Package ‘avesperu’

July 22, 2025

Title Access to the List of Birds Species of Peru

Version 0.0.6

Description Allows access to the data found in the species list featured in the renowned 'List of the Birds of Peru' Plenge, M. A. (2023) <https://sites.google.com/site/boletinunop/checklist>. This publication stands as one of Peru's most comprehensive reviews of bird diversity. The dataset incorporates detailed species accounts and has been meticulously structured for effortless utilization within the R environment.

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Suggests testthat (>= 3.0.0), xml2

Config/testthat/edition 3

Encoding UTF-8

RoxygenNote 7.3.2

URL https://github.com/PaulESantos/avesperu, https://paulesantos.github.io/avesperu/

BugReports https://github.com/PaulESantos/avesperu/issues

Depends R (>= 3.5)

LazyData true

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NeedsCompilation no

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Repository CRAN

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`aves_peru_2025_v3` *aves_peru_2025_v3*

Description

The `aves_peru_2025_v3` dataset provides an updated tibble of bird species recorded in Peru, based on the most recent taxonomic revisions by the South American Checklist Committee (SACC).

Usage

```
aves_peru_2025_v3
```

Format

A tibble with 1,914 rows and 6 columns:

order_name Taxonomic order to which the bird species belongs.

family_name Taxonomic family to which the bird species belongs.

scientific_name Scientific name of the bird species.

english_name English common name of the bird species.

spanish_name Spanish common name of the bird species.

status Category indicating the species' status, based on the following codes:

- `X`: Resident species.
- `E`: Endemic species. A species is considered endemic to Peru until a record outside its borders is published.
- `NB`: Non-breeding (migratory) species. Species that occur regularly in Peru but only during their non-breeding period.
- `V`: Vagrant species. Species that occasionally occur in Peru but are not part of the usual avifauna.
- `IN`: Introduced species. Species introduced to Peru by humans (or have colonized from introduced populations elsewhere) and have established self-sustaining breeding populations.
- `H`: Hypothetical species. Records based only on observations, specimens of dubious origin, or unpublished photographs or recordings kept in private hands.
- `EX`: Extinct or extirpated species. Species that have gone extinct or have been extirpated from Peru.

Details

This version reflects dramatic taxonomic changes and category updates based on published articles, photographs, and sound recordings archived in accredited institutions. It also includes a classification criterion following the SACC guidelines. Species without a specific code are considered resident species, equivalent to the "X" category of the SACC.

- **Total species**: 1,912
- **Distribution by status**:
  - `X`: 1,545 species
  - `E`: 119 species
  - `NB`: 139 species
  - `V`: 85 species
  - `IN`: 3 species
  - `EX`: 0 species
  - `H`: 23 species

These updates reflect the SACC's continuous evaluation process, which now recognizes several former subspecies as full species.

Author(s)

Data compilation: Manuel A. Plenge Package implementation: Paul Efren Santos Andrade

References

Plenge, M. A. Version (23-06-2025) List of the birds of Peru / Lista de las aves del Perú. Unión de Ornitólogos del Perú: `https://sites.google.com/site/boletinunop/checklist`

See Also

For more information about the data, visit: `https://sites.google.com/site/boletinunop/checklist`

Examples

```
# Load the dataset
data("aves_peru_2025_v3")
```

`search_avesperu` *Search for Bird Species Data in the Birds of Peru Dataset*

Description

This function searches for bird species information in the dataset provided by the `avesperu` package, given a list of species names. It supports approximate (fuzzy) matching to handle typographical errors or minor variations in the species names. The function returns detailed information for each species, including taxonomic data, common names, and status.

Usage

```
search_avesperu(splist, max_distance = 0.1)
```

Arguments

`splist`	A character vector containing the names of bird species to search for. Names can include minor variations or typos.
`max_distance`	Numeric. The maximum allowable distance for fuzzy matching, which can either be a proportion (0 < max_distance < 1) or an integer representing the maximum number of allowed differences. Defaults to 0.1.

Details

The function performs the following steps:

1. Validates the input, ensuring that `splist` is a character vector or a factor.
2. Standardizes species names and identifies duplicate entries in the list.
3. For each unique species name, it searches for matches in the dataset using approximate string matching (`agrep`), with a customizable `max_distance`.
4. Retrieves the taxonomic and common name data for the closest matching species.

If no matches are found for a species, the corresponding row in the output will contain `NA` values.

Value

A data frame with the following columns:

name_submitted The species name provided as input.

accepted_name The closest matching species name from the dataset, or `NA` if no match is found.

order_name The taxonomic order of the species.

family_name The taxonomic family of the species.

english_name The common name of the species in English.

spanish_name The common name of the species in Spanish.

status The conservation or other status of the species.

dist The computed distance between the submitted name and the matched name.

Examples

```
# Example: Search for bird species in the dataset
splist <- c("Falco sparverius", "Tinamus osgodi", "Crypturellus soui",
            "Thraupis palmarum", "Thamnophilus praecox")
search_avesperu(splist)
```

`show_progress` *Determine whether to show progress bar Return logical TRUE/FALSE depending on options and interactive session*

Description

Determine whether to show progress bar Return logical TRUE/FALSE depending on options and interactive session

Usage

```
show_progress()
```

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