

# Package ‘iucnr’

November 6, 2024

**Title** IUCN Red List Data

**Version** 0.0.0.1

**Description** Facilitates access to the International Union for Conservation of Nature (IUCN) Red List of Threatened Species, a comprehensive global inventory of species at risk of extinction. This package streamlines the process of determining conservation status by matching species names with Red List data, providing tools to easily query and retrieve conservation statuses. Designed to support biodiversity research and conservation planning, this package relies on data from the 'iucnrdata' package, available on GitHub <<https://github.com/PaulESantos/iucnrdata>>. To install the data package, use `pak::pak('PaulESantos/iucnrdata')`.

**License** MIT + file LICENSE

**Config/testthat/edition** 3

**Encoding** UTF-8

**RoxygenNote** 7.3.2

**URL** <https://github.com/PaulESantos/iucnr>,  
<https://paulesantos.github.io/iucnr/>

**BugReports** <https://github.com/PaulESantos/iucnr/issues>

**Depends** R (>= 2.10)

**Imports** cli, dplyr, stringr

**Suggests** rlang, testthat (>= 3.0.0), iucnrdata

**NeedsCompilation** no

**Author** Paul Efren Santos Andrade [aut, cre]  
(<<https://orcid.org/0000-0002-6635-0375>>)

**Maintainer** Paul Efren Santos Andrade <[paulefrens@gmail.com](mailto:paulefrens@gmail.com)>

**Repository** CRAN

**Date/Publication** 2024-11-06 16:10:05 UTC

## Contents

<code>get_common_name</code> . . . . .	2
<code>get_conservation_status</code> . . . . .	3

---

get_common_name	<i>Retrieve Vernacular Names for a Given Species</i>
-----------------	--

---

## Description

This function retrieves vernacular (common) names for a given species using IUCN data. It filters vernacular names based on matching `internal_taxon_id` and merges them with species metadata.

## Usage

```
get_common_name(splist)
```

## Arguments

`splist` A character vector containing the scientific names of species for which vernacular names are to be retrieved.

## Details

The function retrieves IUCN data for the input species, extracts the corresponding `core_id`, filters the vernacular name dataset using the `core_id`, and concatenates all unique vernacular names for each species.

## Value

A `data.table` or `data.frame` with columns:

**submitted\_name** The scientific name of the species as submitted.

**vernacular\_names** A character string that contains the concatenated vernacular names for each species, separated by " - ".

## Examples

```
species <- c("Panthera uncia", "Cedrela odorata")
result <- get_common_name(splist = species)
print(result)
```

---

`get_conservation_status`*Get Conservation Status of Species*

---

**Description**

This function retrieves the conservation status of species from the `iucn_data` dataset. It is vectorized to handle multiple species names and optimized using `data.table` for performance.

**Usage**

```
get_conservation_status(splist)
```

**Arguments**

`splist` A character vector of species names to search for in the `iucn_data` dataset.

**Value**

A `data.table` with species names and their corresponding conservation status or "no match found".

**Examples**

```
species <- c("Panthera uncia", "Cedrela odorata")
result <- get_conservation_status(splist = species)
print(result)
```

# Index

`get_common_name`, [2](#)  
`get_conservation_status`, [3](#)