Package 'ritalic'

July 23, 2025

Title Interface to the ITALIC Database of Lichen Biodiversity

Version 0.11.0

Maintainer Matteo Conti <matt.ciao@gmail.com>

Description A programmatic interface to the Web Service methods provided by ITALIC (<https://italic.units.it>).
ITALIC is a database of lichen data in Italy and bordering European countries. 'ritalic' includes functions for retrieving information
about lichen scientific names, geographic distribution, ecological data, morpho-functional traits and identification keys.
More information about the data is available at <https://italic.units.it/?procedure=base&t=59&c=60>.
The API documentation is available at <https://italic.units.it/?procedure=api>.

License MIT + file LICENSE

Encoding UTF-8

RoxygenNote 7.3.2

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

URL https://github.com/plant-data/ritalic

BugReports https://github.com/plant-data/ritalic/issues

Depends R (>= 3.5.3)

Imports httr, jsonlite, utils, sf, ggplot2

NeedsCompilation no

Author Matteo Conti [aut, cre] (ORCID:
<https://orcid.org/0009-0003-4917-2639>),
Luana Francesconi [aut],
Alice Musina [aut],
Luca Di Nuzzo [aut],
Gabriele Gheza [aut],
Chiara Pistocchi [aut],
Juri Nascimbene [aut],
Pier Luigi Nimis [aut],
Stefano Martellos [aut]

Repository CRAN

Date/Publication 2025-03-30 21:40:02 UTC

Contents

`italic_checklist` *Get species names in the checklist of the lichens of Italy*

Description

Retrieves the complete list of accepted scientific names from the Checklist of the Lichens of Italy in ITALIC. The function returns all accepted names of species occurring in Italy. If the parameter include_bordering_countries is set to TRUE the function returns all the accepted names of species in ITALIC occurring both in Italy and in bordering countries.

Usage

```
italic_checklist(
  include_bordering_countries = FALSE,
  genus = NULL,
  family = NULL,
  order = NULL,
  class = NULL,
  phylum = NULL
)
```

Arguments

include_bordering_countries	Optional. Default FALSE. If TRUE the result includes also taxa occurring in bordering countries.
genus	Optional. A genus name to filter the checklist.
family	Optional. A family name to filter the checklist.
order	Optional. An order name to filter the checklist.
class	Optional. A class name to filter the checklist.
phylum	Optional. A phylum name to filter the checklist.

Value

A character vector containing all accepted scientific names from the checklist of ITALIC.

References

ITALIC - The Information System on Italian Lichens: checklist https://italic.units.it/index.php?procedure=checklist

Examples

```
## Not run:
# Get the complete checklist of Italy
italic_checklist()
# Get the complete checklist of Italy and bordering countries
italic_checklist(include_bordering_countries=TRUE)
# Get the checklist of the species of genus Lecanora
italic_checklist(genus ="Lecanora")

## End(Not run)
```

---

italic_description *Get descriptions of lichen taxa*

Description

Retrieves morphological descriptions and additional taxonomic or ecological notes about lichen taxa present in the Checklist of the Lichens of Italy. Only accepts names that exist in the database of ITALIC.

Usage

```
italic_description(sp_names)
```

Arguments

sp_names	Character vector of accepted names

Value

A data frame with columns:

scientific_name The scientific name provided as input

description Morphological description

notes Additional taxonomic or ecological information

Note

Before using this function with a list of names, first obtain their accepted names using `italic_match()`. Example workflow:

```
names_matched <- italic_match(your_names)
descriptions <- italic_description(names_matched$accepted_name)
```

Examples

```
## Not run:
italic_description("Cetraria islandica (L.) Ach. subsp. islandica")

## End(Not run)
```

---

italic_distribution_map

Create distribution map of a lichen taxon

Description

Creates a distribution map for a given lichen species based on its commonness/rarity status across Italian ecoregions and presence/absence across administrative regions. The map visually represents the data obtained from `italic_ecoregions_distribution()` and `italic_regions_distribution()`.

Usage

```
italic_distribution_map(sp_name, plot_map = TRUE)
```

Arguments

sp_name	Character string representing the accepted scientific name of a lichen species.
plot_map	If TRUE (default) the function returns a ggplot graph, if FALSE returns a sf object

Details

The function internally utilizes `italic_ecoregions_distribution()` and `italic_regions_distribution()` to retrieve the commonness/rarity status across Italian ecoregions and presence/absence across administrative regions data for the provided species. It then joins this data with a geospatial dataset of Italian regions and ecoregions (included in the package) to generate the map.

Commonness/rarity categories are visualized with a color scale, where each color corresponds to a different level of commonness/rarity ("extremely common", "very common", "common", "rather common", "rather rare", "rare", "very rare", "extremely rare", "absent").

Value

if plot_map = TRUE (default) a `ggplot` object representing the distribution map where Italian areas are colored according to the species' commonness/rarity. If plot_map = FALSE the sf object used to create the plot

Note

Before using this function, ensure that you have obtained the accepted name of the lichen using `italic_match()`. Example workflow:

```
name_matched <- italic_match("Cetraria islandica")
map <- italic_distribution_map(name_matched$accepted_name)
```

References

For more information about Italian ecoregions see ITALIC ecoregions distribution https://italic.units.it/?procedure=base&t=59&c=60#commonness and the scientific publication describing the ecoregions used in ITALIC https://www.mdpi.com/1424-2818/12/8/294

Examples

```
## Not run:
italic_distribution_map("Flavoparmelia caperata (L.) Hale")
italic_distribution_map("Anisomeridium biforme (Schaer.) R.C. Harris")

## End(Not run)
```

---

italic_ecology_traits *Get ecology data and morphological traits of lichen taxa*

Description

Retrieves morpho-functional traits, ecological indicators, altitudinal distribution, and poleotolerance data for lichen taxa. Only accepts names that exist in the database of ITALIC.

Usage

```
italic_ecology_traits(sp_names)
```

Arguments

sp_names	Character vector of accepted names

Value

A data frame with:

scientific_name The scientific name provided as input

substrata Substrate

photobiont Type of photosynthetic partner

growth_form Growth form

phytoclimatic_range Distribution in vegetation zones

special_requirements_for_water Water requirements

reproductive_strategy Main reproductive methods

ph_of_the_substrata_min Minimum pH value (1-5 scale)

ph_of_the_substrata_max Maximum pH value (1-5 scale)

solar_irradiation_min Minimum light requirements (1-5 scale)

solar_irradiation_max Maximum light tolerance (1-5 scale)

aridity_min Minimum aridity tolerance (1-5 scale)

aridity_max Maximum aridity tolerance (1-5 scale)

eutrophication_min Minimum nutrient requirements (1-5 scale)

eutrophication_max Maximum nutrient tolerance (1-5 scale)

altitudinal_distribution_min Minimum altitude zone (1-6 scale)

altitudinal_distribution_max Maximum altitude zone (1-6 scale)

poleotolerance_min Minimum poleotolerance level (1-5 scale)

poleotolerance_max Maximum poleotolerance level (1-5 scale)

Note

Before using this function with a list of names, first obtain their accepted names using `italic_match()`. Example workflow:

```
names_matched <- italic_match(your_names)
data <- italic_ecology_traits(names_matched$accepted_name)
```

References

ITALIC - The Information System on Italian Lichens: data about taxa https://italic.units.it/?procedure=base&t=59&c=60#otherdata

Examples

```
## Not run:
italic_ecology_traits("Cetraria islandica (L.) Ach. subsp. islandica")

## End(Not run)
```

`italic_ecoregions_distribution` *Get distribution of lichen taxa across Italian ecoregions*

Description

Returns the distribution and commonness status of lichen taxa across Italian ecoregions. Only accepts names that exist in the database of ITALIC.

Usage

```
italic_ecoregions_distribution(sp_names, result_data = "rarity")
```

Arguments

`sp_names`	Character vector of accepted names
`result_data`	Character string specifying the output format: "rarity" (default) returns commonness/rarity categories, "presence-absence" returns only values for presence/absence (0/1)

Value

A data frame with:

scientific_name The scientific name provided as input

alpine Status in alpine belt (extremely common to absent)

subalpine Status in subalpine belt (extremely common to absent)

oromediterranean Status in oromediterranean belt (extremely common to absent)

montane Status in montane belt (extremely common to absent)

dry_submediterranean Status in dry submediterranean belt (extremely common to absent)

padanian Status in padanian belt (extremely common to absent)

humid_submediterranean Status in humid submediterranean belt (extremely common to absent)

humid_mediterranean Status in humid mediterranean belt (extremely common to absent)

dry_mediterranean Status in dry mediterranean belt (extremely common to absent)

The possible values of commonness/rarity are: "extremely common", "very common", "common", "rather common", "rather rare", "rare", "very rare", "extremely rare", "absent"

Note

Before using this function with a list of names, first obtain their accepted names using `italic_match()`. Example workflow:

```
  names_matched <- italic_match(your_names)
ecoregions_distribution <- italic_ecoregions_distribution(names_matched$accepted_name)
```

References

For more information about Italian ecoregions see ITALIC ecoregions distribution https://italic.units.it/?procedure=base&t=59&c=60#commonness and the scientific publication describing the ecoregions https://www.mdpi.com/1424-2818/12/8/294

Examples

```
## Not run:
# Get commonness/rarity categories
italic_ecoregions_distribution("Cetraria ericetorum Opiz")

# Get presence/absence data
italic_ecoregions_distribution("Cetraria ericetorum Opiz", result_data="presence-absence")

## End(Not run)
```

`italic_identification_key` *Generate interactive identification keys for lichen taxa*

Description

Creates a URL link to a custom interactive dichotomous key for identifying the specified lichen taxa using the KeyMaker system of ITALIC. Only accepts names that exist in the database of ITALIC.

Usage

```
italic_identification_key(sp_names)
```

Arguments

`sp_names`	Character vector of accepted names

Value

Character string containing the URL to a web-based interactive identification key. The key is uniquely generated for the input taxa and allows step-by-step identification through dichotomous choices.

Note

Before using this function with a list of names, first obtain their accepted names using `italic_match()`. Example workflow:

```
names_matched <- italic_match(your_names)
key_url <- italic_identification_key(names_matched$accepted_name)
```

References

ITALIC - The KeyMaker https://italic.units.it/key-maker/

Examples

```
## Not run:
# Generate key for two species
italic_identification_key(c("Cetraria ericetorum Opiz","Xanthoria parietina (L.) Th. Fr."))

## End(Not run)
```

`italic_match` *Match scientific names of lichens against the database of ITALIC*

Description

Aligns scientific names of lichens against the Checklist of the Lichens of Italy available in ITALIC database. The function handles infraspecific ranks (subspecies, varieties, forms) and returns detailed matching information including nomenclatural status and matching scores.

Usage

```
italic_match(sp_names, subsp_marks = c(), var_marks = c(), form_marks = c())
```

Arguments

`sp_names`	A character vector of scientific names to match
`subsp_marks`	Character vector of markers used to indicate uncommon subspecies rank in the input names (different from "subsp.", "ssp."). For example, to match "Pseudevernia furfuracea b) ceratea", you need to pass "b)" as subsp_mark
`var_marks`	Character vector of markers used to indicate uncommon variety rank in the input names (different from "var.", "v."). For example, to match "Acarospora sulphurata varietas rubescens", you need to pass "varietas" as var_mark
`form_marks`	Character vector of markers used to indicate uncommon form rank in the input names (different from "f.", "form"). For example, to match "Verrucaria nigrescens fo. tectorum", you need to pass "fo." as form_mark

Value

A data frame with the following columns:

input_name Original scientific name provided

matched_name Name matched in ITALIC database

status Nomenclatural status ("accepted" or "synonym")

accepted_name Currently accepted name in ITALIC

name_score Matching score for the name part (0-100)

auth_score Matching score for the authority part (0-100)

Examples

```
## Not run:
# Simple name match
italic_match("Cetraria islandica")

# Name match where the name contains spelling mistakes
italic_match("Xantoria parietina")

# Match where the name contains uncommon marker
italic_match("Acarospora sulphurata varietas rubescens",
                      var_marks = "varietas")

# Match multiple names
italic_match(c("Cetraria islandica", "Xanthoria parietina"))

## End(Not run)
```

---

italic_name_usage *Get details of species names*

Description

Retrieves information for a scientific name used in ITALIC, including name id, taxonomic status, Index Fungorum id and related taxon id.

Usage

```
italic_name_usage(sp_names)
```

Arguments

sp_names	Character vector of matched names or accepted names

Value

A data frame with columns:

input_name The scientific name provided as input

scientific_name_id Unique identifier of ITALIC for the scientific name

index_fungorum_id Corresponding Index Fungorum identifier

scientific_name_full Complete scientific name including authority

scientific_name Scientific name without authority

authorship Author of the name

notes Additional notes about the taxon, if any

rank Taxonomic rank of the name

status Taxonomic status ('accepted', 'synonym' or 'basionym')

related_accepted_name_id ID of the currently accepted name related to the input name in ITALIC

related_accepted_name Full accepted name

related_taxon_id ID of the related taxon in ITALIC

Note

Before using this function with a list of names, first obtain their matched names or accepted names using `italic_match()`. Example workflow:

```
names_matched <- italic_match(your_names)
name_data <- italic_name_usage(names_matched$matched_name)
# or
accepted_name_data <- italic_name_usage(names_matched$accepted_name)
```

Examples

```
## Not run:
italic_name_usage(c("Cetraria islandica (L.) Ach. subsp. islandica", "Secoliga annexa Arnold"))

## End(Not run)
```

`italic_occurrences` *Get occurrence records for lichen taxa*

Description

Retrieves occurrence records from Italian herbarium collections for specified lichen taxa. Only accepts names that exist in the database of ITALIC.

Usage

```
italic_occurrences(sp_names, result_data = "simple")
```

Arguments

sp_names	Character vector of accepted names
result_data	Character string specifying output detail level: "simple" (default) or "extended"

Value

A data frame with occurrence records. Column names follow the Darwin Core standard, with the additional column substratum, which is particularly relevant for lichens. For simple output:

scientificName The scientific name provided as input

decimalLatitude Latitude in decimal degrees

decimalLongitude Longitude in decimal degrees

coordinatesUncertaintyInMeters Spatial uncertainty of the coordinates

substratum Substrate on which the specimen was found

institutionCode Code of the herbarium holding the specimen

eventDate Collection date

Extended output adds:

locality Collection locality

catalogNumber Specimen identifier in the collection

minimumElevationInMeters Lower limit of the elevation range

maximumElevationInMeters Upper limit of the elevation range

verbatimIdentification Scientific name reported on the original label

identifiedBy Person who identified the specimen

Note

Before using this function with a list of names, first obtain their accepted names using `italic_match()`. Example workflow:

```
names_matched <- italic_match(your_names)
occ <- italic_occurrences(names_matched$accepted_name)
```

References

ITALIC - The Information System on Italian Lichens https://italic.units.it

Examples

```
## Not run:
# Get simple occurrence data
italic_occurrences("Cetraria ericetorum Opiz")

# Get extended occurrence data
occ_ext <- italic_occurrences("Cetraria ericetorum Opiz", result_data = "extended")

# Then get citations for the retrieved occurrences
italic_occurrences_references(occ_ext)

## End(Not run)
```

---

italic_occurrences_references

Get scientific references for occurrence data

Description

Retrieves bibliographic references and DOIs for scientific publications describing occurrence datasets from specific herbarium collections.

Usage

```
italic_occurrences_references(occurrences_dataframe)
```

Arguments

`occurrences_dataframe`
: Data frame containing occurrence records, obtained from `italic_occurrences()`. Must include an 'institutionCode' column

Value

A data frame with two columns:

reference Full bibliographic citation of the publication

doi Digital Object Identifier URL

Examples

```
## Not run:
# Get occurrences first
occurrences <- italic_occurrences("Cetraria ericetorum Opiz")

# Then get associated references
italic_occurrences_references(occurrences)
```

```
## End(Not run)
```

`italic_regions_distribution` *Get distribution of lichen taxa in Italy*

Description

Retrieves presence/absence data (1/0) for lichen taxa across all the Italian administrative regions. Only accepts accepted names from the ITALIC database.

Only accepts names that exist in the database of ITALIC.

Usage

```
italic_regions_distribution(sp_names)
```

Arguments

`sp_names`	Character vector of accepted names from ITALIC database

Value

A data frame with columns:

scientific_name The scientific name provided as input
abruzzo Presence (1) or absence (0) in Abruzzo
basilicata Presence (1) or absence (0) in Basilicata
calabria Presence (1) or absence (0) in Calabria
campania Presence (1) or absence (0) in Campania
emilia_romagna Presence (1) or absence (0) in Emilia Romagna
friuli_venezia_giulia Presence (1) or absence (0) in Friuli Venezia-Giulia
lazio Presence (1) or absence (0) in Lazio
liguria Presence (1) or absence (0) in Liguria
lombardia Presence (1) or absence (0) in Lombardia
marche Presence (1) or absence (0) in Marche
molise Presence (1) or absence (0) in Molise
piemonte Presence (1) or absence (0) in Piemonte
puglia Presence (1) or absence (0) in Puglia
sardegna Presence (1) or absence (0) in Sardegna
sicilia Presence (1) or absence (0) in Sicilia
toscana Presence (1) or absence (0) in Toscana
trentino_alto_adige Presence (1) or absence (0) in Trentino Alto-Adige
umbria Presence (1) or absence (0) in Umbria
valle_d_aosta Presence (1) or absence (0) in Valle d'Aosta
veneto Presence (1) or absence (0) in Veneto

Note

Before using this function with a list of names, first obtain their accepted names using `italic_match()`. Example workflow:

```
names_matched <- italic_match(your_names)
distribution <- italic_regions_distribution(names_matched$accepted_name)
```

Examples

```
## Not run:
# First match names
matched <- italic_match("Cetraria islandica")
# Then get distribution in administrative regions
italic_regions_distribution(matched$accepted_name)

## End(Not run)
```

`italic_taxonomy` *Get taxonomic classification of lichen taxa*

Description

Retrieves the complete taxonomic classification of lichen taxa from the ITALIC database. Only accepts names that exist in the database of ITALIC.

Usage

```
italic_taxonomy(sp_names)
```

Arguments

`sp_names`	Character vector of accepted names

Value

A data frame with:

scientific_name The scientific name provided as input

phylum Phylum

class Class

order Order

family Family

genus Genus

Note

Before using this function with a list of names, first obtain their accepted names using `italic_match()`. Example workflow:

```
names_matched <- italic_match(your_names)
taxonomy <- italic_taxonomy(names_matched$accepted_name)
```

Examples

```
## Not run:
italic_taxonomy("Cetraria islandica (L.) Ach. subsp. islandica")

## End(Not run)
```

---

italic_taxon_data *Get data of lichen taxa*

Description

This function returns a dataframe containing taxonomy, ecology_traits, regions_distribution, ecoregions_distribution of the lichen species passed as input. For more info about these parameters see https://italic.units.it/?procedure=base&t=59&c=60#otherdata Only accepts names that exist in the database of ITALIC.

Usage

```
italic_taxon_data(sp_names)
```

Arguments

`sp_names`	A vector containing the scientific names of the lichen species.

Value

A dataframe containing the taxonomy, ecology distribution and rarity of the lichen species passed as input.

Note

Before using this function with a list of names, first obtain their accepted names using `italic_match()`. Example workflow:

```
names_matched <- italic_match(your_names)
italic_taxon_data(names_matched$accepted_name)
```

References

ITALIC - The Information System on Italian Lichens: data about taxa https://italic.units.it/?procedure=base&t=59&c=60#otherdata

Examples

```
## Not run:
italic_taxon_data(c("Cetraria ericetorum Opiz", "Lecanora salicicola H. Magn."))

## End(Not run)
```

---

italic_traits_pa *Get a presence-absence matrix of lichen traits*

Description

This function returns morphological traits of the lichen species passed as input. Only accepts names that exist in the database of ITALIC.

Usage

```
italic_traits_pa(sp_names)
```

Arguments

sp_names	A vector containing scientific names of lichens.

Value

A dataframe containing a series of traits for the lichen species passed as input.

Note

Before using this function with a list of names, first obtain their accepted names using `italic_match()`. Example workflow:

```
names_matched <- italic_match(your_names)
traits <- italic_taits_pa(names_matched$accepted_name)
```

Examples

```
## Not run:
italic_traits_pa("Cetraria ericetorum Opiz")

## End(Not run)
```

Index