Package: BoundaryStats (via r-universe)

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Type Package

Title Boundary Overlap Statistics

Version 2.3.0

Description Analysis workflow for finding geographic boundaries of ecological or landscape traits and comparing the placement of geographic boundaries of two traits. If data are trait values, trait data are transformed to boundary intensities based on approximate first derivatives across latitude and longitude. The package includes functions to create custom null models based on the input data. The boundary statistics are described in: Fortin, Drapeau, and Jacquez (1996) <doi:10.2307/3545584>.

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LazyData true

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`A.delicatus_crs` *Afrixalus delicatus genetic groups projection*

Description

Projection for A.delicatus_matrix

Usage

```
data(A.delicatus)
```

Format

Projection crs object

Source

doi:10.5061/dryad.315km76

References

Barratt et al. (2013) Molecular Ecology 27:4289–4308

A.delicatus_ext *Afrixalus delicatus genetic groups extent*

Description

Extent for A.delicatus_matrix

Usage

```
data(A.delicatus)
```

Format

Numeric vector of length length 4

Source

doi:10.5061/dryad.315km76

References

Barratt et al. (2013) Molecular Ecology 27:4289–4308

A.delicatus_matrix *Afrixalus delicatus genetic groups*

Description

Raster data representing interpolated genetic group assignments for Afrixalus delicatus based on analyses in Barratt et al. 2018.

Usage

```
data(A.delicatus)
```

Format

A matrix to be converted into a SpatRaster object with a EPSG:4210 projection.

Source

doi:10.5061/dryad.315km76

References

Barratt et al. (2013) Molecular Ecology 27:4289–4308

A.sylvaticus_crs *Afrixalus sylvaticus genetic groups projection*

Description

Projection for A.sylvaticus_matrix

Usage

```
data(A.sylvaticus)
```

Format

Projection crs object

Source

doi:10.5061/dryad.315km76

References

Barratt et al. (2013) Molecular Ecology 27:4289–4308

A.sylvaticus_ext *Afrixalus sylvaticus genetic groups extent*

Description

Extent for A.sylvaticus_matrix

Usage

```
data(A.sylvaticus)
```

Format

Numeric vector of length length 4

Source

doi:10.5061/dryad.315km76

References

Barratt et al. (2013) Molecular Ecology 27:4289–4308

A.sylvaticus_matrix *Afrixalus sylvaticus genetic groups*

Description

Raster data representing interpolated genetic group assignments for Afrixalus sylvaticus based on analyses in Barratt et al. 2018.

Usage

```
data(A.sylvaticus)
```

Format

A matrix to be converted into a SpatRaster object with a EPSG:4210 projection.

Source

doi:10.5061/dryad.315km76

References

Barratt et al. (2013) Molecular Ecology 27:4289–4308

`average_min_distance` *Average minimum distance between boundary elements of two variables*

Description

Statistical test for the average minimum distance between boundary elements in two raster layers. Uses Euclidean distance. Boundaries for each trait affect one another reciprocally (x affects y and y affects x).

Usage

```
average_min_distance(x, y, null_distrib)
```

Arguments

`x`	A SpatRaster object with boundary elements.
`y`	A SpatRaster object with boundary elements.
`null_distrib`	A list of probability functions output from overlap_null_distrib().

Value

p-value

Author(s)

Amy Luo

References

Jacquez, G.M., Maruca,I S. & Fortin, M.-J. (2000) From fields to objects: A review of geographic boundary analysis. Journal of Geographical Systems, 3, 221, 241. Fortin, M.-J., Drapeau, P. & Jacquez, G.M. (1996) Quantification of the Spatial Co-Occurrences of Ecological Boundaries. Oikos, 77, 51-60.

Examples

```
data(T.cristatus)
T.cristatus <- terra::rast(T.cristatus_matrix, crs = T.cristatus_crs)
terra::ext(T.cristatus) <- T.cristatus_ext

data(grassland)
grassland <- terra::rast(grassland_matrix, crs = grassland_crs)
terra::ext(grassland) <- grassland_ext

Tcrist_ovlp_null <- overlap_null_distrib(T.cristatus, grassland, rand_both = FALSE,
  x_cat = TRUE, n_iterations = 100, x_model = 'random_cluster')
Tcrist_boundaries <- define_boundary(T.cristatus, cat = TRUE)
```

```
grassland_boundaries <- define_boundary(grassland, cat = FALSE, threshold = 0.1)

average_min_distance(Tcrist_boundaries, grassland_boundaries, Tcrist_ovlp_null)
```

`average_min_x_to_y` *Average minimum distance from x boundary elements to nearest y boundary element.*

Description

Statistical test for the average minimum distance between each boundary element in raster x and the nearest boundary element in raster y. Uses Euclidean distance. The boundaries of trait x depend on the boundaries of trait y.

Usage

```
average_min_x_to_y(x, y, null_distrib)
```

Arguments

`x`	A SpatRaster object with boundary elements.
`y`	A SpatRaster object with boundary elements.
`null_distrib`	A list of probability functions output from overlap_null_distrib().

Value

The average minimum distance and a p-value.

Author(s)

Amy Luo

References

Jacquez, G.M., Maruca,I S. & Fortin,M.-J. (2000) From fields to objects: A review of geographic boundary analysis. Journal of Geographical Systems, 3, 221, 241. Fortin, M.-J., Drapeau, P. & Jacquez, G.M. (1996) Quantification of the Spatial Co-Occurrences of Ecological Boundaries. Oikos, 77, 51-60.

Examples

```
data(T.cristatus)
T.cristatus <- terra::rast(T.cristatus_matrix, crs = T.cristatus_crs)
terra::ext(T.cristatus) <- T.cristatus_ext

data(grassland)
grassland <- terra::rast(grassland_matrix, crs = grassland_crs)
terra::ext(grassland) <- grassland_ext

Tcrist_ovlp_null <- overlap_null_distrib(T.cristatus, grassland, rand_both = FALSE,
  x_cat = TRUE, n_iterations = 100, x_model = 'random_cluster')
Tcrist_boundaries <- define_boundary(T.cristatus, cat = TRUE)
grassland_boundaries <- define_boundary(grassland, cat = FALSE, threshold = 0.1)

average_min_x_to_y(Tcrist_boundaries, grassland_boundaries, Tcrist_ovlp_null)
```

---

boundary_null_distrib *Null distribution for overlap statistics*

Description

Creates custom probability distributions for two boundary statistics (number of subgraphs and length of the longest subgraph). Given a SpatRaster object, simulates n iterations of random raster surfaces from a neutral model.

Usage

```
boundary_null_distrib(
  x,
  calculate_intensity = FALSE,
  cat = FALSE,
  threshold = 0.2,
  n_iterations = 10,
  model = "random",
  p = 0.5,
  progress = TRUE
)
```

Arguments

x	A SpatRaster object.
calculate_intensity	TRUE if x contains numeric trait data from which boundary intensities should be calculated. default = FALSE.
cat	TRUE if the input SpatRaster contains a categorical variable. default = FALSE.

threshold	A value between 0 and 1. The proportion of cells to keep as boundary elements. default = 0.2.
n_iterations	An integer indicating the number of iterations for the function. A value of 100 or 1000 is recommended to produce sufficient resolution for downstream statistical tests. default = 10.
model	Neutral model to use. Options: 'random' (stochastic), 'gaussian' (Gaussian random field), and 'random_cluster' (modified random clusters method)
p	If using modified random clusters, proportion of cells to be marked in percolated raster.Higher values of p produce larger clusters. Default: p = 0.5
progress	If progress = TRUE (default) a progress bar will be displayed.

Value

A list of two probability distribution functions for boundary statistics.

Author(s)

Amy Luo

References

Saura, S. & Martínez-Millán, J. (2000). Landscape patterns simulation with a modified random clusters method. Landscape Ecology, 15:661-678.

Examples

```
data(T.cristatus)
T.cristatus <- terra::rast(T.cristatus_matrix, crs = T.cristatus_crs)
  terra::ext(T.cristatus) <- T.cristatus_ext

T.crist_bound_null <- boundary_null_distrib(T.cristatus, cat = TRUE,
n_iterations = 100, model = 'random_cluster')
```

---

categorical_boundary *Define the boundary elements of a SpatRaster with categorical data*

Description

This function is deprecated. Please use define_boundary

Creates boundary element cells where patches of two categories meet.

Usage

```
categorical_boundary(x)
```

Arguments

x	A SpatRaster object.

Value

A SpatRaster object with cell values 1 for boundary elements and 0 for other cells

Author(s)

Amy Luo

Examples

```
data(grassland)
grassland <- terra::rast(grassland_matrix, crs = grassland_crs)
terra::ext(grassland) <- grassland_ext

grassland_boundaries <- categorical_boundary(grassland)
```

---

define_boundary *Define the boundary elements of a SpatRaster with numeric data or boundary intensities*

Description

Defines boundary elements in a SpatRaster object.

For categorical traits, boundary elements are defined as cells that neighbor a patch with a different value.

If the trait is quantitative, function will keep a proportion of the cells with the highest boundary intensity values, with a threshold chosen by the user. If the SpatRaster contains trait values, boundary intensity values can be calculated (calculate_intensity = T) using a Sobel-Feldman operator.

In some cases, there may be many redundant values for boundary intensity. If the threshold is set to cut off the values at those points, the actual proportion of cells categorized as boundary elements would differ from the intended threshold. The function reports the proportion of cells that are boundary elements, so that users can choose a different value, if necessary.

Usage

```
define_boundary(x, cat = FALSE, threshold = 0.2, calculate_intensity = FALSE)
```

Arguments

x	A SpatRaster object.
cat	TRUE if the input SpatRaster contains a categorical variable. default = FALSE.
threshold	A value between 0 and 1. The proportion of cells to keep as boundary elements. default = 0.2.
calculate_intensity	logical. If TRUE, calculate boundary intensity at each cell from trait data. default = FALSE.

Value

A SpatRaster object with cell values 1 for boundary elements and 0 for other cells

Author(s)

Amy Luo

References

Fortin, M.J. et al. (2000) Issues related to the detection of boundaries. Landscape Ecology, 15, 453-466. Jacquez, G.M., Maruca,I S. & Fortin M.-J. (2000) From fields to objects: A review of geographic boundary analysis. Journal of Geographical Systems, 3, 221, 241.

Examples

```
data(grassland)
grassland <- terra::rast(grassland_matrix, crs = grassland_crs)
terra::ext(grassland) <- grassland_ext

grassland_boundaries <- define_boundary(grassland, threshold = 0.1)
```

---

ecoregions_crs *Ecoregion data for East Africa projection*

Description

Projection for ecoregions_matrix

Usage

```
data(ecoregions)
```

Format

Projection crs object

Source

doi:10.5061/dryad.315km76

References

Barratt et al. (2013) Molecular Ecology 27:4289–4308

---

ecoregions_ext *Ecoregion data for East Africa extent*

Description

Extent for ecoregions_matrix

Usage

```
data(ecoregions)
```

Format

Numeric vector of length length 4

Source

doi:10.5061/dryad.315km76

References

Barratt et al. (2013) Molecular Ecology 27:4289–4308

---

ecoregions_matrix *Ecoregion data for East Africa*

Description

Raster data of ecoregions in East Africa

Usage

```
data(ecoregions)
```

Format

A matrix to be converted into a SpatRaster object with a EPSG:4210 projection.

Source

doi:10.5061/dryad.315km76

References

Barratt et al. (2013) Molecular Ecology 27:4289–4308

`gauss_random_field_sim` *Gaussian random field neutral model*

Description

Simulates a gaussian random field as a neutral landscape of the same extent and resolution as the input raster, using the same spatial autocorrelation range as the input

Usage

```
gauss_random_field_sim(x, autocorr_range)
```

Arguments

`x`	A SpatRaster object.
`autocorr_range`	Distance range of spatial autocorrelation.

Value

A SpatRaster object with boundary elements.

Author(s)

Amy Luo

References

James, P. M. A., Fleming, R.A., & Fortin, M.-J. (2010) Identifying significant scale-specific spatial boundaries using wavelets and null models: Spruce budworm defoliation in Ontario, Canada as a case study. Landscape Ecology, 6, 873-887.

Examples

```
data(grassland)
grassland <- terra::rast(grassland_matrix, crs = grassland_crs)
terra::ext(grassland) <- grassland_ext

simulation <- gauss_random_field_sim(grassland, 3)
terra::plot(simulation)
```

grassland_crs *Grassland land cover projection*

Description

Projection for grassland_matrix

Usage

```
data(grassland)
```

Format

Projection crs object

Source

doi:10.5061/dryad.bk3j9kdhz

References

Cox et al. (2023) Conservation Genetics Radoux et al. (2019) Remote Sens 11:354.

grassland_ext *Grassland land cover extent*

Description

Extent for grassland_matrix

Usage

```
data(grassland)
```

Format

Numeric vector of length length 4

Source

doi:10.5061/dryad.bk3j9kdhz

References

Cox et al. (2023) Conservation Genetics Radoux et al. (2019) Remote Sens 11:354.

grassland_matrix *Grassland land cover*

Description

Raster land cover data from the LifeWatch Wallonia-Brussels ecotope database and used in Cox et al. 2023. Downsampled to match T. cristatus raster

Usage

```
data(grassland)
```

Format

A matrix to be converted into a SpatRaster object with a EPSG:4326 projection.

Source

doi:10.5061/dryad.bk3j9kdhz

References

Cox et al. (2023) Conservation Genetics Radoux et al. (2019) Remote Sens 11:354.

L.concolor_crs *Leptopelis concolor genetic groups projection*

Description

Projection

Usage

```
data(L.concolor)
```

Format

Projection crs object

Source

doi:10.5061/dryad.315km76

References

Barratt et al. (2013) Molecular Ecology 27:4289–4308

L.concolor_ext *Leptopelis concolor genetic groups extent*

Description

Extent for L.concolor_matrix

Usage

```
data(L.concolor)
```

Format

Numeric vector of length length 4

Source

doi:10.5061/dryad.315km76

References

Barratt et al. (2013) Molecular Ecology 27:4289–4308

L.concolor_matrix *Leptopelis concolor genetic groups*

Description

Raster data representing interpolated genetic group assignments for Leptopelis concolor based on analyses in Barratt et al. 2018.

Usage

```
data(L.concolor)
```

Format

A matrix to be converted into a SpatRaster object with a EPSG:4210 projection.

Source

doi:10.5061/dryad.315km76

References

Barratt et al. (2013) Molecular Ecology 27:4289–4308

`L.flavomaculatus_crs` *Leptopelis flavomaculatus genetic groups projection*

Description

Projection for L.flavomaculatus_matrix

Usage

```
data(L.flavomaculatus)
```

Format

Projection crs object

Source

doi:10.5061/dryad.315km76

References

Barratt et al. (2013) Molecular Ecology 27:4289–4308

`L.flavomaculatus_ext` *Leptopelis flavomaculatus genetic groups extent*

Description

Extent for L.flavomaculatus_ext

Usage

```
data(L.flavomaculatus)
```

Format

Numeric vector of length length 4

Source

doi:10.5061/dryad.315km76

References

Barratt et al. (2013) Molecular Ecology 27:4289–4308

L.flavomaculatus_matrix *Leptopelis flavomaculatus genetic groups*

Description

Raster data representing interpolated genetic group assignments for Leptopelis flavomaculatus based on analyses in Barratt et al. 2018.

Usage

```
data(L.flavomaculatus)
```

Format

A matrix to be converted into a SpatRaster object with a EPSG:4210 projection.

Source

doi:10.5061/dryad.315km76

References

Barratt et al. (2013) Molecular Ecology 27:4289–4308

longest_boundary *Length of the longest boundary*

Description

Statistical test for the length of the longest subgraph, or set of contiguous boundary elements.

Usage

```
longest_boundary(x, null_distrib)
```

Arguments

x	A SpatRaster object with boundary elements.
null_distrib	A list of probability functions output from boundary_null_distrib().

Value

The length of the longest subgraph and a p-value.

Author(s)

Amy Luo

References

Jacquez, G.M., Maruca,I S. & Fortin M.-J. (2000) From fields to objects: A review of geographic boundary analysis. Journal of Geographical Systems, 3, 221, 241.

Examples

```
data(T.cristatus)
T.cristatus <- terra::rast(T.cristatus_matrix, crs = T.cristatus_crs)
terra::ext(T.cristatus) <- T.cristatus_ext

Tcrist_boundaries <- define_boundary(T.cristatus, cat = FALSE)
T.crist_bound_null <- boundary_null_distrib(T.cristatus, cat = TRUE, n_iterations = 100,
  model = 'random_cluster')

longest_boundary(Tcrist_boundaries, T.crist_bound_null)
```

---

mod_random_clust_sim *Modified random cluster neutral landscape model*

Description

Simulates a neutral landscape of the same extent and resolution as the input raster, with the same distribution of values.

Usage

```
mod_random_clust_sim(x, p)
```

Arguments

x	A SpatRaster object.
p	The proportion of cells to be marked in percolated raster. Higher values of p produce larger clusters.

Value

A SpatRaster object with boundary elements.

Author(s)

Amy Luo

References

Saura, S. & Martínez-Millán, J. (2000) Landscape patterns simulation with a modified random clusters method. Landscape Ecology, 15, 661 – 678.

Examples

```
data(grassland)
grassland <- terra::rast(grassland_matrix, crs = grassland_crs)
terra::ext(grassland) <- grassland_ext

simulation <- mod_random_clust_sim(grassland, p = 0.6)
terra::plot(simulation)
```

---

n_boundaries *Number of boundaries*

Description

Statistical test the for number of subgraphs, or sets of contiguous boundary elements, in the data.

Usage

```
n_boundaries(x, null_distrib)
```

Arguments

x	A SpatRaster object with boundary elements.
null_distrib	A list of probability functions output from boundary_null_distrib().

Value

The number of subgraphs in the raster and a p-value.

Author(s)

Amy Luo

References

Jacquez, G.M., Maruca,I S. & Fortin M.-J. (2000) From fields to objects: A review of geographic boundary analysis. Journal of Geographical Systems, 3, 221, 241.

Examples

```
data(T.cristatus)
T.cristatus <- terra::rast(T.cristatus_matrix, crs = T.cristatus_crs)
terra::ext(T.cristatus) <- T.cristatus_ext

T.crist_boundaries <- define_boundary(T.cristatus, cat = TRUE)
T.crist_bound_null <- boundary_null_distrib(T.cristatus, cat = TRUE,
n_iterations = 100, model = 'random_cluster')

n_boundaries(T.crist_boundaries, T.crist_bound_null)
```

---

n_overlap_boundaries *Direct overlap between boundary elements.*

Description

Statistical test for the number of directly overlapping boundary elements of two traits.

Usage

```
n_overlap_boundaries(x, y, null_distrib)
```

Arguments

x	A SpatRaster object with boundary elements.
y	A SpatRaster object with boundary elements.
null_distrib	A list of probability functions output from overlap_null_distrib().

Value

The number of directly overlapping boundary elements and a p-value.

Author(s)

Amy Luo

References

Jacquez, G.M., Maruca,I S. & Fortin, M.-J. (2000) From fields to objects: A review of geographic boundary analysis. Journal of Geographical Systems, 3, 221, 241. Fortin, M.-J., Drapeau, P. & Jacquez, G.M. (1996) Quantification of the Spatial Co-Occurrences of Ecological Boundaries. Oikos, 77, 51-60.

Examples

```
data(T.cristatus)
T.cristatus <- terra::rast(T.cristatus_matrix, crs = T.cristatus_crs)
terra::ext(T.cristatus) <- T.cristatus_ext

data(grassland)
grassland <- terra::rast(grassland_matrix, crs = grassland_crs)
terra::ext(grassland) <- grassland_ext

Tcrist_ovlp_null <- overlap_null_distrib(T.cristatus, grassland, rand_both = FALSE,
  x_cat = TRUE, n_iterations = 100, x_model = 'random_cluster')
Tcrist_boundaries <- define_boundary(T.cristatus, cat = TRUE)
grassland_boundaries <- define_boundary(grassland, cat = FALSE, threshold = 0.1)

n_overlap_boundaries(Tcrist_boundaries, grassland_boundaries, Tcrist_ovlp_null)
```

---

overlap_null_distrib *Null distribution for boundary overlap statistics*

Description

Creates custom probability distributions for three boundary overlap statistics (directly overlapping boundary elements, minimum distance between boundary elements in x to y, and minimum distance between elements in x and y). Given two SpatRaster objects with the same extent, projection, and resolution, simulates n iterations of random raster surfaces from neutral model(s).

Usage

```
overlap_null_distrib(
  x,
  y,
  rand_both,
  x_calculate_intensity = FALSE,
  y_calculate_intensity = FALSE,
  x_cat = FALSE,
  y_cat = FALSE,
  threshold = 0.2,
  n_iterations = 10,
  x_model = "random",
  y_model = "random",
  px = 0.5,
  py = 0.5,
  progress = TRUE
)
```

Arguments

x	A SpatRaster object. If rand_both = FALSE, only this raster will be modeled.
y	A SpatRaster object. If rand_both = FALSE, this raster does not change.
rand_both	TRUE if distribution of traits in x and y should be modeled.
x_calculate_intensity	TRUE if x contains numeric trait data from which boundary intensities should be calculated. default = FALSE.
y_calculate_intensity	TRUE if y contains numeric trait data from which boundary intensities should be calculated. default = FALSE.
x_cat	TRUE if x contains a categorical variable. default = FALSE.
y_cat	TRUE if y contains a categorical variable. default = FALSE.
threshold	A value between 0 and 1. The proportion of cells to keep as boundary elements. Default = 0.2.
n_iterations	An integer indicating the number of iterations for the function. A value of 100 or 1000 is recommended to produce sufficient resolution for downstream statistical tests. default = 10.
x_model	Neutral model to use. Options: 'random' (stochastic), 'gaussian' (Gaussian random field), and 'random_cluster' (modified random clusters method)
y_model	Neutral model to use for y.
px	If using modified random clusters for x, proportion of cells to be marked in percolated raster. Higher values of p produce larger clusters. Default = 0.5
py	If using modified random clusters for y, proportion of cells to be marked in percolated raster. Higher values of p produce larger clusters. Default = 0.5
progress	If progress = TRUE (default) a progress bar will be displayed.

Value

A list of probability distribution functions for boundary overlap statistics.

Author(s)

Amy Luo

References

Saura, S. & Martínez-Millán, J. (2000). Landscape patterns simulation with a modified random clusters method. Landscape Ecology, 15:661-678.

Examples

```
data(T.cristatus)
T.cristatus <- terra::rast(T.cristatus_matrix, crs = T.cristatus_crs)
terra::ext(T.cristatus) <- T.cristatus_ext

data(grassland)
```

```
grassland <- terra::rast(grassland_matrix, crs = grassland_crs)
terra::ext(grassland) <- grassland_ext

Tcrist_ovlp_null <- overlap_null_distrib(T.cristatus, grassland, rand_both = FALSE,
  x_cat = TRUE, n_iterations = 100, x_model = 'random_cluster')
```

`plot_boundary` *Map the boundary elements of two raster layers*

Description

This is a wrapper function for ggplot2 that will produce a map of boundary elements for two traits and show where boundary elements intersect.

Usage

```
plot_boundary(x, y, color = NA, trait_names = NA, output_raster = FALSE)
```

Arguments

`x`	A SpatRaster object with boundary elements.
`y`	A SpatRaster object with boundary elements.
`color`	Optional. A character vector of up to three colors (x boundary, y boundary, and overlapping elements).
`trait_names`	Optional. A character vector with up to two elements (legend name for x and legend name for y).
`output_raster`	Returns a SpatRaster object with the boundary elements of each trait and overlapping boundary elements together in a single layer.

Value

A ggplot2 object.

Author(s)

Amy Luo

Examples

```
data(T.cristatus)
T.cristatus <- terra::rast(T.cristatus_matrix, crs = T.cristatus_crs)
terra::ext(T.cristatus) <- T.cristatus_ext

data(grassland)
grassland <- terra::rast(grassland_matrix, crs = grassland_crs)
terra::ext(grassland) <- grassland_ext
```

```
Tcrist_boundaries <- define_boundary(T.cristatus, cat = TRUE)
grassland_boundaries <- define_boundary(grassland, threshold = 0.1)

plot_boundary(Tcrist_boundaries, grassland_boundaries)
```

`random_raster_sim` *Stochastic neutral landscape model*

Description

Simulates a spatially stochastic neutral landscape of the same extent and resolution as the input raster, with the same distribution of values.

Usage

```
random_raster_sim(x)
```

Arguments

`x`	A SpatRaster object.

Value

A SpatRaster object with boundary elements.

Author(s)

Amy Luo

References

James, P. M. A., Fleming, R.A., & Fortin, M.-J. (2010) Identifying significant scale-specific spatial boundaries using wavelets and null models: Spruce budworm defoliation in Ontario, Canada as a case study. Landscape Ecology, 6, 873-887.

Examples

```
data(grassland)
grassland <- terra::rast(grassland_matrix, crs = grassland_crs)
terra::ext(grassland) <- grassland_ext

simulation <- random_raster_sim(grassland)
terra::plot(simulation)
```

sobel_operator *Sobel-Feldman operator for edge detection*

Description

Uses a Sobel-Feldman operator (3x3 kernel) to detect internal edges in a SpatRaster object.

Usage

```
sobel_operator(x)
```

Arguments

x	A SpatRaster object.

Value

A SpatRaster object with boundary values.

Author(s)

Amy Luo

Examples

```
data(T.cristatus)
T.cristatus <- terra::rast(T.cristatus_matrix, crs = T.cristatus_crs)
terra::ext(T.cristatus) <- T.cristatus_ext

edges <- sobel_operator(T.cristatus)
terra::plot(edges)
```

T.cristatus_crs *Triturus cristatus genetic groups projection*

Description

Projection for T.cristatus_matrix

Usage

```
data(T.cristatus)
```

Format

ces Barratt et al. (2013) Molecular Ecology 27:4289–4308

Projection crs object

Source

doi:10.5061/dryad.bk3j9kdhz

References

Cox et al. (2023) Conservation Genetics

`T.cristatus_ext` *Triturus cristatus genetic groups extent*

Description

Extent for T.cristatus_matrix

Usage

```
data(T.cristatus)
```

Format

Numeric vector of length length 4

Source

doi:10.5061/dryad.bk3j9kdhz

References

Cox et al. (2023) Conservation Genetics

`T.cristatus_matrix` *Triturus cristatus genetic groups*

Description

Raster data representing interpolated genetic group assignments for Triturus cristatus based on analyses in Cox et al. 2023

Usage

```
data(T.cristatus)
```

Format

A matrix to be converted into a SpatRaster object with a EPSG:4326 projection.

Source

doi:10.5061/dryad.bk3j9kdhz

References

Cox et al. (2023) Conservation Genetics

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