), value = TRUE),   
 grep("bird" , unique(df$myaxis), value = TRUE),  
 grep("fish" , unique(df$myaxis), value = TRUE),  
 grep("invertebrate", unique(df$myaxis), value = TRUE),  
 grep("mammal", unique(df$myaxis), value = TRUE),  
 grep("reptile", unique(df$myaxis), value = TRUE),  
 grep("angiosperm", unique(df$myaxis), value = TRUE),  
 grep("gymnosperm", unique(df$myaxis), value = TRUE),  
 grep("pteridophytes", unique(df$myaxis), value = TRUE),  
 grep("others" , unique(df$myaxis), value = TRUE)))  
  
df$taxonomic\_group\_simplified<-factor(df$taxonomic\_group\_simplified,   
 levels=c("amphibian", "bird" , "fish" , "invertebrate", "mammal", "reptile",  
 "angiosperm", "gymnosperm", "pteridophytes",  
 "others"))  
  
   
# plot  
p1<-df %>%  
 ggplot(aes(x=myaxis, y=indicator1\_mean, fill=taxonomic\_group\_simplified, color=taxonomic\_group\_simplified)) +  
 geom\_violin(width=1.5, linewidth = 0.2) +  
 geom\_jitter(size=.7, width = 0.1, color="black") +  
 xlab("") + ylab("Proportion of populations within species with Ne>500") +  
 coord\_flip() +  
 scale\_x\_discrete(limits=rev) +  
 scale\_fill\_manual(values= c(rep(grouped\_taxon\_colors[1], 6), # for animals  
 rep(grouped\_taxon\_colors[2], 3), # for platns  
 rep(grouped\_taxon\_colors[3], 1)), # for fungi and others  
 breaks=c(levels(df$taxonomic\_group\_simplified))) +  
 scale\_color\_manual(values= c(rep(grouped\_taxon\_colors[1], 6), # for animals  
 rep(grouped\_taxon\_colors[2], 3), # for platns  
 rep(grouped\_taxon\_colors[3], 1)), # for fungi and others  
 breaks=c(levels(df$taxonomic\_group\_simplified))) +  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="none",  
 text= element\_text(size=15))  
p1

## Warning: `position\_dodge()` requires non-overlapping x intervals

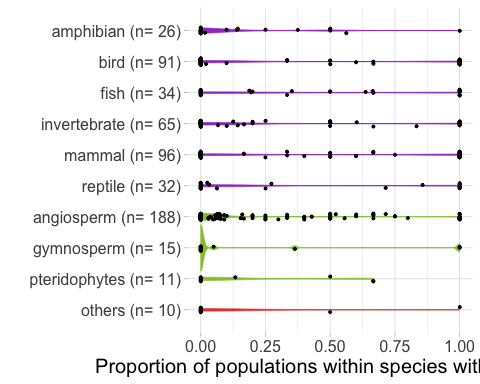


Table with sampling size, mean indicator value and proporiton of taxa where the value is below 0.25, 0.50 and 0.75:

#summary table by taxonomic group  
x <- indicators\_averaged\_one %>%  
 filter(!is.na(indicator1\_mean)) %>%   
 filter(!is.na(taxonomic\_group\_simplified)) %>%   
 group\_by(taxonomic\_group\_simplified) %>%   
 summarize(n=n(),  
 mean=mean(indicator1\_mean),  
 median=median(indicator1\_mean),  
 n.below.75=sum(indicator1\_mean<0.75),  
 n.below.50=sum(indicator1\_mean<0.50),  
 n.below.25=sum(indicator1\_mean<0.25),  
 per.below.25=n.below.25/n\*100,  
 per.below.50=n.below.50/n\*100)  
  
# Calculate total counts and means  
total\_counts <- summarise(x,  
 taxonomic\_group\_simplified = "ALL",  
 n = sum(n),  
 mean= mean(mean),  
 median=median(median),  
 n.below.75 = sum(n.below.75),  
 n.below.50 = sum(n.below.50),  
 n.below.25 = sum(n.below.25),  
 per.below.25 = n.below.25 / n \* 100,  
 per.below.50 = n.below.50 / n \* 100)  
  
# Bind the total row to the summary\_table  
summary\_table <- bind\_rows(x, total\_counts)  
  
# keep taxonomic groups as level in desired order:  
summary\_table$taxonomic\_group\_simplified<-factor(summary\_table$taxonomic\_group\_simplified,  
 levels = c("amphibian", "bird" , "fish" , "invertebrate", "mammal",  
 "angiosperm", "gymnosperm", "reptile", "pteridophytes",  
 "others", "ALL"))  
summary\_table<- summary\_table %>% arrange(taxonomic\_group\_simplified)  
  
# show nice table  
kable(summary\_table, digits=2)

| taxonomic\_group\_simplified | n | mean | median | n.below.75 | n.below.50 | n.below.25 | per.below.25 | per.below.50 |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| amphibian | 26 | 0.16 | 0.00 | 25 | 21 | 19 | 73.08 | 80.77 |
| bird | 91 | 0.32 | 0.00 | 66 | 60 | 58 | 63.74 | 65.93 |
| fish | 34 | 0.39 | 0.20 | 25 | 20 | 18 | 52.94 | 58.82 |
| invertebrate | 65 | 0.28 | 0.00 | 51 | 45 | 44 | 67.69 | 69.23 |
| mammal | 96 | 0.42 | 0.08 | 62 | 54 | 50 | 52.08 | 56.25 |
| angiosperm | 188 | 0.18 | 0.00 | 170 | 154 | 140 | 74.47 | 81.91 |
| gymnosperm | 15 | 0.16 | 0.00 | 13 | 13 | 12 | 80.00 | 86.67 |
| reptile | 32 | 0.29 | 0.00 | 24 | 23 | 21 | 65.62 | 71.88 |
| pteridophytes | 11 | 0.18 | 0.00 | 11 | 8 | 8 | 72.73 | 72.73 |
| others | 10 | 0.15 | 0.00 | 9 | 8 | 8 | 80.00 | 80.00 |
| ALL | 568 | 0.25 | 0.00 | 456 | 406 | 378 | 66.55 | 71.48 |

**Indicator Proportion of maintained populations:**

## prepare data  
# add sampling size  
sample\_size <- indicators\_averaged\_one %>%  
 filter(!is.na(indicator2\_mean)) %>%   
 group\_by(taxonomic\_group\_simplified) %>% summarize(num=n())  
  
# new df   
df<- indicators\_averaged\_one %>%   
 filter(!is.na(indicator2\_mean)) %>%   
 # add sampling size   
 left\_join(sample\_size) %>%  
 mutate(myaxis = paste0(taxonomic\_group\_simplified, " (n= ", num, ")"))

## Joining, by = "taxonomic\_group\_simplified"

# change order of levels so that they are in the desired order  
df$myaxis<-factor(df$myaxis,   
 #grep is used below to get the sample size, which may change depending on the data  
 levels=c(grep("amphibian", unique(df$myaxis), value = TRUE),   
 grep("bird" , unique(df$myaxis), value = TRUE),  
 grep("fish" , unique(df$myaxis), value = TRUE),  
 grep("invertebrate", unique(df$myaxis), value = TRUE),  
 grep("mammal", unique(df$myaxis), value = TRUE),  
 grep("reptile", unique(df$myaxis), value = TRUE),  
 grep("angiosperm", unique(df$myaxis), value = TRUE),  
 grep("gymnosperm", unique(df$myaxis), value = TRUE),  
 grep("pteridophytes", unique(df$myaxis), value = TRUE),  
 grep("others" , unique(df$myaxis), value = TRUE)))  
  
df$taxonomic\_group\_simplified<-factor(df$taxonomic\_group\_simplified,   
 levels=c("amphibian", "bird" , "fish" , "invertebrate", "mammal", "reptile",  
 "angiosperm", "gymnosperm", "pteridophytes",  
 "others"))  
  
   
# plot  
p2<-df %>%  
 ggplot(aes(x=myaxis, y=indicator2\_mean, fill=taxonomic\_group\_simplified, color=taxonomic\_group\_simplified)) +  
 geom\_violin(width=1, linewidth = 0.2) +  
 geom\_jitter(size=.7, width = 0.1, color="black") +  
 xlab("") + ylab("Proportion of maintained populations within species") +  
 coord\_flip() +  
 scale\_x\_discrete(limits=rev) +  
 scale\_fill\_manual(values= c(rep(grouped\_taxon\_colors[1], 6), # for animals  
 rep(grouped\_taxon\_colors[2], 3), # for platns  
 rep(grouped\_taxon\_colors[3], 1)), # for fungi and others  
 breaks=c(levels(df$taxonomic\_group\_simplified))) +  
 scale\_color\_manual(values= c(rep(grouped\_taxon\_colors[1], 6), # for animals  
 rep(grouped\_taxon\_colors[2], 3), # for platns  
 rep(grouped\_taxon\_colors[3], 1)), # for fungi and others  
 breaks=c(levels(df$taxonomic\_group\_simplified))) +  
 theme\_light() +  
 theme(panel.border = element\_blank(), legend.position="none",  
 text= element\_text(size=15))  
p2

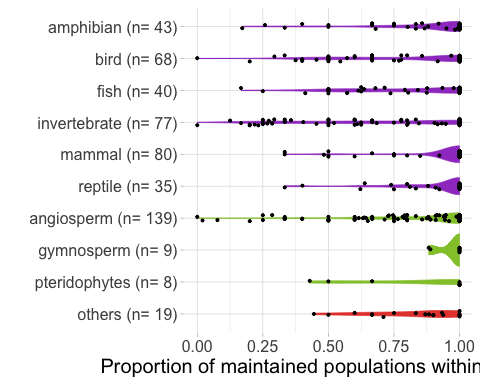


Table with sampling size, mean indicator value and proporiton of taxa where the value is below 0.25, 0.50 and 0.75:

# summary table for taxonomic group:  
x <- indicators\_averaged\_one %>%  
 filter(!is.na(indicator2\_mean)) %>%   
 filter(!is.na(taxonomic\_group\_simplified)) %>%   
 group\_by(taxonomic\_group\_simplified) %>%   
 summarize(n=n(),  
 mean=mean(indicator2\_mean),  
 median=median(indicator2\_mean),  
 n.below.75=sum(indicator2\_mean<0.75),  
 n.below.50=sum(indicator2\_mean<0.50),  
 n.below.25=sum(indicator2\_mean<0.25),  
 per.below.25=n.below.25/n\*100,  
 per.below.50=n.below.50/n\*100)  
  
  
# Calculate total counts and means  
total\_counts <- summarise(x,  
 taxonomic\_group\_simplified = "ALL",  
 n = sum(n),  
 mean = mean(mean),  
 median = median(median),  
 n.below.75 = sum(n.below.75),  
 n.below.50 = sum(n.below.50),  
 n.below.25 = sum(n.below.25),  
 per.below.25 = n.below.25 / n \* 100,  
 per.below.50 = n.below.50 / n \* 100)  
  
# Bind the total row to the summary\_table  
summary\_table <- bind\_rows(x, total\_counts)  
  
# keep taxonomic groups as level in desired order:  
summary\_table$taxonomic\_group\_simplified<-factor(summary\_table$taxonomic\_group\_simplified,  
 levels = c("amphibian", "bird" , "fish" , "invertebrate", "mammal",  
 "angiosperm", "gymnosperm", "reptile", "pteridophytes",  
 "others", "ALL"))  
summary\_table<- summary\_table %>% arrange(taxonomic\_group\_simplified)  
  
# show nice table  
kable(summary\_table, digits=2)

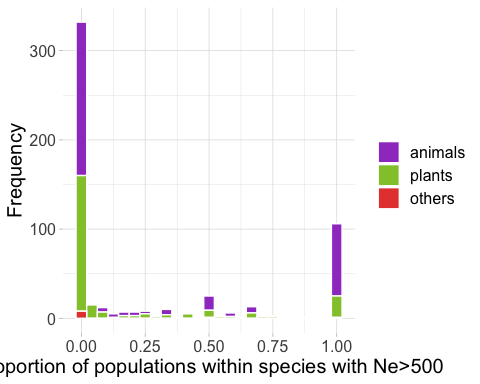
| taxonomic\_group\_simplified | n | mean | median | n.below.75 | n.below.50 | n.below.25 | per.below.25 | per.below.50 |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| amphibian | 43 | 0.85 | 1.00 | 9 | 4 | 1 | 2.33 | 9.30 |
| bird | 68 | 0.79 | 1.00 | 25 | 9 | 2 | 2.94 | 13.24 |
| fish | 40 | 0.78 | 0.86 | 17 | 3 | 1 | 2.50 | 7.50 |
| invertebrate | 77 | 0.67 | 0.67 | 40 | 21 | 7 | 9.09 | 27.27 |
| mammal | 80 | 0.94 | 1.00 | 8 | 3 | 0 | 0.00 | 3.75 |
| angiosperm | 139 | 0.83 | 1.00 | 36 | 13 | 4 | 2.88 | 9.35 |
| gymnosperm | 9 | 0.97 | 1.00 | 0 | 0 | 0 | 0.00 | 0.00 |
| reptile | 35 | 0.90 | 1.00 | 5 | 2 | 0 | 0.00 | 5.71 |
| pteridophytes | 8 | 0.82 | 1.00 | 3 | 1 | 0 | 0.00 | 12.50 |
| others | 19 | 0.82 | 0.88 | 6 | 1 | 0 | 0.00 | 5.26 |
| ALL | 518 | 0.84 | 1.00 | 149 | 57 | 15 | 2.90 | 11.00 |

### Histograms and summary tables by 3 taxonomic groups (animals, plants, others)

By animals, plants, others:

# Create a histogram   
hist\_p1 <- indicators\_averaged\_one %>%  
 ggplot(aes(x = indicator1\_mean, fill = taxonomic\_group\_3)) +  
 geom\_histogram( bins = 25, color="white") + # Adjust the number of bins as needed  
 labs(x = "Proportion of populations within species with Ne>500", y = "Frequency") +  
 scale\_fill\_manual(  
 values = grouped\_taxon\_colors, # Custom colors for animals, plants, and others  
 breaks = c("animals", "plants", "others"),  
 name = "Taxonomic Group")+  
 theme\_light() +  
 theme(panel.border = element\_blank(), text = element\_text(size = 15),   
 legend.position = "right") +  
 guides(fill = guide\_legend(title = NULL))  
  
# plot  
hist\_p1

## Warning: Removed 351 rows containing non-finite values (`stat\_bin()`).

 Summary table for Ne indicator 3 taxonomic groups:

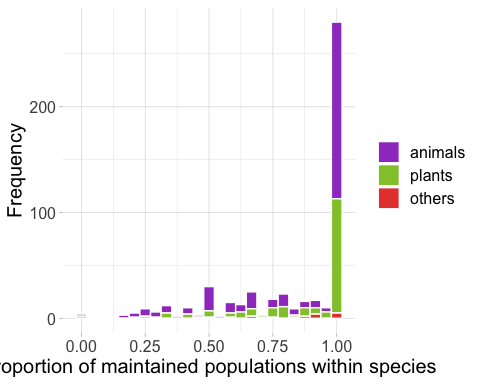
x <- indicators\_averaged\_one %>%  
 filter(!is.na(indicator1\_mean)) %>%   
 filter(!is.na(taxonomic\_group\_3)) %>%   
 group\_by(taxonomic\_group\_3) %>%   
 summarize(n=n(),  
 mean=mean(indicator1\_mean),  
 median=median(indicator1\_mean),  
 per.0=sum(indicator1\_mean==0) / n \*100,  
 per.below.25=sum(indicator1\_mean<0.25) / n \*100,  
 per.below.90=sum(indicator1\_mean<0.90) / n \*100,  
 per.above.75=sum(indicator1\_mean>0.75)/ n \*100,  
 per1=sum(indicator1\_mean==1) / n \*100)  
  
  
  
# Calculate total counts and means  
total\_counts <- indicators\_averaged\_one %>%  
 filter(!is.na(indicator1\_mean)) %>%   
 filter(!is.na(taxonomic\_group\_3)) %>%   
 ungroup() %>%   
 summarize(taxonomic\_group\_3 = "ALL",  
 n= n(),  
 mean = mean(indicator1\_mean),  
 median = median(indicator1\_mean),  
 per.0=sum(indicator1\_mean==0) / n \*100,  
 per.below.25=sum(indicator1\_mean<0.25) / n \*100,  
 per.below.90=sum(indicator1\_mean<0.90) / n \*100,  
 per.above.75=sum(indicator1\_mean>0.75)/ n \*100,  
 per1=sum(indicator1\_mean==1) / n \*100)  
  
# Bind the total row to the summary\_table  
summary\_table <- bind\_rows(x, total\_counts)  
  
# keep taxonomic groups as level in desired order:  
summary\_table$taxonomic\_group\_3<-factor(summary\_table$taxonomic\_group\_3,  
 levels = c("animals", "plants", "others", "ALL"))  
summary\_table<- summary\_table %>% arrange(taxonomic\_group\_3)  
  
kable(summary\_table, digits=2)

| taxonomic\_group\_3 | n | mean | median | per.0 | per.below.25 | per.below.90 | per.above.75 | per1 |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| animals | 312 | 0.34 | 0 | 54.49 | 60.58 | 74.04 | 26.28 | 25.96 |
| plants | 246 | 0.19 | 0 | 61.79 | 73.58 | 90.24 | 10.57 | 9.76 |
| others | 10 | 0.15 | 0 | 80.00 | 80.00 | 90.00 | 10.00 | 10.00 |
| ALL | 568 | 0.27 | 0 | 58.10 | 66.55 | 81.34 | 19.19 | 18.66 |

PM Histogram for animal, plants, others:

# Create a histogram   
hist\_p2 <- indicators\_averaged\_one %>%  
 ggplot(aes(x = indicator2\_mean, fill = taxonomic\_group\_3)) +  
 geom\_histogram(bins = 25, color="white") + # Adjust the number of bins as needed  
 labs(x = "Proportion of maintained populations within species", y = "Frequency") +  
 scale\_fill\_manual(  
 values = grouped\_taxon\_colors, # Custom colors for animals, plants, and others  
 breaks = c("animals", "plants", "others"),  
 name = "Taxonomic Group")+  
 theme\_light() +  
 theme(panel.border = element\_blank(), text = element\_text(size = 15)) +  
 guides(fill = guide\_legend(title = NULL))  
  
# plot  
hist\_p2

## Warning: Removed 401 rows containing non-finite values (`stat\_bin()`).



Summary table for PM indicator 3 taxonomic groups

x <- indicators\_averaged\_one %>%  
 filter(!is.na(indicator2\_mean)) %>%   
 filter(!is.na(taxonomic\_group\_3)) %>%   
 group\_by(taxonomic\_group\_3) %>%   
 summarize(n=n(),  
 mean=mean(indicator2\_mean),  
 median=median(indicator2\_mean),  
 per0=sum(indicator2\_mean==0) / n \*100,  
 per.below.25=sum(indicator2\_mean<0.25) / n \*100,  
 per.below.90=sum(indicator2\_mean<0.90) / n \*100,  
 per.above.75=sum(indicator2\_mean>0.75) / n \*100,  
 per1=sum(indicator2\_mean==1) / n \*100)  
  
# Calculate total counts and means  
total\_counts <- indicators\_averaged\_one %>%  
 filter(!is.na(indicator2\_mean)) %>%   
 filter(!is.na(taxonomic\_group\_3)) %>%   
 ungroup() %>%   
 summarize(taxonomic\_group\_3 = "ALL",  
 n= n(),  
 mean = mean(indicator2\_mean),  
 median = median(indicator2\_mean),  
 per0=sum(indicator2\_mean==0) / n \*100,  
 per.below.25=sum(indicator2\_mean<0.25) / n \*100,  
 per.below.90=sum(indicator2\_mean<0.90) / n \*100,  
 per.above.75=sum(indicator2\_mean>0.75) / n \*100,  
 per1=sum(indicator2\_mean==1) / n \*100)  
  
# Bind the total row to the summary\_table  
summary\_table <- bind\_rows(x, total\_counts)  
  
# keep taxonomic groups as level in desired order:  
summary\_table$taxonomic\_group\_3<-factor(summary\_table$taxonomic\_group\_3,  
 levels = c("animals", "plants", "others", "ALL"))  
summary\_table<- summary\_table %>% arrange(taxonomic\_group\_3)  
  
kable(summary\_table, digits=2)

| taxonomic\_group\_3 | n | mean | median | per0 | per.below.25 | per.below.90 | per.above.75 | per1 |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| animals | 308 | 0.81 | 1.00 | 0.65 | 3.57 | 42.21 | 65.91 | 53.57 |
| plants | 191 | 0.85 | 1.00 | 0.52 | 2.09 | 37.17 | 74.35 | 56.02 |
| others | 19 | 0.82 | 0.88 | 0.00 | 0.00 | 52.63 | 63.16 | 26.32 |
| ALL | 518 | 0.82 | 1.00 | 0.58 | 2.90 | 40.73 | 68.92 | 53.47 |

### Main Figure: Single figure 4 panels for violin plots and histograms for both indicators by taxonomic group

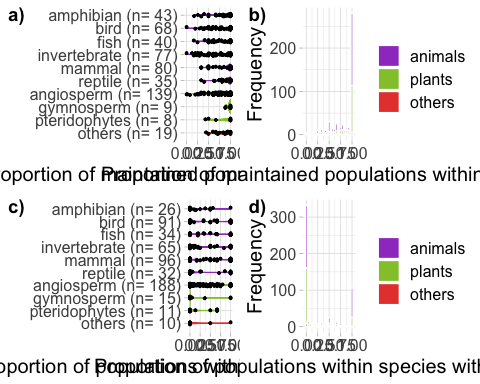
plot\_grid(p2, hist\_p2,   
 p1, hist\_p1,  
 ncol=2, align = "v", labels=c("a)", "b)", "c)", "d)"))

## Warning: Removed 401 rows containing non-finite values (`stat\_bin()`).

## Warning: `position\_dodge()` requires non-overlapping x intervals

## Warning: Removed 351 rows containing non-finite values (`stat\_bin()`).

## Warning: Graphs cannot be vertically aligned unless the axis parameter is set.  
## Placing graphs unaligned.



## Supplementary Figure: Values of indicator 1 and indicator 2 for multiassessed taxa (alternative assessments)

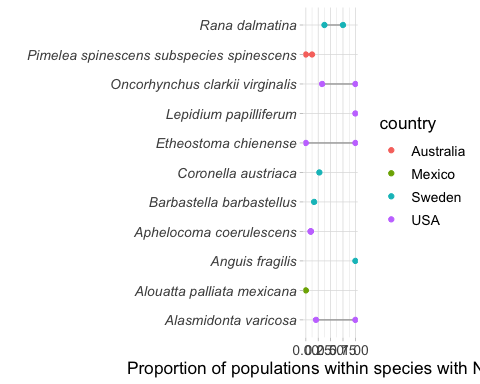
#subset only with taxa assessed multiple times:  
only\_multi<-indicators\_full %>%   
 filter(multiassessment=="multiassessment")

First, check how indicator 1 changes across the multiassessments.

p1<-only\_multi %>%   
 # Keep rows with different values in indicator1 within each taxon group  
 group\_by(taxon) %>%  
 filter(n\_distinct(indicator1) > 1) %>%  
 # plot  
 ggplot(aes(x=taxon, y=indicator1)) +  
 geom\_line(colour="darkgrey") +   
 geom\_point(aes(color=country\_assessment)) +  
 xlab("") + ylab("Proportion of populations within species with Ne>500") +  
 labs(color="country") +  
 ylim(0, 1)+  
 coord\_flip() +  
 theme\_light() +   
 theme(axis.text.y = element\_text(face = "italic"), panel.border = element\_blank(), legend.position="right", text= element\_text(size=13))  
p1

## Warning: Removed 5 rows containing missing values (`geom\_line()`).

## Warning: Removed 6 rows containing missing values (`geom\_point()`).

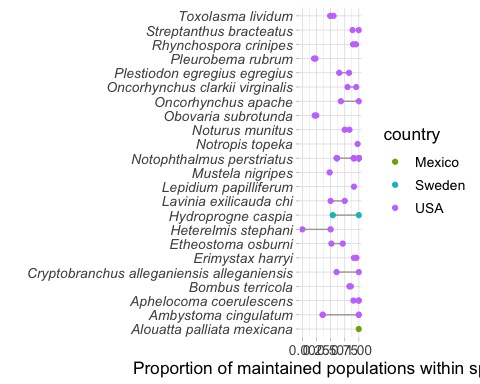


Now check how Proportion of maintained populations (indicator 2) changes across the multiassessments.

p2<-only\_multi %>%   
 # Keep rows with different values in indicator1 within each taxon group  
 group\_by(taxon) %>%  
 filter(n\_distinct(indicator2) > 1) %>%  
   
 ggplot(aes(x=taxon, y=indicator2)) +  
 geom\_line(colour="darkgrey") +   
 geom\_point(aes(color=country\_assessment)) +  
 scale\_color\_manual(values= scales::hue\_pal()(4)[2:4]) + # last 3 colors to make them the same than the other plot  
 xlab("") + ylab("Proportion of maintained populations within species") +  
 labs(color="country") +  
 coord\_flip() +  
 theme\_light() +   
 theme(axis.text.y = element\_text(face = "italic"), panel.border = element\_blank(), legend.position="right", text= element\_text(size=13))  
p2

## Warning: Removed 6 rows containing missing values (`geom\_line()`).

## Warning: Removed 6 rows containing missing values (`geom\_point()`).



Plot together:

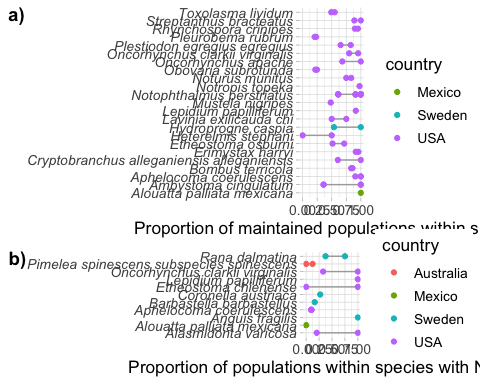
plot\_grid(p2, p1,   
 rel\_heights = c(1.4, 0.8),  
 ncol=1, labels=c("a)", "b)"))

## Warning: Removed 6 rows containing missing values (`geom\_line()`).

## Warning: Removed 6 rows containing missing values (`geom\_point()`).

## Warning: Removed 5 rows containing missing values (`geom\_line()`).

## Warning: Removed 6 rows containing missing values (`geom\_point()`).



## Indicator 3 (number of species with genetic diversity monitoring)

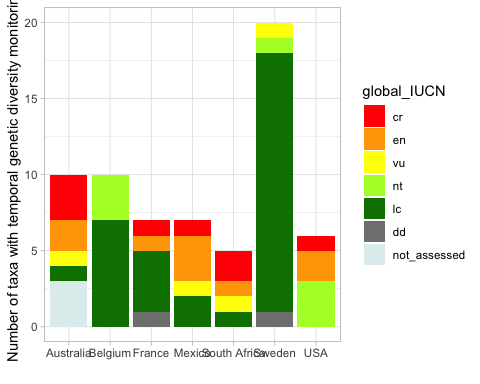
Indicator 3 refers to the number (count) of taxa by country in which genetic monitoring is occurring. This is stored in the variable temp\_gen\_monitoring as a “yes/no” answer for each taxon.

indicator3

## # A tibble: 7 × 2  
## country\_assessment n\_taxon\_gen\_monitoring  
## <chr> <int>  
## 1 australia 10  
## 2 belgium 10  
## 3 france 7  
## 4 mexico 7  
## 5 south\_africa 5  
## 6 sweden 20  
## 7 united\_states 6

Plot by global IUCN redlist status

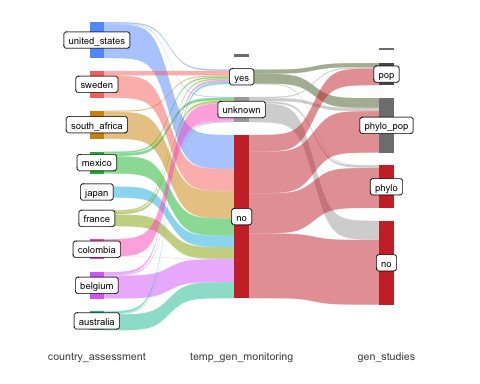
# desired order of levels  
indicators\_full$global\_IUCN<-factor(as.factor(indicators\_full$global\_IUCN), levels=c("cr", "en", "vu", "nt", "lc", "dd", "not\_assessed", "unknown"))  
  
  
## plot  
indicators\_full %>%  
 # keep only one record if the taxon was assessed more than once within the country  
 select(country\_assessment, taxon, temp\_gen\_monitoring, global\_IUCN) %>%  
 filter(!duplicated(.)) %>%  
  
 # count "yes" in tem\_gen\_monitoring by country  
 filter(temp\_gen\_monitoring=="yes") %>%  
ggplot(aes(x=country\_assessment, fill=global\_IUCN)) +  
 geom\_bar() +  
 xlab("") + ylab("Number of taxa with temporal genetic diversity monitoring") +  
 scale\_fill\_manual(values= IUCNcolors, # iucn color codes  
 breaks=levels(as.factor(indicators\_full$global\_IUCN))) +  
 theme\_light()



Relatively few taxa have genetic monitoring, but many have some sort of genetic study. Let’s check that with a Sankey Plot:

# first subset the ind3\_data keeping only taxa assessed a single time, plust the first record of those assessed multiple times.  
ind3\_data\_firstmulti<-ind3\_data[!duplicated(cbind(ind3\_data$taxon, ind3\_data$country\_assessment)), ]  
  
# transform data to how ggsankey wants it  
df <- ind3\_data\_firstmulti %>%  
 make\_long(country\_assessment, temp\_gen\_monitoring, gen\_studies)  
  
# plot  
ggplot(df, aes(x = x,  
 next\_x = next\_x,  
 node = node,  
 next\_node = next\_node,  
 fill = factor(node),  
 label = node)) +  
 geom\_sankey(flow.alpha = 0.5,   
 show.legend = FALSE) +  
 geom\_sankey\_label(size = 2.5, color = "black", fill = "white") +  
 theme\_sankey(base\_size = 10) +  
  
 # manually set flow fill according to desired color  
 # countries  
 scale\_fill\_manual(values=c(scales::hue\_pal()(length(unique(ind3\_data\_firstmulti$country\_assessment))),   
 # traffic light for monitoring  
 c("darkolivegreen", "brown3", "darkgrey"),  
 # nice soft colors for gen\_studies  
 c("grey50", "grey35", "grey50", "brown3")),  
   
 breaks=c(unique(ind3\_data\_firstmulti$country\_assessment),  
 unique(ind3\_data\_firstmulti$temp\_gen\_monitoring),  
 unique(ind3\_data\_firstmulti$gen\_studies))) +  
   
 xlab("")

## Warning: Removed 2 rows containing missing values (`geom\_label()`).



table(ind3\_data\_firstmulti$gen\_studies)

##   
## no phylo phylo\_pop pop   
## 375 190 244 99

Count data:

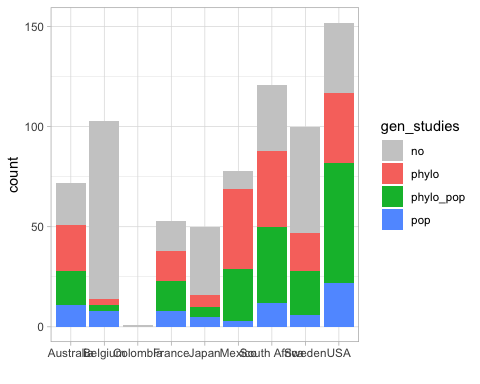
ind3\_data %>%  
 # keep only one record if the taxon was assessed more than once within the country  
 select(country\_assessment, taxon, gen\_studies, temp\_gen\_monitoring) %>%  
 filter(!duplicated(.)) %>%  
  
 group\_by(country\_assessment, temp\_gen\_monitoring, gen\_studies) %>%  
 summarise(n\_studies=n())

## `summarise()` has grouped output by 'country\_assessment',  
## 'temp\_gen\_monitoring'. You can override using the `.groups` argument.

## # A tibble: 65 × 4  
## # Groups: country\_assessment, temp\_gen\_monitoring [23]  
## country\_assessment temp\_gen\_monitoring gen\_studies n\_studies  
## <chr> <chr> <chr> <int>  
## 1 australia no no 21  
## 2 australia no phylo 23  
## 3 australia no phylo\_pop 17  
## 4 australia no pop 11  
## 5 australia unknown no 1  
## 6 australia unknown phylo\_pop 1  
## 7 australia unknown pop 1  
## 8 australia yes phylo\_pop 7  
## 9 australia yes pop 3  
## 10 belgium no no 89  
## # … with 55 more rows

How many genetic studies ara available by country for species without temporal genetic diversity monitoring?

## plot  
indicators\_full %>%  
 # keep only one record if the taxon was assessed more than once within the country  
 select(country\_assessment, taxon, temp\_gen\_monitoring, gen\_studies) %>%  
 filter(!duplicated(.)) %>%  
 # keep only taxa without gen div monitoring  
 filter(temp\_gen\_monitoring=="no")%>%  
  
ggplot(aes(x=country\_assessment, fill=gen\_studies)) +  
 geom\_bar() +  
 scale\_fill\_manual(values=c("grey80", scales::hue\_pal()(3)))+  
 xlab("") +  
 theme\_light()



## Summary table of mean indicator values and n

The tables below show the indicator values and sampling size averaging them by country, taxonomic group, distribution type or IUCN global red list status. For this summary the mean of the multiassessed species was considering and counted as a single entry for the sampling size.

Codes for indicator names:

* **PM.ind**: Proportion of Mantained populations indicator (indicator 2)
* **Ne.ind**: Proportion of populations where Ne>500 indicator (indicator 1)
* **Mon.ind**: Number of species where genetic diversity monitoring is taking place (indicator 3)

Codes for summary stats:

* **n**: sampling size (number of taxa assessed) without missing data
* **mean**: mean value for the indicator value
* **sd**: standar deviation for the indicator value

Summary stats by country:

x<-indicators\_averaged\_one %>%   
 group\_by(country\_assessment) %>%  
 summarise(n.PM.ind=sum(!is.na(indicator2)),   
 mean.PM.ind=mean(indicator2, na.rm=TRUE),  
 sd.PM.ind=sd(indicator2, na.rm=TRUE),  
 n.Ne.ind=sum(!is.na(indicator1)),   
 mean.Ne.ind=mean(indicator1, na.rm=TRUE),  
 sd.Ne.ind=sd(indicator1, na.rm=TRUE),  
 Mon.ind=sum(temp\_gen\_monitoring=="yes"))  
  
# nice table  
kable(x, digits=3)

| country\_assessment | n.PM.ind | mean.PM.ind | sd.PM.ind | n.Ne.ind | mean.Ne.ind | sd.Ne.ind | Mon.ind |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Australia | 28 | 0.903 | 0.178 | 47 | 0.170 | 0.299 | 10 |
| Belgium | 27 | 0.453 | 0.221 | 101 | 0.246 | 0.381 | 10 |
| Colombia | 22 | 0.601 | 0.174 | 43 | 0.326 | 0.474 | NA |
| France | 34 | 0.854 | 0.278 | 55 | 0.416 | 0.471 | 7 |
| Japan | 50 | 0.925 | 0.152 | 50 | 0.077 | 0.180 | 0 |
| Mexico | 28 | 0.936 | 0.135 | 47 | 0.217 | 0.354 | 7 |
| South Africa | 90 | 0.948 | 0.155 | 61 | 0.422 | 0.475 | 5 |
| Sweden | 120 | 0.777 | 0.271 | 83 | 0.188 | 0.331 | 20 |
| USA | 117 | 0.794 | 0.244 | 79 | 0.354 | 0.410 | 6 |

### Taxonomic groups

Summary stats by taxonomic group:

x<-indicators\_averaged\_one %>%   
 group\_by(taxonomic\_group) %>%  
 summarise(n.PM.ind=sum(!is.na(indicator2)),   
 mean.PM.ind=mean(indicator2, na.rm=TRUE),  
 sd.PM.ind=sd(indicator2, na.rm=TRUE),  
 n.Ne.ind=sum(!is.na(indicator1)),   
 mean.Ne.ind=mean(indicator1, na.rm=TRUE),  
 sd.Ne.ind=sd(indicator1, na.rm=TRUE),  
 Mon.ind=sum(temp\_gen\_monitoring=="yes"))  
  
# nice table  
kable(x, digits=3)

| taxonomic\_group | n.PM.ind | mean.PM.ind | sd.PM.ind | n.Ne.ind | mean.Ne.ind | sd.Ne.ind | Mon.ind |
| --- | --- | --- | --- | --- | --- | --- | --- |
| amphibian | 43 | 0.833 | 0.244 | 26 | 0.150 | 0.250 | 9 |
| bird | 67 | 0.789 | 0.265 | 91 | 0.321 | 0.445 | NA |
| fish | 40 | 0.768 | 0.245 | 34 | 0.414 | 0.448 | 11 |
| invertebrate | 77 | 0.671 | 0.309 | 65 | 0.277 | 0.403 | 4 |
| mammal | 80 | 0.937 | 0.161 | 95 | 0.419 | 0.461 | 22 |
| reptile | 35 | 0.902 | 0.176 | 31 | 0.288 | 0.437 | 1 |
| angiosperm | 138 | 0.834 | 0.242 | 188 | 0.177 | 0.311 | 6 |
| bryophyte | 4 | 0.688 | 0.252 | 2 | 0.250 | 0.354 | 0 |
| gymnosperm | 9 | 0.975 | 0.050 | 15 | 0.161 | 0.353 | 0 |
| pteridophytes | 8 | 0.824 | 0.251 | 11 | 0.179 | 0.284 | 0 |
| fungus | 3 | 0.903 | 0.167 | 2 | 0.500 | 0.707 | 0 |
| other | 12 | 0.844 | 0.141 | 6 | 0.000 | 0.000 | 3 |

Detailed table:

x<-indicators\_averaged\_one %>%   
 group\_by(country\_assessment, taxonomic\_group) %>%  
 summarise(n.PM.ind=sum(!is.na(indicator2)),   
 mean.PM.ind=mean(indicator2, na.rm=TRUE),  
 sd.PM.ind=sd(indicator2, na.rm=TRUE),  
 n.Ne.ind=sum(!is.na(indicator1)),   
 mean.Ne.ind=mean(indicator1, na.rm=TRUE),  
 sd.Ne.ind=sd(indicator1, na.rm=TRUE),  
 Mon.ind=sum(temp\_gen\_monitoring=="yes"))

## `summarise()` has grouped output by 'country\_assessment'. You can override  
## using the `.groups` argument.

# nice table  
kable(x, digits=3)

| country\_assessment | taxonomic\_group | n.PM.ind | mean.PM.ind | sd.PM.ind | n.Ne.ind | mean.Ne.ind | sd.Ne.ind | Mon.ind |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Australia | amphibian | 0 | NaN | NA | 1 | 0.000 | NA | 0 |
| Australia | bird | 9 | 1.000 | 0.000 | 9 | 0.167 | 0.264 | 2 |
| Australia | fish | 1 | 1.000 | NA | 2 | 0.500 | 0.707 | 1 |
| Australia | invertebrate | 1 | 0.500 | NA | 0 | NaN | NA | 0 |
| Australia | mammal | 3 | 0.750 | 0.250 | 10 | 0.303 | 0.359 | 3 |
| Australia | reptile | 7 | 0.958 | 0.078 | 5 | 0.050 | 0.112 | 0 |
| Australia | angiosperm | 2 | 0.700 | 0.424 | 15 | 0.115 | 0.276 | 1 |
| Australia | bryophyte | 0 | NaN | NA | 1 | 0.500 | NA | 0 |
| Australia | gymnosperm | 0 | NaN | NA | 2 | 0.000 | 0.000 | 0 |
| Australia | pteridophytes | 0 | NaN | NA | 1 | 0.000 | NA | 0 |
| Australia | other | 5 | 0.887 | 0.141 | 1 | 0.000 | NA | 3 |
| Belgium | amphibian | 3 | 0.310 | 0.170 | 9 | 0.186 | 0.330 | 1 |
| Belgium | fish | 5 | 0.570 | 0.153 | 9 | 0.206 | 0.352 | 2 |
| Belgium | invertebrate | 10 | 0.444 | 0.259 | 30 | 0.323 | 0.416 | 3 |
| Belgium | mammal | 3 | 0.444 | 0.192 | 19 | 0.447 | 0.497 | 4 |
| Belgium | reptile | 0 | NaN | NA | 4 | 0.030 | 0.026 | 0 |
| Belgium | angiosperm | 5 | 0.446 | 0.279 | 26 | 0.093 | 0.219 | 0 |
| Belgium | bryophyte | 1 | 0.444 | NA | 1 | 0.000 | NA | 0 |
| Belgium | gymnosperm | 0 | NaN | NA | 1 | 0.050 | NA | 0 |
| Belgium | pteridophytes | 0 | NaN | NA | 2 | 0.250 | 0.354 | 0 |
| Colombia | amphibian | 2 | 0.625 | 0.177 | 0 | NaN | NA | 0 |
| Colombia | bird | 19 | 0.604 | 0.181 | 31 | 0.419 | 0.502 | NA |
| Colombia | fish | 0 | NaN | NA | 2 | 0.500 | 0.707 | 0 |
| Colombia | mammal | 1 | 0.500 | NA | 1 | 0.000 | NA | 0 |
| Colombia | reptile | 0 | NaN | NA | 2 | 0.000 | 0.000 | 0 |
| Colombia | angiosperm | 0 | NaN | NA | 6 | 0.000 | 0.000 | 0 |
| Colombia | other | 0 | NaN | NA | 1 | 0.000 | NA | 0 |
| France | amphibian | 1 | 1.000 | NA | 1 | 0.000 | NA | 1 |
| France | bird | 11 | 0.852 | 0.259 | 20 | 0.342 | 0.460 | 1 |
| France | fish | 1 | 0.167 | NA | 6 | 0.589 | 0.463 | 2 |
| France | invertebrate | 3 | 0.700 | 0.265 | 7 | 0.405 | 0.508 | 0 |
| France | mammal | 11 | 0.955 | 0.151 | 10 | 0.217 | 0.416 | 3 |
| France | reptile | 1 | 1.000 | NA | 2 | 0.500 | 0.707 | 0 |
| France | angiosperm | 3 | 0.667 | 0.577 | 6 | 0.583 | 0.492 | 0 |
| France | gymnosperm | 1 | 1.000 | NA | 2 | 1.000 | 0.000 | 0 |
| France | fungus | 1 | 1.000 | NA | 1 | 1.000 | NA | 0 |
| France | other | 1 | 0.900 | NA | 0 | NaN | NA | 0 |
| Japan | angiosperm | 39 | 0.931 | 0.130 | 39 | 0.061 | 0.148 | 0 |
| Japan | gymnosperm | 4 | 1.000 | 0.000 | 4 | 0.000 | 0.000 | 0 |
| Japan | pteridophytes | 7 | 0.847 | 0.262 | 7 | 0.210 | 0.316 | 0 |
| Mexico | amphibian | 0 | NaN | NA | 2 | 0.000 | 0.000 | 0 |
| Mexico | bird | 1 | 0.667 | NA | 2 | 0.500 | 0.707 | 1 |
| Mexico | fish | 0 | NaN | NA | 0 | NaN | NA | 0 |
| Mexico | invertebrate | 1 | 1.000 | NA | 0 | NaN | NA | 0 |
| Mexico | mammal | 3 | 0.867 | 0.231 | 3 | 0.000 | 0.000 | 1 |
| Mexico | reptile | 1 | 1.000 | NA | 4 | 0.500 | 0.577 | 0 |
| Mexico | angiosperm | 20 | 0.959 | 0.120 | 29 | 0.236 | 0.339 | 5 |
| Mexico | gymnosperm | 2 | 0.886 | 0.005 | 6 | 0.061 | 0.148 | 0 |
| Mexico | pteridophytes | 0 | NaN | NA | 1 | 0.000 | NA | 0 |
| South Africa | amphibian | 18 | 0.918 | 0.173 | 4 | 0.125 | 0.250 | 2 |
| South Africa | bird | 11 | 1.000 | 0.000 | 11 | 0.327 | 0.467 | 1 |
| South Africa | fish | 9 | 1.000 | 0.000 | 4 | 0.297 | 0.477 | 0 |
| South Africa | invertebrate | 0 | NaN | NA | 0 | NaN | NA | 0 |
| South Africa | mammal | 32 | 0.992 | 0.044 | 31 | 0.608 | 0.480 | 2 |
| South Africa | reptile | 7 | 0.869 | 0.254 | 1 | 1.000 | NA | 0 |
| South Africa | angiosperm | 12 | 0.833 | 0.277 | 10 | 0.060 | 0.190 | 0 |
| South Africa | gymnosperm | 1 | 1.000 | NA | 0 | NaN | NA | 0 |
| Sweden | amphibian | 13 | 0.891 | 0.183 | 9 | 0.192 | 0.219 | 5 |
| Sweden | bird | 11 | 0.696 | 0.385 | 9 | 0.111 | 0.333 | 2 |
| Sweden | fish | 7 | 0.738 | 0.290 | 4 | 0.299 | 0.476 | 4 |
| Sweden | invertebrate | 29 | 0.674 | 0.292 | 20 | 0.078 | 0.225 | 0 |
| Sweden | mammal | 20 | 0.986 | 0.047 | 15 | 0.361 | 0.447 | 8 |
| Sweden | reptile | 7 | 0.983 | 0.045 | 3 | 0.619 | 0.541 | 1 |
| Sweden | angiosperm | 22 | 0.622 | 0.259 | 18 | 0.159 | 0.258 | 0 |
| Sweden | bryophyte | 2 | 0.904 | 0.048 | 0 | NaN | NA | 0 |
| Sweden | pteridophytes | 1 | 0.667 | NA | 0 | NaN | NA | 0 |
| Sweden | fungus | 2 | 0.855 | 0.205 | 1 | 0.000 | NA | 0 |
| Sweden | other | 6 | 0.800 | 0.153 | 4 | 0.000 | 0.000 | 0 |
| USA | amphibian | 6 | 0.754 | 0.267 | 0 | NaN | NA | 0 |
| USA | bird | 5 | 0.741 | 0.205 | 9 | 0.254 | 0.375 | 2 |
| USA | fish | 17 | 0.737 | 0.198 | 7 | 0.615 | 0.448 | 2 |
| USA | invertebrate | 33 | 0.730 | 0.324 | 8 | 0.492 | 0.471 | 1 |
| USA | mammal | 7 | 0.905 | 0.194 | 6 | 0.303 | 0.351 | 1 |
| USA | reptile | 12 | 0.823 | 0.202 | 10 | 0.271 | 0.444 | 0 |
| USA | angiosperm | 35 | 0.867 | 0.181 | 39 | 0.332 | 0.398 | 0 |
| USA | bryophyte | 1 | 0.500 | NA | 0 | NaN | NA | 0 |
| USA | gymnosperm | 1 | 1.000 | NA | 0 | NaN | NA | 0 |

### IUCN

Summary stats:

x<-indicators\_averaged\_one %>%   
 group\_by(global\_IUCN) %>%  
 summarise(n.PM.ind=sum(!is.na(indicator2)),   
 mean.PM.ind=mean(indicator2, na.rm=TRUE),  
 sd.PM.ind=sd(indicator2, na.rm=TRUE),  
 n.Ne.ind=sum(!is.na(indicator1)),   
 mean.Ne.ind=mean(indicator1, na.rm=TRUE),  
 sd.Ne.ind=sd(indicator1, na.rm=TRUE),  
 Mon.ind=sum(temp\_gen\_monitoring=="yes"))  
  
# nice table  
kable(x, digits=3)

| global\_IUCN | n.PM.ind | mean.PM.ind | sd.PM.ind | n.Ne.ind | mean.Ne.ind | sd.Ne.ind | Mon.ind |
| --- | --- | --- | --- | --- | --- | --- | --- |
| CR | 36 | 0.825 | 0.272 | 46 | 0.109 | 0.284 | 8 |
| EN | 59 | 0.786 | 0.254 | 48 | 0.260 | 0.415 | 9 |
| VU | 64 | 0.778 | 0.253 | 66 | 0.310 | 0.414 | 4 |
| NT | 42 | 0.821 | 0.263 | 50 | 0.237 | 0.375 | 7 |
| LC | 152 | 0.845 | 0.251 | 185 | 0.365 | 0.436 | 32 |
| DD | 9 | 0.707 | 0.313 | 10 | 0.442 | 0.490 | 2 |
| NE | 152 | 0.833 | 0.235 | 156 | 0.187 | 0.329 | 3 |
| unknown | 2 | 1.000 | 0.000 | 3 | 0.667 | 0.577 | 0 |
| NA | 0 | NaN | NA | 2 | 0.000 | 0.000 | NA |

Detailed table by IUCN category:

x<-indicators\_averaged\_one %>%   
 group\_by(country\_assessment, global\_IUCN) %>%  
 summarise(n.PM.ind=sum(!is.na(indicator2)),   
 mean.PM.ind=mean(indicator2, na.rm=TRUE),  
 sd.PM.ind=sd(indicator2, na.rm=TRUE),  
 n.Ne.ind=sum(!is.na(indicator1)),   
 mean.Ne.ind=mean(indicator1, na.rm=TRUE),  
 sd.Ne.ind=sd(indicator1, na.rm=TRUE),  
 Mon.ind=sum(temp\_gen\_monitoring=="yes"))

## `summarise()` has grouped output by 'country\_assessment'. You can override  
## using the `.groups` argument.

# nice table  
kable(x, digits=3)

| country\_assessment | global\_IUCN | n.PM.ind | mean.PM.ind | sd.PM.ind | n.Ne.ind | mean.Ne.ind | sd.Ne.ind | Mon.ind |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Australia | CR | 5 | 0.860 | 0.219 | 10 | 0.000 | 0.000 | 3 |
| Australia | EN | 4 | 0.850 | 0.300 | 7 | 0.167 | 0.264 | 2 |
| Australia | VU | 6 | 0.943 | 0.101 | 8 | 0.260 | 0.355 | 1 |
| Australia | NT | 4 | 1.000 | 0.000 | 5 | 0.353 | 0.328 | 0 |
| Australia | LC | 3 | 1.000 | 0.000 | 8 | 0.229 | 0.367 | 1 |
| Australia | NE | 6 | 0.822 | 0.202 | 9 | 0.128 | 0.329 | 3 |
| Australia | unknown | 0 | NaN | NA | 0 | NaN | NA | 0 |
| Belgium | CR | 1 | 0.333 | NA | 2 | 0.500 | 0.707 | 0 |
| Belgium | EN | 1 | 0.455 | NA | 1 | 0.000 | NA | 0 |
| Belgium | VU | 3 | 0.548 | 0.410 | 3 | 0.333 | 0.577 | 0 |
| Belgium | NT | 2 | 0.310 | 0.034 | 13 | 0.030 | 0.058 | 3 |
| Belgium | LC | 19 | 0.466 | 0.215 | 64 | 0.285 | 0.398 | 7 |
| Belgium | DD | 1 | 0.333 | NA | 3 | 0.364 | 0.553 | 0 |
| Belgium | NE | 0 | NaN | NA | 14 | 0.151 | 0.292 | 0 |
| Belgium | unknown | 0 | NaN | NA | 1 | 1.000 | NA | 0 |
| Colombia | CR | 2 | 0.450 | 0.071 | 7 | 0.000 | 0.000 | 0 |
| Colombia | EN | 4 | 0.525 | 0.145 | 3 | 0.667 | 0.577 | 0 |
| Colombia | VU | 11 | 0.659 | 0.195 | 15 | 0.133 | 0.352 | 0 |
| Colombia | NT | 3 | 0.550 | 0.180 | 6 | 0.667 | 0.516 | 0 |
| Colombia | LC | 2 | 0.667 | 0.000 | 10 | 0.600 | 0.516 | 0 |
| Colombia | NA | 0 | NaN | NA | 2 | 0.000 | 0.000 | NA |
| France | CR | 2 | 0.583 | 0.589 | 5 | 0.040 | 0.089 | 1 |
| France | EN | 1 | 1.000 | NA | 3 | 0.333 | 0.577 | 1 |
| France | VU | 4 | 0.725 | 0.320 | 9 | 0.481 | 0.467 | 0 |
| France | NT | 7 | 0.839 | 0.277 | 6 | 0.333 | 0.516 | 0 |
| France | LC | 17 | 0.953 | 0.133 | 28 | 0.476 | 0.482 | 4 |
| France | DD | 0 | NaN | NA | 2 | 1.000 | 0.000 | 1 |
| France | NE | 3 | 0.633 | 0.551 | 2 | 0.000 | 0.000 | 0 |
| Japan | CR | 2 | 1.000 | 0.000 | 2 | 0.000 | 0.000 | 0 |
| Japan | EN | 1 | 1.000 | NA | 1 | 0.000 | NA | 0 |
| Japan | LC | 3 | 1.000 | 0.000 | 3 | 0.021 | 0.036 | 0 |
| Japan | NE | 44 | 0.914 | 0.159 | 44 | 0.086 | 0.190 | 0 |
| Mexico | CR | 4 | 1.000 | 0.000 | 3 | 0.333 | 0.577 | 1 |
| Mexico | EN | 9 | 0.919 | 0.163 | 12 | 0.083 | 0.289 | 3 |
| Mexico | VU | 5 | 0.900 | 0.224 | 5 | 0.000 | 0.000 | 1 |
| Mexico | NT | 1 | 0.889 | NA | 2 | 0.000 | 0.000 | 0 |
| Mexico | LC | 5 | 0.936 | 0.092 | 12 | 0.497 | 0.367 | 2 |
| Mexico | DD | 1 | 1.000 | NA | 1 | 0.333 | NA | 0 |
| Mexico | NE | 3 | 0.958 | 0.072 | 12 | 0.158 | 0.318 | 0 |
| South Africa | CR | 14 | 0.860 | 0.285 | 12 | 0.042 | 0.144 | 2 |
| South Africa | EN | 16 | 0.895 | 0.182 | 9 | 0.467 | 0.469 | 1 |
| South Africa | VU | 14 | 0.982 | 0.067 | 12 | 0.500 | 0.522 | 1 |
| South Africa | NT | 8 | 0.969 | 0.088 | 8 | 0.253 | 0.356 | 0 |
| South Africa | LC | 34 | 1.000 | 0.000 | 18 | 0.667 | 0.485 | 1 |
| South Africa | DD | 1 | 1.000 | NA | 0 | NaN | NA | 0 |
| South Africa | NE | 2 | 0.750 | 0.354 | 1 | 0.000 | NA | 0 |
| South Africa | unknown | 1 | 1.000 | NA | 1 | 1.000 | NA | 0 |
| Sweden | EN | 5 | 0.489 | 0.208 | 2 | 0.050 | 0.071 | 0 |
| Sweden | VU | 7 | 0.685 | 0.247 | 7 | 0.297 | 0.363 | 1 |
| Sweden | NT | 8 | 0.816 | 0.273 | 5 | 0.054 | 0.074 | 1 |
| Sweden | LC | 63 | 0.836 | 0.259 | 41 | 0.247 | 0.374 | 17 |
| Sweden | DD | 4 | 0.549 | 0.299 | 4 | 0.250 | 0.500 | 1 |
| Sweden | NE | 33 | 0.744 | 0.268 | 24 | 0.085 | 0.228 | 0 |
| USA | CR | 6 | 0.828 | 0.164 | 5 | 0.467 | 0.447 | 1 |
| USA | EN | 18 | 0.743 | 0.268 | 10 | 0.300 | 0.483 | 2 |
| USA | VU | 14 | 0.664 | 0.271 | 7 | 0.427 | 0.311 | 0 |
| USA | NT | 9 | 0.796 | 0.289 | 5 | 0.284 | 0.435 | 3 |
| USA | LC | 6 | 0.791 | 0.208 | 1 | 0.000 | NA | 0 |
| USA | DD | 2 | 0.917 | 0.118 | 0 | NaN | NA | 0 |
| USA | NE | 61 | 0.829 | 0.234 | 50 | 0.365 | 0.415 | 0 |
| USA | unknown | 1 | 1.000 | NA | 1 | 0.000 | NA | 0 |

### Distribution type

Summary stats:

x<-indicators\_averaged\_one %>%   
 group\_by(species\_range) %>%  
 summarise(n.PM.ind=sum(!is.na(indicator2)),   
 mean.PM.ind=mean(indicator2, na.rm=TRUE),  
 sd.PM.ind=sd(indicator2, na.rm=TRUE),  
 n.Ne.ind=sum(!is.na(indicator1)),   
 mean.Ne.ind=mean(indicator1, na.rm=TRUE),  
 sd.Ne.ind=sd(indicator1, na.rm=TRUE),  
 Mon.ind=sum(temp\_gen\_monitoring=="yes"))  
  
# nice table  
kable(x, digits=3)

| species\_range | n.PM.ind | mean.PM.ind | sd.PM.ind | n.Ne.ind | mean.Ne.ind | sd.Ne.ind | Mon.ind |
| --- | --- | --- | --- | --- | --- | --- | --- |
| restricted | 309 | 0.795 | 0.266 | 313 | 0.187 | 0.344 | 24 |
| unknown | 14 | 0.760 | 0.259 | 20 | 0.300 | 0.470 | 1 |
| wide ranging | 193 | 0.867 | 0.217 | 231 | 0.384 | 0.432 | 40 |
| NA | 0 | NaN | NA | 2 | 0.000 | 0.000 | NA |

Detailed table by IUCN category:

x<-indicators\_averaged\_one %>%   
 group\_by(country\_assessment, species\_range) %>%  
 summarise(n.PM.ind=sum(!is.na(indicator2)),   
 mean.PM.ind=mean(indicator2, na.rm=TRUE),  
 sd.PM.ind=sd(indicator2, na.rm=TRUE),  
 n.Ne.ind=sum(!is.na(indicator1)),   
 mean.Ne.ind=mean(indicator1, na.rm=TRUE),  
 sd.Ne.ind=sd(indicator1, na.rm=TRUE),  
 Mon.ind=sum(temp\_gen\_monitoring=="yes"))

## `summarise()` has grouped output by 'country\_assessment'. You can override  
## using the `.groups` argument.

# nice table  
kable(x, digits=3)

| country\_assessment | species\_range | n.PM.ind | mean.PM.ind | sd.PM.ind | n.Ne.ind | mean.Ne.ind | sd.Ne.ind | Mon.ind |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Australia | restricted | 14 | 0.865 | 0.224 | 27 | 0.114 | 0.253 | 4 |
| Australia | unknown | 0 | NaN | NA | 1 | 0.000 | NA | 0 |
| Australia | wide ranging | 14 | 0.942 | 0.110 | 19 | 0.260 | 0.347 | 6 |
| Belgium | restricted | 10 | 0.319 | 0.128 | 22 | 0.135 | 0.262 | 1 |
| Belgium | unknown | 2 | 0.456 | 0.062 | 5 | 0.000 | 0.000 | 1 |
| Belgium | wide ranging | 15 | 0.542 | 0.242 | 74 | 0.295 | 0.411 | 8 |
| Colombia | restricted | 16 | 0.614 | 0.193 | 28 | 0.286 | 0.460 | 0 |
| Colombia | unknown | 5 | 0.547 | 0.117 | 10 | 0.500 | 0.527 | 0 |
| Colombia | wide ranging | 1 | 0.667 | NA | 3 | 0.333 | 0.577 | 0 |
| Colombia | NA | 0 | NaN | NA | 2 | 0.000 | 0.000 | NA |
| France | restricted | 14 | 0.741 | 0.336 | 28 | 0.227 | 0.388 | 2 |
| France | wide ranging | 20 | 0.933 | 0.202 | 27 | 0.611 | 0.476 | 5 |
| Japan | restricted | 35 | 0.939 | 0.141 | 35 | 0.080 | 0.180 | 0 |
| Japan | unknown | 1 | 1.000 | NA | 1 | 0.000 | NA | 0 |
| Japan | wide ranging | 14 | 0.884 | 0.179 | 14 | 0.076 | 0.192 | 0 |
| Mexico | restricted | 19 | 0.933 | 0.138 | 31 | 0.094 | 0.267 | 4 |
| Mexico | unknown | 2 | 1.000 | 0.000 | 0 | NaN | NA | 0 |
| Mexico | wide ranging | 7 | 0.926 | 0.150 | 16 | 0.456 | 0.385 | 3 |
| South Africa | restricted | 41 | 0.905 | 0.206 | 29 | 0.217 | 0.391 | 4 |
| South Africa | unknown | 2 | 1.000 | 0.000 | 1 | 1.000 | NA | 0 |
| South Africa | wide ranging | 47 | 0.984 | 0.081 | 31 | 0.595 | 0.475 | 1 |
| Sweden | restricted | 71 | 0.708 | 0.292 | 53 | 0.076 | 0.210 | 6 |
| Sweden | unknown | 2 | 1.000 | 0.000 | 2 | 0.000 | 0.000 | 0 |
| Sweden | wide ranging | 47 | 0.871 | 0.204 | 28 | 0.415 | 0.408 | 14 |
| USA | restricted | 89 | 0.813 | 0.243 | 60 | 0.367 | 0.418 | 3 |
| USA | unknown | 0 | NaN | NA | 0 | NaN | NA | 0 |
| USA | wide ranging | 28 | 0.735 | 0.244 | 19 | 0.314 | 0.393 | 3 |

## Simplified figures and basic stats for text summary and policy brief

### How many species and pops:

How many species:

nrow(indicators\_averaged\_one)

## [1] 919

How many assessments (including species assessed more than once):

nrow(indicators\_full)

## [1] 982

How many populations, including all pops from species that were assessed more than once:

nrow(ind1\_data)

## [1] 5652

How many populations, counting only once populations from taxa assessed more than once:

# This looks for the id of the taxa already keeping only 1 for the multiassessed taxa, and keeps those int he ind1\_data (where the pops data is)  
x<-ind1\_data[ind1\_data$X\_uuid %in% indicators\_averaged\_one$X\_uuid, ]  
  
# the number of rows is the number of pops counting only once multiassessed taxa  
nrow(x)

## [1] 5271

How many multiassesments:

sum(indicators\_full$multiassessment=="multiassessment")

## [1] 107

Which taxa had multiassesments and how many:

x<- indicators\_full %>% filter(multiassessment=="multiassessment") %>%  
 group\_by(taxon) %>%  
 summarise(n=n())  
kable(x)

| taxon | n |
| --- | --- |
| Alasmidonta varicosa | 2 |
| Alouatta palliata mexicana | 2 |
| Ambystoma cingulatum | 4 |
| Anguis fragilis | 2 |
| Aphelocoma coerulescens | 5 |
| Astragalus microcymbus | 2 |
| Barbastella barbastellus | 2 |
| Bombus terricola | 2 |
| Cambarus elkensis | 2 |
| Coronella austriaca | 2 |
| Cryptobranchus alleganiensis alleganiensis | 2 |
| Cryptomastix devia | 2 |
| Erimystax harryi | 2 |
| Etheostoma chienense | 2 |
| Etheostoma osburni | 2 |
| Hemphillia burringtoni | 2 |
| Heterelmis stephani | 2 |
| Hydroprogne caspia | 2 |
| Lavinia exilicauda chi | 2 |
| Lepidium papilliferum | 2 |
| Mustela nigripes | 2 |
| Necturus lewisi | 2 |
| Nicrophorus americanus | 2 |
| Notophthalmus perstriatus | 16 |
| Notropis mekistocholas | 2 |
| Notropis topeka | 2 |
| Noturus munitus | 2 |
| Obovaria subrotunda | 2 |
| Oncorhynchus apache | 2 |
| Oncorhynchus clarkii virginalis | 2 |
| Phonotimpus talquian | 2 |
| Pimelea spinescens subspecies spinescens | 2 |
| Plestiodon egregius egregius | 2 |
| Pleurobema rubrum | 2 |
| Procambarus orcinus | 2 |
| Pseudemys rubriventris | 2 |
| Rana dalmatina | 2 |
| Rhynchospora crinipes | 2 |
| Streptanthus bracteatus | 2 |
| Texella reyesi | 2 |
| Thamnophis sirtalis tetrataenia | 2 |
| Thoburnia atripinnis | 2 |
| Toxolasma lividum | 2 |
| Zapus hudsonius luteus | 2 |

How many taxa with multiassesments?

nrow(x)

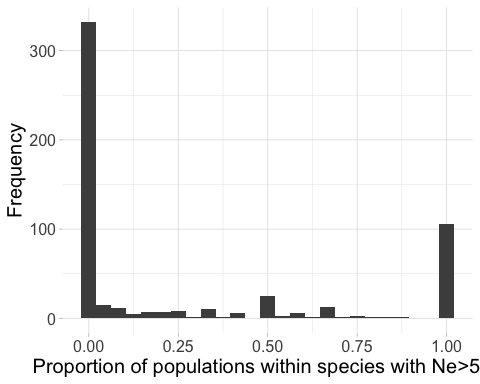
## [1] 44

### Plain Histogram and stats for Ne > 500 indicator

Plain histogram:

# Create a histogram   
hist\_p <- indicators\_averaged\_one %>%  
 ggplot(aes(x = indicator1\_mean)) +  
 geom\_histogram( bins = 25, fill="grey30") + # Adjust the number of bins as needed  
 labs(x = "Proportion of populations within species with Ne>500", y = "Frequency") +  
 theme\_light() +  
 theme(panel.border = element\_blank(), text = element\_text(size = 15)) +  
 guides(fill = guide\_legend(title = NULL))  
  
# plot  
hist\_p

## Warning: Removed 351 rows containing non-finite values (`stat\_bin()`).



Summary stats for the Ne 500 indicator:

x <- indicators\_averaged\_one %>%  
 filter(!is.na(indicator1\_mean)) %>%   
 ungroup() %>%   
 summarize(n=n(),  
 mean=mean(indicator1\_mean),  
 median=median(indicator1\_mean),  
 per.0=sum(indicator1\_mean==0) / n \*100,  
 per.below.25=sum(indicator1\_mean<0.25) / n \*100,  
 per.below.90=sum(indicator1\_mean<0.90) / n \*100,  
 per.above.75=sum(indicator1\_mean>0.75)/ n \*100,  
 per1=sum(indicator1\_mean==1) / n \*100)  
x

## # A tibble: 1 × 8  
## n mean median per.0 per.below.25 per.below.90 per.above.75 per1  
## <int> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>  
## 1 568 0.270 0 58.1 66.5 81.3 19.2 18.7

kable(x, digits = 2)

| n | mean | median | per.0 | per.below.25 | per.below.90 | per.above.75 | per1 |
| --- | --- | --- | --- | --- | --- | --- | --- |
| 568 | 0.27 | 0 | 58.1 | 66.55 | 81.34 | 19.19 | 18.66 |

Data availability for the Ne indicator. At the species level:

sum(!is.na(indicators\_averaged\_one$indicator1\_mean)) / nrow(indicators\_averaged\_one)

## [1] 0.6180631

At the population level:

sum(!is.na(ind1\_data$Ne\_combined)) / nrow(ind1\_data)

## [1] 0.811925

Populations below the Ne 500 threshold

x<- ind1\_data %>%   
 ungroup() %>%   
 summarise(n\_pops = n(),   
 n\_pops\_Ne\_data = sum(!is.na(Ne\_combined)),   
 n\_pops\_more\_500 = sum(Ne\_combined >= 500, na.rm = TRUE),  
 n\_pops\_less\_500 =sum(Ne\_combined < 500, na.rm = TRUE),  
 per\_less\_500 = n\_pops\_less\_500/n\_pops\_Ne\_data)  
kable(x, digits=2)

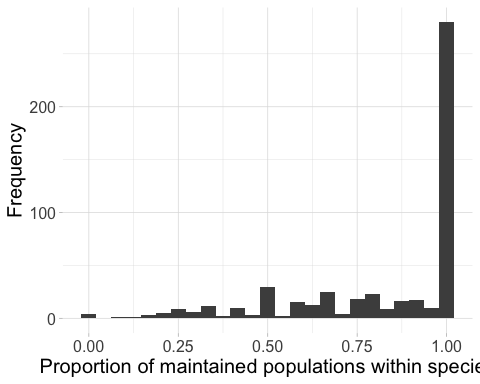
| n\_pops | n\_pops\_Ne\_data | n\_pops\_more\_500 | n\_pops\_less\_500 | per\_less\_500 |
| --- | --- | --- | --- | --- |
| 5652 | 4589 | 604 | 3985 | 0.87 |

### Plain Histogram and stats for Proportion Mantained populations

Plain histogram

# Create a histogram   
hist\_p <- indicators\_averaged\_one %>%  
 ggplot(aes(x = indicator2\_mean)) +  
 geom\_histogram(bins = 25, fill="grey30") + # Adjust the number of bins as needed  
 labs(x = "Proportion of maintained populations within species", y = "Frequency") +  
 theme\_light() +  
 theme(panel.border = element\_blank(), text = element\_text(size = 15)) +  
 guides(fill = guide\_legend(title = NULL))  
  
# plot  
hist\_p

## Warning: Removed 401 rows containing non-finite values (`stat\_bin()`).



Summary stats for the PM indicator:

x <- indicators\_averaged\_one %>%  
 filter(!is.na(indicator2\_mean)) %>%   
 ungroup() %>%   
 summarize(n=n(),  
 mean=mean(indicator2\_mean),  
 median=median(indicator2\_mean),  
 per0=sum(indicator2\_mean==0) / n \*100,  
 per.below.25=sum(indicator2\_mean<0.25) / n \*100,  
 per.below.90=sum(indicator2\_mean<0.90) / n \*100,  
 per.above.75=sum(indicator2\_mean>0.75) / n \*100,  
 per1=sum(indicator2\_mean==1) / n \*100)  
  
kable(x, digits = 2)

| n | mean | median | per0 | per.below.25 | per.below.90 | per.above.75 | per1 |
| --- | --- | --- | --- | --- | --- | --- | --- |
| 518 | 0.82 | 1 | 0.58 | 2.9 | 40.73 | 68.92 | 53.47 |

### Data availability, donuts and plot bars for Ne 500

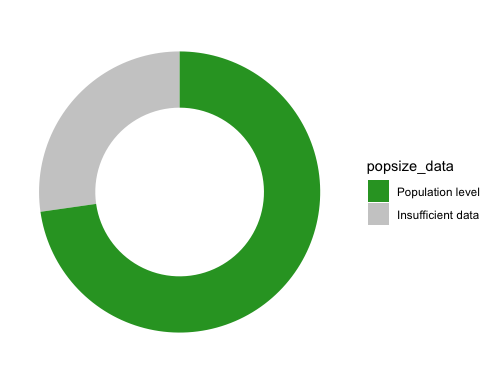
Species level yes/no table with percentages for Ne 500 indicator

df<- indicators\_full %>%  
 group\_by(popsize\_data) %>%  
 summarise(n=n(),  
 percentage = (n / nrow(metadata)) \* 100)  
   
kable(df, digits = 0)

| popsize\_data | n | percentage |
| --- | --- | --- |
| data\_for\_species | 131 | 14 |
| insuff\_data\_species | 230 | 24 |
| yes | 614 | 64 |
| NA | 7 | 1 |

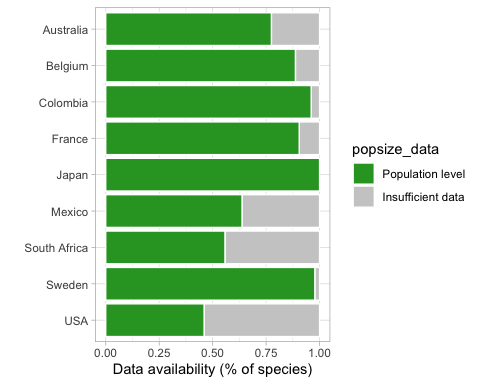
Donut only available data

df<- indicators\_full %>%  
 filter(popsize\_data != "data\_for\_species") %>% # we want to show only data for pops or insufficient  
 group\_by(popsize\_data) %>%  
 summarise(n=n(),  
 percentage = (n / nrow(metadata)) \* 100)  
  
# variable to make change the size of the hole  
hsize <- 2 # to change the size of the hole. larger=bigger   
df <- df %>%   
 mutate(x = hsize)   
  
# donut plot  
p <- ggplot(df, aes(x = hsize, y = n, fill = popsize\_data)) +  
 geom\_col() +  
 coord\_polar(theta = "y") +  
 scale\_fill\_manual(values=c("#2ca02c", "grey80"),  
 breaks=c("yes", "insuff\_data\_species"),  
 labels=c("Population level", "Insufficient data")) +  
  
 xlim(c(0.2, hsize + 0.5)) + theme\_void()  
p



Species level yes/no. Bar plot for Ne 500

indicators\_full %>%  
 filter(popsize\_data != "data\_for\_species") %>% # we want to show only data for pops or insufficient  
 ggplot(aes(x=country\_assessment, fill = popsize\_data)) +  
 geom\_bar(position = "fill", color="white") +  
 scale\_fill\_manual(values=c("#2ca02c", "grey80"),  
 breaks=c("yes", "insuff\_data\_species"),  
 labels=c("Population level", "Insufficient data")) +  
 scale\_x\_discrete(limits=rev) + xlab("") + ylab("Data availability (% of species)") +  
 coord\_flip() +  
 theme\_light()



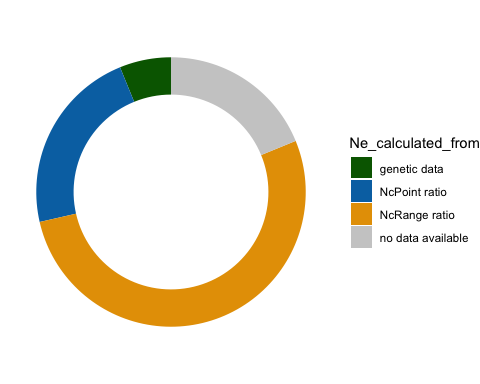
Population level, what kind? Table

# we first need the column numbers  
df<-ind1\_data %>%  
 mutate(Ne\_calculated\_from = replace\_na(Ne\_calculated\_from, "no data available")) %>%  
 group\_by(Ne\_calculated\_from) %>%  
 summarise(n=n(),  
 percentage = (n / nrow(ind1\_data)) \* 100)  
   
kable(df, digits = 0)

| Ne\_calculated\_from | n | percentage |
| --- | --- | --- |
| genetic data | 349 | 6 |
| NcPoint ratio | 1266 | 22 |
| NcRange ratio | 2974 | 53 |
| no data available | 1063 | 19 |

Donut

# variable to make change the size of the hole  
hsize <- 3 # to change the size of the hole. larger=bigger   
df <- df %>%   
 mutate(x = hsize)   
  
# donut plot  
p <- ggplot(df, aes(x = hsize, y = n, fill = Ne\_calculated\_from)) +  
 geom\_col() +  
 coord\_polar(theta = "y") +  
 scale\_fill\_manual(labels=c("genetic data", "NcPoint ratio", "NcRange ratio", "no data available"),  
 breaks=c("genetic data", "NcPoint ratio", "NcRange ratio", "no data available"),  
 values=c("darkgreen", "#0072B2", "#E69F00", "grey80")) +  
 xlim(c(0.2, hsize + 0.5)) + theme\_void()  
p



### Data availability for PM indicator

Total taxa with NA in extinct populations:

sum(is.na(indicators\_full$n\_extint\_populations))

## [1] 417

Percentage of missing data

sum(is.na(indicators\_full$n\_extint\_populations))/nrow(indicators\_full)

## [1] 0.4246436

Total taxa with data availability on extinct pops

sum(!is.na(indicators\_full$n\_extint\_populations))

## [1] 565

Percentage of taxa with data availability on extinct pops (which also includes NA for extant, see above)

sum(!is.na(indicators\_full$n\_extint\_populations))/nrow(indicators\_full)

## [1] 0.5753564

nrow(indicators\_full)

## [1] 982

### Data availability for at least one indicator

Data availability for at least one indicator. Including multiassesments

# number  
x<- indicators\_full %>%  
 filter(popsize\_data=="yes" | !is.na(n\_extint\_populations))  
nrow(x)

## [1] 817

# percentage  
nrow(x) / nrow(indicators\_full)

## [1] 0.8319756

Data availability for at least one indicator. Keeping only one of the multiassesments

# number  
x<- indicators\_averaged\_one %>%  
 filter(popsize\_data=="yes" | !is.na(n\_extint\_populations))  
nrow(x)

## [1] 765

# percentage  
nrow(x) / nrow(indicators\_averaged\_one)

## [1] 0.8324266

## Session Info for reproducibility purposes:

sessionInfo()

## R version 4.2.1 (2022-06-23)  
## Platform: x86\_64-apple-darwin17.0 (64-bit)  
## Running under: macOS Big Sur ... 10.16  
##   
## Matrix products: default  
## BLAS: /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRblas.0.dylib  
## LAPACK: /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRlapack.dylib  
##   
## locale:  
## [1] en\_US.UTF-8/en\_US.UTF-8/en\_US.UTF-8/C/en\_US.UTF-8/en\_US.UTF-8  
##   
## attached base packages:  
## [1] stats graphics grDevices utils datasets methods base   
##   
## other attached packages:  
## [1] glmmTMB\_1.1.7 knitr\_1.39 lme4\_1.1-31 Matrix\_1.5-3   
## [5] cowplot\_1.1.1 viridis\_0.6.3 viridisLite\_0.4.0 alluvial\_0.1-2   
## [9] ggnewscale\_0.4.9 ggsankey\_0.0.99999 ggplot2\_3.4.1 stringr\_1.4.0   
## [13] utile.tools\_0.2.7 readr\_2.1.2 dplyr\_1.0.9 tidyr\_1.2.0   
##   
## loaded via a namespace (and not attached):  
## [1] TMB\_1.9.6 tidyselect\_1.1.2 xfun\_0.31   
## [4] purrr\_0.3.4 splines\_4.2.1 lattice\_0.20-45   
## [7] colorspace\_2.0-3 vctrs\_0.5.2 generics\_0.1.3   
## [10] htmltools\_0.5.5 yaml\_2.3.5 utf8\_1.2.2   
## [13] rlang\_1.0.6 nloptr\_2.0.3 pillar\_1.7.0   
## [16] glue\_1.6.2 withr\_2.5.0 DBI\_1.1.3   
## [19] lifecycle\_1.0.3 munsell\_0.5.0 gtable\_0.3.0   
## [22] evaluate\_0.15 labeling\_0.4.2 tzdb\_0.3.0   
## [25] fastmap\_1.1.0 fansi\_1.0.3 highr\_0.9   
## [28] Rcpp\_1.0.10 scales\_1.2.0 farver\_2.1.1   
## [31] gridExtra\_2.3 hms\_1.1.1 digest\_0.6.29   
## [34] stringi\_1.7.6 numDeriv\_2016.8-1.1 grid\_4.2.1   
## [37] cli\_3.6.0 tools\_4.2.1 magrittr\_2.0.3   
## [40] tibble\_3.1.7 crayon\_1.5.1 pkgconfig\_2.0.3   
## [43] ellipsis\_0.3.2 MASS\_7.3-57 assertthat\_0.2.1   
## [46] minqa\_1.2.5 rmarkdown\_2.14 rstudioapi\_0.13   
## [49] R6\_2.5.1 boot\_1.3-28 nlme\_3.1-157   
## [52] compiler\_4.2.1