

Package: impIndicator (via r-universe)

February 20, 2025

Title Impact Indicators of Alien Taxa

Version 0.0.1

Description Compute impact indicators of alien taxa using GBIF occurrence cube and EICAT assessment of alien species.
Aggregates species impact of various scores due to mecahnism.
Aggregates site impact of various scores due to species.

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BugReports <https://github.com/b-cubed-eu/impIndicator/issues>

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Imports assertthat, b3gbi (>= 0.2.2), cli, dplyr, ggplot2, magrittr, rgbif, rnaturalearth, sf, stats, tibble, tidyr

Remotes b-cubed-eu/b3gbi

Depends R (>= 2.10)

LazyData true

Suggests knitr, rmarkdown, rnaturalearthdata, testthat (>= 3.0.0)

Config/testthat/edition 3

Encoding UTF-8

URL <https://b-cubed-eu.github.io/impIndicator/>

VignetteBuilder knitr

Config/pak/sysreqs libgdal-dev gdal-bin libgeos-dev libicu-dev libxml2-dev libssl-dev libproj-dev libsqlite3-dev libudunits2-dev libx11-dev

Repository <https://b-cubed-eu.r-universe.dev>

RemoteUrl <https://github.com/b-cubed-eu/impIndicator>

RemoteRef HEAD

RemoteSha 5d0fd3c56981c6005dd54fe2f73bf69e1ad11f2e

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eicat_acacia	<i>EICAT data of acacia taxa An example of EICAT data containing species name, impact category and mechanism.</i>
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Description

EICAT data of acacia taxa An example of EICAT data containing species name, impact category and mechanism.

Usage

```
eicat_acacia
```

Format

A dataframe object containing 138 observations and 3 variables

scientific_name species scientific name
impact_category EICAT impact category
impact_mechanism mechanism of impact

Source

Jansen, C., Kumschick, S. A global impact assessment of Acacia species introduced to South Africa. Biol Invasions 24, 175–187 (2022). <https://doi.org/10.1007/s10530-021-02642-0>

See Also

Other Data: [southAfrica_sf](#), [taxa_Acacia](#)

Examples

```
head(eicat_acacia,10)
```

impact_cat	<i>Compute impact categories</i>
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Description

Aggregate species impact categories from impact data.

Usage

```
impact_cat(
  impact_data,
  species_list,
  trans = 1,
  col_category = NULL,
  col_species = NULL,
  col_mechanism = NULL
)
```

Arguments

impact_data	The dataframe of species impact which contains columns of impact_category, scientific_name and impact_mechanism.
species_list	The vector of species' list to aggregate their impact categories
trans	Numeric. The type of transformation to convert the EICAT categories to numerical values. 1 converts ("MC", "MN", "MO", "MR", "MV") to (0,1,2,3,4) 2 converts ("MC", "MN", "MO", "MR", "MV") to (1,2,3,4,5) and 3 converts ("MC", "MN", "MO", "MR", "MV") to (1,10,100,1000,10000)
col_category	The name of the column containing the impact categories. The first two letters each categories must be an EICAT short names (e.g "MC -Minimal concern")
col_species	The name of the column containing species names
col_mechanism	The name of the column containing mechanisms of impact

Value

The dataframe containing the aggregated species impact. max - maximum impact of a species. mean - mean impact of a species. max_mech - sum of maximum impact per categories of a species

See Also

Other Prepare data: [taxa_cube\(\)](#)

Examples

```
# define species list
species_list <- c(
  "Acacia adunca",
  "Acacia baileyana",
  "Acacia binervata",
  "Acacia crassiuscula",
  "Acacia cultriformis",
  "Acacia cyclops",
  "Acacia dealbata",
  "Acacia decurrens",
  "Acacia elata"
)

agg_impact <- impact_cat(
  impact_data = eicat_acacia,
  species_list = species_list,
  trans = 1
)
```

impact_indicator	<i>Impact indicator</i>
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Description

Compute impact indicators of alien taxa

Usage

```
impact_indicator(
  cube,
  impact_data = NULL,
  method = NULL,
  trans = 1,
  col_category = NULL,
  col_species = NULL,
  col_mechanism = NULL
)
```

Arguments

cube	The data cube of class <code>sim_cube</code> or <code>processed_cube</code> from <code>b3gbi::process_cube()</code>
impact_data	The dataframe of species impact which contains columns of <code>impact_category</code> , <code>scientific_name</code> and <code>impact_mechanism</code>
method	The method of computing the indicator. The method used in the aggregation of within and across species in a site. The method can be precautionary, precautionary cumulative, mean, mean cumulative or cumulative.

trans	Numeric. The method of transformation to convert the EICAT categories to numerical values. 1 converts ("MC", "MN", "MO", "MR", "MV") to (0,1,2,3,4) 2 converts ("MC", "MN", "MO", "MR", "MV") to (1,2,3,4,5) and 3 converts ("MC", "MN", "MO", "MR", "MV") to (1,10,100,1000,10000)
col_category	The name of the column containing the impact categories. The first two letters of each categories must be an EICAT short names (e.g "MC - Minimal concern")
col_species	The name of the column containing species names
col_mechanism	The name of the column containing mechanisms of impact

Value

A dataframe of the invasive alien impact trend (class `impact_indicator`)

See Also

Other Indicator function: [site_impact\(\)](#), [species_impact\(\)](#)

Examples

```
acacia_cube <- taxa_cube(
  taxa = taxa_Acacia,
  region = southAfrica_sf,
  res = 0.25,
  first_year = 2010
)
impact_value <- impact_indicator(
  cube = acacia_cube,
  impact_data = eicat_acacia,
  method = "mean cumulative",
  trans = 1
)
```

plot.impact_indicator *Plot impact indicator*

Description

Produces a ggplot object to show the trend of the impact.

Usage

```
## S3 method for class 'impact_indicator'
plot(
  x,
  linewidth = 2,
  colour = "red",
  title_lab = "Impact indicator",
  y_lab = "impact score",
```

```

    text_size = 14,
    ...
  )

```

Arguments

<code>x</code>	A dataframe of impact indicator. Must be a class of "impact_indicator"
<code>linewidth</code>	The width size of the line. Default is 2
<code>colour</code>	The colour of the line Default is "red"
<code>title_lab</code>	Title of the plot. Default is "Impact indicator"
<code>y_lab</code>	Label of the y-axis. Default is "impact score"
<code>text_size</code>	The size of the text of the plot. Default is "14"
<code>...</code>	Additional arguments passed to <code>geom_line</code>

Value

The ggplot object of the impact indicator, with the y- and x-axes representing the impact score and time respectively.

See Also

Other Plot: [plot.site_impact\(\)](#), [plot.species_impact\(\)](#)

Examples

```

# create data_cube
acacia_cube <- taxa_cube(
  taxa = taxa_Acacia,
  region = southAfrica_sf,
  res = 0.25,
  first_year = 2010
)

# compute impact indicator
impact_value <- impact_indicator(
  cube = acacia_cube,
  impact_data = eicat_acacia,
  method = "mean cumulative",
  trans = 1
)

# plot impact indicator
plot(impact_value)

```

plot.site_impact	<i>Plot site impact</i>
------------------	-------------------------

Description

Produces the yearly impact map of a region

Usage

```
## S3 method for class 'site_impact'  
plot(  
  x,  
  region = NULL,  
  first_year = NULL,  
  last_year = NULL,  
  title_lab = "Impact map",  
  text_size = 14,  
  ...  
)
```

Arguments

x	A dataframe of impact indicator. Must be a class of "site_impact"
region	sf or character. The shapefile of the region of study or a character which represent the name of a country. It is not compulsory but makes the plot more comprehensible.
first_year	The first year the impact map should include. Default starts from the first year included in x.
last_year	The last year the impact map should include. Default ends in the last year included in x.
title_lab	Title of the plot. Default is "Impact map"
text_size	The size of the text of the plot. Default is "14"
...	Additional arguments passed to geom_tile

Value

The ggplot of species yearly impact on the region.

See Also

Other Plot: [plot.impact_indicator\(\)](#), [plot.species_impact\(\)](#)

Examples

```

# define cube for taxa
acacia_cube <- taxa_cube(
  taxa = taxa_Acacia,
  region = southAfrica_sf,
  res = 0.25,
  first_year = 2010
)

# compute site impact
siteImpact <- site_impact(
  cube = acacia_cube,
  impact_data = eicat_acacia,
  method = "precautionary cumulative",
  trans = 1
)

# visualise site impact
plot(x=siteImpact,
     region= southAfrica_sf,
     first_year = 2021)

```

plot.species_impact *Plot species impact*

Description

Produces a ggplot to show the trend of the species impact.

Usage

```

## S3 method for class 'species_impact'
plot(
  x,
  alien_species = "all",
  linewidth = 1.5,
  title_lab = "Species impact",
  y_lab = "impact score",
  text_size = 14,
  ...
)

```

Arguments

x A dataframe of impact indicator. Must be a class of "species_impact"

alien_species The character vector containing names of the alien species to be included in the plot. Default is "all" which plot all species in the data frame

linewidth	The width size of the line. Default is 1.5
title_lab	Title of the plot. Default is "Species impact"
y_lab	Label of the y-axis. Default is "impact score"
text_size	The size of the text of the plot. Default is "14"
...	Additional arguments passed to geom_line

Value

The ggplot object of the species impact, with the y- and x-axes representing the impact score and time respectively.

See Also

Other Plot: [plot.impact_indicator\(\)](#), [plot.site_impact\(\)](#)

Examples

```
# create data cube
acacia_cube <- taxa_cube(
  taxa = taxa_Acacia,
  region = southAfrica_sf,
  res = 0.25,
  first_year = 2010
)

# compute species impact
speciesImpact <- species_impact(
  cube = acacia_cube,
  impact_data = eicat_acacia,
  method = "mean",
  trans = 1
)

# visualise species impact
plot(speciesImpact)
```

site_impact

Compute site impact indicator

Description

Compute site impact indicator

Usage

```
site_impact(
  cube,
  impact_data = NULL,
  method = NULL,
  trans = 1,
  col_category = NULL,
  col_species = NULL,
  col_mechanism = NULL
)
```

Arguments

cube	The data cube of class <code>sim_cube</code> or <code>processed_cube</code> from <code>b3gbi::process_cube()</code>
impact_data	The dataframe of species impact which contains columns of <code>impact_category</code> , <code>scientific_name</code> and <code>impact_mechanism</code>
method	The method of computing the indicator. The method used in the aggregation of within and across species in a site. The method can be precautionary, precautionary cumulative, mean, mean cumulative or cumulative.
trans	Numeric. The method of transformation to convert the EICAT categories to numerical values. 1 converts ("MC", "MN", "MO", "MR", "MV") to (0,1,2,3,4) 2 converts ("MC", "MN", "MO", "MR", "MV") to (1,2,3,4,5) and 3 converts ("MC", "MN", "MO", "MR", "MV") to (1,10,100,1000,10000)
col_category	The name of the column containing the impact categories. The first two letters each categories must be an EICAT short names (e.g "MC - Minimal concern")
col_species	The name of the column containing species names
col_mechanism	The name of the column containing mechanisms of impact

Value

The dataframe of impact indicator per sites (class `site_impact`)

See Also

Other Indicator function: [impact_indicator\(\)](#), [species_impact\(\)](#)

Examples

```
# define cube for taxa
acacia_cube <- taxa_cube(
  taxa = taxa_Acacia,
  region = southAfrica_sf,
  res = 0.25,
  first_year = 2010
)

siteImpact <- site_impact(
  cube = acacia_cube,
```

```

    impact_data = eicat_acacia,
    method = "precautionary cumulative",
    trans = 1
  )

```

southAfrica_sf	<i>South African sf An example of region sf for impact indicator.</i>
----------------	---

Description

South African sf An example of region sf for impact indicator.

Usage

```
southAfrica_sf
```

Format

A 'sf' object of South African map

geometry geometry of polygon

See Also

Other Data: [eicat_acacia](#), [taxa_Acacia](#)

Examples

```
sf::plot_sf(southAfrica_sf)
```

species_impact	<i>Compute species impact indicator</i>
----------------	---

Description

Compute species impact indicator

Usage

```

species_impact(
  cube,
  impact_data = NULL,
  method = NULL,
  trans = 1,
  col_category = NULL,
  col_species = NULL,
  col_mechanism = NULL
)

```

Arguments

cube	The data cube of class <code>sim_cube</code> or <code>processed_cube</code> from <code>b3gbi::process_cube()</code>
impact_data	The dataframe of species impact which contains columns of <code>impact_category</code> , <code>scientific_name</code> and <code>impact_mechanism</code>
method	The method of computing the indicator. The method used in the aggregation of within impact of species. The method can be "max", "mean" or "max_mech".
trans	Numeric. The method of transformation to convert the EICAT categories to numerical values. 1 converts ("MC", "MN", "MO", "MR", "MV") to (0,1,2,3,4) 2 converts ("MC", "MN", "MO", "MR", "MV") to (1,2,3,4,5) and 3 converts ("MC", "MN", "MO", "MR", "MV") to (1,10,100,1000,10000)
col_category	The name of the column containing the impact categories. The first two letters each categories must be an EICAT short names (e.g "MC - Minimal concern")
col_species	The name of the column containing species names
col_mechanism	The name of the column containing mechanisms of impact

Value

A dataframe of impact indicator per species (class `species_impact`)

See Also

Other Indicator function: `impact_indicator()`, `site_impact()`

Examples

```
acacia_cube <- taxa_cube(
  taxa = taxa_Acacia,
  region = southAfrica_sf,
  res = 0.25,
  first_year = 2010
)

speciesImpact <- species_impact(
  cube = acacia_cube,
  impact_data = eicat_acacia,
  method = "mean",
  trans = 1
)
```

taxa_Acacia

GBIF occurrences data of acacia in South Africa An example of occurrence data from GBIF containing required column for impact indicator.

Description

GBIF occurrences data of acacia in South Africa An example of occurrence data from GBIF containing required column for impact indicator.

Usage

```
taxa_Acacia
```

Format

A dataframe object containing 19,100 rows and 6 variables

decimalLatitude geographic latitude in decimal

decimalLongitude geographic longitude in decimal

species scientific name of species

speciesKey GBIF species identification number

coordinateUncertaintyInMeters radius of the uncertainty circle around geographic point

year year occurrence was recorded

Source

<https://doi.org/10.15468/dl.b6gda5>

See Also

Other Data: [eicat_acacia](#), [southAfrica_sf](#)

Examples

```
head(taxa_Acacia,10)
```

taxa_cube

Prepare Data Cubes

Description

Prepare data cube to calculate species impact . The function taxa_cube can take in the scientific name of the taxa of interest as in character or GBIF occurrences data containing necessary columns. The GBIF occurrences is downloaded if scientific names is given.

Usage

```
taxa_cube(
  taxa,
  region,
  limit = 500,
  country = NULL,
  res = 0.25,
  first_year = NULL,
  last_year = NULL
)
```

Arguments

taxa	Character or dataframe. The character should be the scientific name of the focal taxa while the dataframe is the GBIF occurrences data which must contain "decimalLatitude", "decimalLongitude", "species", "speciesKey", "coordinateUncertaintyInMeters", "dateIdentified", and "year".
region	sf or character. The shapefile of the region of study or a character which represent the name of a country
limit	Number of records to return from GBIF download. Default is set to 500
country	Two-letter country code (ISO-3166-1) of Country for which the GBIP occurrences data should be downloaded.
res	The resolution of grid cells to be used. Default is 0.25
first_year	The year from which the occurrence should start from
last_year	The year at which the occurrence should end

Value

A data cube of `sim_cubes`

See Also

Other Prepare data: [impact_cat\(\)](#)

Examples

```
acacia_cube <- taxa_cube(
  taxa = taxa_Acacia,
  region = southAfrica_sf,
  first_year = 2010
)
```

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