

# Package ‘ritalic’

March 16, 2026

**Title** Interface to the ITALIC Database of Lichen Biodiversity

**Version** 0.12.0

**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** httr2 (>= 1.1.0), 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** 2026-03-16 09:20:02 UTC

## Contents

italic_checklist . . . . .	2
italic_description . . . . .	3
italic_distribution_map . . . . .	4
italic_ecology_traits . . . . .	5
italic_ecoregions_distribution . . . . .	7
italic_identification_key . . . . .	8
italic_match . . . . .	9
italic_name_usage . . . . .	10
italic_occurrences . . . . .	11
italic_occurrences_references . . . . .	13
italic_regions_distribution . . . . .	14
italic_taxonomy . . . . .	15
italic_taxon_data . . . . .	16
italic_traits_pa . . . . .	17

**Index** **18**

---

italic_checklist	<i>Get species names in the checklist of the lichens of Italy</i>
------------------	---

---

## 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](https://doi.org/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**

<code>sp_names</code>	Character vector of accepted names
<code>result_data</code>	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](https://doi.org/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\_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	<i>Get taxonomic classification of lichen taxa</i>
-----------------	--

---

**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	<i>Get a presence-absence matrix of lichen traits</i>
------------------	---

---

## 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

[italic\\_checklist](#), [2](#)  
[italic\\_description](#), [3](#)  
[italic\\_distribution\\_map](#), [4](#)  
[italic\\_ecology\\_traits](#), [5](#)  
[italic\\_ecoregions\\_distribution](#), [7](#)  
[italic\\_identification\\_key](#), [8](#)  
[italic\\_match](#), [9](#)  
[italic\\_name\\_usage](#), [10](#)  
[italic\\_occurrences](#), [11](#)  
[italic\\_occurrences\\_references](#), [13](#)  
[italic\\_regions\\_distribution](#), [14](#)  
[italic\\_taxon\\_data](#), [16](#)  
[italic\\_taxonomy](#), [15](#)  
[italic\\_traits\\_pa](#), [17](#)