Package ‘taxalight’

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Version 0.1.5

Title A Lightweight and Lightning-Fast Taxonomic Naming Interface

Description Creates a local Lightning Memory-Mapped Database (‘LMDB’) of many commonly used taxonomic authorities and provides functions that can quickly query this data. Supported taxonomic authorities include the Integrated Taxonomic Information System (‘ITIS’), National Center for Biotechnology Information (‘NCBI’), Global Biodiversity Information Facility (‘GBIF’), Catalogue of Life (‘COL’), and Open Tree Taxonomy (‘OTT’). Name and identifier resolution using ‘LMDB’ can be hundreds of times faster than either relational databases or internet-based queries. Precise data provenance information for data derived from naming providers is also included.

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Encoding UTF-8

ByteCompile true

Depends R (>= 4.0)

Imports thor, contentid

Suggests jsonlite, spelling, testthat, covr, knitr, rmarkdown, progress, utf8, crayon

URL https://github.com/cboettig/taxalight

BugReports https://github.com/cboettig/taxalight

Language en-US

RoxygenNote 7.1.1

NeedsCompilation no

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**Description**

Return the accepted taxonomic identifier, acceptedNameUsageID given a scientific name.

**Usage**

```r
get_ids(
    name,
    provider = getOption("tl_default_provider", "itis"),
    version = tl_latest_version(),
    dir = tl_dir()
)
```

**Arguments**

- `name` character vector of scientific names
- `provider` Abbreviation for a known naming provider. Provider data should first be imported with `tl_create`. Note: setting provider to "itis_test" is for testing purposes only, use "itis" for the full ITIS data. See details
- `version` version of the authority to use (e.g. four-digit year)
- `dir` storage location for the LMDB databases

**Value**

A vector of matching accepted identifiers. Note that if the name provided is considered to be a synonym by the provider, then the ID corresponds to the accepted name and not the synonym. (i.e. `get_names(get_ids(synonym))`) will return the accepted name and not the synonym name.
get_names

Examples

# slow initial import
sp <- c("Dendrocygna autumnalis", "Dendrocygna bicolor")
get_ids(sp, "itis_test")  # use "itis_test" test data for example only

get_names  

Return scientificName names given taxonomic identifiers

Description

Return scientificName names given taxonomic identifiers

Usage

get_names(
  id, 
  provider =getOption("tl_default_provider", "itis"),
  version = tl_latest_version(),
  dir = tl_dir()
)

Arguments

id  a character vector of taxonomic identifiers, including provider prefix
provider  Abbreviation for a known naming provider. Provider data should first be im-
  ported with [tl_create]. Note: setting provider to "itis_test" is for testing
  purposes only, use "itis" for the full ITIS data. See details
version  version of the authority to use (e.g. four-digit year)
dir  storage location for the LMDB databases

Value

a vector of matching scientific names

Examples

# slow initial import
get_names(c("ITIS:180092", "ITIS:179913"), "itis_test")  # uses test version
taxalight query: rapidly look up scientific names from a local database

Description

taxalight query: rapidly look up scientific names from a local database

Usage

tl(
  x,
  provider = getOption("tl_default_provider", "itis"),
  version = tl_latest_version(),
  dir = tl_dir()
)

Arguments

x character vector of either scientific names or taxonomic identifiers (with prefix). Can mix and match too.

provider Abbreviation for a known naming provider. Provider data should first be imported with [tl_create]. Note: setting provider to "itis_test" is for testing purposes only, use "itis" for the full ITIS data. See details

version version of the authority to use (e.g. four-digit year)

dir storage location for the LMDB databases

Details

Naming providers currently recognized by taxalight are:

- gbif: Global Biodiversity Information Facility, https://www.gbif.org/
- ott: OpenTree Taxonomy: https://github.com/OpenTreeOfLife/reference-taxonomy
- itis_test: a small subset of ITIS, cached locally for testing purposes only.

The default provider is itis, which can be reconfigured by setting tl_default_provider in [options].

Value

a data.frame in Darwin Core format with rows matching the acceptedNameUsageID or scientificName requested.
See Also
tl_create

Examples

```r
# slow initial import
sp <- c("Dendrocygna autumnalis", "Dendrocygna bicolor")
id <- c("ITIS:180092", "ITIS:179913")

## example uses "itis_test" provider for illustration only:
 tl(sp, "itis_test")
 tl(id, "itis_test")
```
Details

Naming providers currently recognized by taxalight are:

- gbif: Global Biodiversity Information Facility, https://www.gbif.org/
- ott: OpenTree Taxonomy: https://github.com/OpenTreeOfLife/reference-taxonomy
- itis_test: a small subset of ITIS, cached locally for testing purposes only.

The default provider is itis, which can be reconfigured by setting tl_default_provider in [options].

Examples

```r
## example uses "itis_test" for illustration only:

tl_create("itis_test")
```

---

### tl_dir

taxalight data directory

**Description**

taxalight stores data for persistent access in the directory given by tl_dir() by default. All functions can override this choice by passing an alternative path to the dir argument, or configure the location system-wide by setting the environmental variable TAXALIGHT_HOME, eg. in their .Renviron file, see Sys.setenv(). If unset, the default location is the default for the operating system, as provided by the core R function tools::R_user_dir(). Users can manually purge the data storage at any time by deleting this directory.

**Usage**

tl_dir()

**Examples**

tl_dir()
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