Tutorial 2 - Accessing biodiveristy data through web services

In this tutorial we will work with another r-package that can be used to download biodiversity data:

The IUCN redlist package `rredlist`

The IUCN RedList is a collective work of many researchers and conservaionists, which compile information about species population trends, habitats, and evaluations of all applicable threats. This information is used to assign a protection status to each species. You can find more information about the IUCN RedList here (https://www.iucnredlist.org/).

Let's load the `rredlist` package:

```
In [1]: library(rredlist)
```

1. Get your API token

In order to use this package you first need to apply for an API token. You can do that by filling out this form here: https://apiv3.iucnredlist.org/api/v3/token (https://apiv3.iucnredlist.org/api/v3/token).

Since it is hard to predict how long it will take for IUCN to approve your token request, you can get a key from us (just approach us if you're getting to this part of the tutorial and haven't received your token yet).

Then store the API token as a string:

```
In [10]: iucn_api = 'paste_your_api_here'
```

Extra info: If you're interested you can store this key in your R environment. It's not necessary for this exercise but if you want you can check out the documentation of the functions `rl_use_iucn()` and `edit_r_environ()`.

2. Pick a taxon and find synonyms

Now you can again pick a species of your choice, in this example we're working with the tiger *Panthera tigris*.

```
In [38]: taxon_name <- "Panthera tigris" # tiger
```

We can check for synonyms of our species name, using the `rl_synonyms()` function:

```
In [37]: rl_synonyms(taxon_name,key=iucn_api)
```

$name
'Felis tigris'
$count
1
$result

accepted_id	accepted_name	authority	synonym	syn_authority
15955	Panthera tigris	(Linnaeus, 1758)	Felis tigris	Linnaeus, 1758

IUCN standardizes all its' data to one main taxonomy, so you will not find any data associated with the synonyms ooutside of the `accepted_name` . Therefore make sure you continue working with the `accepted_name` .

Similarly as before in the GBIF tutorial, we can extract **popular names (vernacular names)** associated with our chosen taxon in the IUCN database:

```
In [39]: rl_common_names(taxon_name,key=iucn_api)
```

$name
'Panthera tigris'
$result

taxonname	primary	language
Tigre	FALSE	fre
Tiger	TRUE	eng

3. Habitat information

The IUCN `rredlist` package offers several functions to extract information about the chosen taxon. You can check out the available functions and explanation in the official package documentation (https://cran.r-project.org/web/packages/rredlist/rredlist.pdf).

For example we can extract information about the habitats the species is found in using the `rl_habitats()` function.

```
In [40]: rl_habitats(taxon_name,key=iucn_api)
```

$name
'Panthera tigris'
$result

code	habitat	suitability	season	majorimportance
1.1	Forest - Boreal	Suitable	NA	Yes
1.4	Forest - Temperate	Suitable	NA	Yes
1.5	Forest - Subtropical/Tropical Dry	Suitable	NA	Yes
1.6	Forest - Subtropical/Tropical Moist Lowland	Suitable	NA	Yes
1.7	Forest - Subtropical/Tropical Mangrove Vegetation Above High Tide Level	Suitable	NA	Yes
1.9	Forest - Subtropical/Tropical Moist Montane	Marginal	NA	NA
3.5	Shrubland - Subtropical/Tropical Dry	Suitable	NA	Yes
3.6	Shrubland - Subtropical/Tropical Moist	Suitable	NA	Yes
4.5	Grassland - Subtropical/Tropical Dry	Marginal	NA	NA
4.6	Grassland - Subtropical/Tropical Seasonally Wet/Flooded	Marginal	NA	NA

4. Threat status

One of the most interesting and unique information IUCN has to offer are the RedList assessments. Each species is classified into either one of the following categories:

- Least Concern (LC)
- Near threatened (NT)
- Vulnerable (VU)
- Endangered (EN)
- Critically endangered (CR)
- Extinct in the wild (EW)
- Extinct (EX)
- Data deficient (DD)

Let's see how our species is evaluated. We are using the `rl_search()` function which will return all sorts of information, but for now we're only interested in the `category` of the output:

In [41]:
```
threat_data = rl_search(taxon_name,key=iucn_api)
threat_data$result$category
```

'EN'

We can also view the history of IUCN assessments of our species and see if the trends have improved or worsened. Note that older evaluations may contain different categories, since IUCN has changed its' nomenclature several times in history:

In [42]:
```
rl_history(taxon_name,key=iucn_api)
```

$name
'Panthera tigris'
$result

year	code	category
2015	EN	Endangered
2011	EN	Endangered
2010	EN	Endangered
2008	EN	Endangered
2002	EN	Endangered
1996	EN	Endangered
1994	E	Endangered
1990	E	Endangered
1988	E	Endangered
1986	E	Endangered

5. Extract geographic information

Unfortunately it is not possible to download range maps for your species via the package rredlist (to our knowledge), even though IUCN has range maps for most species in their database stored on their server. Precise range maps can instead be downloaded manually via the webpage (https://www.iucnredlist.org/resources/spatial-data-download).

However the `rredlist` package offers a function `rl_occ_country()` which can be used to extract a list of countries where the species exists:

In [43]:
```
occurrence_countries = rl_occ_country(taxon_name,key=iucn_api)
occurrence_countries
```

$name
'Panthera tigris'
$count
24
$result

code	country	presence	origin	distribution_code
AF	Afghanistan	Extinct Post-1500	Native	Regionally Extinct
BD	Bangladesh	Extant	Native	Native
BT	Bhutan	Extant	Native	Native
CN	China	Extant	Native	Native
ID	Indonesia	Extant	Native	Native
IN	India	Extant	Native	Native
IR	Iran, Islamic Republic of	Extinct Post-1500	Native	Regionally Extinct
KG	Kyrgyzstan	Extinct Post-1500	Native	Regionally Extinct
KH	Cambodia	Possibly Extinct	Native	Possibly Extinct
KP	Korea, Democratic People's Republic of	Possibly Extinct	Native	Possibly Extinct
KZ	Kazakhstan	Extinct Post-1500	Native	Regionally Extinct
LA	Lao People's Democratic Republic	Extant	Native	Native
MM	Myanmar	Extant	Native	Native
MY	Malaysia	Extant	Native	Native
NP	Nepal	Extant	Native	Native
PK	Pakistan	Extinct Post-1500	Native	Regionally Extinct
RU	Russian Federation	Extant	Native	Native
SG	Singapore	Extinct Post-1500	Native	Regionally Extinct
TH	Thailand	Extant	Native	Native
TJ	Tajikistan	Extinct Post-1500	Native	Regionally Extinct
TM	Turkmenistan	Extinct Post-1500	Native	Regionally Extinct
TR	Turkey	Extinct Post-1500	Native	Regionally Extinct
UZ	Uzbekistan	Extinct Post-1500	Native	Regionally Extinct
VN	Viet Nam	Possibly Extinct	Native	Possibly Extinct

As you can see, the output also contains the information if the species is extant or extinct in the country where it was once found. In the next step we use this information to plot a world map with countries highlighted where our species has been found, with different coloring depending on if the species is extinct or extant in the respective country.

6. Plotting geographic information

First let's turn the `presence` column, which contain the info if the taxon is extinct/extant in each country, into an array of 0 (extinct) and 1 (extant), in order to use this information for plotting:

In [49]:
```
extant_extinct = occurrence_countries$result$presence
extant_extinct[extant_extinct != "Extant"] <- 0
extant_extinct[extant_extinct == "Extant"] <- 1
```

Now let's extract the list of countries where our species has been found:

In [50]:
```
theCountries <- c(occurrence_countries$result$code) # ISO2 country codes
theCountries
```

```
'AF'  'BD'  'BT'  'CN'  'ID'  'IN'  'IR'  'KG'  'KH'  'KP'  'KZ'  'LA'  'MM'  'MY'  'NP'  'PK'  'RU'
'SG'  'TH'  'TJ'  'TM'  'TR'  'UZ'  'VN'
```

Now let's merge the list with our extinct/extant info with the list of the country names into one dataframe:

In [51]:
```
extDF <- data.frame(country = c(occurrence_countries$result$code),
  extant = c(extant_extinct))
extDF
```

country	extant
AF	0
BD	1
BT	1
CN	1
ID	1
IN	1
IR	0
KG	0
KH	0
KP	0
KZ	0
LA	1
MM	1
MY	1
NP	1
PK	0
RU	1
SG	0
TH	1
TJ	0
TM	0
TR	0
UZ	0
VN	0

Now we will use the `rworldmap` package, which provides a function that allows us to find the countries on the world map based on their ISO2 codes:

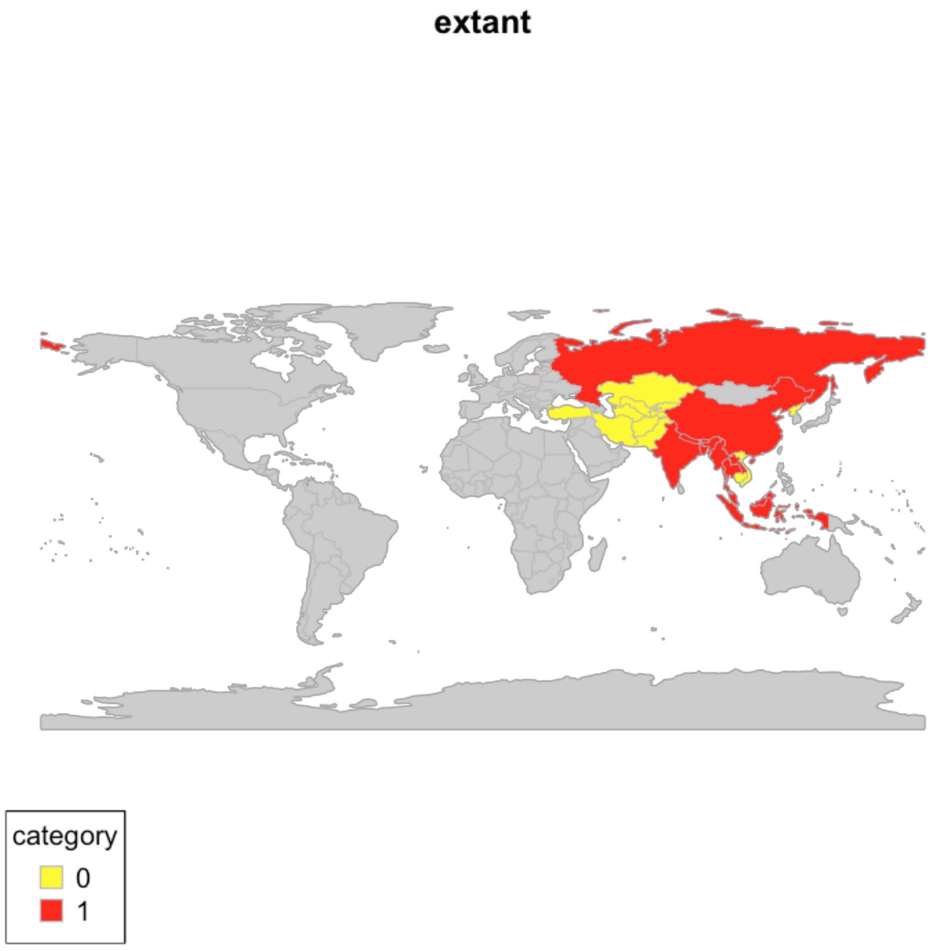
In [52]:
```
library(rworldmap)

extMap <- joinCountryData2Map(extDF, joinCode = "ISO2", nameJoinColumn = "country")
# This will join your data.frame to the country map data
```

```
24 codes from your data successfully matched countries in the map
0 codes from your data failed to match with a country code in the map
219 codes from the map weren't represented in your data
```

Finally we can plot the map with the countries of presence of our species highlighted in red and the countires where the species went extinct in yellow:

In [53]:
```
mapCountryData(extMap, nameColumnToPlot="extant", catMethod = "categorical",
  missingCountryCol = gray(.8))
# And this will plot it, with the trick that the color palette's first
# color is red
```



Resolving taxon names

Often in biology we are confronted with taxon names or lists of taxon names, and we need to somehow retrieve data for these taxa from public databases (as we did in the previous tutorial steps). The challenge here is usually to find the correct species name, since taxonomies can vary between databases and between different authors. Luckily there are great tools to standardize and resolve taxonomic issues in many cases, implemented in the `taxize` package.

The `taxize` package provides access to taxonomic information sourced from many databases, among them the Global Names Resolver (GNR) service provided by the [Encyclopedia of Life (http://eol.org/)](http://eol.org/). The advantage of `taxize` is that it is primarily designed for resolving taxonomic issues and thus has many useful functions for this purpose, compared to some similar but more simplified functionalities of the `rgbif` and `rredlist` packages we have seen in the previous tutorial steps.

Let's first load the package.

In [55]:
```
library(taxize)
```

1. Finding correct taxon name for database

Let's say we have a list of species names and we want to know if our species are spelled correctly.

Here, we are searching for two misspelled names:

In [66]:
```
temp <- gnr_resolve(names = c("Pantera tigrsi", "Homo saapiens"))
temp
```

user_supplied_name	submitted_name	matched_name	data_source_title	score
Pantera tigrsi	Pantera tigrsi	Panthera tigris (Linnaeus, 1758)	Catalogue of Life	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris (Linnaeus, 1758)	ITIS	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris	NCBI	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris (Linnaeus, 1758)	Union 4	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris (Linnaeus, 1758)	The Interim Register of Marine and Nonmarine Genera	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris	Freebase	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris (Linnaeus, 1758)	GBIF Backbone Taxonomy	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris (Linnaeus, 1758)	EOL	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris	EOL	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris (Linnaeus, 1758)	TaxonConcept	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris	AnAge	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris	ARKive	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris (Linnaeus, 1758)	Wikipedia in EOL	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris (Linnaeus, 1758)	EUNIS	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris	CU*STAR	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris (Linnaeus, 1758)	IUCN Red List of Threatened Species	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris (Linnaeus, 1758)	BioLib.cz	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris (Linnaeus, 1758)	nlbif	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris	Index to Organism Names	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris Linnaeus 1758	Index to Organism Names	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris (Linnaeus 1758)	Index to Organism Names	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris (Linnaeus, 1758)	uBio NameBank	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris	uBio NameBank	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris Linnaeus 1758	uBio NameBank	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris	Arctos	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris (Linnaeus 1758)	The Paleobiology Database	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris Linnaeus 1758	The Mammal Species of The World	0.75
Pantera tigrsi	Pantera tigrsi	Panthera tigris	Open Tree of Life Reference Taxonomy	0.75

Here you can find the database you want to download data from and use the according correct species name (can vary between databases).

2. Getting species list for higher taxon

Let's say we have a taxonomic family name and want to find all species belonging to this family, for example all dogs of the family Canidae.

A number of data sources in taxize provide the capability to retrieve higher taxonomic names, we will be using the Catalogue of Life (COL) (http://www.catalogueoflife.org/).

In [82]:
```
species_output = downstream("Canidae", downto = "Species", db = "col")
species_output
```

```
Retrieving data for taxon 'Canidae'



$Canidae
                       childtaxa_id           childtaxa_name childtaxa_rank
1  5f3ddd0e635c5fb11690722f002dbdfa      Atelocynus microtis        species
2  36807bbc8e4efedbea119a1144c0dae3            Canis adustus        species
3  cbc6668c8147b2292e3ab4b57696cc35             Canis anthus        species
4  2d360d349c645ad93fd960ae988101e9             Canis aureus        species
5  04afba115065ca57c2ea8f64fe876579            Canis latrans        species
6  f942db24200d36657e3e0e5d270b66cb           Canis lupaster        species
7  bcd6035778291a7feaad52cb7ac167cb              Canis lupus        species
8  3f5e32547d4f78fbd3e3dd4755a27166          Canis mesomelas        species
9  e2c274e049e7a12fa066f96028092720           Canis simensis        species
10 9491363ed5ec89660e88360f5b26371d          Cerdocyon thous        species
11 0b3e53b24ae32db8b7f60d943b8c3814    Chrysocyon brachyurus        species
12 59a93bdf80e76056b2e314cf0b036f9c             Cuon alpinus        species
13 dd44e931aa3f678a294d10fa7077aec6       Dusicyon australis        species
14 f40aaf906fb148d75061b038ed87d151       Lycalopex culpaeus        species
15 35662d32e85eb35c5924815d886613b3       Lycalopex fulvipes        species
16 9cd7fa30d6d5ee85a659136379561bc6    Lycalopex gymnocercus        species
17 1170f87af3bf43bcf4682cd3afa3ee28       Lycalopex sechurae        species
18 c35e04f0ec502c3ae31d718e14a29d10        Lycalopex vetulus        species
19 52fba5321357578285952cce9c1b6dac            Lycaon pictus        species
20 6ec904764dc49972c516a4e145fe1119 Nyctereutes procyonoides        species
21 53df8909c343b83a85be76d14b33e0bb        Otocyon megalotis        species
22 1c649d85dbd9ca61520070161bbb35b2       Speothos venaticus        species
23 773e517e0d62fa2480d4e98d903bca20 Urocyon cinereoargenteus        species
24 2c067f962be1d8728cdac746468de29e       Urocyon littoralis        species
25 eb30fda8c22c514872dc41db41aa9ee4       Vulpes bengalensis        species
26 20348ff212809ed92379a8fd97ff8603              Vulpes cana        species
27 db657058fc8388992045c700568188b6             Vulpes chama        species
28 7280e26bc93075bc66ffe4d3f92d9f59            Vulpes corsac        species
29 58d469f96f6b40a7f9091b29c117a88b         Vulpes ferrilata        species
30 74f649c50206103b78005228c898e177           Vulpes lagopus        species
31 fab10f7b9fa033416da18dabbb3e00b2          Vulpes macrotis        species
32 65b53deea25e6b58b0eec077888c4094           Vulpes pallida        species
33 db3a8a220f89e6efce06d28e2f183e9b        Vulpes rueppellii        species
34 f7b9a26e37b69782b0d2b4438d46d128             Vulpes velox        species
35 f76554e91aa357dd527f70ed534fa52c            Vulpes vulpes        species
36 0974e2e971e67503122402cf46b5fb1e             Vulpes zerda        species
   childtaxa_extinct
1              FALSE
2              FALSE
3              FALSE
4              FALSE
5              FALSE
6              FALSE
7              FALSE
8              FALSE
9              FALSE
10             FALSE
11             FALSE
12             FALSE
13             FALSE
14             FALSE
15             FALSE
16             FALSE
17             FALSE
18             FALSE
```

You can now extract the list of all species belonging to your chosen family:

```
In [83]: species_list = species_output$Canidae$childtaxa_name
         species_list
```

```
'Atelocynus microtis'   'Canis adustus'   'Canis anthus'   'Canis aureus'   'Canis latrans'   'Canis lupaster'
'Canis lupus'   'Canis mesomelas'   'Canis simensis'   'Cerdocyon thous'   'Chrysocyon brachyurus'
'Cuon alpinus'   'Dusicyon australis'   'Lycalopex culpaeus'   'Lycalopex fulvipes'   'Lycalopex gymnocercus'
'Lycalopex sechurae'   'Lycalopex vetulus'   'Lycaon pictus'   'Nyctereutes procyonoides'
'Otocyon megalotis'   'Speothos venaticus'   'Urocyon cinereoargenteus'   'Urocyon littoralis'
'Vulpes bengalensis'   'Vulpes cana'   'Vulpes chama'   'Vulpes corsac'   'Vulpes ferrilata'   'Vulpes lagopus'
'Vulpes macrotis'   'Vulpes pallida'   'Vulpes rueppellii'   'Vulpes velox'   'Vulpes vulpes'   'Vulpes zerda'
```

Assignment

Now where you have a basic overview over the use of the `rgbif` , `rredlist` , and `taxize` packages, you are ready to approach a bioinformatic task based on biodiversity data:

Your supervisor asks you for help with a project about the cat family `Felidae` . Your task is to **create a map of global occurrences of this family, colored by species**. Further your supervisor asks you to retrieve a **list of IUCN threat statuses for all species of this family** (if you like a challenge, you can also create a second plot, colored by threat status instead of colored by species).

Since these data are supposed to be used in a publication, your supervisor expects you as a properly trained biodiversity data wizard to provide a DOI assigned dataset of `Felidae` occurrence records to be cited in the study.

Tips for assignment:

There are different ways of solving this task, one approach could be:

1. create a download request containing all records assigned to the taxon `Felidae` , using the `rgbif::occ_download()` function
2. download the data and load into R (step 8 in the first tutorial)
3. export the DOI reference of the data download (step 8 in the first tutorial)
4. plot occurrences colored by name (step 8 in the first tutorial)
5. retrieve a species list of the family `Felidae` , using the `taxize` package
6. get the IUCN RedList status for each species, using the `rredlist::rl_search()` function