

# Package ‘bdvis’

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**Type** Package

**Title** Biodiversity Data Visualizations

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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.

**License** CC0

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

**Suggests** rinat

**NeedsCompilation** no

**Repository** CRAN

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

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**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)
```

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bdsummary                    *bdsummary - description*

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**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)
```

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fixstr	<i>fixstr - Fix structure of the data frame to match the key fields to GBIF style data field names</i>
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### Description

fixstr - Fix structure of the data frame to match the key fields to GBIF style data field 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 <a href="#">strptime</a>
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)
```

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getcellid	<i>getcellid - Assigns GBIF style degree Cell ids and Centi degree (0.1) cell ids for each record.</i>
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### 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*

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**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*

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### 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
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## 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)
```

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tempolar	<i>tempolar - Polar plot of temporal data</i>
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## 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. Default is "red".
plottype	plot types of r - lines, p - polygon and s - symbols. Default 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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