

Exploratory results

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Objective

Produce a series of figures that help validate population projection results.

Question

Is *Podocnemis unifilis* an Endangered species?

To answer this question we use population projection matrices to understand the future impacts of current threats to populations. This is an extension of Norris et al 2019 that includes:

- stochastic population projections
- threats caused by human accessibility and actions that reduce river connectivity.

According to the IUCN Redlist criteria A3, population size reduction is a reduction which is projected, inferred or suspected to be met in the future (up to a maximum of 100 years). Here we use population projection matrices to obtain an index of abundance relevant to the taxon (“b”) and consider actual or potential levels of exploitation (“d”).

This assessment is therefore based on criteria - A3bd.

Load packages and data

Packages

```
library(tidyverse)
library(sf)
library(patchwork)
```

Load data

Here we load data created previously in “test_riversections.Rmd”. First dataframes with projection values.

```
sum_diff_current <- readRDS("inst/other/sum_diff_current.rds")
scenario_res_current <- readRDS("inst/other/scenario_res_current.rds")
```

Now load ggplot maps showing spatial patterns in projected changes, created previously in “test_riversections.Rmd”.

```
# load .rds holding ggplot objects. Takes a few minutes.
# Need to include SUBBASI in sum_diff
dirrds <- "C:\\Users\\user\\Documents\\Articles\\2024_Norris_Greenstatus\\TACAR\\inst\\other\\fig_rds"
ffrds <- list.files(dirrds, pattern="\\.rds$", full.names=TRUE)
# Make a vector of file names
file_names <- gsub(pattern = "\\rds$", replacement = "", x = basename(ffrds))
# Dataframe for selecting/joining
dfref <- data.frame(apath = ffrds, aname = file_names) |>
  separate_wider_delim(aname, "_", names = c("a", "b", "BASIN_N", "SUBBASI"),
    cols_remove = FALSE) |>
  select(!c(a, b)) |>
  left_join(scenario_res_current |>
    group_by(BASIN_N, SUBBASI, subbasn) |>
    summarise(acount = n()) |>
    mutate(SUBBASI = as.character(SUBBASI)) |>
    ungroup()) |>
  select(!acount) |>
  arrange(BASIN_N, subbasn)
```

```
## `summarise()` has grouped output by 'BASIN_N', 'SUBBASI'. You can override
## using the `.groups` argument.
## Joining with `by = join_by(BASIN_N, SUBBASI)`
```

```
# Amazon (n=27) = 6 pages , Coastal North (n=21) = 5 pages
# Coastal South = 1 (n=1), Orinoco = 1 (n=3)
dfref |>
  group_by(BASIN_N) |>
  summarise(count_sub = length(unique(subbasn)),
    count_subi = length(unique(SUBBASI)))
```

```
## # A tibble: 4 x 3
##   BASIN_N      count_sub count_subi
##   <chr>          <int>     <int>
## 1 Amazon             27         27
## 2 Coastal North      21         21
## 3 Coastal South        1          1
## 4 Orinoco             3          3
```

Results

For each basin and subbasin there are composite figures that show:

- Projected population changes.
- Projected growth rates.
- Maps of points with 50% population reductions over three generations.

This is a wide ranging species, so it takes several pages to show all the results. Projections are shown by major river basins, including 5 sub-basins per page.

Population change 42 years (3 generations lower estimate)

