Taxonomic Data

with taxize

Cheat Sheet



Use Cases

Get taxonomic IDs

taxize::get ids(name) / taxize::get colid(name)

Puma concolor

2435099

Ursus americanus

2433407

Quercus robur

2878688

Get correct spellings

taxize::tnrs(names) / taxize::gnr resolve(names)

Pumma concolor —— Puma concolor



Retrieve higher taxonomic classification

taxize::classification(names)

Classification for Chironomus riparius

	name	rank	id
1	Animalia	Kingdom	22254411
2 3 4 5 6	Arthropoda	Phylum	22254412
3	Insecta	Class	22254618
4	Diptera	0rder	22254663
5	Chironomidae	Family	22254676
1 -	Chironomus		22350527
7	Chironomus riparius	Species	8663146

Fetch all taxonomic names downstream from a target taxnomic group

taxize::downstream(names)

Species downstream from the genus Apis

	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

Data Sources (hyperlinked)

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 later.



Or, get back certain records.

taxize::get colid(id)

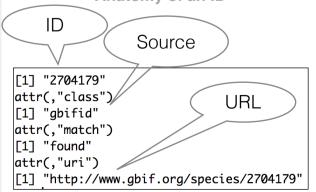
If > 1 result, interactively select by row

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

Get rows 1 through 4

taxize::get_colid_(id) Get all data

Anatomy of an ID



Coerce to Taxonomic ID

With taxonomic IDs, you have a stable reference to a species for a specific source, and you can do many things in taxize with ids (See box to the right for examples).

From: numeric, character, list, or data.frame, e.g.:

taxize::as.colid(8663146)

Validate

Set check=FALSE to not check if ID is valid if **TRUE** we ping the data source to make sure the ID is good.

taxize::as.colid(8663146, check = FALSE)

All taxize::as.*() take one or many Ids

Correct Names

Out of the box frameworks

taxize::gnr resolve(names)

taxize::tnrs(names)

Queries NCBI, Mammals dataset, and iPlant, only fuzzy matching on plants

taxize::iplant_resolve(names)

iPlant has a nice name resolver of course, it only works for plants

Bonus: taxize::resolve(names) is an interface to all three of the resolution functions

DIY correction

There are a lot of functions to search various taxonomic databases - they don't do name resolution per se. But you can use them to achieve the same end as the above functions. Some exmples:

taxize::col_search(names)

Get name synonyms

taxize::nbn search(names)

Search UK Nat. Biodiveristy Network

taxize::tp_search(names)

Search Tropicos

taxize::gni_search(names)

Search Global Names Index

Down-/up-stream, children, and more

Target Taxon

taxize::downstream(name, "species")



taxize::children(names)

Immediate children only



taxize::upstream(names)

Upstream to desired rank



taxize::classification(names)

Kingdom

All upstream names for given taxon

Order

Family

Combine Classification Data

Stack vertically - rbind

out <- taxize::classification(ids, db = "ncbi")</pre>

taxize::rbind(out)

Animalia Kingdom 22254411 Arthropoda Phylum 22254412 Insecta Class 22254618

Combine horizontally - cbind

taxize::rbind(out)

kingdom phylum class Protozoa Euglenophycota Euglenophyceae Euglenales Animalia Platyhelminthes Trematoda Plagiorchiida