

R-code

Required packages

```
library(magrittr)
library(rredlist)
library(readr)
```

Query IUCN data

The IUCN Redlist API is queried using the `rredlist`¹ package. Using this service requires a token (see Link above on how to get access).

```
## load the token. The token is not provided here!
load("RedListAPI.RData")

## NOT RUN: Redo so once taxonomy list is completed!
## list all 1576 taxons
taxon <- lapply(list.files("data/Species_split/", full.names = T), read.csv) %>%
  do.call("rbind",.)
taxon <- taxon[["Species"]] %>% as.character()

## retrieve common names
common.names <- pbapply::pblapply(taxon, function(x) {
  query <- rredlist::rl_common_names(x, key = RedListAPI, parse = T)
  if (length(query[["result"]]) > 0) {
    df <- data.frame(name = query[["name"]],
                     query[["result"]]) %>%
      dplyr::filter(., primary == "TRUE")
    return(df[,c("name", "taxonname")])
  } else {
    df <- data.frame(name = query[["name"]], taxonname = "Unknown")
    return(df)
  }
}) %>%
  do.call("rbind",.) %>%
  ## correct all scientific names before continuing!
  dplyr::filter(., taxonname != "Unknown")

## unknown names
unknown.names <- taxon[-which(taxon %in% common.names$name)]

## retrieve habitats
habitats <- pbapply::pblapply(common.names[["name"]], function(x) {
  query <- rredlist::rl_habitats(as.character(x), key = RedListAPI, parse = T)
  return(query[["result"]])
}) %>% set_names(., value = common.names$name)
```

¹Scott Chamberlain (2018). `rredlist`: 'IUCN' Red List Client. R package version 0.5.0. <https://CRAN.R-project.org/package=rredlist>

```
## retrieve main accounts
redlist <- pbapply::pblapply(common.names[["name"]], function(x) {
  query <- rredlist::rl_search(as.character(x), key = RedListAPI, parse = T)
  return(query[["result"]])
}) %>%
  do.call("rbind",.)

save(redlist, file = "data/redlist.RData")
save(habitats, file = "data/habitats.RData")
save(common.names, file = "data/common.names.RData")
save(unknown.names, file = "data/unknown.names.RData")
```

EltonTraits

Standardised Species-level foraging and diet attributes are available from the EltonTraits 1.0² database. In this dataset, foraging strata and diet types are available on a semi-quantitative scale giving the relative importance for each taxon (values from 0 to 100 in steps of 10).

```
download.file(url = "http://www.esapubs.org/archive/ecol/E095/178/BirdFuncDat.txt",
  destfile = "data/BirdFuncDat.txt",
  quiet = T,
  cacheOK = T)
```

```
BirdFuncDat <-
  read_delim("data/BirdFuncDat.txt", "\t", trim_ws = T, skip_empty_rows = T)
```

AnAge

The AnAge³ Database provides proxies of longevity

```
## download zip file
download.file(url = "http://genomics.senescence.info/species/dataset.zip",
  destfile = "data/AnAge.zip",
  quiet = T)

## extract data table
unzip(zipfile = "data/AnAge.zip", files = "anage_data.txt", exdir = "data")
## delete zip file
unlink("data/AnAge.zip")
```

```
AnAge <-
  read_delim("data/anage_data.txt", "\t", trim_ws = T, skip_empty_rows = T)
AnAge[["taxon.name"]] <- paste(AnAge[["Genus"]], AnAge[["Species"]])
```

Merge data

Bring together all the resources ... and:

²Hamish Wilman, Jonathan Belmaker, Jennifer Simpson, Carolina de la Rosa, Marcelo M. Rivadeneira, and Walter Jetz. 2014. EltonTraits 1.0: Species-level foraging attributes of the world's birds and mammals. Ecology 95:2027. <http://dx.doi.org/10.1890/13-1917.1>

³Tacutu, R., Craig, T., Budovsky, A., Wuttke, D., Lehmann, G., Taranukha, D., Costa, J., Fraifeld, V. E., de Magalhaes, J. P. (2013) "Human Ageing Genomic Resources: Integrated databases and tools for the biology and genetics of ageing." Nucleic Acids Research 41(D1):D1027-D1033

1. Unifying habitats: (e.g. merging related categories & building hierarchical categories)
2. Adding additional RedList variables
3. Adding sample metadata (e.g. coords)
4. Solve taxonomy issues by two columns 'taxon.malavi' and 'taxon.hbw' allowing to match entries in a two-way join.