Package 'bdvis'

January 27, 2015

Type Package

Title Biodiversity Data Visualizations

Version 0.1.0

Date 2014-05-06

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Description Biodiversity data visualizations using R would be helpful to
understand completeness of biodiversity inventory, extent of geographical,
taxonomic and temporal coverage, gaps and biases in data.

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Imports maps, plotrix, sqldf, plyr, taxize, treemap, ggplot2, grid

Suggests rinat

NeedsCompilation no

Repository CRAN

Date/Publication 2014-05-07 07:57:17

R topics documented:

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bdcomplete	*bdcomplete - Computes completeness values for each cell currently returns Chao2*

Description

bdcomplete - Computes completeness values for each cell currently returns Chao2

Usage

```
bdcomplete(indf, recs = 50)
```

Arguments

indf	- Input data frame containing biodiversity data set
recs	- Minimum number of records per grid cell (Default is 50, if the number is too low, might give error)

Value

data.frame with the columns

- "Cell_id"id of the cell
- "Sobs"Number of Observed species
- "Sest"Estimated number of species
- "c"Completeness ratio the cell

Examples

```
## Not run:
bdcomplete(inat)

## End(Not run)
```

---

bdsummary	*bdsummary - description*

Description

bdsummary - description

Usage

```
bdsummary(indf)
```

Arguments

`indf`	input data frame containing biodiversity data set

Examples

```
## Not run:
require(rinat)
inat<-get_inat_obs_project("reptileindia")
bdsummary(inat)

## End(Not run)
```

---

chronohorogram	*chronohorogram - Draws a chronohorogram of records*

Description

chronohorogram - Draws a chronohorogram of records

Usage

```
chronohorogram(indf = NA, title = NA, startyear = 0, endyear = 0,
  colors = c("red", "blue"))
```

Arguments

`indf`	- Input data frame containing biodiversity data set
`title`	- Title of the plot
`startyear`	- Starting year for the plot
`endyear`	- End year for the graph
`colors`	- Colors to build color ramp

References

Arino, A. H., & Otegui, J. (2008). Sampling biodiversity sampling. In Proceedings of TDWG (pp. 77-78). Retrieved from http://www.tdwg.org/fileadmin/2008conference/documents/Proceedings2008.pdf#page=77

Examples

```
## Not run:
chronohorogram(inat)

## End(Not run)
```

---

fixstr   *fixstr - Fix structure of the data frame to match the key fields to GBIF*
                                         style data fireld names

---

Description

fixstr - Fix structure of the data frame to match the key fields to GBIF style data fireld names

Usage

```
fixstr(indf, Latitude = NA, Longitude = NA, DateCollected = NA,
  datefmt = NA, SciName = NA)
```

Arguments

indf	input data frame containing biodiversity data set
Latitude	name of Latitude field in original data frame
Longitude	name of Longitude field in original data frame
DateCollected	name of Date Collected field in original data frame
datefmt	format string for the original date field strptime
SciName	name of Scientific Name field in original data frame

Examples

```
## Not run:
inat = fixstr(inat, DateCollected = "Date.collected", datefmt = "%Y-%m-%d %H:%M:%S")

## End(Not run)
```

---

getcellid   *getcellid - Assigns GBIF style degree Cell ids and Centi degree (0.1)*
                                         cell ids for each record.

Description

getcellid - Assigns GBIF style degree Cell ids and Centi degree (0.1) cell ids for each record.

Usage

```
getcellid(indf)
```

Arguments

indf	input data frame containing biodiversity data set

Examples

```
## Not run:
getcellid(inat)

## End(Not run)
```

---

gettaxo	*gettaxo - Get higher taxonomy fields data*

Description

gettaxo - Get higher taxonomy fields data

Usage

```
gettaxo(indf)
```

Arguments

indf   input data frame containing biodiversity data set

Value

indf with added / updated columns

- "kingdom"Kingdom of the Scientific name
- "phylum"Phylum of the Scientific name
- "order"Order of the Scientific name
- "family"Family of the Scientific name
- "genus"Genus of the Scientific name

Examples

```
## Not run:
inat=gettaxo(inat)

## End(Not run)
```

---

mapgrid   *mapgrid - Maps the data points on the map in grid format*

Description

mapgrid - Maps the data points on the map in grid format

Usage

```
mapgrid(indf = NA, ptype = "records", bbox = NA, title = "",
    mapdatabase = "world", region = ".", customize = NULL)
```

Arguments

indf	- input data frame containing biodiversity data set
ptype	- type of map on the grid valid values are presence, records, species
title	- title for the map
bbox	- Bounding box for the map in format c(xmin,xmax,ymin,ymax)
mapdatabase	- database to be used default world
region	- specify region(s) to map i.e. countries default . for whole world
customize	- customization string

Examples

```
## Not run:
mapgrid(inat,ptype="records")

## End(Not run)
```

---

taxotree   *taxotree - Draws a treemap based on Taxonomic hierarchy of records*

Description

taxotree - Draws a treemap based on Taxonomic hierarchy of records

Usage

```
taxotree(indf)
```

Arguments

indf	input data frame containing biodiversity data set

References

Otegui, J., Arino, A. H., Encinas, M. A., & Pando, F. (2013). Assessing the Primary Data Hosted by the Spanish Node of the Global Biodiversity Information Facility (GBIF). PLoS ONE, 8(1), e55144. doi:10.1371/journal.pone.0055144

Examples

```
## Not run:
taxotree(inat)

## End(Not run)
```

---

tempolar	*tempolar - Polar plot of temporal data*

Description

tempolar - Polar plot of temporal data

Usage

```
tempolar(indf = NA, timescale = NA, title = NA, color = NA,
  plottype = NA)
```

Arguments

indf	input data frame containing biodiversity data set
timescale	Temporal scale of the graph d - daily, w - weekly m - monthly. Default is d.
title	Title for the graph. Default is "Temporal coverage".
color	color of the graph plot. Dafault is "red".
plottype	plot types of r - lines, p - polygon and s - symbols. Dafault is p.

References

Otegui, J., Arino, A. H., Encinas, M. A., & Pando, F. (2013). Assessing the Primary Data Hosted by the Spanish Node of the Global Biodiversity Information Facility (GBIF). PLoS ONE, 8(1), e55144. doi:10.1371/journal.pone.0055144

Examples

```
## Not run:
tempolar(inat)

## End(Not run)
```

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