

Package: EthnoBotaPhyWR (via r-universe)

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Title Infrastructure for Ethnobotanical and Phytochemical Data
Integration with Wikidata

Version 0.0.0.9001

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Description Infrastructure and curated ethnobotanical and phytochemical datasets for analyzing plant families, including phylogenetic integration and visualization tools. Includes vendored functions from the 'cascade' package (<https://github.com/adafede/cascade>) to minimize the dependency tree.

License AGPL (>= 3)

URL <https://github.com/adafede/EthnoBotaPhyWR>,
<https://adafede.github.io/EthnoBotaPhyWR>

BugReports <https://github.com/adafede/EthnoBotaPhyWR/issues>

Depends R (>= 4.5.0)

Imports ape (>= 5.8.1), curl (>= 5.0.0), data.table (>= 1.15.0),
forcats (>= 0.5.4), ggplot2 (>= 4.0.3), ggtext (>= 0.1.2),
ggtree (>= 4.0.5), ggtreeExtra (>= 1.20.1), httr2 (>= 1.0.0),
jsonlite (>= 2.0.0), khroma (>= 1.17.0), logger (>= 0.4.2),
openssl (>= 2.4.2), phangorn (>= 2.12.1), purrr (>= 1.2.2),
rotl (>= 3.1.1), rvest (>= 1.0.5), scales (>= 1.4.0), tibble
(>= 3.3.1), tidytable (>= 0.11.2), tidytree (>= 0.4.8)

Suggests altdoc, gdtools (>= 0.5.2), gt (>= 1.3.0), quarto (>= 1.5.1),
spelling, svglite (>= 2.2.2), systemfonts (>= 1.3.2), testthat
(>= 3.0.0)

ByteCompile TRUE

Collate 'EthnoBotaPhyWR-package.R' 'normalize_ott_ids.R'
'calculate_branches_values.R' 'cascade_colors.R'
'cascade_prepare_hierarchy.R' 'cascade_prepare_plot.R'
'cascade_query_wikidata.R' 'cascade_taxon_name_to_qid.R'
'data.R' 'plot_trees.R' 'get_trees.R' 'get_results_wd.R'
'get_npclassifier_taxonomy.R' 'ethnobotafever_tree.R'
'globals.R'

Config/roxygen2/markdown TRUE
Config/roxygen2/version 8.1.1
Config/testthat/edition 3
Encoding UTF-8
Language en-US
LazyData TRUE
VignetteBuilder quarto
biocViews Ethnobotany, Phytochemistry, Taxonomy, Wikidata
X-schema.org-keywords Ethnobotany, Phytochemistry, Taxonomy, Wikidata
Config/pak/sysreqs libcairo2-dev cmake libfontconfig1-dev libfreetype6-dev libglpk-dev make libicu-dev libjpeg-dev libpng-dev libuv1-dev libxml2-dev libssl-dev
Repository https://adafede.r-universe.dev
Date/Publication 2026-10-27 22:30:57 UTC
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ethnobotafever_tree	<i>Ethnobota fever</i>
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Description

Collects and plots ethnobotanical and phytochemical data for a given taxon. This function performs data retrieval, merging, and logging, and produces summary statistics and outputs for downstream analysis and visualization.

Usage

```
ethnobotafever_tree(  
  taxon_name,  
  n_multiple_genera,  
  n_ethnobotanical_count_min,  
  n_compounds_count_min,  
  example_family_names,  
  path_molecules,  
  path_classes,  
  path_ethnobotanical,  
  export_tree_full,  
  export_tree_phyto,  
  export_tree_phyto_sub,  
  export_table_classified,  
  export_table_counts,  
  export_table_counts_sub,  
  local_cache,  
  log_dir  
)
```

Arguments

taxon_name	Character. Name of the taxon of interest.
n_multiple_genera	Integer. Minimum number of genera for filtering.
n_ethnobotanical_count_min	Integer. Minimum ethnobotanical count for filtering.
n_compounds_count_min	Integer. Minimum compound count for filtering.
example_family_names	Character vector. Example family names for comparison.
path_molecules	Character, data.frame, or NULL. Local molecules file or table.
path_classes	Character, data.frame, or NULL. Local classes file or seed data.
path_ethnobotanical	Character, data.frame, or NULL. Local ethnobotanical file or table.
export_tree_full	Character. Path for the main full-tree PDF figure.
export_tree_phyto	Character. Path for the phytochemical overview PDF figure.
export_tree_phyto_sub	Character. Path for the species-level phytochemical PDF figure.
export_table_classified	Character. Path for the classified compounds export.
export_table_counts	Character. Path for the genus-level summary table export.

export_table_counts_sub	Character or NULL. Path for the filtered species-level counts export.
local_cache	Character. Directory containing .rda tree cache datasets (for example data-raw).
log_dir	Character. Directory for log files.

Details

This function is a pipeline for data collection, merging, and reporting. It logs progress and statistics throughout. All side effects (file writes, logs) are documented inline.

Value

A list containing the rendered plots, exported tables, and the log-file path.

Examples

```
NULL
```

orchids_compound_classes

Orchids Compound Classifications

Description

NPClassifier taxonomy results for SMILES strings found in *Orchidaceae*. Maps each unique SMILES to its pathway, superclass, class, and glycoside status.

Usage

```
orchids_compound_classes
```

Format

A data.frame with 1574 rows and 5 columns:

query Canonical SMILES string
pathway NPClassifier pathway classification
superclass NPClassifier superclass classification
class NPClassifier class classification
glycoside Logical: whether compound is a glycoside

Details

This dataset is a deduplicated lookup table for compound classifications. Use it to quickly retrieve NPClassifier results for a given SMILES string without querying the live API.

Source

NPClassifier Web Service (<https://npclassifier.gnps2.org/>)

Examples

```
data(orchids_compound_classes)
head(orchids_compound_classes)
nrow(orchids_compound_classes)
```

orchids_compounds	<i>Orchids Compound Data</i>
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Description

A dataset containing phytochemical information from *Orchidaceae* species. This is a curated subset linking taxonomic data, chemical structures (SMILES), and NPClassifier taxonomy.

Usage

```
orchids_compounds
```

Format

A data.frame with 3055 rows and 10 columns:

taxon Wikidata QID (Q-identifier) for the species
taxon_name Scientific name of the species
compound Wikidata QID for the chemical compound
compound_smiles_canonical Canonical SMILES representation
compound_inchikey InChIKey chemical identifier
connectivity_layer First block of InChIKey (connectivity skeleton)
pathway NPClassifier pathway classification
superclass NPClassifier superclass classification
class NPClassifier class classification
glycoside Logical: whether compound is a glycoside

Source

Curated from:

- Wikidata (<https://www.wikidata.org/>)
- LOTUS database (<https://lotus.naturalproducts.net/>)
- NPClassifier (<https://npclassifier.gnps2.org/>)

Examples

```
data(orchids_compounds)
head(orchids_compounds)
table(orchids_compounds$superclass)
```

orchids_ethnobotanical

Orchids Ethnobotanical Uses

Description

A dataset of ethnobotanical uses reported for *Orchidaceae* species, linked to their Open Tree of Life (OTT) taxonomy identifiers.

Usage

```
orchids_ethnobotanical
```

Format

A data.frame with 419 rows and 3 columns:

taxon_name Scientific name of the species

taxon Wikidata QID (Q-identifier) for the species

taxon_id_ott Open Tree of Life taxonomy identifier

Details

Each row represents a species with documented ethnobotanical uses. The `taxon_id_ott` field enables integration with phylogenetic analyses via the Open Tree of Life API.

Source

Wikidata (<https://www.wikidata.org/>) and Open Tree of Life (<https://tree.opentreeoflife.org/>)

Examples

```
data(orchids_ethnobotanical)
head(orchids_ethnobotanical)
nrow(orchids_ethnobotanical)
```

trees_5141741f198446414395a45383e3a7ec
Cached Tree Result for Orchidaceae

Description

Precomputed tree cache generated by `get_trees_cached()` for the Orchidaceae pipeline. The .rda file contains a single object named `trees_5141741f198446414395a45383e3a7ec`.

Usage

`trees_5141741f198446414395a45383e3a7ec`

Format

An .rda file containing a list with:

taxa_not_in_tree A tidytable/data.frame of taxa that were not found in the tree

tree_taxa_full A phylo object for the full induced tree

tree_taxa_phyto A phylo object for the phytochemical subset tree

Source

Generated by `get_trees_cached()` from Open Tree of Life queries.

trees_886f2bbc1ee37e9433e35b78f5db91ef
Cached Tree Result for Orchidaceae

Description

Precomputed tree cache generated by `get_trees_cached()` for the Orchidaceae pipeline. The .rda file contains a single object named `trees_886f2bbc1ee37e9433e35b78f5db91ef`.

Usage

`trees_886f2bbc1ee37e9433e35b78f5db91ef`

Format

An .rda file containing a list with:

taxa_not_in_tree A tidytable/data.frame of taxa that were not found in the tree

tree_taxa_full A phylo object for the full induced tree

tree_taxa_phyto A phylo object for the phytochemical subset tree

Source

Generated by `get_trees_cached()` from Open Tree of Life queries.

trees_8cca7de252bc0994398aec413cebdbbc
Cached Tree Result for Orchidaceae

Description

Precomputed tree cache generated by `get_trees_cached()` for the Orchidaceae pipeline. The .rda file contains a single object named `trees_8cca7de252bc0994398aec413cebdbbc`.

Usage

`trees_8cca7de252bc0994398aec413cebdbbc`

Format

An .rda file containing a list with:

taxa_not_in_tree A tidytable/data.frame of taxa that were not found in the tree

tree_taxa_full A phylo object for the full induced tree

tree_taxa_phyto A phylo object for the phytochemical subset tree

Source

Generated by `get_trees_cached()` from Open Tree of Life queries.

trees_9a06c9c148110e62a4e1d2ff8094e462
Cached Tree Result for Orchidaceae

Description

Precomputed tree cache generated by `get_trees_cached()` for the Orchidaceae pipeline. The .rda file contains a single object named `trees_9a06c9c148110e62a4e1d2ff8094e462`.

Usage

`trees_9a06c9c148110e62a4e1d2ff8094e462`

Format

An .rda file containing a list with:

taxa_not_in_tree A tidytable/data.frame of taxa that were not found in the tree

tree_taxa_full A phylo object for the full induced tree

tree_taxa_phyto A phylo object for the phytochemical subset tree

Source

Generated by `get_trees_cached()` from Open Tree of Life queries.

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