

# Package: inatpick (via r-universe)

June 25, 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>](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.

**License** MIT + file LICENSE

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**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

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**Repository** <https://andresarb.r-universe.dev>

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inat_annotatons	<i>iNaturalist annotation term and value IDs</i>
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### 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.

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inat_download	<i>Download photos from iNaturalist observations</i>
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### 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 <a href="#">inat_fetch()</a> .
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 <code>c(term_id, term_value_id)</code> , or NULL. Use labels from <a href="#">inat_annotations</a> (e.g. "flowers", "green_leaves", "alive"). Multiple labels can be passed as <code>c("flowers", "green_leaves")</code> — each is fetched separately and results are combined. See <a href="#">inat_annotations</a> 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_annotatons

## End(Not run)
```

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inat_metadata	<i>Export observation metadata to CSV</i>
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**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 <a href="#">inat_fetch()</a> .
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)
```

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inat_search_place	<i>Search for a place by name on iNaturalist</i>
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## 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)
```

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inat_search_taxon	<i>Search for a taxon by name on iNaturalist</i>
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### 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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