

Package ‘inatpick’

June 24, 2026

Title Download Photos and Metadata from 'iNaturalist'

Version 0.2.2

Description A lightweight interface to the 'iNaturalist' API (<<https://www.inaturalist.org/pages/api+reference>>) for downloading observation photos and exporting metadata to CSV. Supports filtering by taxon, place, user, and annotation. Note that downloaded photos retain their original licenses as set by 'iNaturalist' observers; users are responsible for respecting these licenses.

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Encoding UTF-8

Depends R (>= 4.1.0)

Imports httr, jsonlite, dplyr, tidyr, purrr, rlang, stats, utils

Suggests knitr, rmarkdown, testthat (>= 3.0.0), httpptest2

Config/testthat/edition 3

URL <https://github.com/andresarb/inatpick>,
<https://andresarb.github.io/inatpick/>

BugReports <https://github.com/andresarb/inatpick/issues>

VignetteBuilder knitr

Config/roxygen2/version 8.0.0

NeedsCompilation no

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Repository CRAN

Date/Publication 2026-06-24 08:20:02 UTC

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|-----------------|--|
| inat_annotatons | <i>iNaturalist annotation term and value IDs</i> |
|-----------------|--|

Description

A named lookup table for human-readable annotation labels and their corresponding iNaturalist term_id and term_value_id pairs, for use with [inat_fetch\(\)](#).

Usage

```
inat_annotatons
```

Format

A data frame with columns label, term_id, term_value_id.

Value

A data frame with 20 rows and 3 columns (label, term_id, term_value_id) listing all supported annotation labels and their corresponding iNaturalist API term and term-value IDs.

| | |
|---------------|--|
| inat_download | <i>Download photos from iNaturalist observations</i> |
|---------------|--|

Description

Downloads all photos from a data frame returned by [inat_fetch\(\)](#), and optionally saves observation metadata to a CSV file in the same folder.

Usage

```
inat_download(  
  obs,  
  out_dir,  
  size = "large",  
  metadata = TRUE,  
  overwrite = FALSE,  
  verbose = TRUE  
)
```

Arguments

| | |
|-----------|---|
| obs | Data frame returned by <code>inat_fetch()</code> . |
| out_dir | Character. Directory to save images and metadata. Created if it does not exist. There is no default: you must specify a path, e.g. a folder in your working directory or <code>tempdir()</code> for a temporary location. |
| size | Character. Photo size: "square" (75px), "small" (240px), "medium" (500px), "large" (1024px), or "original". Default "large". The size is appended to the filename (e.g. obs123_456_large.jpg). |
| metadata | Logical. If TRUE (default), automatically saves a metadata.csv file to out_dir alongside the downloaded photos. |
| overwrite | Logical. Re-download files that already exist (default FALSE). |
| verbose | Logical. Print progress messages (default TRUE). |

Value

Invisibly returns a data frame of photo URLs and local file paths.

Examples

```
## Not run:
obs <- inat_fetch(taxon_id = 488444, place_id = 6783,
                 user_login = "someuser")

# Download photos and save metadata.csv to the same folder
inat_download(obs, out_dir = file.path(tempdir(), "my_photos"))

# Download photos only, no metadata
inat_download(obs, out_dir = file.path(tempdir(), "my_photos"),
             metadata = FALSE)

## End(Not run)
```

inat_fetch

Fetch observations from the iNaturalist API

Description

Retrieves all observations matching the given filters, handling pagination automatically. Multiple annotations can be passed as a character vector; each is fetched separately and the results combined.

Usage

```
inat_fetch(
  taxon_id,
  place_id = NULL,
  user_login = NULL,
  annotation = NULL,
  quality_grade = "any",
  year = NULL,
  month = NULL,
  licensed = NULL,
  per_page = 200,
  verbose = TRUE
)
```

Arguments

| | |
|---------------|---|
| taxon_id | Integer. iNaturalist taxon ID (e.g. 488444 for <i>Caiophora chuquitensis</i>). |
| place_id | Integer or NULL. iNaturalist place ID (e.g. 6783 for Bolivia). |
| user_login | Character or NULL. iNaturalist username. |
| annotation | Character vector of annotation labels, or a single integer vector c(term_id, term_value_id), or NULL. Use labels from inat_annotatons (e.g. "flowers", "green_leaves", "alive"). Multiple labels can be passed as c("flowers", "green_leaves") — each is fetched separately and results are combined. See inat_annotatons for all valid labels. |
| quality_grade | Character. One of "research", "needs_id", or "any" (default). |
| year | Integer or NULL. Filter by observation year. |
| month | Integer (1–12) or NULL. Filter by observation month. |
| licensed | Logical or NULL. If TRUE, return only observations with a CC photo license. |
| per_page | Integer. Results per API page (max 200). |
| verbose | Logical. Print progress messages (default TRUE). |

Value

A data frame of observations with list-column photos.

See Also

[inat_annotatons](#) for all annotation labels and IDs.

Examples

```
## Not run:
# Single annotation
obs <- inat_fetch(taxon_id = 488444, place_id = 6783,
                 annotation = "flowers")
```

```
# Multiple annotations
obs <- inat_fetch(taxon_id = 51935, place_id = 6857,
                 annotation = c("flowers", "green_leaves"))

# See all available annotation labels
inat_annotatations

## End(Not run)
```

| | |
|---------------|---|
| inat_metadata | <i>Export observation metadata to CSV</i> |
|---------------|---|

Description

Extracts key fields from observations returned by `inat_fetch()` and writes them to a CSV file. Use path to save the CSV in the same folder as your downloaded photos.

Usage

```
inat_metadata(obs, path, extra_cols = NULL)
```

Arguments

| | |
|------------|---|
| obs | Data frame returned by <code>inat_fetch()</code> . |
| path | Character. Output CSV file path. There is no default: you must specify a path, e.g. a file in your working directory or <code>tempfile(fileext = ".csv")</code> for a temporary location. To save alongside downloaded photos, use <code>path = file.path(out_dir, "metadata.csv")</code> . |
| extra_cols | Character vector of additional column names from obs to include, if present. |

Value

Invisibly returns the metadata data frame.

Note

The `common_name` column reflects iNaturalist's `preferred_common_name`, which is typically in English but may vary depending on the taxon and iNaturalist's locale settings.

Examples

```
## Not run:
obs <- inat_fetch(taxon_id = 488444, place_id = 6783,
                 user_login = "someuser")

# Save photos and metadata to the same folder
inat_download(obs, out_dir = file.path(tempdir(), "my_photos"))
```

```
inat_metadata(obs, path = file.path(tempdir(), "my_photos", "metadata.csv"))  
## End(Not run)
```

inat_search_place *Search for a place by name on iNaturalist*

Description

Returns matching places from iNaturalist, useful for finding the place ID to pass to [inat_fetch\(\)](#).

Usage

```
inat_search_place(name, n = 10)
```

Arguments

name Character. Place name to search.
n Integer. Maximum number of results to return (default 10).

Value

A data frame with columns id, name, display_name, and place_type.

Examples

```
## Not run:  
inat_search_place("United Kingdom")  
inat_search_place("Bolivia")  
  
## End(Not run)
```

inat_search_taxon *Search for a taxon by name on iNaturalist*

Description

Returns matching taxa from iNaturalist, useful for finding the taxon ID to pass to [inat_fetch\(\)](#).

Usage

```
inat_search_taxon(name, rank = NULL, n = 10)
```

Arguments

| | |
|------|---|
| name | Character. Taxon name to search (common or scientific). |
| rank | Character or NULL. Filter results by taxonomic rank, e.g. "genus", "species", "family". Default NULL returns all ranks. |
| n | Integer. Maximum number of results to return (default 10). |

Value

A data frame with columns `id`, `name`, `common_name`, `rank`, and `observations_count`, ordered by number of observations.

Note

The `common_name` field reflects iNaturalist's `preferred_common_name`, which is typically in English but may vary depending on the taxon and iNaturalist's locale settings.

Examples

```
## Not run:  
inat_search_taxon("Drosera rotundifolia")  
inat_search_taxon("Drosera", rank = "genus")  
inat_search_taxon("sundew", rank = "species")  
  
## End(Not run)
```

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