Package 'redbookperu'

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Title Access and Analyze Data from the Red Book of Endemic Plants of Peru

Version 0.1.0

Description Provides access to and analysis of data from ``The Red Book of Endemic Plants of Peru" (León, B., Roque, J., Ulloa, C., Jorgensen, P.M., Pitman, N., Cano, A. 2006) <doi:10.15381/rpb.v13i2.1782>. This package offers comprehensive taxonomic, geographic, and conservation information about Peru's endemic plant species. It includes functions to verify species inclusion, obtain updated taxonomic details, and explore the dataset.

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Suggests testthat (>= 3.0.0), arrow, wcvpmatch

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LazyData true

LazyDataCompression xz

Encoding UTF-8

URL https://github.com/PaulESantos/redbookperu, https://paulesantos.github.io/redbookperu/

BugReports https://github.com/PaulESantos/redbookperu/issues

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Imports tibble

Maintainer Paul E. Santos Andrade <paulefrens@gmail.com>

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Author Paul E. Santos Andrade [aut, cre] (ORCID: <https://orcid.org/0000-0002-6635-0375>), Lucely L. Vilca Bustamante [aut] (ORCID: <https://orcid.org/0000-0002-5559-1296>)

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`check_redbooklist` *Check Species Names in the Red Book of Endemic Plants of Peru*

Description

This function checks a list of species names against the Red Book of Endemic Plants of Peru database and provides information about whether a species was recorded as endemic, and checks for misspelling typos (fuzzy match).

Usage

```
check_redbooklist(
  splist,
  dist = 0.02,
  output = c("status", "detailed"),
  quiet = FALSE
)
```

Arguments

`splist`	A character vector containing the species names to be checked.
`dist`	Maximum allowed distance for fuzzy matching of species names.
`output`	Output type. `"status"` returns the legacy character vector; `"detailed"` returns row-level matching diagnostics.
`quiet`	If `TRUE`, suppresses summary messages.

Details

This function checks each species name in the provided list against the Red Book of Endemic Plants of Peru database using fuzzy matching based on the specified maximum distance (`dist`). It provides information about the endemic status of each species and flags if the recorded name needs updating. It also counts the number of exact and fuzzy matches found.

Value

With `output = "status"`, a character vector indicating whether each input name is listed as endemic. With `output = "detailed"`, a tibble with row-level matching diagnostics.

References

Red Book of Endemic Plants of Peru The World Checklist of Vascular Plants, a continuously updated resource for exploring global plant diversity. Taxonomic Name Resolution Service - TNRS Plants of the World Online - Facilitated by the Royal Botanic Gardens - Kew.

Examples

```
# Example usage of the function
splist <- c("Aphelandra cuscoenses",
            "Piper stevensi",
            "Sanchezia ovata",
            "Verbesina andina",
            "Festuca dentiflora",
            "Eucrosia bicolor var. plowmanii",
            "Hydrocotyle bonplandii var. hirtipes",
            "Persea americana")

# Basic usage
check_redbooklist(splist = splist, dist = 0.2)

# Using base R with a data frame
plant_list <- data.frame(splist = splist)
plant_list$label <- check_redbooklist(plant_list$splist, dist = 0.2)
plant_list
```

---

get_redbook_data *Get Red Book Data for Given Species List*

Description

This function retrieves comprehensive information from the Red Book of Endemic Plants of Peru database for a provided list of species. It associates the provided species names with their corresponding updated taxonomic information and descriptions recorded in the original publication.

Usage

```
get_redbook_data(
  splist,
  dist = 0.1,
  unmatched = c("NA", "placeholder"),
  quiet = FALSE
)
```

Arguments

splist	A character vector containing the species names to be queried.
dist	Maximum allowed distance for fuzzy matching of species names.

`unmatched`	How unmatched or invalid rows are represented. `"NA"` uses missing values; `"placeholder"` uses the historical `"---"` placeholder.
`quiet`	If `TRUE`, suppresses summary messages.

Details

This function checks each species name in the provided list against the Red Book of Endemic Plants of Peru database using fuzzy matching based on the specified maximum distance (`dist`). For each species, it retrieves and combines taxonomic information (accepted name, accepted family, accepted name author) with additional descriptive data recorded in the original publication, such as IUCN conservation category, bibliographic reference, collector, herbariums, common name, departmental registrations, ecological regions, protected natural areas (SINANPE), Peruvian herbaria, and additional remarks.

Value

A tibble containing comprehensive information about the provided species, including updated taxonomic details and descriptions.

References

Red Book of Endemic Plants of Peru The World Checklist of Vascular Plants, a continuously updated resource for exploring global plant diversity. Taxonomic Name Resolution Service - TNRS Plants of the World Online - Facilitated by the Royal Botanic Gardens - Kew.

See Also

`check_redbooklist` function for a more focused check of species endemic status.

Examples

```
# Example illustrating how to use the get_redbook_data function
species_list <- c("Aphelandra cuscoensis", "Sanchezia ovata", "Piper stevensii")
redbook_data <- get_redbook_data(species_list)
head(redbook_data)
```

`match_redbook_names` *Match Submitted Names Against the Red Book of Endemic Plants of Peru*

Description

`match_redbook_names()` returns one row per submitted name with matching diagnostics, endemicity status, and taxonomic context from the bundled Red Book data.

Usage

```
match_redbook_names(
  splist,
  dist = 0.1,
  method = "osa",
  parser = c("wcvpmatch", "legacy"),
  allow_duplicates = TRUE,
  output = c("detailed", "summary")
)
```

Arguments

splist	A character vector of submitted taxon names.
dist	Maximum allowed edit distance for fuzzy matching. Values between 0 and 1 are interpreted as a fraction of the submitted name length.
method	Distance method. Currently only base R Levenshtein distance is used internally; the argument is reserved for compatibility with the planned wcvpmatch integration.
parser	Parser preference. "legacy" uses the bundled parser. "wcvpmatch" uses wcvpmatch::classify_spname when available and falls back to the legacy parser otherwise.
allow_duplicates	Logical. Kept for API compatibility; duplicated inputs are preserved in all cases.
output	Output detail level. "detailed" returns the full diagnostic table. "summary" returns a compact subset.

Value

A tibble with one row per input name.

Examples

```
# Accepted name, spelling error, absent name, and missing input.
submitted <- c("Sanchezia ovata", "Verbesina andinaa",
               "Persea americana", NA_character_)
matches <- match_redbook_names(submitted, dist = 0.2,
                               parser = "legacy", output = "summary")
matches[, c("name_submitted", "input_valid", "redbook_name",
            "endemic_status", "match_status", "match_distance")]

# Inspect the taxonomic context and how an accepted name was matched.
details <- match_redbook_names("Sanchezia ovata", parser = "legacy")
details[, c("name_submitted", "redbook_name", "accepted_name",
            "matched_via", "name_update_status")]
```

redbook_position — *List of the number positions of the first 3 letters of the species name in the redbook_tab*

Description

The 'redbook_position' reports the position (in term of number of rows) of the first three letters (triphthong) for the plant names stored in the variable 'accepted_name' of the table 'redbook_tab'. This indexing system speeds up of the search on the largest list using the package.

Usage

```
redbook_position
```

Format

A data frame with 978 observations on the following 3 variables:

position A character vector. The position of the first three letters of the species name in the `redbook_tab`.

triphthong A character vector. The first three letters of the species name in the `redbook_tab`.

genus A character vector. The corresponding genus name.

Details

Positions of Species Names in The Red Book of Endemic Plants of Peru

The `redbook_position` dataset provides the positions of the first three letters of each species name listed in the `redbook_tab`.

Examples

```
data("redbook_position")
head(redbook_position)
```

redbook_sps_class — *List of Species Names in redbook_sps_class Separated by Category*

Description

The `redbook_sps_class` dataset includes all species names separated by genus, epithet, author, subspecies, variety, and their position (ID) in the `redbook_tab`.

Usage

```
redbook_sps_class
```

Format

A data.frame with the following columns:

species A character vector. The full species name.

genus A character vector. The genus of the species.

epithet A character vector. The specific epithet of the species.

input_subspecies_epitheton A character vector. The infraspecific epithet of the species, if applicable.

rank A character vector. The taxonomic rank (e.g., "species", "subspecies", "variety").

subspecies A character vector. The subspecies name, if applicable.

variety A character vector. The variety name, if applicable.

hybrid A character vector. Indicates if the species is a hybrid.

id A character vector. The ID of the species in the `redbook_tab`.

Examples

```
data("redbook_sps_class")
head(redbook_sps_class)
```

`redbook_sp_data` *Database of the Red Book of Endemic Plants of Peru*

Description

This database contains comprehensive information regarding the endemic plant species listed in the Red Book of Endemic Plants of Peru. Each endemic taxon is accompanied by corresponding variables that detail its taxonomic status, IUCN conservation category, bibliographic references, type collection details, common names, departmental registrations, ecological regions, protected natural areas (SINANPE), and Peruvian herbaria where the specimens are deposited, as recorded in the original book.

Usage

```
redbook_sp_data
```

Format

A data frame with the following variables:

redbook_id Unique identifier for each species in the Red Book of Endemic Plants of Peru.

redbook_name Scientific name of the endemic species.

iucn Conservation category assigned according to IUCN.

publication Bibliographic reference where the taxon was originally described.

collector Name(s) of the collector(s) of the type specimen.

herbariums Acronyms of the institutions where the type specimens of the taxon are deposited.

common_name Common names of the species as mentioned in the literature.

dep_registry Abbreviations of the departments where the taxon has been recorded.

ecological_regions Abbreviations of the ecological regions proposed by Zamora (1996).

sinampe Abbreviation of the Protected Natural Area where the taxon was recorded.

peruvian_herbariums Acronyms of the Peruvian institutions where both type and non-type specimens are deposited.

remarks Observations and additional information about the endemic taxon.

Details

This database provides essential information for research and conservation efforts related to Peru's endemic flora, offering access to the data presented in the corresponding book.

References

León, Blanca, et.al. 2006. "The Red Book of Endemic Plants of Peru". Revista Peruana De Biología 13 (2): 9s-22s. https://revistasinvestigacion.unmsm.edu.pe/index.php/rpb/issue/view/153

Examples

```
# Example illustrating how to load and explore the database
data("redbook_sp_data")
head(redbook_sp_data)
```

`redbook_tab` *Species Names Listed in The Red Book of Endemic Plants of Peru*

Description

The `redbook_tab` contains records for all species listed in The Red Book of Endemic Plants of Peru.

Usage

```
redbook_tab
```

Format

A tibble with the following columns:

redbook_id The fixed species ID of the input taxon in The Red Book of Endemic Plants of Peru.

redbook_name A character vector. The species name as listed in The Red Book of Endemic Plants of Peru.

input_genus A character vector. The input genus of the corresponding species name listed.

input_epitheton A character vector. The specific epithet of the corresponding species name listed.

rank A character vector. The taxonomic rank (e.g., "species", "subspecies", "variety") of the corresponding species name listed.

input_subspecies_epitheton A character vector. The infraspecific epithet of the corresponding species name listed, if applicable.

accepted_name A character vector. The accepted plant taxa names according to the World Checklist of Vascular Plants (WCVP).

accepted_family A character vector. The corresponding family name of the accepted name.

accepted_name_author A character vector. The author of the accepted name.

accepted_name_rank A character vector. The rank of the accepted name (e.g., species, subspecies).

tag_subsp_wcvp A character vector. A tag indicating if the subspecies is recognized in the WCVP.

genus_ephitethon_wcvp A character vector. The genus part of the name according to the WCVP.

species_ephitethon_wcvp A character vector. The specific epithet part of the name according to the WCVP.

subspecies_ephitethon_wcvp A character vector. The infraspecific epithet part of the name according to the WCVP, if applicable.

wcvp_matched_name The taxon name matched in the WCVP backbone.

wcvp_matched_author The authors of the matched WCVP taxon.

wcvp_taxon_status The WCVP taxonomic status of the matched taxon.

wcvp_matched_plant_name_id The WCVP identifier of the matched taxon.

accepted_plant_name_id The WCVP identifier of the accepted taxon.

wcvp_is_accepted_name Whether the matched WCVP name is accepted.

wcvp_matched Whether WCVP returned a match.

taxonomy_source The source and reconciliation method used for the update.

taxonomy_updated_at UTC timestamp of the taxonomy update.

References

León, Blanca, et.al. 2006. “The Red Book of Endemic Plants of Peru”. Revista Peruana De Biología 13 (2): 9s-22s. https://doi.org/10.15381/rpb.v13i2.1782.

Examples

```
data("redbook_tab")
head(redbook_tab)
```

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