Using **plantR** to Manage Animal Taxonomy with the CTFB Backbone

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Contents

1 Installing `plantR`

Install the packages from GitHub if needed and load `plantR`.

```
if (!requireNamespace("remotes"))
  install.packages("remotes")
library(remotes)

if (!requireNamespace("plantR"))
  install_github("LimaRAF/plantR")

if (!requireNamespace("plantRdata"))
  install_github("LimaRAF/plantRdata")

library(plantR)
```

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2 A practical example

We will start with a small list of **names of animal species** that includes common issues (misspellings, synonyms, wrong capitalization, invalid names). We will save it in an objects called `names`:

```
names <- c(
  "Apis mellifera Linnaeus, 1758",                # name accepted with author
  "Apis melifera",                                # misspelling
  "Apis cf. mellifera",                           # open nomenclature
  "Ancyloscelis armatus",                         # synonym of Ancyloscelis apiformis (Fabricius, 179
  "Centris aenea",                                # name accepted without author
  "Centris rufa",                                 # synonym of Centris aenea Lepeletier, 1841
  "Centris Rhodoprocta Moure & Seabra, 1960",     # wrong capitalization
  "Lutjanus purpureus",                           # synonym of Lutjanus campechanus (Poey, 1860)
  "Parotocinclus amazonensis",                    # invalid in CTFB; no synonym for this name
  "Panthera onca",                                # name accepted without author
  "Solenopsis bicolor (Emery, 1906)",             # name accepted with author
  "Eucopricus columbi MacLeay, 1819",             # synonym of Sulcophanaeus columbi (MacLeay, 1819)
  "Eucopricus sp.1"                               # incomplete identification
)
```

---

3 Preparing names using `fixSpecies()`

`fixSpecies()` formats and cleans names (notation, casing, authorship split, notation flags). It accepts either a character vector or a data frame (default `scientificName` column).

```
names_fixed <- fixSpecies(names)
names_fixed[,-c(2,4)]
```

```
#>                              scientificName        scientificName.new
#> 1             Apis mellifera Linnaeus, 1758            Apis mellifera
#> 2                              Apis melifera             Apis melifera
#> 3                         Apis cf. mellifera            Apis mellifera
#> 4                       Ancyloscelis armatus      Ancyloscelis armatus
#> 5                              Centris aenea             Centris aenea
#> 6                               Centris rufa              Centris rufa
#> 7  Centris Rhodoprocta Moure & Seabra, 1960       Centris rhodoprocta
#> 8                           Lutjanus purpureus        Lutjanus purpureus
#> 9                 Parotocinclus amazonensis Parotocinclus amazonensis
#> 10                             Panthera onca             Panthera onca
#> 11         Solenopsis bicolor (Emery, 1906)        Solenopsis bicolor
#> 12         Eucopricus columbi MacLeay, 1819        Eucopricus columbi
#> 13                           Eucopricus sp.1           Eucopricus sp.1
#>                 scientificNameStatus
#> 1                     name_w_authors
#> 2                        possibly_ok
#> 3                           conferre
#> 4                        possibly_ok
#> 5                        possibly_ok
#> 6                        possibly_ok
#> 7  name_w_wrong_case|name_w_authors
```

```
#> 8                        possibly_ok
#> 9                        possibly_ok
#> 10                       possibly_ok
#> 11                    name_w_authors
#> 12                    name_w_authors
#> 13                            indet
```

3.1 Internal functions

For this specific list, some functions may not change anything (which is fine). The goal is to illustrate correct usage of the internal functions on the **same** input vector of names.

```
fixIndet(names)       # detects undetermined names (e.g., "sp.", "indet")
fixCase(names)        # fixes casing (e.g., "Centris Rhodoprocta")
fixAuthors(names)     # splits taxon and author names, if present
```

---

4 Validating taxon names using `prepSpecies()`

Next, validate names against the CTFB backbone (ctfbNames) from plantRdata by loading it into the Global Environment and passing it to db.

```
# load the CTFB backbone (ctfbNames) into the Global Environment
utils::data("ctfbNames", package = "plantRdata")

# validate against CTFB
names_valid <- prepSpecies(
  names_fixed,
  tax.names = c("scientificName.new", "scientificNameAuthorship.new"),
  db = ctfbNames)

names_valid[,-c(2,3,4,9,11)]
```

```
#>                               scientificName             scientificNameStatus
#> 1             Apis mellifera Linnaeus, 1758                   name_w_authors
#> 2                              Apis melifera                      possibly_ok
#> 3                         Apis cf. mellifera                         conferre
#> 4                       Ancyloscelis armatus                      possibly_ok
#> 5                              Centris aenea                      possibly_ok
#> 6                               Centris rufa                      possibly_ok
#> 7  Centris Rhodoprocta Moure & Seabra, 1960 name_w_wrong_case|name_w_authors
#> 8                            Lutjanus purpureus                   possibly_ok
#> 9                  Parotocinclus amazonensis                      possibly_ok
#> 10                             Panthera onca                      possibly_ok
#> 11         Solenopsis bicolor (Emery, 1906)                   name_w_authors
#> 12         Eucopricus columbi MacLeay, 1819                   name_w_authors
#> 13                            Eucopricus sp.1                           indet
#>    suggestedFamily             suggestedName  suggestedAuthorship
#> 1           Apidae            Apis mellifera       Linnaeus, 1758
#> 2           Apidae            Apis mellifera       Linnaeus, 1758
#> 3           Apidae            Apis mellifera       Linnaeus, 1758
```

```
#> 4           Apidae    Ancyloscelis apiformis    (Fabricius, 1793)
#> 5           Apidae             Centris aenea     Lepeletier, 1841
#> 6           Apidae             Centris aenea     Lepeletier, 1841
#> 7           Apidae       Centris rhodoprocta Moure & Seabra, 1960
#> 8       Lutjanidae      Lutjanus campechanus          (Poey, 1860)
#> 9     Loricariidae Parotocinclus amazonensis      Garavello, 1977
#> 10         Felidae             Panthera onca     (Linnaeus, 1758)
#> 11      Formicidae        Solenopsis bicolor        (Emery, 1906)
#> 12    Scarabaeidae     Sulcophanaeus columbi      (MacLeay, 1819)
#> 13    Scarabaeidae             Sulcophanaeus   d'Olsoufieff, 1924
#>               tax.notes                         scientificNameFull
#> 1         name accepted             Apis mellifera Linnaeus, 1758
#> 2       name misspelled             Apis mellifera Linnaeus, 1758
#> 3         name accepted             Apis mellifera Linnaeus, 1758
#> 4      replaced synonym  Ancyloscelis apiformis (Fabricius, 1793)
#> 5         name accepted            Centris aenea Lepeletier, 1841
#> 6      replaced synonym            Centris aenea Lepeletier, 1841
#> 7         name accepted  Centris rhodoprocta Moure & Seabra, 1960
#> 8      replaced synonym         Lutjanus campechanus (Poey, 1860)
#> 9  synonym not replaced Parotocinclus amazonensis Garavello, 1977
#> 10        name accepted            Panthera onca (Linnaeus, 1758)
#> 11        name accepted          Solenopsis bicolor (Emery, 1906)
#> 12     replaced synonym     Sulcophanaeus columbi (MacLeay, 1819)
#> 13     replaced synonym          Sulcophanaeus d'Olsoufieff, 1924
```

Tip 1: for large name lists, consider altering the argument `split.letters`, `parallel`, and `cores`. The minimal fuzzy similarity is controlled by `sug.dist`.

Tip 2: The maximum distance in fuzzy matching (defaults to 10%) is controlled by the argument `sug.dist`.

4.1 Internal functions

`nameMatching()` is the internal function used for exact and fuzzy matching. Below, we demonstrate it using the same names (reference names are the "accepted/standardized" targets):

```
input_names <- c(
  "Apis mellifera Linnaeus, 1758",
  "Apis mellifica",
  "Ancyloscelis apiformis",
  "Centris aenea",
  "Lutjanus purpureus",
  "Parotocinclus amazonensis",
  "Eucopricus columbi MacLeay, 1819"
)

ref_names <- c(
  "Apis mellifera Linnaeus, 1758",
  "Ancyloscelis apiformis (Fabricius, 1793)",
  "Centris aenea",
  "Centris rhodoprocta Moure & Seabra, 1960",
  "Lutjanus campechanus (Poey, 1860)",
  "Panthera onca",
```

```
  "Coelonertus baridioides Solari & Solari, 1906",
  "Solenopsis bicolor (Emery, 1906)",
  "Sulcophanaeus columbi (MacLeay, 1819)"
)

nameMatching(input_names, ref_names)
```

```
#> [1]  1  1  2  3  5 NA  9
```

---

5 Validating family names using `prepFamily()`

plantR contains an internal dictionary of valid family names which can be used via the function `prepFamily()`. Currently, valid family names are available only for plants. But a similar procedure will be included for animals in the near future. So, for now, the fuction does not change the input family names.

```
names_valid <- prepFamily(names_valid,
                          fam.name = "suggestedFamily",
                          spp.name = "scientificName.new",
                          kingdom = "animalia",
                          db = ctfbNames)
```

6 Brief code summary

A compact two-step workflow (CTFB-only):

```
# 1) Standardize
names_fixed <- fixSpecies(names)

# 2) Validate agaisnt the CTFB backbone
utils::data("ctfbNames", package = "plantRdata")
names_valid <- prepSpecies(
  names_fixed,
  tax.names = c("scientificName.new", "scientificNameAuthorship.new"),
  db = ctfbNames
)

names_valid[, c("scientificName.new","scientificNameFull","tax.notes")]
```

```
#>           scientificName.new                        scientificNameFull
#> 1             Apis mellifera             Apis mellifera Linnaeus, 1758
#> 2              Apis melifera             Apis mellifera Linnaeus, 1758
#> 3             Apis mellifera             Apis mellifera Linnaeus, 1758
#> 4       Ancyloscelis armatus  Ancyloscelis apiformis (Fabricius, 1793)
#> 5              Centris aenea            Centris aenea Lepeletier, 1841
#> 6               Centris rufa            Centris aenea Lepeletier, 1841
#> 7        Centris rhodoprocta  Centris rhodoprocta Moure & Seabra, 1960
#> 8         Lutjanus purpureus         Lutjanus campechanus (Poey, 1860)
#> 9  Parotocinclus amazonensis Parotocinclus amazonensis Garavello, 1977
#> 10             Panthera onca            Panthera onca (Linnaeus, 1758)
```

```
#> 11        Solenopsis bicolor          Solenopsis bicolor (Emery, 1906)
#> 12        Eucopricus columbi     Sulcophanaeus columbi (MacLeay, 1819)
#> 13           Eucopricus sp.1          Sulcophanaeus d'Olsoufieff, 1924
#>                tax.notes
#> 1         name accepted
#> 2       name misspelled
#> 3         name accepted
#> 4      replaced synonym
#> 5         name accepted
#> 6      replaced synonym
#> 7         name accepted
#> 8      replaced synonym
#> 9  synonym not replaced
#> 10        name accepted
#> 11        name accepted
#> 12     replaced synonym
#> 13     replaced synonym
```

Or, even simpler, using the wrapper `formatTax()`:

```
names_df <- data.frame(scientificName = names)
names_df_valid <- formatTax(names_df,
                            db = ctfbNames,
                            kingdom = "animalia")
```

---

7 Citation

If you use **plantR**, please cite it as:

> Lima, R.A.F., Sánchez-Tapia, A., Mortara, S.R., ter Steege, H., Siqueira, M.F. (2021). *plantR*: An R package and workflow for managing species records from biological collections. Methods in Ecology and Evolution 14(2): 332–339. https://doi.org/10.1101/2021.04.06.437754

And please also cite the taxonomic backbones that you used:

> Boeger, W., & Valim, M. P. (2024). Brazilian Zoology Group 2023 (version 1.1) [Data set]. Zenodo. https://doi.org/10.5281/zenodo.10498290