

# Package ‘GapAnalysis’

August 10, 2020

**Title** Conservation Indicators using Spatial Information

**Version** 1.0.1

**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 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>

**Depends** R (>= 3.5.0), raster (>= 3.0)

**Imports** base (>= 3.5), utils (>= 3.5), data.table, sp (>= 1.4.1), tmap (>= 2.3), sf (>= 0.8), methods (>= 3.5), geosphere (>= 1.5), dataverse (>= 0.2.0), fasterize (>= 1.0.0), rmarkdown (>= 2.1)

**Suggests** knitr, rgdal (>= 1.2-3), rgeos (>= 0.5), kableExtra (>= 1.1.0), DT

**License** GPL-3

**LazyData** true

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**Author** Dan Carver [aut, cph] (<<https://orcid.org/0000-0002-1344-6357>>),  
Chrystian Sosa [aut, cph] (<<https://orcid.org/0000-0002-3734-3248>>),  
Colin Khoury [aut, cph] (<<https://orcid.org/0000-0001-7893-5744>>),  
Julian Ramirez-Villegas [aut, cre, cph]  
(<<https://orcid.org/0000-0002-8044-583X>>),  
Valentin Stefan [ctb],  
Harold Achicanoy [ctb, cph],  
Maria Victoria Diaz [ctb, cph],  
Steven Sotelo [ctb, cph],  
Nora Castaneda-Alvarez [ctb, cph],  
Kaue De Sousa [ctb]

**Maintainer** Julian Ramirez-Villegas <J.R.Villegas@cgiar.org>

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GapAnalysis-package	<i>GapAnalysis: An R package to calculate conservation indicators using spatial information</i>
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## Description

GapAnalysis is a an R package used to calculate ex situ and in situ conservation indicators

## Details

Package: GapAnalysis  
 Type: Package  
 Version: 1.0.1  
 Date: 2020-07-13  
 License: GPL-3

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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 1184 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**

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

**References**

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

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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**

CucurbitaRasters

**Format**

raster files

**Source**

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

**References**

Khoury et al. (2019) Diversity and Distributions 26(2):209-225. doi: 10.1111/DDI.1300

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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](http://maps.tnc.org/gis_data.html)

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ERSex	<i>Ecological representativeness score ex situ</i>
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**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(
  Species_list,
  Occurrence_data,
  Raster_list,
  Buffer_distance = 50000,
  Ecoregions_shp = NULL,
  Gap_Map = FALSE
)
```

**Arguments**

Species_list	A vector of characters with the species names to calculate the GRSex metrics.
Occurrence_data	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 of rasters representing the species distribution models for the species list provided in <i>Species_list</i> . The order of rasters in this list must match the same order as <i>Species_list</i> .
Buffer_distance	Geographical distance used to create circular buffers around germplasm. Default: 50000 (50 km) around germplasm accessions (CA50)
Ecoregions_shp	A shapefile representing Ecoregions information with a field ECO_ID_U representing Ecoregions Ids. If Ecoregions=NULL the function will use a shapefile provided for use after running GetDatasets()
Gap_Map	logical, if TRUE the function will calculate gap maps for each species analyzed and will return a list with with two slots ERSex and gap_maps, or three slots ERSex, buffer_list, and gap_maps

**Value**

This function returns a dataframe as main result with two columns:

species	Species name
ERSex	ERSex value calculated

**References**

Castaneda-Alvarez et al. (2016) Nature Plants 2(4):16022. doi: 10.1038/nplants.2016.22  
 Khoury et al. (2019) Ecological Indicators 98:420-429. doi: 10.1016/j.ecolind.2018.11.016  
 The Nature Conservancy Geospatial Conservation Atlas. 2019. Terrestrial Ecoregions

**Examples**

```
##Obtaining occurrences from example
data(CucurbitaData)
Cucurbita_splist <- unique(CucurbitaData$species)
## Obtaining rasterList object. ##
data(CucurbitaRasters)
CucurbitaRasters <- raster::unstack(CucurbitaRasters)
##Obtaining ecoregions shapefile
data(ecoregions)
#Running ERSex
ERSex_df <- ERSex(Species_list = Cucurbita_splist,
                  Occurrence_data = CucurbitaData,
                  Raster_list = CucurbitaRasters,
                  Buffer_distance = 50000,
                  Ecoregions_shp=ecoregions,
```

Gap\_Map=FALSE)

---

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. This function uses a thresholded species distribution model, an ecoregions file, and a protected areas file

### Usage

```
ERSin(
  Species_list,
  Occurrence_data,
  Raster_list,
  Pro_areas = NULL,
  Ecoregions_shp = NULL,
  Gap_Map = FALSE
)
```

### Arguments

Species_list	A vector of characters with the species names to calculate the GRSex metrics.
Occurrence_data	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 of rasters representing the species distribution models for the species list provided in <i>Species_list</i> . The order of rasters in this list must match the same order as <i>Species_list</i> .
Pro_areas	A raster file representing protected areas information. If Pro_areas=NULL the function will use a protected area raster file provided for your use after run GetDatasets()
Ecoregions_shp	A shapefile representing Ecoregions_shp information with a field ECO_NUM representing Ecoregions_shp Ids. If Ecoregions_shp=NULL the function will use a protected area raster file provided for your use after run GetDatasets()
Gap_Map	logical, if TRUE the function will calculate gap maps for each species analyzed and will return a list with two slots ERSin and gap_maps

**Value**

This function returns a dataframe as main result with two columns:

species	Species name
ERSin	ERSin value calculated

## References

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

## Examples

```
##Obtaining occurrences from example
data(CucurbitaData)
##Obtaining species names from the data
Cucurbita_splist <- unique(CucurbitaData$species)
##Obtaining Raster_list
data(CucurbitaRasters)
CucurbitaRasters <- raster::unstack(CucurbitaRasters)
##Obtaining protected areas raster
data(ProtectedAreas)
##Obtaining ecoregions shapefile
data(ecoregions)
#Running ERSin
ERSin_df <- ERSin(Species_list = Cucurbita_splist,
                  Occurrence_data = CucurbitaData,
                  Raster_list = CucurbitaRasters,
                  Pro_areas= ProtectedAreas,
                  Ecoregions_shp=ecoregions,
                  Gap_Map=FALSE)
```

---

FCSc\_mean

*Combining ex situ and in situ gap analyses*

---

## Description

This function creates a final combined conservation score by averaging the FCSEX and FCSin It also assigns priority categories based on quantitative results

## Usage

```
FCSc_mean(FCSEX_df, FCSin_df)
```

## Arguments

FCSEX_df	A data frame or a list object result of the function FCSEX
FCSin_df	A data frame or a list object result of the function FCSin

## Value

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



species	Species name
FCSex	Final conservation score ex situ
FCSin	Final conservation score in situ
FCS_min	Final conservation score (minimum value among FCSin and FCSex)
FCS_max	Final conservation score (maximum value among FCSin and FCSex)
FCSc_mean	Final conservation score combined (average value between FCSin and FCSex)
FCS_min_class	Final conservation category using FCS_min value
FCS_max_class	Final conservation category using FCS_max value
FCSc_mean_class	Final conservation category using FCSc_mean value

## References

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

## Examples

```
##Obtaining occurrences from example
data(CucurbitaData)
##Obtaining species names from the data
Cucurbita_splist <- unique(CucurbitaData$species)
##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 FCSex function
FCSex_df <- FCSex(Species_list=Cucurbita_splist,
                  Occurrence_data=CucurbitaData,
                  Raster_list=CucurbitaRasters,
                  Buffer_distance=50000,
                  Ecoregions_shp=ecoregions,
                  Gap_Map=FALSE)

#Running all three in situ gap analysis steps using FCSin function
FCSin_df <- FCSin(Species_list=Cucurbita_splist,
                  Occurrence_data=CucurbitaData,
                  Raster_list=CucurbitaRasters,
                  Ecoregions_shp=ecoregions,
                  Pro_areas=ProtectedAreas,
                  Gap_Map=FALSE)

## Combine gap analysis metrics
FCSc_mean_df <- FCSc_mean(FCSex_df = FCSex_df,FCSin_df = FCSin_df)
```

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(
  Species_list,
  Occurrence_data,
  Raster_list,
  Buffer_distance = 50000,
  Ecoregions_shp = NULL,
  Gap_Map = FALSE
)
```

**Arguments**

Species_list	A vector of characters with the species names to calculate the GRSex metrics.
Occurrence_data	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 of rasters representing the species distribution models for the species list provided in <i>Species_list</i> . The order of rasters in this list must match the same order as <i>Species_list</i> .
Buffer_distance	Geographical distance used to create circular buffers around germplasm. Default: 50000 (50 km) around germplasm accessions (CA50)
Ecoregions_shp	A shapefile representing Ecoregions information with a field ECO_ID_U representing Ecoregions Ids. If Ecoregions=NULL the function will use a shapefile provided for use after running GetDatasets()
Gap_Map	logical, if TRUE the function will calculate gap maps for each species analyzed and will return a list with three slots: FCSex, GRSex_maps, and ERSex_maps

**Value**

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

species	Species name
SRSex	Sampling representativeness score ex situ
GRSex	Geographical representativeness score ex situ
ERSex	Ecological representativeness score ex situ
FCSex	Final conservation score ex situ

## References

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

## Examples

```
##Obtaining occurrences from example
data(CucurbitaData)
##Obtaining species names from the data
Cucurbita_splist <- unique(CucurbitaData$species)
##Obtaining raster_list
data(CucurbitaRasters)
CucurbitaRasters <- raster::unstack(CucurbitaRasters)
##Obtaining ecoregions shapefile
data(ecoregions)
#Running all three Ex-situ gap analysis steps using a unique function
FCSex_df <- FCSex(Species_list=Cucurbita_splist,
                  Occurrence_data=CucurbitaData,
                  Raster_list=CucurbitaRasters,
                  Buffer_distance=50000,
                  Ecoregions_shp=ecoregions,
                  Gap_Map=TRUE)
```

---

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(
  Species_list,
  Occurrence_data,
  Raster_list,
  Ecoregions_shp = NULL,
  Pro_areas = NULL,
  Gap_Map = FALSE
)
```

## Arguments

**Species\_list** A vector of characters with the species names to calculate the GRSex metrics.

**Occurrence\_data** 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 of rasters representing the species distribution models for the species list provided in <i>Species_list</i> . The order of rasters in this list must match the same order as <i>Species_list</i> .
Ecoregions_shp	A shapefile representing Ecoregions_shp information with a field ECO_NUM representing Ecoregions_shp Ids.If Ecoregions_shp=NULL the function will use an ecoregions raster file provided for your use
Pro_areas	A raster file representing protected areas information.If Pro_areas=NULL the function will use a protected area raster file provided for your use after run Get-Datasets()
Gap_Map	logical, if TRUE the function will calculate gap maps for each species analyzed and will return a list with four slots FCSin, SRSin_maps,GRSin_maps,and ERSin_maps

### Value

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

species	Species name
SRSin	Sampling representativeness score in situ
GRSin	Geographical representativeness score in situ
ERSin	Ecological representativeness score in situ
FCSin	Final conservation score in situ

### References

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

### Examples

```
##Obtaining occurrences from example
data(CucurbitaData)
##Obtaining species names from the data
Cucurbita_splist <- unique(CucurbitaData$species)
##Obtaining Raster_list
data(CucurbitaRasters)
CucurbitaRasters <- raster::unstack(CucurbitaRasters)
##Obtaining protected areas raster
data(ProtectedAreas)
##Obtaining Ecoregions_shpions shapefile
data(ecoregions)
#Running all three In-situ gap analysis steps using a unique function
FCSin_df <- FCSin(Species_list=Cucurbita_splist,
                  Occurrence_data=CucurbitaData,
                  Raster_list=CucurbitaRasters,
                  Ecoregions_shp=ecoregions,
                  Pro_areas=ProtectedAreas,
                  Gap_Map=FALSE)
```

---

`GetDatasets`*Preparing datasets to run GapAnalysis functions*

---

**Description**

This function creates the `data_preloaded` folder. It downloads datasets from dataverse to allow the `gapAnalysis` package to 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 installing the package.

**References**

Khoury et al. (2019) Data in Brief 22:90-97. doi: 10.1016/j.dib.2018.11.125. Khoury et al. (2019) Diversity and Distributions 26(2):209-225. doi: 10.1111/DDI.1300

**Examples**

```
GetDatasets()
```

---

`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(  
  Species_list,  
  Occurrence_data,  
  Raster_list,  
  Buffer_distance = 50000,  
  Gap_Map = FALSE  
)
```

**Arguments**

Species_list	A vector of characters with the species names to calculate the GRSex metrics.
Occurrence_data	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 of rasters representing the species distribution models for the species list provided in <i>Species_list</i> . The order of rasters in this list must match the same order as <i>Species_list</i> .
Buffer_distance	Geographical distance used to create circular buffers around germplasm. Default: 50000 (50 km) around germplasm accessions (CA50)
Gap_Map	logical, if TRUE the function will calculate gap maps for each species analyzed and will return a list with two slots GRSex and gap_maps. If any value is provided, the function will assume that Gap_Map = TRUE

**Value**

This function returns a data frame with two columns:

species	Species name
GRSex	GRSex value calculated

**References**

Ramirez-Villegas et al. (2010) PLOS ONE, 5(10), e13497. doi: 10.1371/journal.pone.0013497  
 Khoury et al. (2019) Ecological Indicators 98:420-429. doi: 10.1016/j.ecolind.2018.11.016

**Examples**

```
##Obtaining occurrences from example
data(CucurbitaData)
Cucurbita_splist <- unique(CucurbitaData$species)
## Obtaining rasterList object. ##
data(CucurbitaRasters)
CucurbitaRasters <- raster::unstack(CucurbitaRasters)
#Running GRSex
GRSex_df <- GRSex(Species_list = Cucurbita_splist,
                  Occurrence_data = CucurbitaData,
                  Raster_list = CucurbitaRasters,
                  Buffer_distance = 50000,
                  Gap_Map = TRUE)
```

**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(
  Species_list,
  Occurrence_data,
  Raster_list,
  Pro_areas = NULL,
  Gap_Map = FALSE
)
```

**Arguments**

Species_list	A vector of characters with the species names to calculate the GRSex metrics.
Occurrence_data	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 of rasters representing the species distribution models for the species list provided in <i>Species_list</i> . The order of rasters in this list must match the same order as <i>Species_list</i> .
Pro_areas	A raster file representing protected areas information. If Pro_areas=NULL the function will use a protected area raster file provided for your use after run Get-Datasets()
Gap_Map	logical, if TRUE the function will calculate gap maps for each species analyzed and will return a list with two slots ERSin and gap_maps

**Value**

This function returns a data frame with two columns:

species	Species name
GRSin	GRSin value calculated

**References**

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

**Examples**

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

```

##Obtaining species names from the data
Cucurbita_splist <- unique(CucurbitaData$species)
##Obtaining Raster_list
data(CucurbitaRasters)
CucurbitaRasters <- raster::unstack(CucurbitaRasters)
##Obtaining protected areas raster
data(ProtectedAreas)
#Running GRSin
GRSin_df <- GRSin(Species_list = Cucurbita_splist,
                  Occurrence_data = CucurbitaData,
                  Raster_list = CucurbitaRasters,
                  Pro_areas=ProtectedAreas,
                  Gap_Map=FALSE)

```

---

indicator

*Conservation indicator across taxa based on gap analysis results*

---

### Description

This function uses a data.frame resulting from the function FCSc\_mean and computes a conservation indicator across taxa.

### Usage

```
indicator(FCSc_mean_df)
```

### Arguments

FCSc\_mean\_df    A data frame object result of the function FCSc\_mean

### Value

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

opt	Final conservation score option
count_HP	Count of taxa high priority for conservation action
count_MP	Count of taxa medium priority for conservation action
count_LP	Count of taxa low priority for conservation action
count_SC	Count of taxa sufficiently conserved
count_LP_SC	Count of taxa low priority for conservation action or sufficiently conserved
proportion_HP	Proportion of taxa high priority for conservation action
proportion_MP	Proportion of taxa medium priority for conservation action
proportion_LP	Proportion of taxa low priority for conservation action
proportion_SC	Proportion of taxa sufficiently conserved
proportion_LP_SC	Proportion of taxa low priority for conservation action or sufficiently conserved (indicator)



## References

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

## Examples

```
##Obtaining occurrences from example
data(CucurbitaData)
##Obtaining species names from the data
Cucurbita_splist <- unique(CucurbitaData$species)
##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 FCSEX function
FCSEX_df <- FCSEX(Species_list=Cucurbita_splist,
                  Occurrence_data=CucurbitaData,
                  Raster_list=CucurbitaRasters,
                  Buffer_distance=50000,
                  Ecoregions_shp=ecoregions)
#Running all three in situ gap analysis steps using FCSIN function
FCSIN_df <- FCSIN(Species_list=Cucurbita_splist,
                  Occurrence_data=CucurbitaData,
                  Raster_list=CucurbitaRasters,
                  Ecoregions_shp=ecoregions,
                  Pro_areas=ProtectedAreas)
## Combine gap analysis metrics
FCSC_mean_df <- FCSC_mean(FCSEX_df = FCSEX_df, FCSIN_df = FCSIN_df)
#Running indicator function
indicator_df <- indicator(FCSC_mean_df)
```

---

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

Raster file

**Source**

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

**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(Species_list, Occurrence_data)
```

**Arguments**

`Species_list` A species list to calculate the SRSex metrics.

`Occurrence_data`

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:

<code>species</code>	Species name
<code>SRSex</code>	SRSex value calculated

**References**

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

**Examples**

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

```
##Obtaining species names from the data
Cucurbita_splist <- unique(CucurbitaData$species)
#Running SRSex
SRSex_df <- SRSex(Species_list = Cucurbita_splist,
                  Occurrence_data = 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(
  Species_list,
  Occurrence_data,
  Raster_list,
  Pro_areas = NULL,
  Gap_Map = FALSE
)
```

### Arguments

Species_list	A vector of characters with the species names to calculate the GRSex metrics.
Occurrence_data	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 of rasters representing the species distribution models for the species list provided in <i>Species_list</i> . The order of rasters in this list must match the same order as <i>Species_list</i> .
Pro_areas	A raster file representing protected areas information. If Pro_areas=NULL the function will use a protected area raster file provided for your use after run Get-Datasets()
Gap_Map	logical, if TRUE the function will calculate gap maps for each species analyzed and will return a list with two slots SRSin and gap_maps

### Value

This function returns a data frame with two columns:

species	Species name
SRSin	SRSin value calculated

## References

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

## Examples

```
##Obtaining occurrences from example
data(CucurbitaData)
##Obtaining species names from the data
Cucurbita_splist <- unique(CucurbitaData$species)
##Obtaining Raster_list
data(CucurbitaRasters)
CucurbitaRasters <- raster::unstack(CucurbitaRasters)
##Obtaining protected areas raster
data(ProtectedAreas)
#Running SRSin
SRSin_df <- SRSin(Species_list = Cucurbita_splist,
                  Occurrence_data = CucurbitaData,
                  Raster_list=CucurbitaRasters,
                  Pro_areas=ProtectedAreas,
                  Gap_Map=FALSE)
```

---

SummaryHTML

*Creating a summary HTML document for each taxon*

---

## Description

Calls the summaryHTML rmd file information and displays the quantitative and spatial results content.

## Usage

```
SummaryHTML(
  Species_list,
  Occurrence_data,
  Raster_list,
  Buffer_distance = 50000,
  Ecoregions_shp = NULL,
  Pro_areas = NULL,
  Output_Folder,
  writeRasters
)
```

## Arguments

**Species\_list** A species list to calculate metrics.

**Occurrence\_data**

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 as the species list.
Buffer_distance	Geographical distance used to create circular buffers around germplasm. Default: 50000 that is 50 km around germplasm accessions (CA50)
Ecoregions_shp	A shapefile representing Ecoregions information with a field ECO_ID_U representing Ecoregions Ids. If Ecoregions=NULL the function will use a shapefile provided for use after running GetDatasets()
Pro_areas	A raster file representing protected areas information. If Pro_areas=NULL the function will use a protected area raster file provided for your use after run GetDatasets()
Output_Folder	A path to save the HTML file resulting of this function
writeRasters	Boolean field (default=FALSE) to indicate if raster files should be saved

### Value

This function returns a data frame file saved at a specified folder

### References

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

### Examples

```
##Obtaining occurrences from example
data(CucurbitaData)
##Obtaining species names from the data
Cucurbita_splist <- unique(CucurbitaData$species)
##Obtaining raster_list
data(CucurbitaRasters)
CucurbitaRasters <- raster::unstack(CucurbitaRasters)
##Obtaining protected areas raster
data(ProtectedAreas)
##Obtaining ecoregions shapefile
data(ecoregions)
##Get datasets
GetDatasets()
##Running SummaryHTML function
summaryHTML_file <- SummaryHTML(Species_list=Cucurbita_splist,
                                Occurrence_data = CucurbitaData,
                                Raster_list=CucurbitaRasters,
                                Pro_areas=ProtectedAreas,
                                Buffer_distance=50000,
                                Ecoregions_shp=ecoregions,
                                Output_Folder=tempdir(),
                                writeRasters=FALSE)
```

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