

NCBITaxonomy.jl - rapid biological names finding and reconciliation

Timothée Poisot^{1,2} Rory Gibb^{3,4} Sadie J. Ryan^{5,6,7} Colin J. Carlson^{8,9}

¹ Université de Montréal, Département de Sciences Biologiques, Montréal QC, Canada ² Québec Centre for Biodiversity Science, Montréal, QC, Canada ³ Centre on Climate Change and Planetary Health, London School of Hygiene and Tropical Medicine, London, UK ⁴ Centre for Mathematical Modelling of Infectious Diseases, London School of Hygiene and Tropical Medicine, London, UK ⁵ Emerging Pathogens Institute, University of Florida, Gainesville, FL, United States of America ⁶ School of Life Sciences, University of KwaZulu-Natal, Durban, South Africa ⁷ Department of Geography, University of Florida, Gainesville, FL, United States of America ⁸ Department of Microbiology and Immunology, Georgetown University Medical Center, Georgetown University, Washington, D.C., United States of America ⁹ Center for Global Health Science and Security, Georgetown University Medical Center, Georgetown University, Washington, D.C., United States of America

Correspondance to:

Timothée Poisot — timothee.poisot@umontreal.ca

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NCBITaxonomy.jl is a package designed to facilitate the reconciliation and cleaning of taxonomic names, using a local copy of the NCBI taxonomic backbone (Federhen 2012, Schoch et al. 2020); The basic search functions are coupled with quality-of-life functions including case-insensitive search and custom fuzzy string matching to facilitate the amount of information that can be extracted automatically while allowing efficient manual curation and inspection of results. NCBITaxonomy.jl works with version 1.6 of the Julia programming language (Bezanson et al. 2017), and relies on the Apache Arrow format to store a local copy of the NCBI raw taxonomy files. The design of NCBITaxonomy.jl has been inspired by similar efforts, like the R package taxadb (Norman et al. 2020), which provides an offline alternative to packages like taxize (Chamberlain and Szöcs 2013).

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9 taxize (Chamberlain and Szöcs 2013).

10 **Statement of need**

11 Unambiguously identifying species is a far more challenging task than it may appear. There are a vast
12 number of reasons for this. Different databases keep different taxonomic “backbones,” *i.e.* different data
13 structures in which names are mapped to species, and organised in a hierarchy. Not all names are unique
14 identifiers to groups. For example, *Io* can either refer to a genus of plants from the aster family, or to a
15 genus of molluscs; the genus *Mus* (of which the house mouse *Mus musculus* is a species), contains a
16 sub-genus *also* named *Mus*. Conversely, the same species can have several names, which are valid
17 synonyms: for example, the domestic cow *Bos taurus* admits *Bos primigenius taurus* as a valid synonym.
18 Taxonomic nomenclature also changes regularly, with groups being split, merged, or moved to a new
19 position in the tree of life; this is, notably, a common occurrence with viral taxonomy, each subsequent
20 version of which can differ markedly from the last; compare, *e.g.* Lefkowitz et al. (2018) to Walker et al.
21 (2020).

22 To add to the complexity, one must also consider that most taxa names are at some point manually typed,
23 which has the potential to introduce additional mistakes in raw data; it is likely to expect that such
24 mistakes may arise when attempting to write down the (perfectly valid) names of the bacterial isolate
25 known as *Myxococcus llanfairpwllgwyngyllgogerychwyrndrobwllllantysiliogogochensis*, or of the crowned
26 slaty flycatcher *Griseotyrannus aurantioatrocristatus*. These mistakes are more likely when dealing with
27 hyper-diverse samples, like plant census (Dauncey et al. 2016, Wagner 2016, Conti et al. 2021). In addition
28 to binomial names, the same species can be known by many vernacular (common) names, which are

language or even region-specific: *Ovis aries*, for example, has valid English vernaculars including lamb, sheep, wild sheep, and domestic sheep.

All these considerations are actually important when matching species names both within and across datasets. Let us consider the following species survey of individual fishes, European chub, *Cyprinus cephalus*, *Leuciscus cephalus*, *Squalius cephalus*: all are the same species (*S. cephalus*), referred to as one of the vernacular (European chub) and two formerly accepted names now classified as synonyms. A cautious estimate of diversity based on the user-supplied names would give $n = 4$ species, when there is in fact only one.

A package with the ability to handle the sources of errors outlined above, and especially while provide an authoritative classification, can accelerate the work of consuming large volumes of biodiversity data. For example, this package was used in the process of developing the *CLOVER* database (Gibb et al. 2021) of host-virus associations, by reconciling the names of viruses and mammals from four different sources, where all of the issues described above were present.

Overview of functionalities

An up-to-date version of the documentation for `NCBITaxonomy.jl` can be found online at <https://docs.ecojulia.org/NCBITaxonomy.jl/stable/>, including examples and a documentation of every method. The package is released under the MIT license. Contributions can be made in the form of issues (bug reports, questions, features suggestions) and pull requests. The package can be checked out and installed anonymously from the central Julia repository:

```
using Pkg

# This line should go in the Julia configuration file - note that the path
# will be created if it doesn't exist, and will be used to store the
# raw taxonomic table
ENV["NCBITAXONOMY_PATH"] = joinpath(homedir(), "data", "NCBITaxonomy.jl")

Pkg.add("NCBITaxonomy") # Downloading the files may take a long time
```

48 The package will download the most recent version of the NCBI taxonomy database, and transform in into
49 a set of Apache Arrow files ready for use. Note that the NCBITAXONOMY_PATH can specified on a per-project
50 basis, and as long as the package is not re-built, the local set of tables downloaded from NCBI will not
51 change; this way, users can re-run an analysis with a guarantee that the underlying taxonomic backbone
52 has not changed.

53 **Improved name matching**

54 Name finding is primarily done through the `taxon` function, which admits either a unique NCBI identifier
55 (e.g. `taxon(36219)` for the bogue *Boops boops*), a string (`taxon("Boops boops")`), or a data frame with a
56 restricted list of names (see the next section). The `taxon` method has additional arguments to perform
57 fuzzy matching in order to catch possible typos (`taxon("Boops bops"; strict=false)`), to perform a
58 lowercase search (useful when alphanumeric codes are part of the taxon name, like for some viruses), and
59 to restrict the the search to a specific taxonomic rank.

60 The lowercase search can be a preferable alternative to fuzzy string matching. Consider the string
61 Adeno-associated virus 3b - it has three names with equal distance (under the Levensthein string
62 distance function):

```
julia> similarnames("Adeno-associated virus 3b"; threshold=0.95)
3-element Vector{Pair{NCBITaxon, Float64}}:
  Adeno-associated virus - 3 (ncbi:46350) => 0.96
  Adeno-associated virus 3B (ncbi:68742) => 0.96
  Adeno-associated virus 3A (ncbi:1406223) => 0.96
```

63 Depending on the operating system, either of these three names can be returned; compare to the output of
64 a case insensitive name search:

```
julia> taxon("Adeno-associated virus 3b"; casesensitive=false)
Adeno-associated virus 3B (ncbi:68742)
```

65 This returns the correct name.

66 Name matching output and error handling

67 The `taxon` function will either return a `NCBITaxon` object (made of a name and id), or throw either a
68 `NameHasNoDirectMatch` (with instructions about how to possibly solve it, using the `similarnames`
69 function), or a `NameHasMultipleMatches` (listing the possible valid matches, and suggesting to use
70 `alternativetaxa` to find the correct one). Therefore, the common way to work with the `taxon` function
71 would be to wrap it in a `try/catch` statement:

```
try
  taxon(name)
  # Additional operations with the matched name
catch err
  if isa(err, NameHasNoDirectMatch)
    # What to do if no match is found
  elseif isa(err, NameHasMultipleMatches)
    # What to do if there are multiple matches
  else
    # What to do in case of another error that is not NCBITaxonomy specific
  end
end
```

72 These functions will not demand any user input in the form of key presses (though they can be wrapped in
73 additional code to allow it), as they are intended to run on clusters without supervision. The `taxon`
74 function has good scaling using multiple threads. For convenience in rapidly getting a `taxon` for
75 demonstration purposes, we also provide a string macro, whereby e.g. `ncbi"Procyon lotor"` will return
76 the `taxon` object for the raccoon.

77 Name filtering functions

78 As the full NCBI names table has over 3 million entries at the time of writing, we have provided a number
79 of functions to restrict the scope of names that are searched. These are driven by the NCBI *divisions*. For
80 example `nf = mammalfilter(true)` will return a data frame containing the names of mammals, inclusive

81 of rodents and primates, and can be used with *e.g.* `taxon(nf, "Pan")`. This has the dual advantage of
 82 making search faster, but also of avoiding matching on names that are shared by another taxonomic group
 83 (which is not an issue with *Pan*, but is an issue with *e.g.* *Io* as mentioned in the introduction).

84 Note that the use of a restricted list of names can have significant performance consequences: compare,
 85 for example, the time taken to return the taxon *Pan* (ID 9596) in the entire database, in all mammals, and
 86 in all primates:

Names list	Fuzzy matching	Time (ms)	Allocations	Memory allocated
all	no	23	34	2 KiB
	yes	105	2580	25 MiB
mammalfilter(true)	no	0.55	32	2 KiB
	yes	1.9	551	286 KiB
primatefilter()	no	0.15	33	2 KiB
	yes	0.3	92	27 KiB

87 Clearly, the optimal search strategy is to (i) rely on name filters to ensure that search are conducted within
 88 the appropriate NCBI division, and (ii) only rely on fuzzy matching when the strict or lowercase match
 89 fails to return a name, as fuzzy matching can result in order of magnitude more run time and memory
 90 footprint. These numbers were obtained on a single Intel i7-8665U CPU (@ (1.90GHz). Using
 91 "chimpanzees" as the search string (the NCBI recognized vernacular for *Pan*) gave qualitatively similar
 92 results, suggesting that there is no performance cost associated with working with synonyms or vernacular
 93 input data.

94 **Quality of life functions**

95 In order to facilitate working with names, we provide the `authority` function (gives the full taxonomic
 96 authority for a name), `synonyms` (to get alternative valid names), `vernacular` (for English common
 97 names), and `rank` (for the taxonomic rank).

98 **Taxonomic lineages navigation**

99 The children function will return all nodes that are directly descended from a taxon; the descendants
100 function will recursively apply this function to all descendants of these nodes, until only terminal leaves
101 are reached. The parent function is an “upwards” equivalent, giving that taxon from which a taxon
102 descends; the lineage function chains calls to parent until either taxon(1) (the taxonomy root) or an
103 arbitrary ancestor is reached.

104 The taxonomicdistance function (and its in-place equivalent, taxonomicdistance!, which uses
105 memory-efficient re-allocation if the user needs to change the distance between taxonomic ranks) uses the
106 Shimatani (2001) approach to reconstruct a matrix of distances based on taxonomy, which can serve as a
107 rough proxy when no phylogenies are available.

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