Package 'ritalic'

October 13, 2026

Title Interface to the ITALIC Database of Lichen Biodiversity

Version 0.13.1

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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>.

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Encoding UTF-8

Suggests ellmer (>= 0.3.0), knitr, mcptools, rmarkdown, testthat (>= 3.0.0), webfakes

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 httr2 (>= 1.1.0), jsonlite, utils, sf, ggplot2

Config/roxygen2/version 8.1.1

NeedsCompilation no

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Repository CRAN

Date/Publication 2026-10-13 08:30:02 UTC

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`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. If multiple names are provided, a list is returned.
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 one name is provided: if plot_map = TRUE (default), a `ggplot` object; if plot_map = FALSE, the `sf` object used to create the plot. If multiple names are provided, a named list of `ggplot` or `sf` objects, one for each input name.

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 doi:10.3390/d12080294

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 doi:10.3390/d12080294

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_mcp_server *Run the ITALIC MCP server*

Description

Runs a local MCP server that lets AI assistants (Claude, Cursor, ...) work with ITALIC through the functions of ritalic: aligning names, retrieving the data of the taxa, searching taxa and creating identification keys. The tools are listed in `italic_mcp_tools()`.

The server communicates over stdin/stdout and is meant to be started by the MCP client, not in an interactive session. Requires the packages `mcptools` and `ellmer`.

Usage

```
italic_mcp_server(...)
```

Arguments

`...`	Further arguments passed to `mcptools::mcp_server()`.

Value

Does not return: it serves the tools until the client closes the connection.

Connecting an assistant

Claude Code:

```
claude mcp add ritalic -- Rscript -e "ritalic::italic_mcp_server()"
```

Claude Desktop, in `claude_desktop_config.json`:

```
{
  "mcpServers": {
    "ritalic": {
      "command": "Rscript",
      "args": ["-e", "ritalic::italic_mcp_server()"]
    }
  }
}
```

Use the full path of `Rscript` if it is not found (e.g. the output of `file.path(R.home("bin"), "Rscript")`).

See Also

`italic_mcp_tools()`

`italic_mcp_tools` *Tools of the ITALIC MCP server*

Description

Returns the functions of ritalic as tools for AI assistants, created with `ellmer::tool()`. They can be served to Claude, Positron or other MCP clients with `italic_mcp_server()`, or registered in an `ellmer` chat with `chat$register_tools(italic_mcp_tools())`.

The tools are:

italic_match Aligns scientific names to ITALIC, dropping the matches below a minimum score

italic_taxon_data Taxonomy, ecology and traits, distribution in regions and ecoregions, description and functional traits of the taxa, as a table

italic_search Searches the taxa by distribution, ecology, traits and taxonomy

italic_search_filters Lists the filters of the search and the meaning of their values

italic_identification_key Creates an interactive identification key with the KeyMaker

italic_checklist Lists the accepted names of the checklist

Each tool returns JSON text; errors are returned as `{"error": "..."}`.

Usage

```
italic_mcp_tools()
```

Value

A list of `ellmer` tool definitions.

See Also

`italic_mcp_server()`

Examples

```
## Not run:
# Use the tools in an ellmer chat
chat <- ellmer::chat_anthropic()
chat$register_tools(italic_mcp_tools())
chat$chat("Which saxicolous lichens with cyanobacteria grow in Sardegna?")

## 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_search` *Search lichen taxa by distribution, ecology, traits and taxonomy*

Description

Returns the taxa of ITALIC that satisfy a set of filters: administrative regions and ecoregions of Italy, commonness-rarity, substratum, photobiont, growth form, reproductive strategy, ecological indicators (pH, solar irradiation, aridity, eutrophication, poleotolerance, altitudinal distribution) and taxonomy. Different filters are combined with AND, multiple values of the same filter with OR.

Use `italic_search_filters()` to list the filters, their allowed values and what each value means.

Usage

```
italic_search(...)
```

Arguments

`...`	Filters as named arguments. Values are readable words (e.g. `substrata = "saxicolous"`), case-insensitive, with spaces and hyphens equivalent. The filters are:

List filters `region`, `ecoregion`, `substrata`, `photobiont`, `growth_form`, `reproductive_strategy`, `phytoclimatic_range`, `special_requirements_for_water`, `genus`, `family`, `order`, `class`, `phylum`: a character vector, the taxa matching any of the values are returned

Range filters `commonness`, `ph_of_the_substrata`, `solar_irradiation`, `aridity`, `eutrophication`, `poleotolerance`, `altitudinal_distribution`: pass `<filter>_min` and/or `<filter>_max` with a single value (for the ecological indicators also its number, e.g. `ph_of_the_substrata_min = 4`); the taxa whose range overlaps the requested one are returned

Logical filters `in_italy`, `coastal`, `parasitic`, `pioneer`, `metal_rich`, `lichenized`: `TRUE` returns only those taxa, `FALSE` excludes them

Value

A data frame with one row per taxon and columns:

taxon_id Identifier of the taxon in ITALIC

scientific_name Accepted name, that can be passed to the other functions of the package

family Family of the taxon

References

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

Examples

```
## Not run:
# Saxicolous lichens of Friuli Venezia Giulia with cyanobacteria
italic_search(region = "friuli-venezia-giulia",
              substrata = "saxicolous",
              photobiont = "cyanobacteria")

# Epiphytic species of slightly basic substrata in the alpine or subalpine ecoregions
italic_search(substrata = "epiphytic",
              ph_of_the_substrata_min = "slightly-basic",
              ecoregion = c("alpine", "subalpine"))

# Rare species of the family Teloschistaceae
italic_search(family = "Teloschistaceae", commonness_max = "rare")

# Then get the data of the taxa found
found <- italic_search(genus = "Peltigera", region = "sardegna")
italic_taxon_data(found$scientific_name)

## End(Not run)
```

---

italic_search_filters *List the filters of the taxa search*

Description

Lists the filters accepted by italic_search(), with their allowed values and the meaning of each value as explained on the ITALIC website.

Usage

```
italic_search_filters(filter = NULL)
```

Arguments

filter	Optional. Name of a filter (e.g. "substrata") or of one of its parameters (e.g. "ph_of_the_substrata_min"): only this filter is returned.

Value

A data frame with one row per allowed value of each filter, and columns:

filter Name of the filter

type `list` (one or more values), `range` (`_min` / `_max` parameters) or `boolean` (`TRUE` / `FALSE`)

parameters Arguments of `italic_search()` for this filter

value Allowed value (`NA` for boolean filters and for `genus`, whose values are too many to be listed)

number Numeric level of the value, accepted in place of the value by the ranges of the ecological indicators

label Meaning of the value

description Description of the filter

Examples

```
## Not run:
# All the filters
italic_search_filters()

# Values of the pH of the substrata
italic_search_filters("ph_of_the_substrata")

## 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 data frame with one row for each name in `sp_names` (in the same order) and the columns:

scientific_name The scientific name provided as input

phylum, class, order, family, genus Taxonomy, see `italic_taxonomy()`

substrata, ..., poleotolerance_max Ecology and traits, see `italic_ecology_traits()`

abruzzo, ..., veneto Presence (1) or absence (0) in the Italian administrative regions, see `italic_regions_distribution()`

alpine, ..., dry_mediterranean Commonness/rarity in the Italian ecoregions, see `italic_ecoregions_distribution()`

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)
```

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