

Package ‘GapAnalysis’

May 5, 2020

Type Package

Title An R package to calculate conservation indicators using spatial information

Date 2019-12-10

Version 1.0

Author Dan Carver, Chrystian Sosa, Colin Khoury, Julian Ramirez-Villegas

Maintainer CIAT Decision and policy analysis research area <J.R.Villegas@cgiar.org>

Description This R library provides a consistent pipeline to calculate ex situ and in situ conservation indicators.

Also, it provides basic functions to allow run the gap analysis methodology based on the gap analysis methodology used in developed by Ramirez-

Villegas et al. (2010) and used in Khoury et al., (2019). Please note, that this library does not include methods for modeling species distribution models. Predicted habitats must be provided by users.

Depends R (>= 3.5.0)

Imports tmap (>= 2.3), dplyr (>= 0.4.0), tidyselect (>= 0.4.0), raster (>= 3.0), rgdal (>= 1.4-8), sf (>= 0.8), rlang (>= 0.4.6), lwgeom (>= 0.2), utils (>= 3.5), base (>= 3.5), methods (>= 3.5), magrittr (>= 1.5), geosphere (>= 1.5), dataverse (>= 0.2.0), data.table (>= 1.12), sp (>= 1.4.1), redlistr (>= 1.0.3), fasterize (>= 1.0.0), tidyr (>= 1.0.2), devtools (>= 2.2.0), usethis (>= 1.6.0), rmarkdown (>= 2.1)

Suggests knitr

License GPL-3

LazyData true

Encoding UTF-8

RoxygenNote 7.1.0

NeedsCompilation no

R topics documented:

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GapAnalysis-package	<i>GapAnalysis: A gap analysis and conservation status tool</i>
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Description

GapAnalysis is a package to provide easy calculation for conservation scores

Details

Package:	GapAnalysis
Type:	Package
Version:	1.0.0
Date:	2020-04-8
License:	GPL-3

Author(s)

CIAT Decision and Policy Analysis research area
email: <J.R.Villegas@cgiar.org>

cucurbitaData	<i>Cucurbita occurrences dataset</i>
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Description

This dataset is a subset of the original dataset for: *C. cordata*, *C. digitata* and *C. palmata* used in Khoury et al., 2020

Usage

```
cucurbitaData
```

Format

A data frame with 1184 rows and 4 variables:

taxon 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

<https://dataverse.harvard.edu/dataverse/GapAnalysisR>

References

Khoury, CK, Carver, D, Kates, HR, et al. Distributions, conservation status, and abiotic stress tolerance potential of wild cucurbita (*Cucurbita* L.). *Plants, People, Planet.* 2019; 00: 1– 15. <https://doi.org/10.1002/ppp3.10085>

cucurbitaRasters

Cucurbita species distribution models dataset

Description

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

Usage

```
cucurbitaRasters
```

Format

raster files

Source

<https://dataverse.harvard.edu/dataverse/GapAnalysisR>

References

Khoury, CK, Carver, D, Kates, HR, et al. Distributions, conservation status, and abiotic stress tolerance potential of wild cucurbita (*Cucurbita* L.). *Plants, People, Planet.* 2019; 00: 1– 15. <https://doi.org/10.1002/ppp3.10085>

ecoregions	<i>Ecoregions shapefile</i>
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Description

This dataset is a subset of the Terrestrial Ecoregions shapefile made by the Nature Conservancy

Usage

```
ecoregions
```

Format

Shapefile

Source

http://maps.tnc.org/gis_data.html

eooAoo	<i>IUCN conservations status using Area of occupancy (AOO) and extent of occurrence (EOO) (IUCN Redlist)</i>
--------	--

Description

This function calculates the species conservation status according IUCN parameters using Area of occupancy (AOO) Area and extent of occurrence (EOO)

Usage

```
eooAoo(species_list, occurrenceData)
```

Arguments

species_list	An species list to calculate metrics.
occurrenceData	A data frame object with the species name, geographical coordinates, and type of records (G or H) for a given species

Value

This function returns a data frame with the following columns:

species	Species name
EOO Status	IUCN conservation status (EOO)
AOO Status	IUCN conservation status (AOO)

Author(s)

Dan Carver

References

Bland, Lucie & Keith, David & Miller, Rebecca & Murray, Nicholas & Rodríguez, Jon. (2017). Guidelines for the application of IUCN Red List of Ecosystems Categories and Criteria, version 1.1. 10.2305/IUCN.CH.2016.RLE.3.en.

Lee, C. K. F., Keith, D. A., Nicholson, E. and Murray, N. J. 2019. Redlistr: tools for the IUCN Red Lists of ecosystems and threatened species in R. – *Ecography* 42: 1050–1055 (ver. 0).

Examples

```
data(cucurbitaData)
##Obtaining species names from the data
speciesList <- unique(cucurbitaData$taxon)
## Obtaining A00 and E00 ##
eooAoo <- GapAnalysis::eooAoo(species_list = speciesList,
                              occurrenceData = cucurbitaData)
```

ERSex	<i>Environmental representativeness score estimation (Ex-situ conservation)</i>
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Description

This function performs an estimation of the environmental representativeness score for ex-situ gap analysis (ERSex) using Ramirez-Villegas et al., (2010) methodology. ERSex is calculated as:

$$ERSex = \min(100, (Numberofecoregionswith50kmofGOccurrences/NumberofEcoregionsPresentwithint$$

Usage

```
ERSex(species_list, occurrenceData, raster_list, bufferDistance, ecoReg)
```

Arguments

species_list	An species list to calculate the ERSex metrics.
occurrenceData	A data frame object with the species name, geographical coordinates, and type of records (G or H) for a given species
raster_list	A list representing the species distribution models for the species list provided loaded in raster format. This list must match the same order of the species list.
bufferDistance	Geographical distance used to create circular buffers around germplasm. Default: 50000 that is 50 km around germplasm accessions (CA50)
ecoReg	A shapefile representing ecoregions information with a field ECO_NUM representing ecoregions Ids. If ecoReg=NULL the function will use a shapefile provided for your use after run GetDataSets()

Value

This function returns a data frame with two columns:

species	Species name
ERSex	ERSex value calculated

References

- Ramirez-Villegas, J., Khoury, C., Jarvis, A., Debouck, D. G., & Guarino, L. (2010). A Gap Analysis Methodology for Collecting Crop Genepools: A Case Study with Phaseolus Beans. PLOS ONE, 5(10), e13497. Retrieved from <https://doi.org/10.1371/journal.pone.0013497>
- Khoury, C. K., Amariles, D., Soto, J. S., Diaz, M. V., Sotelo, S., Sosa, C. C., ... Jarvis, A. (2019). Comprehensiveness of conservation of useful wild plants: An operational indicator for biodiversity and sustainable development targets. Ecological Indicators. <https://doi.org/10.1016/j.ecolind.2018.11.016>

Examples

```
##Obtaining occurrences from example
data(cucurbitaData)
speciesList <- unique(cucurbitaData$taxon)
## Obtaining rasterList object. ##
data(cucurbitaRasters)
cucurbitaRasters <- raster::unstack(cucurbitaRasters)
##Obtaining ecoregions shapefile
data(ecoregions)

ERSex_df <- ERSex(species_list = speciesList,
                  occurrenceData = cucurbitaData,
                  raster_list = cucurbitaRasters,
                  bufferDistance = 50000,
                  ecoReg=ecoregions)
```

ERSin	<i>Environmental representativeness score estimation (In-situ conservation)</i>
-------	---

Description

This function performs an estimation of germplasm representativeness score for in-situ gap analysis (GRSin) using Khoury et al., (2019) methodology This function uses a germplasm buffer raster file (e.g. CA50), a thresholded species distribution model, and a raster file of protected areas

$$ERSin = \min(100, (Numberofecoregionsofgermplasmoccurrencesinprotectedareas/Numberofecoregionsofgermplasmoccurrencesinprotectedareas))$$

Usage

```
ERSin(species_list, occurrenceData, raster_list, proArea, ecoReg)
```

Arguments

- | | |
|----------------|--|
| species_list | An species list to calculate the ERSin metrics. |
| occurrenceData | A data frame object with the species name, geographical coordinates, and type of records (G or H) for a given species |
| raster_list | A list representing the species distribution models for the species list provided loaded in raster format. This list must match the same order of the species list. |
| proArea | A raster file representing protected areas information. If proArea=NULL the funtion will use a protected area raster file provided for your use after run Get-Datasets() |

ecoReg A shapefile representing ecoregions information with a field ECO_NUM representing ecoregions Ids. If ecoReg=NULL the function will use a shapefile provided for your use after run GetDatasets()

Value

This function returns a data frame with two columns:

species	Species name
ERSin	ERSin value calculated

References

Ramirez-Villegas, J., Khoury, C., Jarvis, A., Debouck, D. G., & Guarino, L. (2010). A Gap Analysis Methodology for Collecting Crop Genepools: A Case Study with Phaseolus Beans. PLOS ONE, 5(10), e13497. Retrieved from <https://doi.org/10.1371/journal.pone.0013497>

Khoury, C. K., Amariles, D., Soto, J. S., Diaz, M. V., Sotelo, S., Sosa, C. C., ... Jarvis, A. (2019). Comprehensiveness of conservation of useful wild plants: An operational indicator for biodiversity and sustainable development targets. Ecological Indicators. <https://doi.org/10.1016/j.ecolind.2018.11.016>

Examples

```
##Obtaining occurrences from example
data(cucurbitaData)
##Obtaining species names from the data
speciesList <- unique(cucurbitaData$taxon)
##Obtaining raster_list
data(cucurbitaRasters)
cucurbitaRasters <- raster::unstack(cucurbitaRasters)
##Obtaining protected areas raster
data(protectedAreas)
##Obtaining ecoregions shapefile
data(ecoregions)

ERSin_df <- ERSin(species_list = speciesList,
                  occurrenceData = cucurbitaData,
                  raster_list = cucurbitaRasters,
                  proArea= protectedAreas,
                  ecoReg=ecoregions)
```

ExsituCompile

Ex-situ gap analysis calculation (Ex-situ conservation)

Description

This function allows calculate all the three Ex situ gap analysis scores in one unique function returning a final conservation score summary table

Usage

```
ExsituCompile(
  species_list,
  occurrenceData,
  raster_list,
  bufferDistance,
  ecoReg
)
```

Arguments

species_list	A species list to calculate metrics.
occurrenceData	A data frame object with the species name, geographical coordinates, and type of records (G or H) for a given species
raster_list	A list representing the species distribution models for the species list provided loaded in raster format. This list must match the same order of the species list.
bufferDistance	Geographical distance used to create circular buffers around germplasm. Default: 50000 that is 50 km around germplasm accessions (CA50)
ecoReg	A shapefile representing ecoregions information with a field ECO_NUM representing ecoregions Ids. If ecoReg=NULL the function will use a shapefile provided for your use after run GetDatasets()

Value

This function returns a data frame summarizing the ex-situ gap analysis scores:

species	Species name
SRSex	Ex-situ sample representativeness score
GRSex	Ex-situ germplasm representativeness score
ERSex	Ex-situ environmental representativeness score
FCSex	Ex-situ final conservation score

References

Ramirez-Villegas, J., Khoury, C., Jarvis, A., Debouck, D. G., & Guarino, L. (2010). A Gap Analysis Methodology for Collecting Crop Genepools: A Case Study with Phaseolus Beans. PLOS ONE, 5(10), e13497. Retrieved from <https://doi.org/10.1371/journal.pone.0013497>

Khoury, C. K., Amariles, D., Soto, J. S., Diaz, M. V., Sotelo, S., Sosa, C. C., ... Jarvis, A. (2019). Comprehensiveness of conservation of useful wild plants: An operational indicator for biodiversity and sustainable development targets. Ecological Indicators. <https://doi.org/10.1016/j.ecolind.2018.11.016>

Examples

```
##Obtaining occurrences from example
data(cucurbitaData)
##Obtaining species names from the data
speciesList <- unique(cucurbitaData$taxon)
##Obtaining raster_list
data(cucurbitaRasters)
cucurbitaRasters <- raster::unstack(cucurbitaRasters)
##Obtaining ecoregions shapefile
```



```
data(ecoregions)

#Running all three Ex situ gap analysis steps using ExsituCompile function
exsituGapMetrics <- ExsituCompile(species_list=speciesList,
                                   occurrenceData=cucurbitaData,
                                   raster_list=cucurbitaRasters,
                                   bufferDistance=50000,
                                   ecoReg=ecoregions)
```

FCSc_mean

Combining Ex-situ and In-situ gap analysis results in one comprehensive conservation score (Summary Assessments)

Description

This function concatenates ex-situ conservation scores (SRSex, GRSex, ERSex, FCSEX), and in situ scores (SRSin, GRSin, ERSin, FCSin) in one unique table and calculate the final conservation score for a species using Khoury et al., (2019) methodology.

Usage

```
FCSc_mean(fcsEx, fcsIn)
```

Arguments

fcsEx	A data frame object result of the functions ExsituCompile or fcs_exsitu
fcsIn	A data frame object result of the functions InsituCompile or fcs_insitu

Value

this function returns a data frame object with the following columns:

species	Species name
FCSEX	Ex-situ final conservation score
FCSin	In-situ final conservation score
FCSc_min	Final conservation score (minimum value between FCSin and FCSEX)
FCSc_max	Final conservation score (maximum value between FCSin and FCSEX)
FCSc_mean	Final conservation score (average value between FCSin and FCSEX)
FCSc_min_class	Final conservation category using FCSc_min value
FCSc_max_class	Final conservation category using FCSc_max value
FCSc_mean_class	Final conservation category using FCSc_mean value

References

Ramirez-Villegas, J., Khoury, C., Jarvis, A., Debouck, D. G., & Guarino, L. (2010). A Gap Analysis Methodology for Collecting Crop Genepools: A Case Study with Phaseolus Beans. PLOS ONE, 5(10), e13497. Retrieved from <https://doi.org/10.1371/journal.pone.0013497>

Khoury, C. K., Amariles, D., Soto, J. S., Diaz, M. V., Sotelo, S., Sosa, C. C., ... Jarvis, A. (2019). Comprehensiveness of conservation of useful wild plants: An operational indicator for biodiversity and sustainable development targets. Ecological Indicators. <https://doi.org/10.1016/j.ecolind.2018.11.016>

Examples

```
##Obtaining occurrences from example
data(cucurbitaData)
##Obtaining species names from the data
speciesList <- unique(cucurbitaData$taxon)
##Obtaining raster_list
data(cucurbitaRasters)
cucurbitaRasters <- raster::unstack(cucurbitaRasters)
##Obtaining protected areas raster
data(protectedAreas)
##Obtaining ecoregions shapefile
data(ecoregions)

#Running all three Ex-situ gap analysis steps using ExsituCompile function
exsituGapMetrics <- ExsituCompile(species_list=speciesList,
                                occurrenceData=cucurbitaData,
                                raster_list=cucurbitaRasters,
                                bufferDistance=50000,
                                ecoReg=ecoregions)

#Running all three In-situ gap analysis steps using InsituCompile function
insituGapMetrics <- InsituCompile(species_list=speciesList,
                                occurrenceData=cucurbitaData,
                                raster_list=cucurbitaRasters,
                                proArea=protectedAreas,
                                ecoReg=ecoregions)

fcsCombine <- FCSc_mean(fcsEx = exsituGapMetrics,fcsIn = insituGapMetrics)
```

FCSex

Final ex situ conservation score estimation (Ex-situ conservation)

Description

This function concatenates the SRSex, GRSex, and ERSex values in an unique dataframe object to calculate a final priority score as the average of the SRSex, GRSex, and ERSex values:

$$FCSex = mean(SRSex, GRSex, ERSex)$$

Usage

```
FCSex(srsDF, grsDF, ersDF)
```

Arguments

srsDF	A dataframe object result of the SRSex function
grsDF	A dataframe object result of the GRSex function
ersDF	A dataframe object result of the ERSex function

Value

This function returns a data frame with the follows information summarizing the ex situ gap analysis scores:

species	Species name
SRSex	Ex-situ sample representativeness score
GRSex	Ex-situ germplasm representativeness score
ERSex	Ex-situ environmental representativeness score
FCSex	Ex-situ final conservation score

References

Ramirez-Villegas, J., Khoury, C., Jarvis, A., Debouck, D. G., & Guarino, L. (2010). A Gap Analysis Methodology for Collecting Crop Genepools: A Case Study with Phaseolus Beans. PLOS ONE, 5(10), e13497. Retrieved from <https://doi.org/10.1371/journal.pone.0013497>

Khoury, C. K., Amariles, D., Soto, J. S., Diaz, M. V., Sotelo, S., Sosa, C. C., ... Jarvis, A. (2019). Comprehensiveness of conservation of useful wild plants: An operational indicator for biodiversity and sustainable development targets. Ecological Indicators. <https://doi.org/10.1016/j.ecolind.2018.11.016>

Examples

```
##Obtaining occurrences from example
data(cucurbitaData)
##Obtaining species names from the data
speciesList <- unique(cucurbitaData$taxon)
##Obtaining raster_list
data(cucurbitaRasters)
cucurbitaRasters <- raster::unstack(cucurbitaRasters)
##Obtaining ecoregions shapefile
data(ecoregions)

#Calculating SRSex value
SRSex_df <- SRSex(species_list = speciesList,
                  occurrenceData = cucurbitaData)

#Calculating GRSex value
GRSex_df <- GRSex(species_list = speciesList,
                  occurrenceData = cucurbitaData,
                  raster_list = cucurbitaRasters)

#Calculating ERSex value
ERSex_df <- ERSex(species_list = speciesList,
                  occurrenceData = cucurbitaData,
                  raster_list = cucurbitaRasters,
                  bufferDistance = 50000,
                  ecoReg=ecoregions
                  )

#Calculating final conservation for ex-situ gap analysis

FCSex_df <- FCSex(srsDF = SRSex_df, grsDF = GRSex_df, ersDF = ERSex_df)
```

FCSin	<i>Final in-situ conservation score estimation (In-situ conservation)</i>
-------	---

Description

This function concatenates the SRSin, GRSin, and ERSin values in an unique dataframe object to calculate a final priority score as the average of the SRSin, GRSin, and ERSin values:

$$FCSin = mean(SRSin, GRSin, ERSin)$$

Usage

```
FCSin(srsDF, grsDF, ersDF)
```

Arguments

srsDF	A dataframe object result of the SRSin function
grsDF	A dataframe object result of the GRSin function
ersDF	A dataframe object result of the ERSin function

Value

This function returns a data frame with the follows information summarizing the in-situ gap analysis scores:

species	Species name
SRSin	In-situ sample representativeness score
GRSin	In-situ germplasm representativeness score
ERSin	In-situ environmental representativeness score
FCSin	In-situ final conservation score

References

Ramirez-Villegas, J., Khoury, C., Jarvis, A., Debouck, D. G., & Guarino, L. (2010). A Gap Analysis Methodology for Collecting Crop Genepools: A Case Study with Phaseolus Beans. PLOS ONE, 5(10), e13497. Retrieved from <https://doi.org/10.1371/journal.pone.0013497>

Khoury, C. K., Amariles, D., Soto, J. S., Diaz, M. V., Sotelo, S., Sosa, C. C., ... Jarvis, A. (2019). Comprehensiveness of conservation of useful wild plants: An operational indicator for biodiversity and sustainable development targets. Ecological Indicators. <https://doi.org/10.1016/j.ecolind.2018.11.016>

Examples

```
##Obtaining occurrences from example
data(cucurbitaData)
##Obtaining species names from the data
speciesList <- unique(cucurbitaData$taxon)
##Obtaining raster_list
data(cucurbitaRasters)
cucurbitaRasters <- raster::unstack(cucurbitaRasters)
##Obtaining protected areas raster
```

```

data(protectedAreas)
##Obtaining ecoregions shapefile
data(ecoregions)
#Calculating SRSin value
SRSin_df <- SRSin(species_list = speciesList,
                  occurrenceData = cucurbitaData,
                  raster_list = cucurbitaRasters,
                  proArea=protectedAreas)

#Calculating GRSin value
GRSin_df <- GRSin(species_list = speciesList,
                  occurrenceData = cucurbitaData,
                  raster_list = cucurbitaRasters,
                  proArea=protectedAreas)

#Calculating ERSin value
ERSin_df <- ERSin(species_list = speciesList,
                  occurrenceData = cucurbitaData,
                  raster_list = cucurbitaRasters,
                  proArea=protectedAreas,
                  ecoReg=ecoregions)

#Calculating final conservation for ex-situ gap analysis

FCSin_df <- FCSin(srsDF = SRSin_df, grsDF = GRSin_df, ersDF = ERSin_df)

```

GetDatasets

Preparing datasets to run GapAnalysis functions

Description

This function creates the data_preloaded folder and it downloads datasets from dataverse to allow run gapAnalysis package function.

Usage

```
GetDatasets()
```

Value

This function downloads data required to run a full gap analysis. It creates the folder data_preloaded into the GapAnalysis. Please run this function after install the package.

References

Khoury, CK, Carver, D, Kates, HR, et al. Distributions, conservation status, and abiotic stress tolerance potential of wild cucurbits (*Cucurbita* L.). *Plants, People, Planet*. 2019; 00: 1– 15. <https://doi.org/10.1002/ppp3.10085>

Examples

```
## Not run:
GetDatasets()

## End(Not run)
```

GRSex	<i>Geographical representativeness score estimation (Ex-situ conservation)</i>
-------	--

Description

This function performs an estimation of the geographical representativeness score for ex-situ gap analysis (GRSex) using Ramirez-Villegas et al., (2010) methodology. GRS ex-situ score is calculated as:

$$GRSex = \min(100, (MaskedAreaofBufferedGOccurrences/TotalAreaofPredictedHabitat)*100)$$

Usage

```
GRSex(occurrenceData, species_list, raster_list, bufferDistance)
```

Arguments

occurrenceData	A data frame object with the species name, geographical coordinates, and type of records (G or H) for a given species
species_list	An species list to calculate the GRSex metrics.
raster_list	A list representing the species distribution models for the species list provided loaded in raster format. This list must match the same order of the species list.
bufferDistance	Geographical distance used to create circular buffers around germplasm. Default: 50000 that is 50 km around germplasm accessions (CA50)

Value

This function returns a data frame with two columns:

species	Species name
GRSex	GRSex value calculated

References

Ramirez-Villegas, J., Khoury, C., Jarvis, A., Debouck, D. G., & Guarino, L. (2010). A Gap Analysis Methodology for Collecting Crop Genepools: A Case Study with Phaseolus Beans. PLOS ONE, 5(10), e13497. Retrieved from <https://doi.org/10.1371/journal.pone.0013497>

Khoury, C. K., Amariles, D., Soto, J. S., Diaz, M. V., Sotelo, S., Sosa, C. C., ... Jarvis, A. (2019). Comprehensiveness of conservation of useful wild plants: An operational indicator for biodiversity and sustainable development targets. Ecological Indicators. <https://doi.org/10.1016/j.ecolind.2018.11.016>

Hijmans, R.J. and Spooner, D.M. (2001). Geographic distribution of wild potato species. Am. J. Bot., 88: 2101-2112. doi:10.2307/3558435

Examples

```
##Obtaining occurrences from example
data(cucurbitaData)
speciesList <- unique(cucurbitaData$taxon)
## Obtaining rasterList objet. ##
data(cucurbitaRasters)
cucurbitaRasters <- raster::unstack(cucurbitaRasters)
#Calculating GRSEX value
GRSEX_df <- GRSEX(species_list = speciesList,
                  occurrenceData = cucurbitaData,
                  raster_list = cucurbitaRasters,
                  bufferDistance = 50000)
```

GRSin	<i>Geographical representativeness score estimation (In-situ conservation)</i>
-------	--

Description

This function performs an estimation of germplasm representativeness score for in-situ gap analysis (GRSin) using Khoury et al., (2019) methodology # GRSEX is calculated as:

$$GRSin = \min(100, (PredictedHabitatwithinprotectedareas/TotalAreaofPredictedHabitat)*100)$$

Usage

```
GRSin(species_list, occurrenceData, raster_list, proArea)
```

Arguments

species_list	An species list to calculate the GRSEX metrics.
occurrenceData	A data frame object with the species name, geographical coordinates, and type of records (G or H) for a given species
raster_list	A list representing the species distribution models for the species list provided loaded in raster format. This list must match the same order of the species list.
proArea	A raster file representing protected areas information. If proArea=NULL the function will use a protected area raster file provided for your use after run Get-Datasets()

Value

This function returns a data frame with two columns:

species	Species name
GRSin	GRSEX value calculated

References

- Ramirez-Villegas, J., Khoury, C., Jarvis, A., Debouck, D. G., & Guarino, L. (2010). A Gap Analysis Methodology for Collecting Crop Genepools: A Case Study with Phaseolus Beans. PLOS ONE, 5(10), e13497. Retrieved from <https://doi.org/10.1371/journal.pone.0013497>
- Khoury, C. K., Amariles, D., Soto, J. S., Diaz, M. V., Sotelo, S., Sosa, C. C., ... Jarvis, A. (2019). Comprehensiveness of conservation of useful wild plants: An operational indicator for biodiversity and sustainable development targets. Ecological Indicators. <https://doi.org/10.1016/j.ecolind.2018.11.016>

Examples

```
##Obtaining occurrences from example
data(cucurbitaData)
##Obtaining species names from the data
speciesList <- unique(cucurbitaData$taxon)
##Obtaining raster_list
data(cucurbitaRasters)
cucurbitaRasters <- raster::unstack(cucurbitaRasters)
##Obtaining protected areas raster
data(protectedAreas)

GRSin_df <- GRSin(species_list = speciesList,
                  occurrenceData = cucurbitaData,
                  raster_list = cucurbitaRasters,
                  proArea=protectedAreas)
```

InsituCompile

In-situ gap analysis calculation (In-situ conservation)

Description

This function allows calculating all the three In-situ gap analysis scores in one unique function returning a final conservation score summary table

Usage

```
InsituCompile(species_list, occurrenceData, raster_list, proArea, ecoReg)
```

Arguments

- | | |
|----------------|--|
| species_list | An species list to calculate metrics. |
| occurrenceData | A data frame object with the species name, geographical coordinates, and type of records (G or H) for a given species |
| raster_list | A list representing the species distribution models for the species list provided loaded in raster format. This list must match the same order of the species list. |
| proArea | A raster file representing protected areas information. If proArea=NULL the function will use a protected area raster file provided for your use after run GetDatasets() |
| ecoReg | A shapefile representing ecoregions information with a field ECO_NUM representing ecoregions Ids. If ecoReg=NULL the function will use a shapefile provided for your use after run GetDatasets() |

Value

This function returns a data frame summarizing the in-situ gap analysis scores:

species	Species name
SRSin	In-situ sample representativeness score
GRSin	In-situ germplasm representativeness score
ERSin	In-situ environmental representativeness score
FCSin	In-situ final conservation score

References

Ramirez-Villegas, J., Khoury, C., Jarvis, A., Debouck, D. G., & Guarino, L. (2010). A Gap Analysis Methodology for Collecting Crop Genepools: A Case Study with Phaseolus Beans. PLOS ONE, 5(10), e13497. Retrieved from <https://doi.org/10.1371/journal.pone.0013497>

Khoury, C. K., Amariles, D., Soto, J. S., Diaz, M. V., Sotelo, S., Sosa, C. C., ... Jarvis, A. (2019). Comprehensiveness of conservation of useful wild plants: An operational indicator for biodiversity and sustainable development targets. Ecological Indicators. <https://doi.org/10.1016/j.ecolind.2018.11.016>

Examples

```
##Obtaining occurrences from example
data(cucurbitaData)
##Obtaining species names from the data
speciesList <- unique(cucurbitaData$taxon)
##Obtaining raster_list
data(cucurbitaRasters)
cucurbitaRasters <- raster::unstack(cucurbitaRasters)
##Obtaining protected areas raster
data(protectedAreas)
##Obtaining ecoregions shapefile
data(ecoregions)

#Running all three In situ gap analysis steps using InsituCompile function
insituGapMetrics <- InsituCompile(species_list=speciesList,
                                occurrenceData=cucurbitaData,
                                raster_list=cucurbitaRasters,
                                proArea=protectedAreas,
                                ecoReg=ecoregions)
```

OccurrenceCounts

Generating Species Count Data Frame

Description

This function creates a summary file the summarizes the total number of germplasm and herbarium occurrences

Usage

```
OccurrenceCounts(species, occurrenceData)
```

Arguments

- `species` The name of a species
- `occurrenceData` A data frame object with the species name, geographical coordinates, and type of records (G or H) for a given species

Value

This function returns a data frame object with the following columns:

<code>species</code>	Species name
<code>totalRecords</code>	Total records available
<code>hasLat</code>	Number of occurrences with latitude
<code>hasLon</code>	Number of occurrences with longitude
<code>totalUseful</code>	Number of occurrences with longitude
<code>totalGRecords</code>	Number of occurrences with longitude
<code>totalGUseful</code>	Number of occurrences with longitude
<code>totalHRecords</code>	Number of occurrences with longitude
<code>totalHUseful</code>	Number of occurrences with longitude

References

Ramirez-Villegas, J., Khoury, C., Jarvis, A., Debouck, D. G., & Guarino, L. (2010). A Gap Analysis Methodology for Collecting Crop Genepools: A Case Study with Phaseolus Beans. PLOS ONE, 5(10), e13497. Retrieved from <https://doi.org/10.1371/journal.pone.0013497>

Khoury, C. K., Amariles, D., Soto, J. S., Diaz, M. V., Sotelo, S., Sosa, C. C., ... Jarvis, A. (2019). Comprehensiveness of conservation of useful wild plants: An operational indicator for biodiversity and sustainable development targets. Ecological Indicators. <https://doi.org/10.1016/j.ecolind.2018.11.016>

Examples

```
data(cucurbitaData)
##Obtaining species names from the data
speciesList <- unique(cucurbitaData$taxon)
countDF <- OccurrenceCounts(speciesList[[1]],cucurbitaData)
```

<code>protectedAreas</code>	<i>Protected areas dataset in raster format</i>
-----------------------------	---

Description

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

Usage

```
protectedAreas
```

Format

Raster file

Source

<https://www.protectedplanet.net/>

References

Khoury, C. K., Amariles, D., Soto, J. S., Diaz, M. V., Sotelo, S., Sosa, C. C., ... Jarvis, A. (2019). Comprehensiveness of conservation of useful wild plants: An operational indicator for biodiversity and sustainable development targets. *Ecological Indicators*. <https://doi.org/10.1016/j.ecolind.2018.11.016>

SRSex

Sample representativeness score estimation (Ex-situ conservation)

Description

This function performs an estimation of sample representativeness score for ex-situ gap analysis (SRSex) using Ramirez-Villegas et al., (2010) methodology using information from herbarium and germplasm occurrences. SRS ex-situ score is calculated as:

$$SRSex = \text{Number of germplasm occurrences} / \text{Number of herbarium occurrences}$$

Usage

```
SRSex(species_list, occurrenceData)
```

Arguments

species_list An species list to calculate the SRSex metrics.

occurrenceData A data frame object with the species name, geographical coordinates, and type of records (G or H) for a given species

Value

This function returns a data frame with two columns:

species	Species name
SRSex	SRSex value calculated

References

Ramirez-Villegas, J., Khoury, C., Jarvis, A., Debouck, D. G., & Guarino, L. (2010). A Gap Analysis Methodology for Collecting Crop Genepools: A Case Study with Phaseolus Beans. *PLOS ONE*, 5(10), e13497. Retrieved from <https://doi.org/10.1371/journal.pone.0013497>

Khoury, C. K., Amariles, D., Soto, J. S., Diaz, M. V., Sotelo, S., Sosa, C. C., ... Jarvis, A. (2019). Comprehensiveness of conservation of useful wild plants: An operational indicator for biodiversity and sustainable development targets. *Ecological Indicators*. <https://doi.org/10.1016/j.ecolind.2018.11.016>

Examples

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

```
##Obtaining species names from the data
speciesList <- unique(cucurbitaData$taxon)
SRSex_df <- SRSex(species_list = speciesList,
                  occurrenceData = cucurbitaData)
```

SRSin

Sample representativeness score estimation (In-situ conservation)

Description

This function performs an estimation of the sample representativeness score for in situ gap analysis (SRSin) using Khoury et al., (2019) methodology. SRSin is calculated as:

$$SRSin = \text{Number of occurrences in protected areas} / \text{Total number of occurrences}$$

Usage

```
SRSin(species_list, occurrenceData, raster_list, proArea)
```

Arguments

<code>species_list</code>	An species list to calculate the SRSin metrics.
<code>occurrenceData</code>	A data frame object with the species name, geographical coordinates, and type of records (G or H) for a given species
<code>raster_list</code>	A list representing the species distribution models for the species list provided loaded in raster format. This list must match the same order of the species list.
<code>proArea</code>	A raster file representing protected areas information. If <code>proArea=NULL</code> the function will use a protected area raster file provided for your use after run <code>Get-Datasets()</code>

Value

This function returns a data frame with two columns:

<code>species</code>	Species name
<code>SRSin</code>	srsInsitu value calculated

References

Ramirez-Villegas, J., Khoury, C., Jarvis, A., Debouck, D. G., & Guarino, L. (2010). A Gap Analysis Methodology for Collecting Crop Genepools: A Case Study with Phaseolus Beans. *PLOS ONE*, 5(10), e13497. Retrieved from <https://doi.org/10.1371/journal.pone.0013497>

Khoury, C. K., Amariles, D., Soto, J. S., Diaz, M. V., Sotelo, S., Sosa, C. C., ... Jarvis, A. (2019). Comprehensiveness of conservation of useful wild plants: An operational indicator for biodiversity and sustainable development targets. *Ecological Indicators*. <https://doi.org/10.1016/j.ecolind.2018.11.016>

Examples

```
##Obtaining occurrences from example
```

```

data(cucurbitaData)
##Obtaining species names from the data
speciesList <- unique(cucurbitaData$taxon)
##Obtaining raster_list
data(cucurbitaRasters)
cucurbitaRasters <- raster::unstack(cucurbitaRasters)
##Obtaining protected areas raster
data(protectedAreas)
SRSin_df <- SRSin(species_list = speciesList,
                  occurrenceData = cucurbitaData,
                  raster_list=cucurbitaRasters,
                  proArea=protectedAreas)

```

summary_HTML

Creating a summary HTML document for gap analysis

Description

Calls the summaryHTML rmd file information from all in situ, ex situ, and EOO AOO summaries and displays The content. The code also produces in situ and ex situ gap maps which can be written out to disk.

Usage

```

summary_HTML(
  species_list,
  occurrenceData,
  raster_List,
  proArea,
  bufferDistance,
  insituSummary,
  exsituSummary,
  fcsSummary,
  eooAooSummary,
  outputFolder,
  writeRasters
)

```

Arguments

species_list	A species list to calculate metrics.
occurrenceData	A data frame object with the species name, geographical coordinates, and type of records (G or H) for a given species
raster_List	A list representing the species distribution models for the species list provided loaded in raster format. This list must match the same order of the species list.
proArea	A raster file representing protected areas information. If proArea=NULL the funtion will use a protected area raster file provided for your use after run Get-Datasets()
bufferDistance	Geographical distance used to create circular buffers around germplasm. Default: 50000 that is 50 km around germplasm accessions (CA50)

[illegible]

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