

Package ‘AntClassify’

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Type Package

Title Functional Guilds, Invasion Status, Endemism, and Rarity of Ants

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Description Provides functions for the analysis of ant communities, aiming to standardize workflows in myrmecology. The package automates the assignment of species to functional guilds based on trophic strategies, feeding habits, and foraging behavior, using established classification frameworks (Silva et al., 2015 <[doi:10.7476/9788574554419](https://doi.org/10.7476/9788574554419)>; Silvestre et al., 2003 <[isbn:9588151236](https://doi.org/10.1007/978-1-4020-0123-6)>; Delabie et al., 2000 <https://www.researchgate.net/publication/44961742_Sampling_Ground-Dwelling_Ants_Case_Studies_from_the_World%27s_Rain_Forests>), and also includes a novel classification system implemented within the package, developed from ant species occurring in urban environments. It also includes routines to flag exotic species of Brazil (Vieira, 2025, unpublished master's thesis), identify endemic species (Silva et al., 2025 <[doi:10.37885/250920259](https://doi.org/10.37885/250920259)>), and classify species rarity and rarity forms of the Atlantic Forest (Silva et al., 2024 <[doi:10.1016/j.biocon.2024.110640](https://doi.org/10.1016/j.biocon.2024.110640)>). The package reduces manual effort and improves reproducibility, supporting research and biodiversity management of Neotropical ant communities.

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URL <https://github.com/cogdebora/AntClassify>

BugReports <https://github.com/cogdebora/AntClassify/issues>

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Suggests knitr, rmarkdown, testthat (>= 3.0.0)

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antclassify	<i>AntClassify Full Ecological Pipeline</i>
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Description

Runs all ecological classification functions of the package.

Usage

```
antclassify(comm, verbose = TRUE, plot = TRUE, validate = TRUE, delay = 0.5)
```

Arguments

comm	Community matrix (samples x species). Species names as columns, samples as rows.
verbose	Logical; if TRUE, displays progress messages.
plot	Logical; if TRUE, displays guild proportion plots (passed to assign_guild_ants).
validate	Logical; if TRUE, validates species names using GBIF.
delay	Numeric; seconds between API calls (if validate = TRUE).

Value

A list containing results from all analyses (guilds, exotic, endemic, rarity).

Examples

```
## Not run:
# Load the built-in example dataset
data(ant_community)

# Run the full pipeline (validation disabled for speed)
results <- antclassify(ant_community, validate = FALSE, plot = FALSE)

# Inspect the results
names(results)
head(results$guilds$table)
results$exotic$table
results$endemic$table
results$rarity$table

## End(Not run)
```

antclassify_community *Classify Ant Communities Across Multiple Sites*

Description

Applies the AntClassify pipeline to each site (row) of a community matrix and returns aggregated guild abundance and richness matrices.

Usage

```
antclassify_community(comm, guild_col = "antclassify_guild", ...)
```

Arguments

comm	A community matrix with sites as rows and species as columns. Species names must match the nomenclature used in the internal databases.
guild_col	Character string giving the name of the guild column to use for aggregation. Must be one of "antclassify_guild", "silva_guild", "delabie_guild", or "silvestre_guild". Default is "antclassify_guild".
...	Additional arguments passed to assign_guild_ants (for example, validate, delay). Note that plot is always set to FALSE inside this function to avoid displaying one plot per site.

Value

A list with three components:

- by_site A list of length equal to nrow(comm). Each element contains the full output of `assign_guild_ants` for the corresponding site.
- guild_abundance A matrix of guild abundances (sites × guilds).
- guild_richness A numeric vector of length nrow(comm) giving the number of distinct guilds found at each site.

Examples

```
# Small community matrix with two sites and six species
comm <- matrix(c(5, 0, 2, 0, 1, 3,
                2, 4, 0, 2, 0, 0),
              nrow = 2, byrow = TRUE,
              dimnames = list(c("Site1", "Site2"),
                              c("Atta sexdens", "Camponotus atriceps",
                                "Pheidole megacephala", "Wasmannia auropunctata",
                                "Solenopsis saevissima", "Nylanderia fulva")))

# Run the classification (validate = FALSE to avoid GBIF calls in examples)
results <- antclassify_community(comm, guild_col = "antclassify_guild",
                                validate = FALSE)

results$guild_abundance
results$guild_richness
```

ant_community	<i>Ant community example</i>
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Description

A sample community matrix of ant species abundances with 3 sites and 6 species. Rows represent sites, columns represent species.

Usage

```
data(ant_community)
```

Format

A data frame with 3 rows and 6 columns:

Atta sexdens abundance of *Atta sexdens*

Camponotus atriceps abundance of *Camponotus atriceps*

Pheidole megacephala abundance of *Pheidole megacephala*

Wasmannia auropunctata abundance of *Wasmannia auropunctata*

Solenopsis saevissima abundance of *Solenopsis saevissima*

Nylanderia fulva abundance of *Nylanderia fulva*

Source

Simulated data for package examples.

Examples

```
data(ant_community)
head(ant_community)
```

assign_guild_ants	<i>Assign Functional Guilds for Ants</i>
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Description

Classifies ants into functional guilds using four different ecological databases.

Usage

```
assign_guild_ants(  
  comm,  
  verbose = TRUE,  
  plot = TRUE,  
  validate = TRUE,  
  delay = 0.5  
)
```

Arguments

comm	A community matrix where species are columns and samples are rows.
verbose	Logical; if TRUE, displays progress messages.
plot	Logical; if TRUE, displays guild proportion plots.
validate	Logical; if TRUE, validates species names using GBIF before analysis.
delay	Numeric; seconds to wait between GBIF API calls when validate = TRUE.

Value

Invisibly returns a list with two elements:

table	A data frame containing species, abundance, percentage, and guild assignments from each system.
plots	A list of four ggplot2 objects, one for each guild classification system.

`check_endemic_atlantic_ants`*Identify Endemic Ant Species (Atlantic Forest)*

Description

Checks a community matrix for ant species endemic to the Brazilian Atlantic Forest based on Silva et al. (2025).

Usage

```
check_endemic_atlantic_ants(  
  comm,  
  verbose = TRUE,  
  plot = TRUE,  
  plot_type = c("status", "species"),  
  validate = TRUE,  
  delay = 0.5  
)
```

Arguments

<code>comm</code>	A community matrix where species are columns and samples are rows.
<code>verbose</code>	Logical; if TRUE, displays progress messages.
<code>plot</code>	Logical; if TRUE, displays a plot (type controlled by <code>plot_type</code>).
<code>plot_type</code>	Character; type of plot to display. "status" (default) shows a bar plot comparing endemic vs. other species abundance proportions. "species" shows a bar plot of individual endemic species abundances as a proportion of the total community.
<code>validate</code>	Logical; if TRUE, validates species names using GBIF before analysis.
<code>delay</code>	Numeric; seconds to wait between GBIF API calls when <code>validate = TRUE</code> .

Value

Invisibly returns a list with two elements:

<code>table</code>	A data frame containing endemic species detected, with columns species, abundance, and percentage.
<code>plot</code>	A ggplot2 object.

check_exotic_ants	<i>Identify Exotic Ant Species (Brazil)</i>
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Description

Checks a community matrix for known exotic ant species in Brazil sourced from Vieira (2025).

Usage

```
check_exotic_ants(  
  comm,  
  verbose = TRUE,  
  plot = TRUE,  
  plot_type = c("status", "species"),  
  validate = TRUE,  
  delay = 0.5  
)
```

Arguments

comm	A community matrix where species are columns and samples are rows.
verbose	Logical; if TRUE, displays progress messages.
plot	Logical; if TRUE, displays a plot (type controlled by plot_type).
plot_type	Character; type of plot to display. "status" (default) shows a bar plot comparing exotic vs. native abundance proportions. "species" shows a bar plot of individual exotic species abundances as a proportion of the total community.
validate	Logical; if TRUE, validates species names using GBIF before analysis.
delay	Numeric; seconds to wait between GBIF API calls when validate = TRUE.

Value

Invisibly returns a list with two elements:

table	A data frame containing exotic species detected, with columns species, abundance, and percentage.
plot	A ggplot2 object.

`check_rarity_atlantic_ants`*Identify Ant Rarity Forms (Atlantic Forest)*

Description

Checks a community matrix for ant rarity forms in the Brazilian Atlantic Forest based on Silva et al. (2024).

Usage

```
check_rarity_atlantic_ants(  
  comm,  
  verbose = TRUE,  
  plot = TRUE,  
  plot_type = c("status", "species"),  
  validate = TRUE,  
  delay = 0.5  
)
```

Arguments

<code>comm</code>	A community matrix where species are columns and samples are rows.
<code>verbose</code>	Logical; if TRUE, displays progress messages.
<code>plot</code>	Logical; if TRUE, displays a plot (type controlled by <code>plot_type</code>).
<code>plot_type</code>	Character; type of plot to display. "status" (default) shows a bar plot of rarity form abundance proportions. "species" shows a bar plot of individual rare species abundances as a proportion of the total community, colored by rarity form.
<code>validate</code>	Logical; if TRUE, validates species names using GBIF before analysis.
<code>delay</code>	Numeric; seconds to wait between GBIF API calls when <code>validate = TRUE</code> .

Value

Invisibly returns a list with two elements:

<code>table</code>	A data frame containing rare species detected, with columns <code>species</code> , <code>rarity_form</code> , <code>abundance</code> , and <code>percentage</code> .
<code>plot</code>	A <code>ggplot2</code> object.

`validate_species_names`*Validate Species Names Using GBIF API*

Description

Checks species names against the GBIF taxonomic backbone. If an exact match is found, the accepted name (or canonical name) is used. If no exact match is found, the original name is kept and a warning is issued, indicating that the name may be outdated or misspelled.

Usage

```
validate_species_names(comm, verbose = TRUE, delay = 0.5)
```

Arguments

<code>comm</code>	A community matrix (rows = sites, columns = species).
<code>verbose</code>	Logical; if TRUE, displays progress messages.
<code>delay</code>	Numeric; seconds to wait between API calls (default 0.5).

Value

A community matrix with updated column names (accepted names when available).

Examples

```
## Not run:  
data(ant_community)  
comm_validated <- validate_species_names(ant_community, verbose = TRUE)  
  
## End(Not run)
```

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