

# Package ‘mtsta’

May 9, 2026

**Title** Accessing the Red List of Montane Tree Species of the Tropical Andes

**Version** 0.0.0.1

**Description** Access the 'Red List of Montane Tree Species of the Tropical Andes' Tejedor Garavito et al.(2014, ISBN:978-1-905164-60-8). This package allows users to search for globally threatened tree species within the andean montane forests, including cloud forests and seasonal (wet) forests above 1500 m a.s.l.

**License** MIT + file LICENSE

**Suggests** dplyr, forcats, ggplot2, janitor, knitr, rmarkdown, stringr, testthat, tibble, tidyr

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**Encoding** UTF-8

**LazyData** true

**LazyDataCompression** xz

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**URL** <https://github.com/PaulESantos/mtsta>

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

**VignetteBuilder** knitr

**Depends** R (>= 2.10)

**NeedsCompilation** no

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**Repository** CRAN

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mtsta_distribution	<i>mtsta_distribution: Distribution Data for Species in mtsta_tab</i>
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## Description

This dataset contains distribution data for species included in A Regional Red List of Montane Tree Species of the Tropical Andes - 2014. It provides information on the current accepted names, distribution range, and taxonomic status for each species. The data is original distribution data and the updated distribution information for the included species.

## Usage

```
mtsta_distribution
```

## Format

A tibble

**accepted\_name** Character vector with the current accepted name of the species.

**distribution** Character vector indicating the distribution range of the species.

**distribution\_wcvp** Character vector indicating the distribution according to the World Checklist of Vascular Plants (**WCVP**).

**taxonomic\_status** Character vector indicating the taxonomic status of the species of the submitted name (e.g., "Accepted").

## Details

The dataset contains information on the distribution of species in A Regional Red List of Montane Tree Species of the Tropical Andes - 2014. The distribution data includes the geographical range of each species, including countries where the species can be found.

## Examples

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

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`mtsta_tab`*Montane Tree Species of the Tropical Andes - Base Data*

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### Description

This is the curated base data of montane tree species found in the Tropical Andes region. The data is stored as a tibble with 132 rows and 11 columns. Each row represents a species and contains information such as the species name, accepted name, accepted family, accepted genus, IUCN status, distribution, elevation range, assessor, description, and taxonomic status.

### Usage

```
mtsta_tab
```

### Format

A tibble with 132 rows and 11 columns.

### Details

The columns in the base data tibble are as follows:

- `species_name`: The scientific name of the species.
- `accepted_name`: The currently accepted name for the species.
- `accepted_family`: The family to which the species belongs.
- `accepted_genus`: The genus to which the species belongs.
- `taxonomic_status`: The taxonomic status of the species.
- `iucn`: The conservation status of the species according to the IUCN Red List Categories.
- `distribution`: The distribution range of the species.
- `unsure_distribution`: Information about the uncertainty in the distribution data.
- `elevation`: The elevation range where the species is found.
- `assessor`: The person or group responsible for assessing the species.
- `description`: Additional information or description of the species.

The base species list used in the `mtsta` package has been carefully reviewed and validated with the assistance of the Taxonomic Name Resolution Service (TNRS). By utilizing the TNRS, the base species list in the `mtsta` package guarantees accuracy and consistency in the representation of species names, enhancing the reliability of the package's functionalities.

### Source

The data for this package was obtained from [A Regional Red List of Montane Tree Species of the Tropical Andes - 2014](#).

**See Also**

Use `search_mtsta()` function to search and match species names using this base data.

**Examples**

```
data("mtsta_tab")
```

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search_mtsta	<i>Search for Matching Species Names in the Red List of Montane Tree Species of the Tropical Andes</i>
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**Description**

This function searches for matching species names in the Red List of Montane Tree Species of the Tropical Andes (`mtsta` package) based on a provided list of species names. The function performs approximate matching using the Levenshtein distance algorithm to find similar names within a specified maximum distance.

**Usage**

```
search_mtsta(splist, max_distance = 0.1, ...)
```

**Arguments**

splist	A character vector containing the species names to be matched.
max_distance	The distance used is a generalized Levenshtein distance that indicates the total number of insertions, deletions, and substitutions allowed to match the two names. It can be expressed as an integer or as the fraction of the binomial name. A value between 0 and 1 will be treated as a percentage of the string length. A value greater than 1 will be treated as an absolute number of allowed changes. For example, a name with length 10, and a <code>max_distance = 0.1</code> , allow only one change (insertion, deletion, or substitution). A <code>max_distance = 2</code> , allows two changes.
...	Additional arguments (currently unused).

**Value**

A data frame with the following columns:

- `name_submitted`: The submitted species names.
- `name_matched`: The matched species names from the `mtsta` data.
- `accepted_name`: The accepted scientific name of the matched species.
- `accepted_family`: The accepted family name of the matched species.
- `accepted_genus`: The accepted genus name of the matched species.

- `taxonomic_status`: The taxonomic status of the matched species.
- `iucn`: The conservation status of the matched species according to the IUCN Red List Categories.
- `distribution`: The distribution range of the matched species.
- `unsure_distribution`: Information about the uncertainty in the distribution data.
- `elevation`: The elevation range where the species is found.
- `assessor`: The person or group responsible for assessing the species.
- `description`: Additional information or description of the species.
- `distance`: The Levenshtein distance between the submitted name and the matched name.

If no match is found, the `name_matched` column will contain "null", and the other columns will be empty.

### See Also

`mtsta::mtsta_tab`

### Examples

```
# Assuming you have the mtsta package loaded with the necessary data
search_result <- search_mtsta(c("Aphelandra acantasa",
                               "Saurauia lehmani",
                               "Saurauia bullosaa",
                               "Schinus meyerii",
                               "Ilex colombiana",
                               "Ilex rimbachii",
                               "Ilex scopulorum"),
                             max_distance = 0.1)
```

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`search_mtsta_distribution`

*Search Species Distribution of A Regional Red List of Montane Tree Species of the Tropical Andes*

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### Description

This function searches the Montane Tree Species of the Tropical Andes distribution database for a list of submitted species names and returns their distribution information. The search allows for approximate string matching within a given maximum distance.

### Usage

```
search_mtsta_distribution(splist, max_distance = 0.1, typedf = "main")
```

**Arguments**

splist	Character vector of submitted plant species names for which distribution data is to be searched.
max_distance	Numeric value representing the maximum allowed distance for approximate string matching. The default value is 0.1.
typedf	"main" return a selected columns in from mtsta_distribution "full" return all data

**Details**

The function uses approximate string matching with a maximum distance specified by the `max_distance` argument. It searches the `mtsta` distribution database for submitted species names that match the provided names within the given distance. The function then retrieves distribution information, including the accepted name, distribution region, unsure distribution (if available), distribution from the World Check-list of Vascular Plants (WCVP), taxonomic status, and the Levenshtein distance between submitted and matched species names.

**Value**

A data frame with the following columns:

**name\_submitted** Character vector with the submitted species names.

**name\_matched** Character vector with the matched species names in the database.

**accepted\_name** Character vector with the accepted names of the matched species.

**distribution** Character vector with the distribution of the matched species.

**unsure\_distribution** Character vector with information about unsure distribution (if available).

**distribution\_wcvp** Character vector with the distribution from the World Check-list of Vascular Plants (WCVP) database for the matched species.

**taxonomic\_status** Character vector indicating the taxonomic status of the matched species.

**distance** Numeric vector with the Levenshtein distance between submitted and matched species names.

**See Also**

[mtsta\\_distribution](#)

**Examples**

```
# Example usage of search_mtsta_distribution function
species_list <- c("Escallonia mirtilloides", "Ilex rimbachii", "Saurauia lehmannii")
distribution_data <- search_mtsta_distribution(species_list, max_distance = 0.2)
print(distribution_data)
```

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