Package ‘GapAnalysis’

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Title Conservation Indicators Using Spatial Information

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Description Supports the assessment of the degree of conservation of taxa in conservation systems, both in ex situ (in genebanks, botanical gardens, and other repositories), and in situ (in protected natural areas). Methods are described in Carver et al. (2021) <doi:10.1111/ecog.05430>, building on Khoury et al. (2020) <doi:10.1073/pnas.2007029117>, Khoury et al. (2019) <doi:10.1016/j.ecolind.2018.11.016>, Khoury et al. (2019) <doi:10.1111/DDI.13008>, Castaneda-Alvarez et al. (2016) <doi:10.1038/nplants.2016.22>, and Ramirez-Villegas et al. (2010) <doi:10.1371/journal.pone.0013497>.

URL `https://github.com/CIAT-DAPA/GapAnalysis`

BugReports `https://github.com/CIAT-DAPA/GapAnalysis/issues`

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Imports dataverse, dplyr, leaflet, terra

License GPL-3

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Repository CRAN

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Contents

`checkEcoregion` *Quality check of ecoregion dataset*

Description

Checks the class, crs, if the idColumn is a unique ID,

Usage

```
checkEcoregion(ecoregion, sdm, idColumn)
```

Arguments

`ecoregion`	A terra vect object the contains spatial information on all ecoregions of interests
`sdm`	a terra rast object that represented the expected distribution of the species
`idColumn`	A character vector that notes what column within the ecoregions object should be used as a unique ID

Value

ecoregions : A terra vect object the contains spatial information on all ecoregions of interests

References

Khoury et al. (2019) Ecological Indicators 98:420-429. doi:10.1016/j.ecolind.2018.11.016 Carver et al. (2021) GapAnalysis: an R package to calculate conservation indicators using spatial information

Examples

```
##Obtaining Raster_list
```

`checkOccurrences` *Quality check on occurrences data*

Description

Checks the column names, column data types, valid lat lon, and can optionally remove any duplicated lat lon records per species. The cleaned and formated dataframe is returned as well as a map object show a quick reference of the points in space.

Usage

```
checkOccurrences(csv, taxon, removeDuplicated = FALSE)
```

Arguments

`csv`	A dataframe holding the occurrence data
`taxon`	A character object that defines the name of the species as listed in the occurrence dataset
`removeDuplicated`	: Binary parameter. TRUE == duplication values are remove. Set to FALSE as default

Value

A list object containing 1. data : a data frames of values of occurrence data in the required format 2. map : a leaflet object showing the spatial results of the function

References

Khoury et al. (2019) Ecological Indicators 98:420-429. doi:10.1016/j.ecolind.2018.11.016 Carver et al. (2021) GapAnalysis: an R package to calculate conservation indicators using spatial information

Examples

```
# example code

##Obtaining occurrences from example
```

`checkProtectedAreas` *Quality check on protected areas dataset*

Description

Checks the class, values, crs, and cell size of the protected areas raster to ensure these elements match those required by gap analysis functions.

Usage

```
checkProtectedAreas(protectedAreas, sdm)
```

Arguments

`protectedAreas`	A terra rast object the contian spatial location of protected areas.
`sdm`	a terra rast object that represented the expected distribution of the species

Value

protectedAreas : a terra rast object representing protected areas

References

Khoury et al. (2019) Ecological Indicators 98:420-429. doi:10.1016/j.ecolind.2018.11.016 Carver et al. (2021) GapAnalysis: an R package to calculate conservation indicators using spatial information

Examples

```
##Obtaining Raster_list
```

`checksdm` *Quality check on sdm imagery*

Description

Evaluates the class, crs, and values are standardizes to what the following gap analysis functions are required.

Usage

```
checksdm(sdm)
```

Arguments

`sdm`	a terra rast object that represented the expected distribution of the species

Value

sdm : a terra rast object that is in the correct CRS

References

Khoury et al. (2019) Ecological Indicators 98:420-429. doi:10.1016/j.ecolind.2018.11.016 Carver et al. (2021) GapAnalysis: an R package to calculate conservation indicators using spatial information

Examples

```
##Obtaining Raster_list
```

`CucurbitaData` *Cucurbita occurrences dataset*

Description

This dataset is a subset of the original dataset for: C. cordata, C. digitata and C. palmata used in Khoury et al. (2019)

Usage

```
CucurbitaData
```

Format

A data frame with 1203 rows and 4 variables:

species character: Species name

latitude numeric:Latitude in decimal format

longitude numeric: Longitude in decimal format

type character: Source of the record,germplasm (G) or herbarium (H)

Source

doi:10.7910/DVN/B8YOQL

References

Khoury et al. (2019) Plants, People, Planet 2(3):269-283. doi:10.1002/ppp3.10085

`CucurbitaRasters` *Cucurbita species distribution models dataset*

Description

This dataset is a subset of species distribution models for: C. cordata, C. digitata and C. palmata used in Khoury et al., 2020

Usage

```
CucurbitaRasts
```

Format

terra rast object stored as a PackedSpatRaster

Source

doi:10.7910/DVN/B8YOQL

References

Khoury et al. (2019) Diversity and Distributions 26(2):209-225. doi:10.1111/DDI.13008

`ecoregions` *Ecoregions vector*

Description

This dataset is a subset of the Terrestrial Ecoregions of the World shapefile was made available by the world wildlife foundation

Usage

```
ecoregions
```

Format

SpatVector

Source

doi:10.7910/DVN/B8YOQL

`ERSex` *Ecological representativeness score ex situ*

Description

The ERSex process provides an ecological measurement of the proportion of a species range that can be considered to be conserved in ex situ repositories. The ERSex calculates the proportion of terrestrial ecoregions (The Nature Conservancy Geospatial Conservation Atlas 2019) represented within the G buffered areas out of the total number of ecoregions occupied by the distribution model.

Usage

```
ERSex(taxon, sdm, occurrenceData, gBuffer, ecoregions, idColumn)
```

Arguments

`taxon`	A character object that defines the name of the species as listed in the occurrence dataset
`sdm`	a terra rast object that represented the expected distribution of the species
`occurrenceData`	a data frame of values containing columns for the taxon, latitude, longitude, and type
`gBuffer`	A terra vect which encompases a specific buffer distance around all G points
`ecoregions`	A terra vect object the contains spatial information on all ecoregions of interests
`idColumn`	A character vector that notes what column within the ecoregions object should be used as a unique ID

Value

A list object containing 1. results : a data frames of values summarizing the results of the function 2. ecogaps : a terra vect object showing the ecoregions with no area within the g buffer objects 3. map : a leaflet object showing the spatial results of the function

References

Khoury et al. (2019) Ecological Indicators 98:420-429. doi:10.1016/j.ecolind.2018.11.016 Carver et al. (2021) GapAnalysis: an R package to calculate conservation indicators using spatial information

Examples

```
##Obtaining occurrences from example
data(CucurbitaData)
##Obtaining Raster_list
data(CucurbitaRasts)
## ecoregion features
data(ecoregions)

# convert the dataset for function
taxon <- "Cucurbita_cordata"
sdm <- terra::unwrap(CucurbitaRasts)$cordata
ecoregions <- terra::vect(ecoregions)
#Running generateGBuffers
gBuffer <- generateGBuffers(taxon = taxon,
                    occurrenceData = CucurbitaData,
                    bufferDistM = 50000
                    )
#Running ERSex
ers_exsitu <- ERSex(taxon = taxon,
                    sdm = sdm,
                    occurrenceData = CucurbitaData,
                   gBuffer = gBuffer,
                   ecoregions = ecoregions,
                   idColumn = "ECO_NAME"
                   )
```

`ERSin` *Ecological representativeness score in situ*

Description

The ERSin process provides an ecological measurement of the proportion of a species range that can be considered to be conserved in protected areas. The ERSin calculates the proportion of ecoregions encompassed within the range of the taxon located inside protected areas to the ecoregions encompassed within the total area of the distribution model, considering comprehensive conservation to have been accomplished only when every ecoregion potentially inhabited by a species is included within the distribution of the species located within a protected area.

Usage

```
ERSin(taxon, sdm, occurrenceData, protectedAreas, ecoregions, idColumn)
```

Arguments

`taxon`	A character object that defines the name of the species as listed in the occurrence dataset
`sdm`	a terra rast object that represented the expected distribution of the species
`occurrenceData`	a data frame of values containing columns for the taxon, latitude, longitude, and type
`protectedAreas`	A terra rast object the contian spatial location of protected areas.
`ecoregions`	A terra vect object the contains spatial information on all ecoregions of interests
`idColumn`	A character vector that notes what column within the ecoregions object should be used as a unique ID

Value

A list object containing 1. results : a data frames of values summarizing the results of the function 2. missingEcos : a terra vect object showing all the ecoregions within the distribution with no protected areas present 3. map : a leaflet object showing the spatial results of the function

References

Khoury et al. (2019) Ecological Indicators 98:420-429. doi:10.1016/j.ecolind.2018.11.016 Carver et al. (2021) GapAnalysis: an R package to calculate conservation indicators using spatial information

Examples

```
##Obtaining occurrences from example
data(CucurbitaData)
##Obtaining Raster_list
data(CucurbitaRasts)
##Obtaining protected areas raster
data(ProtectedAreas)
## ecoregion features
data(ecoregions)

# convert the dataset for function
taxon <- "Cucurbita_cordata"
sdm <- terra::unwrap(CucurbitaRasts)$cordata
protectedAreas <- terra::unwrap(ProtectedAreas)
ecoregions <- terra::vect(ecoregions)
```

```
#Running ERSin
ers_insitu <- ERSin(taxon = taxon,
                    sdm = sdm,
                    occurrenceData = CucurbitaData,
                    protectedAreas = protectedAreas,
                    ecoregions = ecoregions,
                    idColumn = "ECO_NAME"
                    )
```

`FCSc_mean` *Final Conservation Score measure*

Description

Compiles all tabular data from the individual metrics and generate the final results

Usage

```
FCSc_mean(taxon, fcsin, fcsex)
```

Arguments

`taxon`	A character object that defines the name of the species as listed in the occurrence dataset
`fcsin`	A data frame containing summary results from the fcsin function
`fcsex`	A data frame containing summary results from the fcsex function

Value

data_comb : a data frame which aggreates final result summaries

References

Khoury et al. (2019) Ecological Indicators 98:420-429. doi:10.1016/j.ecolind.2018.11.016 Carver et al. (2021) GapAnalysis: an R package to calculate conservation indicators using spatial information

Examples

```
##Obtaining occurrences from example
data(CucurbitaData)
##Obtaining Raster_list
data(CucurbitaRasts)
##Obtaining protected areas raster
data(ProtectedAreas)
## ecoregion features
data(ecoregions)
```

```
# convert the dataset for function
taxon <- "Cucurbita_cordata"
sdm <- terra::unwrap(CucurbitaRasts)$cordata
occurrenceData <- CucurbitaData
protectedAreas <- terra::unwrap(ProtectedAreas)
ecoregions <- terra::vect(ecoregions)


# generate exsitu conservation summaries
srs_exsitu <- SRSex(taxon = taxon,
                    occurrenceData  = CucurbitaData
                    )

gBuffer <- generateGBuffers(taxon = taxon,
                    occurrenceData = occurrenceData,
                    bufferDistM = 50000
                    )#'

grs_exsitu <- GRSex(taxon = taxon,
                    sdm = sdm,
                    gBuffer = gBuffer
                    )

ers_exsitu <- ERSex(taxon = taxon,
                    sdm = sdm,
                    occurrenceData = occurrenceData,
                    gBuffer = gBuffer,
                    ecoregions = ecoregions,
                    idColumn = "ECO_NAME"
                    )

#Running fcsex
fcs_exsitu <- FCSex(taxon = taxon,
                    srsex = srs_exsitu,
                    grsex = grs_exsitu,
                    ersex = ers_exsitu
                    )



# generate insitu conservation summaries
srs_insitu <- SRSin(taxon = taxon,
                    sdm = sdm,
                    occurrenceData = CucurbitaData,
                    protectedAreas = protectedAreas
                    )

grs_insitu <- GRSin(taxon = taxon,
                    sdm = sdm,
                    protectedAreas = protectedAreas
                    )
```

```
ers_insitu <- ERSin(taxon = taxon,
                    sdm = sdm,
                    occurrenceData = occurrenceData,
                    protectedAreas = protectedAreas,
                    ecoregions = ecoregions,
                    idColumn = "ECO_NAME"
                    )

#Running fcsin
fcs_insitu <- FCSin(taxon = taxon,
                    srsin = srs_insitu,
                    grsin = grs_insitu,
                    ersin = ers_insitu
                    )

fsc_combine <- FCSc_mean(taxon = taxon,
                         fcsin = fcs_insitu,
                         fcsex = fcs_exsitu)
```

`FCSex` *Final conservation score ex situ*

Description

This function calculates the average of the three ex situ conservation metrics returning a final conservation score summary table. It also assigns conservation priority categories

Usage

```
FCSex(taxon, srsex, grsex, ersex)
```

Arguments

`taxon`	A character object that defines the name of the species as listed in the occurrence dataset
`srsex`	A dataframe contain the results from the srsex function
`grsex`	A dataframe contain the results from the grsex function
`ersex`	A dataframe contain the results from the ersex function

Value

out_df : a data frames of values summarizing the results of the function

References

Khoury et al. (2019) Ecological Indicators 98:420-429. doi:10.1016/j.ecolind.2018.11.016 Carver et al. (2021) GapAnalysis: an R package to calculate conservation indicators using spatial information

Examples

```
##Obtaining occurrences from example
data(CucurbitaData)
##Obtaining Raster_list
data(CucurbitaRasts)
##Obtaining protected areas raster
data(ProtectedAreas)
## ecoregion features
data(ecoregions)

# convert the dataset for function
taxon <- "Cucurbita_cordata"
sdm <- terra::unwrap(CucurbitaRasts)$cordata
occurrenceData <- CucurbitaData
protectedAreas <- terra::unwrap(ProtectedAreas)
ecoregions <- terra::unwrap(ecoregions)
# generate exsitu conservation summaries
srs_exsitu <- SRSex(taxon = taxon,
                    occurrenceData = CucurbitaData
                    )

gBuffer <- generateGBuffers(taxon = taxon,
                    occurrenceData = occurrenceData,
                    bufferDistM = 50000
                    )#'

grs_exsitu <- GRSex(taxon = taxon,
                    sdm = sdm,
                    gBuffer = gBuffer
                    )

ers_exsitu <- ERSex(taxon = taxon,
                    sdm = sdm,
                    occurrenceData = occurrenceData,
                    gBuffer = gBuffer,
                    ecoregions = ecoregions,
                    idColumn = "ECO_NAME"
                    )

#Running fcsex
fcs_exsitu <- FCSex(taxon = taxon,
                    srsex = srs_exsitu,
                    grsex = grs_exsitu,
                    ersex = ers_exsitu)
```

`FCSin` *Final conservation score in situ*

Description

This function calculates the average of the three in situ conservation metrics and assigns a priority category based on the results

Usage

```
FCSin(taxon, srsin, grsin, ersin)
```

Arguments

`taxon`	A character object that defines the name of the species as listed in the occurrence dataset
`srsin`	A dataframe contain the results from the srsin function
`grsin`	A dataframe contain the results from the grsin function
`ersin`	A dataframe contain the results from the ersin function

Value

out_df : a data frames of values summarizing the results of the function

References

Khoury et al. (2019) Ecological Indicators 98:420-429. doi:10.1016/j.ecolind.2018.11.016 Carver et al. (2021) GapAnalysis: an R package to calculate conservation indicators using spatial information

Examples

```
##Obtaining occurrences from example
data(CucurbitaData)
##Obtaining Raster_list
data(CucurbitaRasts)
##Obtaining protected areas raster
data(ProtectedAreas)
## ecoregion features
data(ecoregions)

# convert the dataset for function
taxon <- "Cucurbita_cordata"
sdm <- terra::unwrap(CucurbitaRasts)$cordata
occurrenceData <- CucurbitaData
protectedAreas <- terra::unwrap(ProtectedAreas)
ecoregions <- terra::vect(ecoregions)

# generate insitu conservation summaries
srs_insitu <- SRSin(taxon = taxon,
                    sdm = sdm,
                    occurrenceData = occurrenceData,
                    protectedAreas = protectedAreas
                    )
```

```
grs_insitu <- GRSin(taxon = taxon,
                    sdm = sdm,
                    protectedAreas = protectedAreas
                    )

ers_insitu <- ERSin(taxon = taxon,
                    sdm = sdm,
                    occurrenceData = occurrenceData,
                    protectedAreas = protectedAreas,
                    ecoregions = ecoregions,
                    idColumn = "ECO_NAME"
                    )

#Running fcsin
FCSin <- FCSin(taxon = taxon,
                    srsin = srs_insitu,
                    grsin = grs_insitu,
                    ersin = ers_insitu
                    )
```

`generateCounts` *Generate initial counts of the occurrence data*

Description

Performs data cleaning to generate a summary of all input occurrence data. These values area used in the SRSex function.

Usage

```
generateCounts(taxon, occurrenceData)
```

Arguments

`taxon`	A character object that defines the name of the species as listed in the occurrence dataset
`occurrenceData`	a data frame of values containing columns for the taxon, latitude, longitude, and type

Value

countsData : a data frames of values summarizing the results of the function

References

Khoury et al. (2019) Ecological Indicators 98:420-429. doi:10.1016/j.ecolind.2018.11.016 Carver et al. (2021) GapAnalysis: an R package to calculate conservation indicators using spatial information

Examples

```
##Obtaining occurrences from example
data(CucurbitaData)

# convert the dataset for function
taxon <- "Cucurbita_cordata"
occurrenceData <- CucurbitaData

#Running generateCounts
counts <- generateCounts(taxon = taxon,
                    occurrenceData = occurrenceData
                    )
```

`generateEcoSelection` *Select relivent ecoregions*

Description

Utilizes the occurrence data location to select all ecoregions that intersect with thoses points. Helpful as it reduces the overall file size of the ecoregion object.

Usage

```
generateEcoSelection(taxon, occurrenceData, ecoregions, idColumn)
```

Arguments

`taxon`	A character object that defines the name of the species as listed in the occurrence dataset
`occurrenceData`	a data frame of values containing columns for the taxon, latitude, longitude, and type
`ecoregions`	A terra vect object the contains spatial information on all ecoregions of interests
`idColumn`	A character vector that notes what column within the ecoregions object should be used as a unique ID

Value

selectedEcos : a terra vect that contains the selected ecoregion features

References

Khoury et al. (2019) Ecological Indicators 98:420-429. doi:10.1016/j.ecolind.2018.11.016 Carver et al. (2021) GapAnalysis: an R package to calculate conservation indicators using spatial information

Examples

```
##Obtaining occurrences from example
data(CucurbitaData)
## ecoregion features
data(ecoregions)

# convert the dataset for function
taxon <- "Cucurbita_cordata"
occurrenceData <- CucurbitaData
ecoregions <- terra::vect(ecoregions)

#Running generateEcoSelection
selectedEcos <- generateEcoSelection(taxon = taxon,
                    occurrenceData = occurrenceData,
                    ecoregions = ecoregions,
                    idColumn = "ECO_NAME"
                    )
```

`generateGBuffers` *Generate buffer of G type occurrences*

Description

Produces a terra vect object representing the area around the G type occurrences

Usage

```
generateGBuffers(taxon, occurrenceData, bufferDistM)
```

Arguments

`taxon`	A character object that defines the name of the species as listed in the occurrence dataset
`occurrenceData`	a data frame of values containing columns for the taxon, latitude, longitude, and type
`bufferDistM`	Distance in meters. Used to set the size of the buffered objects.

Value

A list object containing 1. data : a terra vect object showing all the buffered areas around the G type occurrences 2. map : a leaflet object showing the spatial results of the function

References

Khoury et al. (2019) Ecological Indicators 98:420-429. doi:10.1016/j.ecolind.2018.11.016 Carver et al. (2021) GapAnalysis: an R package to calculate conservation indicators using spatial information

Examples

```
##Obtaining occurrences from example
data(CucurbitaData)

# convert the dataset for function
taxon <- "Cucurbita_cordata"
occurrenceData <- CucurbitaData

#Running generateGBuffers
gBuffer <- generateGBuffers(taxon = taxon,
                    occurrenceData = occurrenceData,
                    bufferDistM = 50000
                    )
```

`getDatasets` *Download datasets from the harvard dataverse repo*

Description

Ecoregions and protected area data base are stored on a harvard dataverse repository. This functions check to see if those datasets have been download and will download them if not present.

Usage

```
getDatasets()
```

Value

A message confirming the datasets were downloaded, along with saving the files to the package's data directory.

References

Khoury et al. (2019) Ecological Indicators 98:420-429. doi:10.1016/j.ecolind.2018.11.016 Carver et al. (2021) GapAnalysis: an R package to calculate conservation indicators using spatial information

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`GRSex` *Geographical representativeness score ex situ*

Description

The GRSex process provides a geographic measurement of the proportion of a species' range that can be considered to be conserved in ex situ repositories. The GRSex uses buffers (default 50 km radius) created around each G coordinate point to estimate geographic areas already well collected within the distribution models of each taxon, and then calculates the proportion of the distribution model covered by these buffers.

Usage

```
GRSex(taxon, sdm, gBuffer)
```

Arguments

`taxon`	A character object that defines the name of the species as listed in the occurrence dataset
`sdm`	a terra rast object that represented the expected distribution of the species
`gBuffer`	A terra vect which encompases a specific buffer distance around all G points

Value

A list object containing 1. results : a data frames of values summarizing the results of the function 2. gGaps : a terra vect object showing buffered area about g points 3. map : a leaflet object showing the spatial results of the function

References

Khoury et al. (2019) Ecological Indicators 98:420-429. doi:10.1016/j.ecolind.2018.11.016 Carver et al. (2021) GapAnalysis: an R package to calculate conservation indicators using spatial information

Examples

```
##Obtaining occurrences from example
data(CucurbitaData)
##Obtaining Raster_list
data(CucurbitaRasts)
##Obtaining protected areas raster
data(ProtectedAreas)
## ecoregion features
data(ecoregions)

# convert the dataset for function
taxon <- "Cucurbita_cordata"
sdm <- terra::unwrap(CucurbitaRasts)$cordata
```

```
occurrenceData <- CucurbitaData

# generate the g buffer object
gBuffer <- generateGBuffers(taxon = taxon,
                            occurrenceData = occurrenceData,
                            bufferDistM = 50000)

#Running GRSex
grs_exsitu <- GRSex(taxon = taxon,
                    sdm = sdm,
                    gBuffer = gBuffer
                    )
```

`GRSin` *Geographical representativeness score in situ*

Description

The GRSin process provides a geographic measurement of the proportion of a species' range that can be considered to be conserved in protected areas. The GRSin compares the area of the distribution model located within protected areas versus the total area of the model, considering comprehensive conservation to have been accomplished only when the entire distribution occurs within protected areas.

Usage

```
GRSin(taxon, sdm, protectedAreas)
```

Arguments

`taxon`	A character object that defines the name of the species as listed in the occurrence dataset
`sdm`	a terra rast object that represented the expected distribution of the species
`protectedAreas`	A terra rast object the contian spatial location of protected areas.

Value

A list object containing 1. results : a data frames of values summarizing the results of the function 2. protectAreaMask : a terra rast object showing all the protected areas within the distribution 3. map : a leaflet object showing the spatial results of the function

References

Khoury et al. (2019) Ecological Indicators 98:420-429. doi:10.1016/j.ecolind.2018.11.016 Carver et al. (2021) GapAnalysis: an R package to calculate conservation indicators using spatial information

Examples

```
##Obtaining Raster_list
data(CucurbitaRasts)
##Obtaining protected areas raster
data(ProtectedAreas)

# convert the dataset for function
taxon <- "Cucurbita_cordata"
sdm <- terra::unwrap(CucurbitaRasts)$cordata
protectedAreas <- terra::unwrap(ProtectedAreas)

#Running GRSin
grs_insitu <- GRSin(taxon = taxon,
                    sdm = sdm,
                    protectedAreas = protectedAreas
                    )
```

`ProtectedAreas` *Protected areas dataset in raster format*

Description

This dataset is a raster version of the world protected areas dataset used in Khoury et al., (2019)

Usage

`ProtectedAreas`

Format

terra rast object

Source

`https://www.protectedplanet.net/en`

References

Khoury et al. (2019) Ecological Indicators 98:420-429. doi:10.1016/j.ecolind.2018.11.016

`SRSex` *Sampling representativeness score ex situ*

Description

The SRSex process provides a general indication of the completeness of ex situ conservation collections, calculating the ratio of germplasm accessions (G) available in ex situ repositories to reference (H) records for each taxon, making use of all compiled records, regardless of whether they include coordinates, with an ideal (i.e., comprehensive) conservation ratio of 1:1. In this and in the subsequent measurements, if no G or H records exist, taxa are automatically considered to be of high priority for further conservation action and assigned a value of 0. If there are more G than H records, SRSex is set to 100.

Usage

```
SRSex(taxon, occurrenceData)
```

Arguments

`taxon`	A character object that defines the name of the species as listed in the occurrence dataset
`occurrenceData`	a data frame of values containing columns for the taxon, latitude, longitude, and type

Value

out_df : a data frames of values summarizing the results of the function

References

Khoury et al. (2019) Ecological Indicators 98:420-429. doi:10.1016/j.ecolind.2018.11.016 Carver et al. (2021) GapAnalysis: an R package to calculate conservation indicators using spatial information

Examples

```
##Obtaining occurrences from example
data(CucurbitaData)

# convert the dataset for function
taxon <- "Cucurbita_cordata"

#Running SRSex
srs_exsitu <- SRSex(taxon = taxon,
                    occurrenceData = CucurbitaData
                    )
```

`SRSin` *Sampling representativeness score in situ*

Description

The SRSin process calculates the proportion of all occurrences of a taxon falling within the distribution model that also fall within a protected area

Usage

```
SRSin(taxon, sdm, occurrenceData, protectedAreas)
```

Arguments

`taxon`	A character object that defines the name of the species as listed in the occurrence dataset
`sdm`	a terra rast object that
`occurrenceData`	a data frame of values containing columns for the taxon, latitude, longitude, and type
`protectedAreas`	A terra rast object the contian spatial location of protected areas.

Value

A list object containing 1. results : a data frames of values summarizing the results of the function 2. points : a terra vect object showing all the points present within protected areas 3. map : a leaflet object showing the spatial results of the function

References

Khoury et al. (2019) Ecological Indicators 98:420-429. doi:10.1016/j.ecolind.2018.11.016 Carver et al. (2021) GapAnalysis: an R package to calculate conservation indicators using spatial information

Examples

```
##Obtaining occurrences from example
data(CucurbitaData)
##Obtaining Raster_list
data(CucurbitaRasts)
##Obtaining protected areas raster
data(ProtectedAreas)

# convert the dataset for function
taxon <- "Cucurbita_cordata"
sdm <- terra::unwrap(CucurbitaRasts)$cordata
occurrenceData <- CucurbitaData
protectedAreas <- terra::unwrap(ProtectedAreas)
#Running SRSin
```

```
srs_insitu <- SRSin(taxon = taxon,
                    sdm = sdm,
                    occurrenceData = occurrenceData,
                    protectedAreas = protectedAreas
                    )
```

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