concordance=TRUE

taxize - taxonomic search and retrieval in R

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I. INTRODUCTION

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II. THE CASE FOR TAXIZE

There are a large suite of applications developed around the problem of searching for, resolving, and getting higher taxonomy for species names. For example, Linnaeus http://linnaeus.sourceforge.net/ provides ability to search for taxonomic names in documents and normalize names. In addition, there are many web interfaces to search for and normalize names such as Encyclopedia of Life's Global Names Resolver http://resolver.globalnames.org/, uBio tools http://www.ubio.org/index.php?pagename=sample_tools, and iPlant's Taxonomic Name Resolution Service http://tnrs.iplantcollaborative.org/.

All of these tools provide great ways to search for taxonomic names and resolve them in some cases. However, scientists ideally need a tool that can be used programmatically, and thus be made reproducible, and highly customizeable. The goal of taxize is to make it easy to create reproducible and easy to use workflows for searching for taxonomic names, resolving them, getting higher taxonomic names, and other tasks related to research dealing with species.

III. DATA SOURCES

taxize uses many data sources, and more can easily be added.

TABLE I. Data sources used in taxize

Source name	Name search	Name resolution	Phylogeny	URL
Encyclopedia of Life	Yes	See GNR below	No	http://eol.org/
Integrated Taxonomic Resolution Service	Yes	Synonyms	No	X
iPlant Taxonomic Name Resolution Service	Yes	Yes	No	X
Phylomatic	No	X	No	X
uBio	Yes	X	No	X
Global Names Resolver	Yes	X	No	X
Global Names Index	Yes	X	No	X
IUCN Red List	Yes	X	No	X
Tropicos	Yes	X	No	X
Plantminer	Yes	X	No	X
Theplantlist.org	Yes	X	No	X
Catalogue of Life	Yes	X	No	X
National Center for Biotechnology Information (NCBI)	Yes	X	No	X

IV. USE CASES

There are a variety of use cases for which taxize is ideally suited, and few side cases in which taxize can be useful. We discuss five ideal use cases for taxize at length, and highlight the side cases in brief.

A. Installing taxize

First, let's install taxize. There are two versions of taxize, a stable release that can be installed from the R package repository, CRAN, and from GitHub, where the code is developed.

Installing from CRAN or GitHub

```
## From CRAN
install.packages("taxize")

## From GitHub
```

```
install_github("taxize_", "ropensci")
```

Loading into your R session

```
library(taxize)
```

B. Resolve taxonomic names

This is a common task in biology. We often have a list of species names and we want to know if a) we have the most up to date names, b) our names are spelled correctly, and c) if we have common names, we likely need the scientific names. One way to resolve names is via the Global Names Resolver service provided by the Encyclopedia of Life (http://resolver.globalnames.org/).

```
# Here, we are searching for two misspelled names
temp <- gnr_resolve(names = c("Helianthos annus", "Homo saapiens"), returndf = TRUE)

# let's take a peek at the data, excluding the data source ID and score
# columns
temp[, -c(1, 4)]

    submitted_name                 name_string                    title
1 Helianthos annus        Helianthus annuus L.       Catalogue of Life
3 Helianthos annus            Helianthus annus GBIF Taxonomic Backbone
4 Helianthos annus            Helianthus annus                     EOL
5 Helianthos annus         Helianthus annus L.                     EOL
6 Helianthos annus            Helianthus annus           uBio NameBank
2    Homo saapiens Homo sapiens Linnaeus, 1758       Catalogue of Life
```

Looks like the correct spellings are *Helianthus annuus* and *Homo sapiens*, cool!

Another approach is using the Taxonomic Name Resolution Service via the Taxosaurus API (http://taxosaurus.org/).

```
# Lets set our list of species names
mynames <- c("Helianthus annuus", "Pinus contort", "Poa anua", "Abis magnifica",
    "Rosa california", "Festuca arundinace", "Sorbus occidentalos", "Madia sateva")

# And we'll call the API with the tnrs function
tnrs(query = mynames)[, -c(5:7)]

data frame with 0 columns and 0 rows
```

It looks like there are a few corrections: e.g., *Madia sateva* should be *Madia sativa*, and *Rosa california* should be *Rosa californica*.

C. Retrieve higher taxonomic names

Another task biologists often face is wanting to get higher taxonomic names for their list of taxa. If you have the higher taxonomy you can put in to context the relationships of your list (i.e., Species A and B are in Family X), as opposed to not knowing that Species A and B are closely related. A number of data sources provide this type of capability. First, let's take a look at the Integrated Taxonomic Information Service (ITIS).

```
specieslist <- c("Abies procera", "Pinus contorta")
classification(get_tsn(specieslist, "sciname"))
```

```
Retrieving data for species ' Abies procera '

Retrieving data for species ' Pinus contorta '
[[1]]
        parentName parentTsn      rankName       taxonName    tsn
1                                  Kingdom         Plantae 202422
2          Plantae    202422    Subkingdom  Viridaeplantae 846492
3   Viridaeplantae    846492  Infrakingdom    Streptophyta 846494
4     Streptophyta    846494      Division    Tracheophyta 846496
5     Tracheophyta    846496   Subdivision Spermatophytina 846504
6  Spermatophytina    846504 Infradivision    Gymnospermae 846506
7     Gymnospermae    846506         Class       Pinopsida 500009
8        Pinopsida    500009         Order         Pinales 500028
9          Pinales    500028        Family        Pinaceae  18030
10        Pinaceae     18030         Genus           Abies  18031
11           Abies     18031       Species   Abies procera 181835

[[2]]
        parentName parentTsn      rankName       taxonName    tsn
1                                  Kingdom         Plantae 202422
2          Plantae    202422    Subkingdom  Viridaeplantae 846492
3   Viridaeplantae    846492  Infrakingdom    Streptophyta 846494
4     Streptophyta    846494      Division    Tracheophyta 846496
5     Tracheophyta    846496   Subdivision Spermatophytina 846504
6  Spermatophytina    846504 Infradivision    Gymnospermae 846506
7     Gymnospermae    846506         Class       Pinopsida 500009
8        Pinopsida    500009         Order         Pinales 500028
9          Pinales    500028        Family        Pinaceae  18030
10        Pinaceae     18030         Genus           Pinus  18035
11           Pinus     18035       Species  Pinus contorta 183327
```

It turns out both species are in the family Pinaceae. You can also get this type of information from the NCBI by doing *classification(get_uid(specieslist))*

Instead of a full classification, you may only wan a single name, say a family name for your species of interest. The function *tax_name* is built just for this purpose. And you can specify the data source you retrieve the taxonomic name from with the *db* parameter.

```
tax_name(query = "Helianthus annuus", get = "family", db = "itis")


Retrieving data for species ' Helianthus annuus '
      family
1 Asteraceae

tax_name(query = "Helianthus annuus", get = "family", db = "ncbi")


Retrieving data for species ' Helianthus annuus '
      family
1 Asteraceae
```

D. Retrieve a phylogeny

There is an increasingly common use case: many biologists are not adequately trained in reconstructing phylogenies. However, so-called *taxonomic phylogenies* can be constructed from simply knowing the higher taxonomic classification of a set of taxa. There are few taxon groups for which we can get phylogenies simply based on taxonomy; one of these

is for angiosperms, called Phylomatic [**?**]. We have created a workflow in taxize that lets you input a simple species list, and then taxize does work behind the scenes to get higher taxonomic names, which are required by Phylomatic to get a phylogeny. Here is a short example.

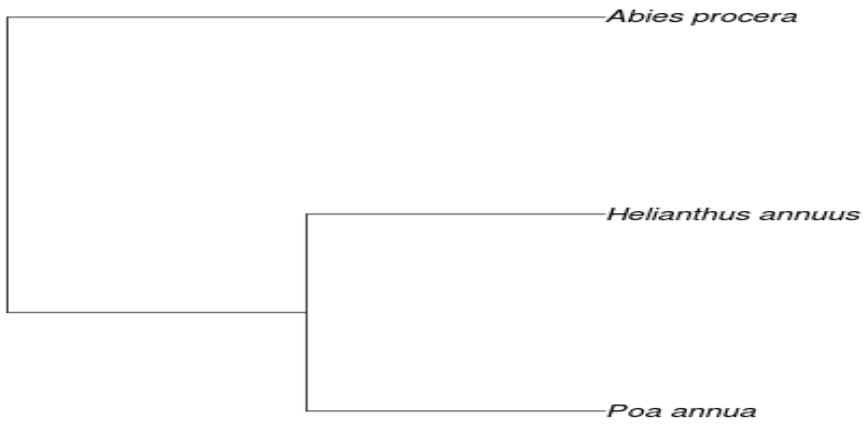
```
library(doMC)
registerDoMC(cores = 4)

# input the taxonomic names
taxa <- c("Poa annua", "Abies procera", "Helianthus annuus")

# fetch the tree - the formatting of names and higher taxonmy is done
# within the function
tree <- phylomatic_tree(taxa = taxa, get = "POST", informat = "newick", method = "phylomatic",
    storedtree = "R20120829", taxaformat = "slashpath", outformat = "newick",
    clean = "true")

tree$tip.label <- capwords(tree$tip.label)

# plot the tree
plot(tree, cex = 1.2)
```



E. What taxa are in children of my taxon of interest?

If you aren't a taxonomic specialist on a particular taxon you likely don't know what children taxa are within a family, or within a genus. You can of course go to a website like Wikispecies (http://species.wikimedia.org/wiki/Main_Page) or Encyclopedia of Life (http://eol.org/). taxize provides an easy way for you to search for downstream taxa, both for the Catalogue of Life (CoL; http://www.catalogueoflife.org/) and the Integrated Taxanomic Information Database (http://www.itis.gov/). Here is a short example using the CoL in which we want to find all the species within the genus *Apis* (honey bees).

```
col_downstream(name = "Apis", downto = "Species")[[1]]

  childtaxa_id     childtaxa_name childtaxa_rank
1      6971712 Apis andreniformis        Species
2      6971713        Apis cerana        Species
3      6971714       Apis dorsata        Species
4      6971715        Apis florea        Species
```

```
5      6971716 Apis koschevnikovi        Species
6      6845885     Apis mellifera        Species
7      6971717   Apis nigrocincta        Species
```

F. IUCN Status

There are a number of things we can do once we have the correct taxonomic names. One thing we can do is ask about the conservation status of a species. We have provided a set of functions, *iucn_summary* and *iucn_status*, to search for species names, and extract the status information, respectively. Here, we search for the Panther and Lynx.

```
ia <- iucn_summary(c("Panthera uncia", "Lynx lynx"))
iucn_status(ia)

Panthera uncia      Lynx lynx
          "EN"           "LC"
```

It turns out that the Panther is endangered (EN) and the Lynx is of least concern (LN).

V. CONCLUSION

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VI. FUNDING

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