

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

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## 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, 1793)
  "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	scientificNameSt
#> 1	Apis mellifera Linnaeus, 1758	Apis mellifera	name_w_aut
#> 2	Apis melifera	Apis melifera	possibl
#> 3	Apis cf. mellifera	Apis mellifera	conf
#> 4	Ancyloscelis armatus	Ancyloscelis armatus	possibl
#> 5	Centris aenea	Centris aenea	possibl
#> 6	Centris rufa	Centris rufa	possibl
#> 7	Centris Rhodoprocta Moure & Seabra, 1960	Centris rhodoprocta	name_w_wrong_case name_w_aut
#> 8	Lutjanus purpureus	Lutjanus purpureus	possibl
#> 9	Parotocinclus amazonensis	Parotocinclus amazonensis	possibl
#> 10	Panthera onca	Panthera onca	possibl
#> 11	Solenopsis bicolor (Emery, 1906)	Solenopsis bicolor	name_w_aut
#> 12	Eucopricus columbi MacLeay, 1819	Eucopricus columbi	name_w_aut
#> 13	Eucopricus sp.1	Eucopricus sp.1	i

### 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")
```

```
#> [1] "Apis mellifera Linnaeus, 1758"      "Apis melifera"
#> [3] "Apis cf. mellifera"                "Ancyloscelis armatus"
#> [5] "Centris aenea"                     "Centris rufa"
#> [7] "Centris Rhodoprocta Moure & Seabra, 1960" "Lutjanus purpureus"
#> [9] "Parotocinclus amazonensis"        "Panthera onca"
#> [11] "Solenopsis bicolor (Emery, 1906)"    "Eucopricus columbi MacLeay, 1819"
#> [13] "Eucopricus sp.1"
```

```
fixCase(names)      # fixes casing (e.g., "Centris Rhodoprocta")
```

```
#>      Apis mellifera Linnaeus, 1758      Apis melifera
#>      "Apis mellifera Linnaeus, 1758"    "Apis melifera"
#>      Ancyloscelis armatus                Centris aenea
#>      "Ancyloscelis armatus"              "Centris aenea"
#>      Centris Rhodoprocta Moure & Seabra, 1960      Lutjanus purpureus
#>      "Centris rhodoprocta Moure & Seabra, 1960"    "Lutjanus purpureus"
#>      Panthera onca                      Solenopsis bicolor (Emery, 1906)      Eu
#>      "Panthera onca"                    "Solenopsis bicolor (Emery, 1906)"    "Euc
#>      Eucopricus sp.1
#>      "Eucopricus sp.1"
```

```
fixAuthors(names)   # splits taxon and author names, if present
```

```
#>      orig.name      tax.name      tax.au
#> 1      Apis mellifera Linnaeus, 1758      Apis mellifera      Linnaeus,
#> 2      Apis melifera      Apis melifera
#> 3      Apis cf. mellifera      Apis cf.      Melli
#> 4      Ancyloscelis armatus      Ancyloscelis armatus
#> 5      Centris aenea      Centris aenea
#> 6      Centris rufa      Centris rufa
#> 7      Centris Rhodoprocta Moure & Seabra, 1960      Centris Rhodoprocta Moure & Seabra,
#> 8      Lutjanus purpureus      Lutjanus purpureus
#> 9      Parotocinclus amazonensis      Parotocinclus amazonensis
#> 10      Panthera onca      Panthera onca
#> 11      Solenopsis bicolor (Emery, 1906)      Solenopsis bicolor      (Emery, 1
#> 12      Eucopricus columbi MacLeay, 1819      Eucopricus columbi      MacLeay,
#> 13      Eucopricus sp.1      Eucopricus sp.1
```

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

```

```

"Parotocinclus amazonensis",
"Panthera onca",
"Coelonertus baridioides Solari & Solari, 1906",
"Solenopsis bicolor (Emery, 1906)",
"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 3 4 5 NA 6 7 8 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 function does not change the input family names.

```

names_valid <- prepFamily(names_valid,
  fam.name = "suggestedFamily",
  spp.name = "scientificName.new",
  kingdom = "animalia")
#> Warning: Synonyms for the input kingdom are currently not available. Returning the input family na

```

## 6 Brief code summary

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

```

# 1) Standardize
names_fixed <- fixSpecies(names)

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

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

```
names_df <- data.frame(scientificName = names)
names_df_valid <- formatTax(names_df, db = ctfbNames)
#> The following family names were automatically replaced:
#>
#> |Genus      |Old fam.      |New fam.      |
#> |:-----|:-----|:-----|
#> |Ancyloscelis |Apidae      |Araceae      |
#> |Apis         |Apidae      |Fabaceae      |
#> |Centris      |Apidae      |Melastomataceae |
#> |Lutjanus     |Lutjanidae  |Fabaceae      |
#> |Panthera     |Felidae     |Fabaceae      |
#> |Parotocinclus |Loricariidae |Cactaceae     |
#> |Solenopsis   |Formicidae  |Campanulaceae |
#> |Sulcophanaeus |Scarabaeidae |Elaeocarpaceae |
```

---

## 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>