

# Package ‘ritalic’

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

**Version** 0.10.1

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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>>.

**License** MIT + file LICENSE

**Encoding** UTF-8

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**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

**NeedsCompilation** no

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italic_checklist	<i>Get the list of 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 and in bordering countries

### Usage

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

### Arguments

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: National Checklist <https://italic.units.it/index.php?procedure=checklist>

## Examples

```
## Not run:  
# Get the complete checklist  
checklist <- italic_checklist()  
# Get the checklist of the species of genus Lecanora  
check_lecanora <- italic_checklist(genus = "Lecanora")  
  
## End(Not run)
```

---

italic\_description      *Get descriptions of lichen taxa*

---

## Description

Retrieves the morphological description 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** Scientific name

**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)`

**Examples**

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

## 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** Scientific name  
**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_names)`

### 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:
traits <- 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** Scientific name with authorities

**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)`

**References**

ITALIC - The Information System on Italian Lichens: ecoregions distribution <https://italic.units.it/?procedure=base&t=59&c=60#commonness>

**Examples**

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

# Get presence/absence data
edist <- italic_ecoregions_distribution("Cetraria ericetorum Opiz", "presence-absence")

## End(Not run)
```

---

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

---

**Description**

Creates 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 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_names)`

**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 lichen scientific names 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 matching
result <- italic_match("Cetraria islandica")

# Name matching with spelling mistakes
result <- italic_match("Xantoria parietina")
```



```
# Matching with uncommon marker
result <- italic_match("Acarospora sulphurata varietas rubescens",
                      var_marks = "varietas")

# Matching multiple names
result <- c("Cetraria islandica", "Xanthoria parietina")

## 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** Full scientific name  
**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
occ <- italic_occurrences("Cetraria ericetorum Opiz")

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

## 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, 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
occ <- italic_occurrences("Cetraria ericetorum Opiz")

# Then get associated references
refs <- italic_occurrences_references(occ)

## 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** Scientific name

**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_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 hierarchy for 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** Scientific name

**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_`

**Examples**

```
## Not run:
taxonomy <- 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 classification, description, ecology 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)` `descriptions <- italic_taxon_data(names_matched$accepted_`

**Examples**

```
italic_taxon_data(c("Cetraria ericetorum Opiz", "Lecanora cenisia Ach."))
```

---

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

---

**Description**

This function returns the functional 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 the ecology 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)` `descriptions <- italic_taits_pa(names_matched$accepted_`

**Examples**

```
italic_traits_pa("Cetraria ericetorum Opiz")
```

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