

Package: eidosapi (via r-universe)

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Type Package

Title Connect to the Taxonomic Services of the Spanish Inventory of Natural Patrimony and Biodiversity

Version 1.2.1

Description Provides access to 'EIDOS'
<<https://iepnb.gob.es/areas-tematicas/especies-silvestres/eidos>>,
the taxonomic information service from the Spanish Inventory of
Natural Patrimony and Biodiversity. This package includes a
suite of functions that help retrieve species' taxonomic and
conservation information from 'EIDOS' and match taxa names
against the checklists available in the database. More
information can be found at Miranda Cebrián, H. (2025)
<[doi:10.7818/ECOS.3134](https://doi.org/10.7818/ECOS.3134)>.

License GPL (>= 3)

Encoding UTF-8

Imports jsonlite, fuzzyjoin, http

URL <https://github.com/hmirceb/eidosapi>

BugReports <https://github.com/hmirceb/eidosapi/issues>

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eidos_clean_checklist	<i>Get the Spanish checklist with synonyms</i>
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Description

Get the Spanish checklist with synonyms

Usage

eidos_clean_checklist()

Value

A data frame with the Spanish checklist with synonyms in a long format ready to use in other functions in the *eidos_api* package.

Examples

eidos_clean_checklist()

eidos_conservation_by_id	<i>Get conservation information from EIDOS</i>
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Description

Get the conservation information from IEPNB (*Inventario Español del Patrimonio Natural y de la Biodiversidad*) for a given taxon using its unique identifier from the IEPNB database. Identifiers can be retrieved using the `eidos_fuzzy_names()` or `eidos_taxon_by_name()` functions. By default de API does not return taxonomic information. If needed, the function retrieves that information using `eidos_taxon_by_id()`.

Usage

```
eidos_conservation_by_id(taxon_id)
```

Arguments

taxon_id An integer. A unique taxon identifier from IEPNB

Value

A data frame with the conservation information of each taxa.

Examples

```
eidos_conservation_by_id(taxon_id = 1)
```

eidos_example_data	<i>Sample species data</i>
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Description

A sample of species data included in the Biotrend project

Usage

```
eidos_example_data
```

Format

eidos_example_data:

A data frame with 500 rows and 4 columns:

taxon Full taxon name

genus Genus

species Specific epithet

subspecies Subspecific epithet

Source

<https://biotrend.es/>

Description

Matches a data frame or vector with species names to any names in the Spanish checklist of Wildlife Species (*Lista Patrón de Especies Silvestres*). Uses fuzzy matching to allow spelling errors. In addition, you can filter by higher taxonomic levels to refine the match.

Usage

```
eidos_fuzzy_names(
  taxa_list,
  checklist = eidos_clean_checklist(),
  maxdist = 0.1,
  method = "jw",
  mode = "left",
  distance_col = "dist",
  kingdom = NULL,
  phylum = NULL,
  class = NULL,
  order = NULL,
  family = NULL
)
```

Arguments

taxa_list	A data frame or vector with taxonomic information to match with the Checklist. Must include at least the genus and species columns. Subspecies is optional. Additional taxonomic levels from kingdom to family can be supplied to filter any possible conflicts. These can be provided as columns with the corresponding name in the data frame or as function arguments if the supplied data was a vector of names. Taxonomic authorities are not supported yet.
checklist	A data frame. The result of running the <code>eidos_clean_checklist()</code> function.
maxdist	A number. Maximum dissimilarity distance between taxa names to match. Default for "jw" is 0.1 (10%)
method	A string. Method to calculate the distance between names inherited from <code>fuzzyjoin::stringdist_join</code> . One of "osa", "lv", "dl", "hamming", "lcs", "qgram", "cosine", "jaccard", "jw" or "soundex". Default is "jw".
mode	A string. Type of join, one of "inner", "left", "right", "full", "semi" or "anti" inherited from <code>fuzzyjoin::stringdist_join</code> .
distance_col	A string. Name of the column to display the dissimilarity distance between matched names. Set NULL to omit the column.
kingdom	A vector of strings of length = <code>taxa_list</code> with the kingdom of each supplied taxon.
phylum	A vector of strings of length = <code>taxa_list</code> with the phylum of each supplied taxon.

class	A vector of strings of length = taxa_list with the class of each supplied taxon.
order	A vector of strings of length = taxa_list with the order of each supplied taxon.
family	A vector of strings of length = taxa_list with the family of each supplied taxon.

Value

A data frame

Examples

```

checklist <- eidos_clean_checklist()
taxa_vector <- c("Bordere chouardii", "Alts cisternasii")
matched_names <- eidos_fuzzy_names(taxa_list = taxa_vector, checklist = checklist)

# Some names have conflicts when using fuzzy matching.
# This returns two matches for two different genera,
# Lanius (our species of interest, a bird) and Lasius (an ant).
taxa_df <- data.frame(genus = "Lanius", species = "meridionalis")
matched_names <- eidos_fuzzy_names(taxa_list = taxa_df, checklist = checklist)

# We can refine the search by including higher taxonomic levels:
taxa_df <- data.frame(class = "Aves", genus = "Lanius", species = "meridionalis")
refined_matched_names <- eidos_fuzzy_names(taxa_list = taxa_df, checklist = checklist)

# Or using a vector instead
taxa_vector <- c("Lanius meridionalis")
class_vector <- c("Aves")
refined_matched_names <- eidos_fuzzy_names(taxa_list = taxa_vector,
                                           checklist = checklist,
                                           class = class_vector)

```

eidos_legal_status_by_id

Get legal status from EIDOS

Description

Retrieves the legal status of a given taxon identifier from the EIDOS database. Identifiers can be retrieved using the eidos_fuzzy_names() or eidos_taxon_by_name() functions.

Usage

```
eidos_legal_status_by_id(taxon_id)
```

Arguments

taxon_id	An integer. A valid taxon identifier from EIDOS.
----------	--

Value

A data frame.

Examples

```
eidos_legal_status_by_id(taxon_id = 1)
```

eidos_tables	<i>Retrieve one of the tables related to the Spanish Checklist of Wildlife Species</i>
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Description

The tables are downloaded verbatim from the API. This means that column names may not match those in other tables from EIDOS. The exception are the Checklists. Due to limits in the download size of files from the API these are downloaded to the disk as xlsx files and then loaded to environment.

Usage

```
eidos_tables(
  eidos_table = c("comunidades_autonomas", "listapatronespecie",
    "listapatronespecie_sinonimos", "listapatronespecie_normas",
    "listapatronespecie_codigos", "componente_tema", "regbiogeograf_termar", "pais",
    "norma")
)
```

Arguments

eidos_table	Name of the table to query. The function is case insensitive, admits whitespaces and has partial matching for arguments, but these must match one of "comunidades_autonomas", "listapatronespecie_codigos", "listapatronespecie", "componente_tema", "regbiogeograf_termar", "listapatronespecie_sinonimos", "pais", "norma" or "listapatronespecie_normas".
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Value

A data.frame with the desired table from the EIDOS API

Examples

```
eidos_tables(eidos_table = "comunidades_autonomas")
```

eidos_taxon_by_id	<i>Get taxonomic information from EIDOS</i>
-------------------	---

Description

Retrieves the taxonomic information for a given taxon identifier from the EIDOS database. Identifiers can be retrieved using the `eidos_fuzzy_names()` or `eidos_taxon_by_name()` functions.

Usage

```
eidos_taxon_by_id(taxon_id)
```

Arguments

taxon_id	An integer or vector of integers. Valid taxon identifiers from EIDOS.
----------	---

Value

A data frame.

Examples

```
eidos_taxon_by_id(taxon_id = 1)
```

eidos_taxon_by_name	<i>Retrieve taxonomic information by name from EIDOS</i>
---------------------	--

Description

Connects to the EIDOS API and retrieves taxonomic information for the given taxa. Invalid names will return nothing. Note that if the supplied data is a vector, prior to querying the names the function removes all traces of "subsp.", "var." "f." and scientific authorships. Names have to be properly written, although the default API admits some common spelling errors like "i" instead of "ii" (e.g. *Borderea chouardi* instead of *chouardii*). For anything else use `eidos_fuzzy_names()`

Usage

```
eidos_taxon_by_name(taxa_list)
```

Arguments

taxa_list	A vector or data.frame with taxa names. The data frame needs at least 2 columns: "genus" and "species". Optional columns are "subspecies", "scientificnameauthorship."
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Value

A data.frame with the supplied data and the taxonomic information from EIDOS for any matching taxa

Examples

```
example_taxo <- data.frame(genus = "Alytes", species = "cisternasii", subspecies = NA)
eidos_taxon_by_name(taxa_list = example_taxo)
eidos_taxon_by_name(taxa_list = c("Alytes cisternasii", "Pinus nigra subsp. salzmannii"))
```

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