Package 'RDH'

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Type Package

Title Range Data Helper

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Description A collection of functions for help in analyzing spatial data available from Birdlife International and NatureServe

Depends sp, maptools, ape, rgeos, raster

License GPL-3

R topics documented:

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RDH-package	*Range Data Helper*

Description

A collection of functions for help in analyzing spatial data available from Birdlife International and NatureServe

Details

Package:	RDH
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Version:	1.0
Date:	2014-24-01
License:	GPL-3

Author(s)

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See Also

rgeos, raster

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example.phylogeny	*Example phylogenetic data for nine species*

Description

Example phylogenetic data for nine species

Usage

```
data(example.phylogeny)
```

Format

A phylogeny of class phylo

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example.shapefiles *Example species range information*

Description

Example range information for nine species

Usage

```
data(example.shapefiles)
```

Format

A `list` with each component being an object of class `SpatialPolygonsDataFrame`.

Source

BirdLife International and Natureserve, 2012, Bird species distribution maps of the world, BirdLife International, Cambridge, UK and NatureServe, Arlington, USA

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nameFix *Birdlife & NatureServe Name Fix*

Description

Cleans the names of shapefiles downloaded from Birdlife International and NatureServe, leaving only Genus and species names

Usage

```
nameFix(x, as.list=FALSE)
```

Arguments

x	A character string. Can either be a single value or a list of names.
as.list	Logical. Should the output be returned in the format of a list?

Details

The format of the input values needs to be unchanged from the format used by Birdlife International and NatureServe.

Value

Returns a character string of the same length as the input

Author(s)

Nicholas M A Crouch

Examples

```
# Using the filename for Accipiter collaris

shp.name <- "Accipiter_collaris_3443_NS.shp"
require(RDH)

nameFix(shp.name)

#Accipiter_collaris
```

---

num.polygons	*Number of Polygons*

Description

Counts the number of unique polygons that make up a shapefile

Usage

```
num.polygons(x, return.sizes=FALSE)
```

Arguments

x	A vector containing one or more shapefiles of class "SpatialPolygonsDataFrame"
return.sizes	Logical. If TRUE, output returns the sizes of the polygons contained within a shapefile

Details

Counts the number of unique polygons that make up a shapefile. Using return.sizes=TRUE means that the sizes of each polygon is returned, rather than the number of files.

Value

If return.sizes=FALSE, the default, then function returns numeric string of the same length as the number of shapefiles passed to the function.

If return.sizes=TRUE, then a data.frame will be returned containing the size of each polygon within the shapefile will be retuned.

Use lapply when passing a list of shapefiles to the function, see examples. When using lapply, a list will be returned will be returned where each element is either a numeric value of polygons with the shapefile, or a data.frame containing the size of each polygon within the shapefile.

Author(s)

Nicholas M A Crouch

Examples

```
library(RDH)
require(maptools)
require(rgeos)
require(sp)

data(example.shapefiles)

shp <- example.shapefiles[[1]]

#Number of polygons within the shapefile
num.polygons(shp)

#Sizes of the polygons within a shapefile
num.polygons(shp, return.sizes=TRUE)
```

---

pairwise.range.overlap

Pairwise percentage range overlap

Description

Calculate what percentage of each species' range is shared with every other species.

Usage

```
pairwise.range.overlap(x)
```

Arguments

x   A list of shapefiles

Details

A value of 0 signifies that the species in that row, shares none of its range with the species in the corresponding column. A value of 100 would signify it shares all of its range.

Important! Some species spatial data provided by Birdlife International and NatureServe have some slight anomalies which might need to be fixed before using this function. See polygon.cleaning.

Value

Returns a data.frame where the rows correspond to the species being analyzed, and columns to each other species in the set.

Author(s)

Nicholas M A Crouch

References

BirdLife International and NatureServe, 2012, Bird species distribution maps of the world, BirdLife International, Cambridge, UK and NatureServe, Arlington, USA

Examples

```
library(RDH)

data(example.shapefiles)


# An initial run reveals two shapefiles have some problems
## Not run:
output <- pairwise.range.overlap(example.shapefiles)

## End(Not run)

example.shapefiles[[5]] <- polygon.cleaning(example.shapefiles[[5]])
example.shapefiles[[8]] <- polygon.cleaning(example.shapefiles[[8]])

output <- pairwise.range.overlap(example.shapefiles)
```

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polygon.cleaning   *Polygon Cleaner*

Description

Cleans polygon files to remove any errors caused by missing data/intersecting nodes

Usage

```
polygon.cleaning(x, resolution=0.5)
```

Arguments

x   A shapefile

resolution   Amount of detail of original polygon retained during process, see Details

Details

Due to some problems encountered with functions in other packages, this function will clean a polygon through a rasterization process. The `resolution` argument describes how much of the detail of the original shapefile will be retained. Note: increasing the resolution (a lower value passed to the function) can result in huge amounts of memory required to perform the task, due to the large shapefiles used for avian ranges. Set at 0.5, a satisfactory amount of resolution is retained for large ranges. For smaller, particularily island ranges, I recommend lowering this value to 0.1, see Examples for comparisons.

Author(s)

Nicholas M A Crouch

References

BirdLife International and NatureServe, 2012, Bird species distribution maps of the world, BirdLife International, Cambridge, UK and NatureServe, Arlington, USA

Examples

```
library(RDH)

data(example.shapefiles)

shp <- example.shapefiles[[1]]

shp.clean <- polygon.cleaning(shp)

par(mfrow=c(1,2))

plot(shp, col=rgb(1,0,0,1/2))
title("Original Shapefile")

plot(shp.clean, col=rgb(0,0,1,1/2))
title("After Cleaning Process")
```

---

rangeOverlaps.phyloDist

Range overlaps and species phylogentic distances

Description

For a group of species, counts the number of times each species range overlaps with every other species. Also calculates the total phylogenetic distance between species with overlapping ranges.

Usage

```
rangeOverlaps.phyloDist(shapefiles, phylo, weight.relatives=TRUE)
```

Arguments

shapefiles	A `list` containing species shapefiles.
phylo	A phylogeny of class `phylo` where the tips correspond to the species shapefiles contained within `shapefiles`. Can be `NUll`, see details.
weight.relatives	
	Logical. Should more closely related species be weighted more than more distantly related species? Defaults to `TRUE`. When `TRUE`, performs 1/ `dist`, where `dist` is the patristic distance between two species.

Details

Progress will be returned whilst the function is running. If `phylo = NULL` then only number of overlapping ranges will be returned. When running with phylogenetic information, function will check whether all species with range data appear in the phylogeny. If species are missing from the phylogeny, an error message is returned. When calculating phylogenetic distance, running time for the function is increased.

Value

If `phylo = NULL`, returns a `data.frame` with two columns: species ID and the number of overlapping ranges. If phylogenetic data included, returns a `data.frame` with three columns: species ID, total phylogenetic distance and the number of overlapping ranges.

Author(s)

Nicholas M A Crouch

References

BirdLife International and NatureServe, 2012, Bird species distribution maps of the world, BirdLife International, Cambridge, UK and NatureServe, Arlington, USA

Examples

```
library(RDH)

data(example.shapefiles)
data(example.phylogeny)

# With phylogeny
output <- rangeOverlaps.phyloDist(example.shapefiles, example.phylogeny)

output

# Without phylogeny
```

```
output1 <- rangeOverlaps.phyloDist(example.shapefiles, phylo=NULL)

output1
```

---

raster.extract   *Raster extraction*

Description

Extracts data for a given species range from a raster file and returns statistical test based on that extracted values.

Usage

```
raster.extract(x, raster.layer, stat.test="mean",na.val=NULL)
```

Arguments

x	A shapefile
raster.layer	An object of class `rasterLayer`
stat.test	Character string specifying the test to perform on the extracted values. Defaults to `mean`
na.val	Raster files can contain specific values which correspond to missing data. Passing a numeric value to `na.val` will remove all instances corresponding to missing data before performing the specified statistical test

Details

Can pass to a `list` of shapefiles using `lapply`, will return a `list` of numeric values.

Value

Returns a numeric value based on the statistical test used.

Author(s)

Nicholas M A Crouch

References

Hijmans, R. J., S. E. Cameron, J. L. Parra, P. G. Jones, and A. Jarvis, 2005. Very high resolution interpolated climate surfaces for global land areas. International journal of Climatology 25:1965–1978. URL www.worldclim.org

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seasonal.distribution.ranges

Seasonal range distribution

Description

Breaks down a species range into new shapefiles which represent the breeding and wintering ranges respectively

Usage

```
seasonal.distribution.ranges(x)
```

Arguments

x   A shapefile

Details

If you are unsure about which seasonal values are present for a species, you can use the function seasonal.values. When x is a list, use lapply followed by unlist, this is to put all sub-lists into one single list, see examples.

Value

Returns a list of shapefiles with species broken down into wintering and breeding ranges

Author(s)

Nicholas M A Crouch

References

BirdLife International and NatureServe, 2012, Bird species distribution maps of the world, BirdLife International, Cambridge, UK and NatureServe, Arlington, USA

Examples

```
require(RDH)

data(example.shapefiles)

# Using a single file
s <- example.shapefiles[[1]]

output <- seasonal.distribution.ranges(s)

# Using a list
output.from.list <- lapply(example.shapefiles, seasonal.distribution.ranges)
```

```
# Without using unlist

length(output.from.list)

#Correcting

corrected.output.from.list <- unlist(output.from.list)

length(corrected.output.from.list)

# All new shapefiles are in a single list
```

---

seasonal.values   *Seasonal values*

Description

Returns description of which discrete seasonal occurances are recorded for a species, given its range information

Usage

```
seasonal.values(x)
```

Arguments

x   A shapefile

Value

Returns a character string with specified seasonal occurances of each species

Author(s)

Nicholas M A Crouch

References

BirdLife International and NatureServe, 2012, Bird species distribution maps of the world, BirdLife International, Cambridge, UK and NatureServe, Arlington, USA

Examples

```
library(RDH)

data(example.shapefiles)

shp <- example.shapefiles[[1]]
```

```
seasonal.values(shp)
```

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