taxonomic data with taxize

Cheat Sheet



Use Cases

A few common use cases to give you a sense for what taxize can be used for:

1. Get taxonomic IDs for your species.

some diagram of this

2. Get correct spellings for your species.

some diagram of this

3. Retrieve higher taxonomic classification names.

some diagram of this

4. Fetch all taxonomic names downstream from a target taxnomic group.

some diagram of this

Data Sources

Encylopedia of Life

Taxonomic Name Resolution Service

Integrated Taxonomic Information Service

Phylomatic

uBio

Global Names Resolver

Global Names Index

IUCN Red List

Tropicos

Plantminer

Theplantlist

Catalogue of Life

Global Invasive Species Database

National Center for Biotechnology Information

CANADENSYS Vascan name search API

International Plant Names Index (IPNI)

Barcode of Life Data Systems (BOLD)

National Biodiversity Network (UK)

Get taxonomic IDs

Options



Interactively select names.



Or, get back all names to process



Or, get back certain records.

For example

taxize::get_colid(<id>)

If > 1 result, interactively select by row

taxize::get_colid_(<id>)

Get all data

taxize::get_colid(<id>, rows = 1:4)

Get rows 1 through 4

Correct Names

Get names up or downstream

Out of the box frameworks

Global Names Resolver

taxize::get colid(<id>)

If > 1 result, interactively select by row

taxize::get colid (<id>)

Get all data

taxize::get_colid(<id>, rows = 1:4)

Get rows 1 through 4

Others

touch on the others briefly...

DIY correction

There are a lot of functions to search various taxonomic databases - they don't do name resolution per se.

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taxize::get_colid(<id>, rows = 1:4)

Get rows 1 through 4