

# Package ‘spatialwarnings’

October 14, 2022

**Type** Package

**Title** Spatial Early Warning Signals of Ecosystem Degradation

**Version** 3.0.3

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**Description** Tools to compute and assess significance of early-warnings signals (EWS) of ecosystem degradation on raster data sets. EWS are metrics derived from the observed spatial structure of an ecosystem -- e.g. spatial autocorrelation -- that increase before an ecosystem undergoes a non-linear transition (Genin et al. (2018) <doi:10.1111/2041-210X.13058>).

**URL** <https://github.com/spatial-ews/spatialwarnings>

**Depends** R (>= 3.3.0), future

**Imports** Rcpp, ggplot2, plyr, stats, utils, future.apply, gsl,  
segmented

**Suggests** moments, powerLaw, reshape2, testthat, covr, acss, mgcv,  
gstat, sp, raster

**LinkingTo** Rcpp, RcppArmadillo

**LazyData** true

**RoxygenNote** 7.1.2

**Encoding** UTF-8

**NeedsCompilation** yes

**Repository** CRAN

**Date/Publication** 2022-03-21 13:00:02 UTC

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---

arizona

*A list of classified aerial images of vegetation*


---

**Description**

A list of classified aerial images of vegetation

**Usage**

arizona

**Format**

A list of logical matrices which were obtained through the classification of aerial images of vegetation taken in Arizona (USA).

**Source**

Derived from the images provided in the Supplementary Material of Rodriguez et al. (2017).

**References**

Rodriguez, F., A. G. Mayor, M. Rietkerk, and S. Bautista. 2017. A null model for assessing the cover-independent role of bare soil connectivity as indicator of dryland functioning and dynamics. *Ecological Indicators*.

---

coarse\_grain

*Matrix coarse-graining*


---

**Description**

This function averages the spatial data locally. It divides the input matrix into submatrices of dimension `subsize` and averages the spatial data in these submatrices. By doing this, the dimension of resultant matrix is reduced by a factor of `subsize`.

**Usage**

```
coarse_grain(mat, subsize)
```

**Arguments**

<code>mat</code>	A matrix
<code>subsize</code>	Dimension of the submatrix. This has to be a positive integer smaller than the dimension of input matrix.

## Details

If the data is classified into discrete units, the calculation of variance and skewness can give spurious results irrelevant to the proximity to transition. Therefore, discrete data should be 'coarse-grained' before calculating the spatial early warning signals. However, this can also be applied to continuous state data.

## Value

A matrix of reduced dimension.

## References

Sankaran, S., Majumder, S., Kefi, S. and Guttal, V. (2017). Implications of being discrete and spatial for detecting early warning signals of regime shifts. *Ecological Indicators*.

## See Also

[generic\\_sews](#)

## Examples

```
rmat <- matrix(runif(20*10) > .5,  
              ncol = 20, nrow = 10)  
rmat.cg <- coarse_grain(rmat, subsize = 2)  
  
par(mfrow = c(1, 2))  
image(rmat)  
title('Raw matrix')  
image(rmat.cg)  
title('Coarse-grained matrix')
```

---

convert\_to\_matrix      *Convert an object to a matrix*

---

## Description

This function is mainly for internal use by the [spatialwarnings](#) package to convert objects before they are processed by \*\_sews functions.

## Usage

```
convert_to_matrix(object, ...)
```

## Arguments

object	An object (typically, a matrix or a list of matrices)
...	Additional arguments (currently ignored)

**Details**

This generic function is here so that other packages can extend it. For example, `spatialwarningsGis` will provide methods so that GIS objects can be handled (e.g. `RasterLayer` from package `raster`).

**Examples**

```
# this does nothing
convert_to_matrix(serengeti[2:3])
```

---

create_indicator	<i>Custom Spatial Early-Warning signals</i>
------------------	---

---

**Description**

Computation, significance assessment and display of trends of a custom, user-defined indicator.

**Usage**

```
create_indicator(fun, taskname = as.character(substitute(fun)))

compute_indicator(mat, fun, taskname = as.character(substitute(fun)), ...)
```

**Arguments**

fun	A function that takes a matrix as input and returns a vector of numerical values. If the function returns a named vector, then the names will be used in plots and summaries. The function may also accept extra arguments.
taskname	The task name. A character string used used for plots and textual summaries that describes the indicator (or set of indicators) being computed. If a task name cannot be derived from fun, then default name is used.
mat	A matrix or a list of matrices.
...	Additional arguments being passed to the function fun

**Details**

`spatialwarnings` provides "workflow functions", named `*_sews`, that assist the user in computing, displaying and assessing the significance of indicator values. The functions `create_indicator` and `compute_indicator` provides such workflow for any arbitrary function.

`create_indicator` takes a function 'fun' and returns another function that can be used as an indicator similar to the `*_sews` functions. The results of this function can be assessed for significance using `indictest` and trends can be displayed using `plot`, `summary`, etc. (see Examples). `compute_indicator` does the same but without needing an intermediate indicator function.

**Value**

create\_indicator returns a function that can be used in the same way than the other \*\_sews functions (e.g. generic\_sews). This function as well as compute\_indicator will return [simple\\_sews\\_\\*](#) objects.

**See Also**

[simple\\_sews](#)

**Examples**

```
# Use the maximum patch size as indicator of degradation
maxpatchsize <- function(mat) {
  max(patchsizes(mat))
}

# Create the indicator function
maxpatch_sews <- create_indicator(maxpatchsize)

# Then work with this function as if it were a function from the *_sews
# family.
mp_indic <- maxpatch_sews(forestgap)
summary(mp_indic)

## Not run:
# Assess significance and display trends
mp_test <- indictest(mp_indic, nulln = 49)
plot(mp_test)

## End(Not run)

# Try spatial coefficient of variation as a spatial EWS. This function can
# have arguments.
spatial_cv <- function(mat, subsize) {
  matc <- coarse_grain(mat, subsize)
  return( sd(matc) / mean(matc) )
}

# Create indicator function
cv_sews <- create_indicator(spatial_cv)

# Compute and display trends
cv_indic <- cv_sews(serengeti, subsize = 3)
plot(cv_indic, along = serengeti.rain)

# We can do the same work in one run using compute_indicator
cv_indic2 <- compute_indicator(serengeti, spatial_cv, subsize = 3)
plot(cv_indic2, along = serengeti.rain)
```

```
## Not run:  
indicest(cv_indic, nulln = 99)  
  
## End(Not run)
```

---

display\_matrix      *Plot a matrix*

---

## Description

Display a matrix or a list of matrices in a plot

## Usage

```
display_matrix(object, palette = "RdYlBu", along = NULL, ...)
```

## Arguments

object	A matrix, a list of matrices, an object produced by *_sews functions or indicest()
palette	A color palette to use in the plot. It can be any color palette understood by <a href="#">scale_fill_brewer</a> .
along	A vector of values used in facet headers. If object is a matrix, this is ignored.
...	Other arguments are ignored.

## Details

This function will plot a matrix using ggplot2, using the provided palette. Its use-case is very much like image(), but it produces nicer plots by default (image() is much faster, however).

## Value

A ggplot2 object, which is printed when this function is used interactively.

## Examples

```
# display_matrix works with single matrices or lists of matrices  
display_matrix(serengeti[2:3])  
  
# display_matrix is compatible with "*_sews" objects  
indics <- compute_indicator(serengeti[2:3], raw_moran)  
display_matrix(indics)
```

---

extract_spectrum	<i>Extract the r-spectrum from objects</i>
------------------	--

---

**Description**

Extract the r-spectrum from objects produced by `spectral_sews`.

**Usage**

```
extract_spectrum(x, ...)
```

**Arguments**

x	An object produced by <code>spectral_sews</code> or the result of the <code>indicte</code> function called on such object
...	Other arguments are ignored

**Value**

The empirical r-spectrum as a `data.frame`

**See Also**

[spectral\\_sews](#)

**Examples**

```
# Extract the r-spectrum after computing indicators
indics <- spectral_sews(serengeti[2:3])
extract_spectrum(indics)
```

---

extract_variogram	<i>extract_variogram() method for variogram_sews objects</i>
-------------------	--

---

**Description**

Extract the empirical variogram from a `variogram_sews` object

**Usage**

```
extract_variogram(x, ...)
```



**Arguments**

`x`                    An object produced by `variogram_sews`, or `indictest`  
`...`                    Additional arguments (ignored)

**Value**

A data.frame containing the variogram with the distances (column `dist`), the empirical semivariance values (`gamma`), and if object contains more than one matrix, a column named `matrixn`.

**See Also**

[variogram\\_sews](#)

**Examples**

```
## Not run:
vario_indics <- variogram_sews(serengeti)
predict(vario_indics)
vario_test <- indictest(vario_indics, nulln = 19)
predict(vario_test) # same result

## End(Not run)
```

---

flowlength_sews	<i>Flowlength connectivity indicator (uniform topography)</i>
-----------------	---

---

**Description**

Measures the connectivity of runoff-source areas as determined by vegetation patterns and (uniform) topography

**Usage**

```
flowlength_sews(mat, slope = 20, cell_size = 1)
```

**Arguments**

`mat`                    The input matrix (must be a logical matrix)  
`slope`                    The slope of the area documented by the matrix (in degree).  
`cell_size`                The horizontal size of a cell in the matrix (as viewed from above).

## Details

This function computes Flowlength, a simple metric that measures the potential hydrological connectivity of runoff-source areas (e.g., bare soil) considering vegetation cover, vegetation patterns and topography. Flowlength is defined as the average length of all the potential runoff pathways in the target area. Thus, a higher value of the index indicates a higher hydrologic connectivity of runoff source areas. This function is designed for an idealized uniform hillslope (e.g., with constant slope angle, the direction of maximum slope being from the top to the bottom of the input matrices).

The deviations of Flowlength from its expected values under random or aggregated-pattern null models can be used as an indicator of imminent transition to a degraded state (Rodriguez et al. 2017) in the context of arid drylands. An increased deviation of flowlength compared to its null values is expected as a possible transition gets closer. This deviation can be computed using any null model provided by `spatialwarnings` (see `indictest` for more details), but a specific null model is provided for Flowlength based on a much-faster analytical approximation, using the argument `null_method = "approx_rand"` when calling `indictest` (see examples below).

In general, Flowlength can be used as indicator of dryland functional status by assessing potential water and soil losses in patchy landscapes (Mayor et al. 2008, Moreno-de las Heras et al. 2012, Mayor et al. 2013, Okin et al. 2015). Finally, the combination of observed and expected Flowlength under null models for random or aggregated vegetation cover can be used for assessing the cover-independent role of bare- soil connectivity (Rodriguez et al. 2018).

## Value

A ‘`simple_sews`’ object containing the flow length value, among other things, see `simple_sews_object` for more information.

## References

- Rodriguez, F., A. G. Mayor, M. Rietkerk, and S. Bautista. 2017. A null model for assessing the cover-independent role of bare soil connectivity as indicator of dryland functioning and dynamics. *Ecological Indicators*.
- Mayor, A.G., Bautista, S., Small, E.E., Dixon, M., Bellot, J., 2008. Measurement of the connectivity of runoff source areas as determined by vegetation pattern and topography: a tool for assessing potential water and soil losses in drylands. *Water Resour. Res.* 44, W10423.
- Mayor, A.G., Kefi, S., Bautista, S., Rodriguez, F., Carteni, F., Rietkerk, M., 2013. Feedbacks between vegetation pattern and resource loss dramatically decrease ecosystem resilience and restoration potential in a simple dryland model. *Landscape Ecol.* 28, 931-942.
- Moreno-de las Heras, M., Saco, P.M., Willgoose, G.R., Tongway, D.J., 2012. Variations in hydrological connectivity of Australian semiarid landscapes indicate abrupt changes in rainfall-use efficiency of vegetation. *J. Geophys. Res.* 117, G03009.
- Okin, G.S., Moreno-de las Heras, M., Saco, P.M., Throop, H.L., Vivoni, E.R., Parsons, A.J., Wainwright, J., Peters, D.P.C., 2015. Connectivity in dryland landscapes: shifting concepts of spatial interactions. *Front. Ecol. Environ.* 13 (1), 20-27.

## See Also

`raw_flowlength_uniform`, `indictest` to test the significance of indicator values.

## Examples

```
## Not run:
fl_result <- flowlength_sews(arizona, slope = 20, cell_size = 1)

# Compute the Z-score (standardized deviation to null distribution) and plot
# its variations along the gradient. This Z-score is suggested by
# Rodriguez et al. (2017) as an indicator of degradation.
fl_test <- indictest(fl_result, nulln = 19)
plot(fl_test, what = "z_score")

# Use the analytical approximation suggested in Rodriguez et al. (2017),
# instead of permuting the original values in the matrix (much faster)
fl_test <- indictest(fl_result, null_method = "approx_rand")
plot(fl_test, what = "z_score")

## End(Not run)
```

---

forestgap

*A list of binary matrices and their associated parameters*

---

## Description

A list of binary matrices and their associated parameters

## Usage

forestgap

forestgap.pars

## Format

A list of logical matrices which are the end results of simulations from Kubo's Forest Gap model along a gradient of increasing values of stress (see references).

The parameters used for the simulations, as a data frame.

## Details

Kubo's forest gap model has three parameters,  $\alpha$  that controls the reproductive rate of trees,  $d$  controls the non-spatialized mortality and  $\delta$  the increased mortality due to the presence of a neighboring gap.

## Source

Generated using the implementation of Kubo's model in caspr 0.2.0 <https://github.com/fdschneider/caspr>.

## References

Kubo, T., Iwasa, Y., & Furumoto, N. (1996). Forest spatial dynamics with gap expansion: Total gap area and gap size distribution. *Journal of Theoretical Biology*, 180(3), 229-246. doi: [10.1006/jtbi.1996.0099](https://doi.org/10.1006/jtbi.1996.0099)

---

generic\_sews

*Generic Spatial Early-Warning signals*

---

## Description

Computation, significance assessment and display of spatial generic early warning signals (Moran's I, variance and skewness)

## Usage

```
generic_sews(
  mat,
  subsize = 4,
  abs_skewness = FALSE,
  moranI_coarse_grain = FALSE
)
```

## Arguments

mat	A matrix (quantitative data), a binary matrix (TRUE/FALSE data), or a list of those
subsize	The subsize used for the coarse-graining phase (see Details)
abs_skewness	Should the absolute skewness be used instead of its raw values ?
moranI_coarse_grain	Should the input matrix be coarse-grained before computing the Moran's I indicator value ?

## Details

The Generic Early warning signal are based on the property of a dynamical system to "slow down" when approaching a critical point, that is take more time to return to equilibrium after a perturbation. This is expected to be reflected in several spatial characteristics: the variance, the spatial autocorrelation (at lag-1) and the skewness. This function provides a convenient workflow to compute these indicators, assess their significance and display the results.

Before computing the actual indicators, the matrix can be "coarse-grained". This process reduces the matrix by averaging the nearby cells using a square window defined by the subsize parameter. This makes spatial variance and skewness reflect actual spatial patterns when working with binary (TRUE/FALSE data), but is optional when using continuous data. Keep in mind that it effectively reduces the size of the matrix by approximately subsize on each dimension.

The significance of generic early-warning signals can be estimated by reshuffling the original matrix (function `indictest`). Indicators are then recomputed on the shuffled matrices and the values

obtained are used as a null distribution. P-values are obtained based on the rank of the observed value in the null distribution. A small P-value means that the indicator is significantly above the null values, as expected before a critical point.

The `plot` method can displays the results graphically. A text summary can be obtained using the `summary` method.

## Value

`generic_sews` returns an object of class `generic_sews_single` (actually a list) if `mat` is a single matrix or an object of class `generic_sews_list` if `mat` is a list.

`indictest` returns an object of class `generic_test` (actually a data.frame).

`plot` methods return `ggplot` objects, usually immediately displayed when R is being used interactively.

## References

Kefi, S., Guttal, V., Brock, W.A., Carpenter, S.R., Ellison, A.M., Livina, V.N., et al. (2014). Early Warning Signals of Ecological Transitions: Methods for Spatial Patterns. *PLoS ONE*, 9, e92097.

Dakos, V., van Nes, E. H., Donangelo, R., Fort, H., & Scheffer, M. (2010). Spatial correlation as leading indicator of catastrophic shifts. *Theoretical Ecology*, 3(3), 163-174.

Guttal, V., & Jayaprakash, C. (2008). Spatial variance and spatial skewness: leading indicators of regime shifts in spatial ecological systems. *Theoretical Ecology*, 2(1), 3-12.

## See Also

`indictest`, to test the significance of indicator values. Individual indicators: [raw\\_cg\\_moran](#) [raw\\_cg\\_variance](#), [raw\\_cg\\_skewness](#), [simple\\_sews](#)

## Examples

```
data(serengeti)
gen_indic <- generic_sews(serengeti, subsize = 5,
                        moranI_coarse_grain = TRUE)

# Display results
summary(gen_indic)

# Display trends along the varying model parameter
plot(gen_indic, along = serengeti.rain)

# Compute significance (long)
## Not run:
gen_test <- indictest(gen_indic, nulln = 199)

print(gen_test)

# Display the trend, now with a grey ribbon indicating the 5%-95% quantile
# range of the null distribution
```

```

plot(gen_test, along = serengeti.rain)

# Display the effect size compared to null distribution
plot(gen_test, along = serengeti.rain, what = "z_score")

# Note that plot() method returns a ggplot object that can be modified
# for convenience
if ( require(ggplot2) ) {
  plot(gen_test, along = serengeti.rain) +
    geom_vline(xintercept = 733, color = "red", linetype = "dashed") +
    xlab('Annual rainfall') +
    theme_minimal()
}

## End(Not run)

```

---

generic\_spews

*(DEFUNCT) Generic Spatial Early-Warning signals*

---

### Description

Computation, significance assesment and display of spatial generic early warning signals (Moran's I, variance and skewness)

### Usage

```

generic_spews(
  mat,
  subsize = 4,
  abs_skewness = FALSE,
  moranI_coarse_grain = FALSE
)

```

### Arguments

mat	A matrix (quantitative data), a binary matrix (TRUE/FALSE data), or a list of those
subsize	The subsize used for the coarse-graining phase (see Details)
abs_skewness	Should the absolute skewness be used instead of its raw values ?
moranI_coarse_grain	Should the input matrix be coarse-grained before computing the Moran's I indicator value ?

### Details

generic\_spews has been renamed, please use [generic\\_sews](#) instead.

---

indicator\_moran      *(DEFUNCT) Moran's Index at lag of 1*

---

### Description

This functions computes the Moran's spatial correlation index (with lag one). It also computes a null value obtained by randomizing the matrix.

### Usage

```
indicator_moran(input, subsize = 1, nulln = 99)
```

### Arguments

input	An matrix or a list of matrix object. It should be a square matrix
subsize	logical. Dimension of the submatrix used to coarse-grain the original matrix (set to 1 for no coarse-graining).
nulln	Number of replicates to produce to estimate null distribution of index (default: 999).

### Value

A list (or a list of those if input is a list of matrix object) of:

- 'value': Spatial autocorrelation of the matrix

If nulln is above 2, then the list has the following additional components :

- 'null\_mean': Mean autocorrelation of the null distribution
- 'null\_sd': SD of autocorrelation in the null distribution
- 'z\_score': Z-score of the observed value in the null distribution
- 'pval': p-value based on the rank of the observed autocorrelation in the null distribution.

### References

Dakos, V., van Nes, E. H., Donangelo, R., Fort, H., & Scheffer, M. (2010). Spatial correlation as leading indicator of catastrophic shifts. *Theoretical Ecology*, 3(3), 163-174.

Legendre, P., & Legendre, L. F. J. (2012). *Numerical Ecology*. Elsevier Science.

### Examples

```
## Not run:  
data(serengeti)  
  
# One matrix  
indicator_moran(serengeti[[1]])
```

```
# Several matrices
indicator_moran(serengeti)

## End(Not run)
```

---

indicator\_plrange      *Power-law range indicator*

---

### Description

Compute the power-law range of a matrix

### Usage

```
indicator_plrange(mat, merge = FALSE, xmin_bounds = NULL)
```

### Arguments

mat	A logical matrix, or a list of logical matrices
merge	Controls whether the patch-size distributions of the input matrices are merged together before computing the power-law range. Setting this value to TRUE makes the function return a single value even if multiple matrices are given as input.
xmin_bounds	A vector of two integer values, defining a range in which to search for the best xmin (see Details).

### Details

Some ecosystems show typical changes in their patch-size distribution as they become more and more degraded. In particular, an increase in the truncation of the patch-size distribution (PSD) is expected to occur. The power-law range (PLR) measures the truncation of the PSD in a single value (see also [patchdistr\\_sews](#) for more details).

To compute the PLR, power-laws are fitted with a variable minimum patch size (xmin) and the one with the lowest Kolmogorov-Smirnov distance to the empirical distribution is retained. PLR is then computed using this best-fitting xmin:

$$\frac{\log(x_{max}) - \log(x_{min})}{\log(x_{max}) - \log(x_{smallest})}$$

where  $x_{max}$  is the maximum observed patch size, and  $x_{smallest}$  is the minimum observed patch size.

### Value

A data.frame with columns minsize, maxsize which are the observed minimum and maximum patch sizes. The estimated  $x_{min}$  and the value of the power-law range. If multiple matrices were provided, then a list of data.frames is returned



## References

Clauset, A., Shalizi, C. R., & Newman, M. E. (2009). Power-law distributions in empirical data. *SIAM review*, 51(4), 661-703.

Berdugo, M., Kefi, S., Soliveres, S. & Maestre, F.T. (2017). Plant spatial patterns identify alternative ecosystem multifunctionality states in global drylands. *Nature in Ecology and Evolution*.

## See Also

[patchdistr\\_sews](#)

## Examples

```
## Not run:
forestgap.plr <- indicator_plrange(forestgap)
do.call(rbind, forestgap.plr) # convert results to data.frame

# Restrict to small xmins
forestgap.plr2 <- indicator_plrange(forestgap, xmin_bounds = c(1, 10))
do.call(rbind, forestgap.plr2)

## End(Not run)
```

---

indicator_psdtype	<i>Change in patch-size distributions types</i>
-------------------	---

---

## Description

This functions fits different patch size distributions types (power-law, log-normal, exponential and truncated power-law) to the patches contained in a matrix. The distributions are returned with their corresponding AIC, BIC and AICc to select the best fit.

## Usage

```
indicator_psdtype(  
  x,  
  xmin = 1,  
  merge = FALSE,  
  fit_lnorm = FALSE,  
  xmin_bounds = NULL,  
  best_by = "AIC",  
  wrap = FALSE  
)
```

**Arguments**

x	A logical (TRUE/FALSE values) matrix or a list of these.
xmin	The xmin to be used to fit the patch size distributions. Use the special values "estimate" to use an estimated xmin for each fit
merge	The default behavior is to produce indicators values for each matrix. If this parameter is set to TRUE then the patch size distributions are pooled together for fitting.
fit_lnorm	Fit also a log-normal distribution
xmin_bounds	Restrict the possible xmins in this range (defaults to the whole range of observed patch sizes)
best_by	The criterion used to select the best distribution type (one of "AIC", "BIC" or "AICc").
wrap	Determines whether patches are considered to wrap around the matrix when reaching the side

**Details**

Patterned ecosystems can exhibit a change in their spatial structure as they become more and more stressed. It has been suggested that this should be reflected in changes in the observed patch size distributions (PSD). The following sequence is expected to occur (Kefi et al. 2011) as patterned ecosystems become more and more degraded:

- Percolation of vegetation patches occurs (a patch has a width or height equal to the size of the system)
- The patch-size distribution follows a power-law
- The patch-size distribution deviates from a power-law as larger patches break down
- The patch-size distribution is closer to an exponential distribution

This indicator fits the observed patch size distribution based on maximum-likelihood (following Clauset et al. 2009 recommendations), then select the best model using AIC, BIC (default) or AICc.

**Value**

A data.frame (or a list of these if x is a list) with the following columns:

- 'method' the method used for fitting (currently: only log-likelihood is implemented, "ll")
- 'type' the type of distribution fit
- 'npars' the number of parameters of the distribution type
- 'AIC', 'AICc' and 'BIC' the values for Akaike Information Criterion (or the corrected for small samples equivalent AICc), and Bayesian Information Criterion (BIC)
- 'best' A logical vector indicating which distribution is the best fit
- 'plexpo', 'cutoff', 'meanlog', 'sdlog' the estimates for distribution parameters (see [pl\\_fit](#))
- 'percolation' A logical value indicating whether there is [percolation](#) in the system.

## References

Kefi, S., Rietkerk, M., Roy, M., Franc, A., de Ruiter, P.C. & Pascual, M. (2011). Robust scaling in ecosystems and the meltdown of patch size distributions before extinction: Patch size distributions towards extinction. *Ecology Letters*, 14, 29-35.

Kefi, S., Rietkerk, M., Alados, C.L., Pueyo, Y., Papanastasis, V.P., ElAich, A., et al. (2007). Spatial vegetation patterns and imminent desertification in Mediterranean arid ecosystems. *Nature*, 449, 213-217.

Clauset, A., Shalizi, C. R., & Newman, M. E. (2009). Power-law distributions in empirical data. *SIAM review*, 51(4), 661-703.

## See Also

[patchdistr\\_sews](#)

[patchdistr\\_sews](#)

## Examples

```
data(forestgap)

# One logical matrix only
indicator_psdtype(forestgap[[1]])

# A list of these matrices
## Not run:
indicator_psdtype(forestgap)

## End(Not run)
```

---

indicator\_sdr                      *(DEFUNCT) Density Ratio (SDR) indicator*

---

## Description

Compute the ratio of low frequencies over high frequencies of the r-spectrum. It also computes a null value obtained by randomizing the matrix.

## Usage

```
indicator_sdr(input, sdr_low_range = NULL, sdr_high_range = NULL, nulln = 99)
```

**Arguments**

input	A matrix or a logical matrix (TRUE/FALSE), or a list of these.
sdr_low_range	The range of values (in proportion) to use for the computation of the spectral density ratio. For example, for the lowest 20% (default value), set sdr_low_range to <code>c(0, .2)</code> .
sdr_high_range	The range of values (in proportion) to use for the computation of the spectral density ratio. For example, for the highest 20% (default value), set sdr_high_range to <code>c(.8, 1)</code> .
nulln	The number of simulations to compute for the null distribution

**Details**

SDR measures the increase in long-range correlations before a critical point. It is the ratio of the average low frequency value over high frequency values. In this implementation, an increase in SDR implies a "reddening" of the [r-spectrum](#). See also [spectral\\_sews](#) for a more complete description.

Low and high frequencies are averaged in order to compute the SDR. The parameters `sdr_low_range` and `sdr_high_range` control which frequencies are selected for averaging. For example `sdr_low_range = c(0, .2)` (default) uses the lower 20 the average of low frequencies. `sdr_high_range = c(.8, 1)` uses the higher 20

**Value**

A list (or a list of lists if input was a list of matrices) with components:

- 'value': SDR of the matrix

If `nulln` is above 2, then the list has the following additional components :

- 'null\_mean': Mean SDR of the null distribution
- 'null\_sd': SD of SDR in the null distribution
- 'z\_score': Z-score of the observed value in the null distribution (value minus the null mean and divided by null standard deviation)
- 'pval': p-value based on the rank of the observed SDR in the null distribution. A low p-value means that the indicator value is significantly higher than the null values.

**References**

Carpenter, S.R. & Brock, W.A. (2010). Early warnings of regime shifts in spatial dynamics using the discrete Fourier transform. *Ecosphere*

**See Also**

`spectral_sews`, `rspectrum`

**Examples**

```
## Not run:
serengeti.sdr <- indicator_sdr(serengeti, nulln = 499)
do.call(rbind, serengeti.sdr) # convert results to data.frame

## End(Not run)
```

---

indicator\_skewness      *(DEFUNCT) Skewness indicator*

---

**Description**

Compute the spatial skewness of spatial data. It also computes a null value obtained by randomizing the matrix.

**Usage**

```
indicator_skewness(input, subsize = 5, absolute = TRUE, nulln = 99)
```

**Arguments**

input	A matrix or a list of matrices. The matrix values can be logical, with FALSE (empty) or TRUE (occupied) values. The entries can also be continuous (like NDVI or EVI data).
subsize	Dimension of the submatrix used to coarse-grain the original matrix. This must be an integer less than size of the full matrix. Coarse-graining reduces the size of the matrix by a factor subsize in each dimension of the matrix. Skewness is calculated on the coarse-grained matrix.
absolute	Should the function return the absolute value or raw value of skewness ?
nulln	Number of simulations used to produce the null distribution of indicator values.

**Details**

Spatial skewness is a measure of fluctuations in space; specifically, it measures if fluctuations are getting biased (skewed) in one direction. Based on the theory of critical slowing down, when systems approach critical points they are expected to show increased fluctuations in space. Thus, increasing spatial skewness is proposed as an early warning signal of impending critical transitions.

Computing spatial skewness is straightforward. However, detecting trends of skewness that correspond to critical slowing down can be tricky, especially if data come from discrete classification of state variable.

For example, many high resolution spatial data are classified as FALSE (empty) or TRUE (occupied by plant). In such cases, spatial skewness captures just the skewness in data, but not that of spatial structure. To resolve the issue, this function employs a method called coarse-graining, proposed

in Kefi et al (2014), and described in detail in Sankaran et al. (2017). One must specify a subsize above one for binary valued data sets to obtain meaningful values.

subsize has to be an integer. It has to be less than or equal to half of matrix size (N). subsize must also be preferably a divisor of N. If it is not a divisor of N, the remainder rows and columns are discarded when computing coarse-graining matrices.

Null model evaluations are also done on coarse-grained matrices.

## Value

A list (or a list of lists if input was a list of matrices) with components:

- ‘value’: Spatial skewness of the matrix

If nulln is above 2, then the list has the following additional components :

- ‘null\_mean’: Mean skewness of the null distribution
- ‘null\_sd’: SD of skewness in the null distribution
- ‘z\_score’: Z-score of the observed value in the null distribution (value minus the null mean and divided by null standard deviation)
- ‘pval’: p-value based on the rank of the observed skewness in the null distribution. A low p-value means that the indicator value is significantly higher than the null values.

## References

Guttal, V., and Jayaprakash, C. (2009). Spatial variance and spatial skewness: leading indicators of regime shifts in spatial ecological systems. *Theoretical Ecology*, 2(1), 3-12.

Kefi, S., Guttal, V., Brock, W.A., Carpenter, S.R., Ellison, A.M., Livina, V.N., et al. (2014). Early Warning Signals of Ecological Transitions: Methods for Spatial Patterns. *PLoS ONE*, 9, e92097.

Sankaran, S., Majumder, S., Kefi, S., and Guttal, V. (2017). Implication of being discrete and spatial in detecting early warning signals of regime shifts. *Ecological indicators*.

## Examples

```
## Not run:  
data(serengeti)  
indicator_skewness(serengeti)  
  
## End(Not run)
```

---

indicator\_variance      *(DEFUNCT) Spatial variance indicator*

---

### Description

This functions computes the spatial variance of spatial data. It also computes a null value obtained by randomizing the matrix.

### Usage

```
indicator_variance(input, subsize = 5, nulln = 99)
```

### Arguments

input	A matrix or a list of matrices. The matrix values can be logical, with FALSE (empty) or TRUE (occupied) values. The entries can also be continuous (like NDVI or EVI data).
subsize	Dimension of the submatrix used to coarse-grain the original matrix. This must be an integer less than size of the full matrix. Coarse-graining reduces the size of the matrix by a factor subsize in each dimension of the matrix. Variance is calculated on the coarse-grained matrix.
nulln	Number of simulations used to produce the null distribution of indicator values.

### Details

Spatial variance is a measure of fluctuations in space. Based on the theory of critical slowing down, when systems approach critical points they are expected to show increased fluctuations in space. Thus, increasing spatial variance is proposed as an early warning signal of impending critical transitions.

For example, many high resolution spatial data are classified as FALSE (empty) or TRUE (occupied by plant). In such cases, spatial variance captures just the variance in data, but not that of spatial structure. To resolve the issue, this function employs a method called coarse-graining, proposed in Kefi et al (2014), and described in detail in Sankaran et al. (2017). One must specify a subsize above one for binary valued data sets to obtain meaningful values.

subsize has to be an integer. It has to be less than or equal to half of matrix size (N). subsize must also be preferably a divisor of N. If it is not a divisor of N, the remainder rows and columns are discarded when computing coarse-graining matrices.

Null model evaluations are also done on coarse-grained matrices.

### Value

A list (or a list of lists if input was a list of matrices) with components:

- ‘value’: Spatial variance of the matrix

If nulln is above 2, then the list has the following additional components :

- ‘null\_mean’: Mean spatial variance of the null distribution
- ‘null\_sd’: SD of spatial variance in the null distribution
- ‘z\_score’: Z-score of the observed value in the null distribution (value minus the null mean and divided by null standard deviation)
- ‘pval’: p-value based on the rank of the observed spatial variance in the null distribution. A low p-value means that the indicator value is significantly higher than the null values.

## References

Guttal, V., and Jayaprakash, C. (2009). Spatial variance and spatial skewness: leading indicators of regime shifts in spatial ecological systems. *Theoretical Ecology*, 2(1), 3-12.

Kefi, S., Guttal, V., Brock, W.A., Carpenter, S.R., Ellison, A.M., Livina, V.N., et al. (2014). Early Warning Signals of Ecological Transitions: Methods for Spatial Patterns. *PLoS ONE*, 9, e92097.

Sankaran, S., Majumder, S., Kefi, S., and Guttal, V. (2017). Implication of being discrete and spatial in detecting early warning signals of regime shifts. *Ecological Indicators*.

## Examples

```
data(serengeti)
## Not run:
indicator_variance(serengeti, nulln = 499)

## End(Not run)
```

---

indicest

*Significance-assessment of spatial early-warning signals*

---

## Description

Assess the significance of spatial early-warning indicators

## Usage

```
indicest(x, nulln = 999, null_method = "perm", null_control = NULL, ...)
```

## Arguments

x	A spatial warning object such as one produced by the *_sews functions, or <a href="#">compute_indicator</a>
nulln	The number of values to compute to produce the null distribution
null_method	The method used to produce the null values (see Details)
null_control	List of arguments used to control the generation of null matrices. If NULL, then arguments then sensible defaults are chosen (see Details)
...	Additional arguments are ignored



## Details

`indicest` is used to test the significance of early-warning signals against 'null matrices', which represent the expected spatial structure in the absence of the biological process of interest.

For a given indicator, a null distribution is obtained by producing a set of 'null' matrices, from which indicator values are recomputed. This produces a null distribution of null indicator values against which the observed value is tested.

Several methods are available to produce the set of null matrices. If `null_method` is set to "perm", the original matrix is reshuffled to obtain a null matrix. If `null_method` is set to "intercept", then a generalized linear model of the form  $y \sim 1$  (where  $y$  represents the values of the matrix) is fitted, then values are drawn from this model. If `null_method` is set to "smooth", then a smooth surface is fitted based on a generalized additive model (using `gam`) to the matrix, then values are drawn from this model. When using the "intercept" or "smooth" null models, it is important to make sure the model 'family' corresponds to the type of values present in the matrix. By default, if a matrix contains TRUE/FALSE values, a 'binomial()' family is used, otherwise a 'gaussian()' family is used. More information about null models is available in the [spatialwarnings FAQ](#).

Please note that specific null methods may exist for some indicators, such as `flowlength`. These are often based on analytical approximation and allow faster computations.

If a matrix has attributes, then these are preserved and passed to the function used to compute the indicator value, except when using the null method 'perm', in which case matrix attributes are discarded.

The list `null_control` can be used to adjust the computation of null matrices. It can have the following components:

- 'family' The family used in the model used to produce the null matrices. Typically, it is one of `binomial()`, `binomial()`, etc.
- 'qinf' The lower quantile to compute from the null distribution and display in summaries/plots. A numeric value between 0 and 1.
- 'qsup' The upper quantile to compute from the null distribution and display in summaries/plots. A numeric value between 0 and 1.

## Value

An object with a class ending in `*_sews_test`, whose exact class depends on the input object. `plot`, summary methods are available to display the results of computations, and additional methods may be available depending on the input object (e.g. see `patchdistr_sews_plot`).

## References

Kefi, S., Guttal, V., Brock, W.A., Carpenter, S.R., Ellison, A.M., Livina, V.N., et al. (2014). Early Warning Signals of Ecological Transitions: Methods for Spatial Patterns. PLoS ONE, 9, e92097

## See Also

[generic\\_sews](#), [spectral\\_sews](#), [kbdm\\_sews](#), [compute\\_indicator](#), [flowlength\\_sews](#)

---

`kbdm_sews`*Indicator based on Kolmogorov Complexity*

---

### Description

Computes the Kolmogorov Complexity on a set of matrices, using the Block Decomposition Method.

### Usage

```
kbdm_sews(mat, subsize = 3)
```

### Arguments

<code>mat</code>	A logical matrix (TRUE/FALSE values) or a list of logical matrices
<code>subsize</code>	A submatrix size to carry out the Block Decomposition Method (must be between 1 and 3)

### Details

be a useful indicator to anticipate transitions in model ecological systems (Dakos and Soler-Toscano, 2017). When close to the transition critical point, the complexity is expected to decrease.

The Kolmogorov complexity cannot be computed directly for large strings (i.e. matrices). However, the complexity of smaller submatrices can be estimated, then combined to obtain an approximation of the complexity of the whole matrix. This method, the Block Decomposition Method is implemented in this indicator following Dakos and Soler-Toscano (2017).

### Value

`kbdm_sews` returns an object of class `simple_sews_single` (a list) if `mat` is a single matrix, and an object of class `simple_sews_list` if `mat` is a list of matrices. These objects can be used with generic methods `indictest` (to test significance) or `plot` (to display trends), see also the examples below.

### References

Dakos, V., and F. Soler-Toscano. 2017. Measuring complexity to infer changes in the dynamics of ecological systems under stress. *Ecological Complexity* 32:144-155.

### See Also

[raw\\_kbdm](#), [acss](#), [indictest](#), to test the significance of indicator values.

## Examples

```
## Not run:

kbdm_result <- kbdm_sews(serengeti, subsize = 3)
plot(kbdm_result, along = serengeti.rain)

kbdm_test <- indictest(kbdm_result, nulln = 49)
plot(kbdm_test, along = serengeti.rain)

# Plot deviation to null expectation
plot(kbdm_test, along = serengeti.rain, what = "z_score")

## End(Not run)
```

---

label

*Labelling of unique patches and detection of percolation.*

---

## Description

Label each patch with a number in a binary matrix

percolation() detects whether percolation occurs in the matrix (i.e. a patch has a width or a height equal to the size of the matrix)

## Usage

```
label(
  mat,
  nbmask = matrix(c(0, 1, 0, 1, 0, 1, 0, 1, 0), ncol = 3),
  wrap = FALSE
)
```

```
percolation(mat, nbmask = matrix(c(0, 1, 0, 1, 0, 1, 0, 1, 0), ncol = 3))
```

## Arguments

mat	A binary matrix
nbmask	a "neighboring mask": a matrix with odd dimensions describing which cells are to be considered as neighbors around a cell (see examples).
wrap	Whether to wrap around lattice boundaries ('TRUE'/'FALSE'), effectively using periodic boundaries.

**Details**

The label function "label" the patches of a binary (TRUE/FALSE) matrix. It returns a matrix of similar height and width, with integer values representing the ID of each unique patch (contiguous cells). Empty cells are labelled as NA.

**Value**

A matrix containing ID numbers for each connected patch. Default parameters assume 4-cell neighborhood and periodic boundaries. The distribution of patch sizes is returned as the attribute "psd" and the percolation status as "percolation" (whether a TRUE patch has a width or height equal to the size of the matrix).

**See Also**

[patchsizes](#), [patchdistr\\_sews](#)

**Examples**

```
data(forestgap)

rmat <- matrix(rnorm(100) > .1, ncol = 10)
display_matrix(label(rmat))

# With 8-way neighborhood mask and no wrapping around borders
nbmask8 <- matrix(c(1,1,1,
                    1,0,1,
                    1,1,1), ncol=3)
display_matrix(label(rmat, nbmask8, wrap = FALSE))

# On real data:
display_matrix(label(forestgap[[5]], nbmask8, wrap = FALSE))
```

---

patchdistr\_sews

*Early-warning signals based on patch size distributions*

---

**Description**

Compute early-warning signals based on patch size distributions

**Usage**

```
patchdistr_sews(
  mat,
  merge = FALSE,
  fit_lnorm = FALSE,
  best_by = "BIC",
```

```

    xmin = 1,
    xmin_bounds = NULL,
    wrap = FALSE
)

```

### Arguments

mat	A logical matrix (TRUE/FALSE values) or a list of these
merge	The default behavior is to produce indicators values for each matrix. If this parameter is set to TRUE then the patch size distributions are pooled together before fitting, yielding only one final indicator value for the set of matrices.
fit_lnorm	When patch size distributions are compared, should we consider lognormal type ? (see details)
best_by	The criterion to use to select the best fit (one of "AIC", "BIC" or "AICc")
xmin	The xmin to be used to fit the patch size distributions. Use the special value "estimate" to compute first the xmin that produces the best power-law fit, then use this estimated value to fit all distributions.
xmin_bounds	Bounds when estimating the xmin for power-law distributions
wrap	Determines whether patches are considered to wrap around the matrix when reaching the side

### Details

Patterned ecosystems can exhibit a change in their spatial structure as they become more and more stressed. It has been suggested that this should be reflected in changes in the observed patch size distributions (PSD). The following sequence is expected to occur (Kefi et al. 2011) as patterned ecosystems become more and more degraded:

- Percolation of vegetation patches occurs (a patch has a width or height equal to the size of the system)
- The patch-size distribution follows a power-law
- The patch-size distribution deviates from a power-law as larger patches break down
- The patch-size distribution is closer to an exponential distribution

Additionally, it has been suggested that these changes in patch size distribution shape should be reflected in the power-law range (PLR). This function carries out all the required computations and helps display the results in a convenient form.

The fitting of PSDs is based on maximum-likelihood following Clauset et al.'s procedure. The best discrete distribution is estimated among these candidates: a power-law  $x^\lambda$ , an exponential  $exp(\alpha x)$ , a truncated power-law and  $x^\lambda exp(\alpha x)$ , and optionally, a log-normal. Each distribution parameter is estimated using maximum-likelihood, with a minimum patch size (xmin) fixed to one. The best distribution is selected based on BIC by default. In raw results, plexpo refers to the power-law exponent ( $\lambda$  in the previous equations) and cutoff refers to the exponential decay rate  $\alpha$ .

To compute the Power-law range (PLR), power-laws are fitted with a variable minimum patch size (xmin) and the one with the lowest Kolmogorov-Smirnov distance to the empirical distribution is retained. PLR is then computed using this best-fitting xmin:

$$\frac{\log(x_{max}) - \log(x_{min})}{\log(x_{max}) - \log(x_{smallest})}$$

Results can be displayed using the text-based summary and print, but graphical options are also available to plot the trends (plot) and the fitted distributions ( `plot_distr`). Plotting functions are documented in a [separate page](#). Observed and fitted distributions can be produced using the predict function, as documented in [this page](#).

### Value

A list object of class 'psdfit' containing among other things - the observed patch size distribution data - the model outputs for the candidate distribution fits - the power-law range values - the percolation values (if several matrices were provided and 'merge' was TRUE, then the average percolation value is returned)

### References

- Kefi, S., Rietkerk, M., Alados, C. L., Pueyo, Y., Papanastasis, V. P., ElAich, A., & De Ruiter, P. C. (2007). Spatial vegetation patterns and imminent desertification in Mediterranean arid ecosystems. *Nature*, 449(7159), 213-217.
- Kefi, S., Rietkerk, M., Roy, M., Franc, A., de Ruiter, P.C. & Pascual, M. (2011). Robust scaling in ecosystems and the meltdown of patch size distributions before extinction: Patch size distributions towards extinction. *Ecology Letters*, 14, 29-35.
- Berdugo, M, Sonia Kefi, Santiago Soliveres, and Fernando T. Maestre. (2017) Plant Spatial Patterns Identify Alternative Ecosystem Multifunctionality States in Global Drylands. *Nature in Ecology and Evolution*, no. 1.
- Clauset, A., Shalizi, C. R., & Newman, M. E. (2009). Power-law distributions in empirical data. *SIAM review*, 51(4), 661-703.

### See Also

[patchsizes](#), [plot\\_distr](#), [predict](#), [plot](#),  
[indicstest](#), to test the significance of indicator values.

### Examples

```
data(forestgap)

## Not run:
psd_indic <- patchdistr_sews(forestgap)

summary(psd_indic)
plot(psd_indic)

# Plots can be modified using ggplot2 directives
if ( require(ggplot2) ) {
```

```

    plot(psd_indic) +
      theme_minimal()
  }

  # Export results to a data.frame
  psd_indic_export <- as.data.frame(psd_indic)
  head(psd_indic_export)

  ## End(Not run)

```

---

patchdistr\_sews\_plot *Early-warning signals based on patch size distributions*

---

## Description

Plot early-warning signals based on patch size distributions

## Usage

```

## S3 method for class 'patchdistr_sews'
plot(x, along = NULL, ...)

plot_distr(x, along = NULL, best_only = TRUE, plrange = TRUE)

```

## Arguments

x	An object as produced by <code>patchdistr_sews</code> , or the result of <code>indictest</code> called on such object
along	A vector providing values along which the indicator trends will be plotted. If NULL then the values are plotted sequentially in their original order.
...	Ignored
best_only	Plot only the best fit the empirical (inverse cumulative) patch-size distribution with an overlay of the estimated fits.
plrange	Plot the power-law range

## Details

The `plot` function will produce a figure summarizing the changes in patch size distributions along a set of values. The figure has two panels:

- the upper panel shows the percolation status of empty (FALSE) and occupied cells (TRUE), and shows the mean value (proportion of TRUE values). The background shows the proportion of each type of distribution for each unique values of the `along` vector.
- the bottom panel displays the power-law range

The `plot_distr` function displays each distribution in an individual facet, with an overlay of the best distribution fit and a blue bar showing the power-law range. If appropriate, a grey ribbon is used to display the expected distribution given the null expectation (i.e. when `plot_distr` is called on the results of `indictest()`). This function can produce quite crowded graphs, but it displays in full the shape of the distributions, and can be useful e.g. to assess the quality of the fits.

### See Also

[patchdistr\\_sews](#)

### Examples

```
## Not run:
data(forestgap)
psd_indic <- patchdistr_sews(forestgap)

plot(psd_indic, along = forestgap.pars[ , "d"])

# When along is non-numeric, bars are used for display
plot(psd_indic, along = as.factor(forestgap.pars[ , "d"]))

# Display individual distributions
plot_distr(psd_indic, along = forestgap.pars[ , "d"])

# We can display the distributions along with the null expectation after
# indictest() is run
psd_test <- indictest(psd_indic, nulln = 19)
plot_distr(psd_test, along = forestgap.pars[ , "d"])

## End(Not run)
```

---

patchdistr\_sews\_predict

*predict method for patchdistr\_sews objects*

---

### Description

Export the observed and fitted patch size distributions

### Usage

```
## S3 method for class 'patchdistr_sews_single'
predict(object, ..., newdata = NULL, best_only = FALSE, xmin_rescale = FALSE)
```



**Arguments**

object	An <code>patchdistr_sews</code> object
...	Additional arguments (ignored)
newdata	A vector of patch sizes at which the fit is returned (default to 200 regularly-spaced values).
best_only	Return values for only the best fit of each element (matrix) in object, or return the values for all fitted distribution.
xmin_rescale	If the xmin value used for fits is above one, then setting this to TRUE will rescale the predicted probabilities so that they align on the cumulative distribution of the observed patch sizes

**Details**

The function `patchdistr_sews` fits competing distribution models to the observed patch size distributions. This functions is able to export the observed values and the fitted values altogether.

**Value**

A list with component obs, a data.frame containing the observed distribution values and pred, a data.frame containing the fitted values.

**See Also**

`patchdistr_sews`

**Examples**

```
## Not run:
patch_indics <- patchdistr_sews(forestgap)

predict(patch_indics)

## End(Not run)
```

---

patchdistr\_spews      *(DEFUNCT) Early-warning signals based on patch size distributions*

---

**Description**

Compute early-warnings based on patch size distributions and review/plot the results

**Usage**

```

patchdistr_spews(
  x,
  merge = FALSE,
  fit_lnorm = FALSE,
  best_by = "BIC",
  xmin = 1,
  xmin_bounds = NULL,
  wrap = FALSE
)

```

**Arguments**

x	A logical matrix (TRUE/FALSE values) or a list of these
merge	The default behavior is to produce indicators values for each matrix. If this parameter is set to TRUE then the patch size distributions are pooled together for fitting.
fit_lnorm	When patch size distributions are compared, should we consider lognormal type ? (see details)
best_by	The criterion to use to select the best fit (one of "AIC", "BIC" or "AICc")
xmin	The xmin to be used to fit the patch size distributions. Use the special value "estimate" to compute first the xmin that produces the best power-law fit, then use this estimated value to fit all distributions.
xmin_bounds	Bounds when estimating the xmin for power-law distributions
wrap	Determines whether patches are considered to wrap around the matrix when reaching the side

**Details**

patchdistr\_spews has been renamed, please use [patchdistr\\_sews](#) instead.

---

patchsizes

*Get patch sizes.*

---

**Description**

Get the distribution of patch sizes from a logical matrix

**Usage**

```

patchsizes(
  mat,
  merge = FALSE,
  nbmask = matrix(c(0, 1, 0, 1, 0, 1, 0, 1, 0), ncol = 3),
  wrap = FALSE
)

```

**Arguments**

mat	A logical matrix or a list of such matrices.
merge	Controls whether the obtained patch size distributions are to be pooled together if mat is a list of matrices.
nbmask	a square matrix with an odd number of lines and columns that describes which neighbors are to be considered around a cell. Default is 4-way neighborhood (the neighborhood of a cell comprises the cell above, below, on the right and on the left of the target cell).
wrap	Whether to wrap around lattice boundaries ('TRUE'/'FALSE'), effectively using periodic boundaries.

**Value**

If mat is a logical matrix, then the function returns a vector of patch sizes. If mat is a list of logical matrices, then it returns a list of vectors of patch sizes: this list is flattened if merge is TRUE.

**See Also**

[label](#)

**Examples**

```
data(forestgap)
patchsizes(forestgap[[5]]) # Use a single matrix

# Compute the average patch size of each matrix
list_patches <- patchsizes(forestgap) # get the patch size for each matrix
print( sapply(list_patches, mean)) # print the average patch size

# Example with 8-way neighborhood
nbmask8 <- matrix(c(1,1,1,
                    1,0,1,
                    1,1,1), ncol = 3)
patchsizes(forestgap[[5]], nbmask = nbmask8)
```

---

plot.simple\_sews\_test *Spatial early-warning signals: display of trends*

---

**Description**

Spatial early-warning signals: display of trends

**Usage**

```
## S3 method for class 'simple_sews_test'
plot(x, along = NULL, what = "value", display_null = TRUE, ...)

## S3 method for class 'simple_sews_list'
plot(x, along = NULL, ...)
```

**Arguments**

x	A <code>simple_sews_test</code> object (as provided by <code>**_sews</code> functions, such as <code>generic_sews()</code> )
along	A vector providing values over which the indicator trend will be plotted. If <code>NULL</code> then the values are plotted sequentially in their original order.
what	The trendline to be displayed. Defaults to the indicator's values ("value") but other metrics can be displayed. Accepted values are "value", "pval" or "z_score".
display_null	Chooses whether a grey ribbon should be added to reflect the null distribution. Note that it can not be displayed when the trend line reflects something else than the indicator values (when <code>what</code> is not set to "value").
...	Other arguments are ignored.

**Details**

Note that the produced plot is adjusted depending on whether `along` is numeric or not.

---

plot_spectrum	<i>Display the r-spectrum of a spectral_sews object</i>
---------------	---

---

**Description**

Display the r-spectrum (or multiple spectra) that are contained in an object returned by `spectral_sews` object (or the result of `indictest` applied on such object).

**Usage**

```
plot_spectrum(x, along = NULL, log = TRUE, display_null = TRUE, ...)
```

**Arguments**

x	An object produced by <code>spectral_sews</code> or the result returned by <code>indictest</code> applied on such object
along	A vector providing numerical or categorical values along which the indicator trends will be plotted. If <code>NULL</code> then the indicator values are plotted sequentially in their original order.
log	Whether to use a log scale or a linear scale on the y axis
display_null	Whether to display null information. This argument is ignored if <code>x</code> has not been produced through <code>indictest</code> (and thus does not contain data regarding the null model)
...	Other arguments are ignored

**See Also**

[rspectrum](#), [spectral\\_sews](#), [extract\\_spectrum](#)

---

pl\_fit

*Distribution-fitting functions*

---

**Description**

These functions fit parametric distributions to a set of discrete values.

**Usage**

```
pl_fit(dat, xmin = 1)
```

```
exp_fit(dat, xmin = 1)
```

```
lnorm_fit(dat, xmin = 1)
```

```
tpl_fit(dat, xmin = 1)
```

**Arguments**

dat	The set of values to which the distribution are fit
xmin	The minimum possible value to consider when fitting the distribution

**Details**

These functions will fit distributions to a set of values using maximum-likelihood estimation. In the context of the 'spatialwarnings' package, they are most-often used to fit parametric distributions on patch size distributions. As a result, these functions assume that the data contains only integer, strictly positive values. The type of distribution depends on the prefix of the function: 'pl' for power-law, 'tpl' for truncated power-law, 'lnorm' for lognormal and 'exp' for an exponential distribution.

In the context of distribution-fitting, 'xmin' represents the minimum value that a distribution can take. It is often used to represent the minimum scale at which a power-law model is appropriate (Clauset et al. 2009), and can be estimated on an empirical distribution using [xmin\\_estim](#). Again, please note that the fitting procedure assumes here that xmin is equal or greater than one.

Please note that a best effort is made to have the fit converge, but it may sometimes fail when the parameters are far from their usual range. It is good practice to make sure the fits are sensible when convergence warnings are reported.

For reference, the shape of the distributions is as follow:

- power-law  $x^{-a}$  where a is the power-law exponent
- exponential  $exp(-bx)$  where b is the truncation rate of the exponential
- truncated power-law  $x^{-a}exp(-bx)$  where a and b are the exponent of the power law and the rate of truncation

The lognormal form follows the [standard definition](#).

**Value**

A list containing at list the following components:

- type: The type of distribution fitted (as a character string)
- method: The method used for the fit - here, maximum likelihood, 'll'
- ll: The negative log likelihood at the estimated parameter values
- xmin: The value of xmin used for the fit
- npars: The number of parameters of the distribution

Additionally, this list may have one or more of the following parameters depending on the type of distribution that has been fitted:

- plexpo: The exponent of the power-law
- cutoff: The rate of truncation, for truncated power law and exponential fits
- meanlog: The mean of the lognormal distribution
- sdlog: The s.d. of the lognormal distribution

**References**

Clauset, Aaron, Cosma Rohilla Shalizi, and M. E. J. Newman. 2009. "Power-Law Distributions in Empirical Data." *SIAM Review* 51 (4): 661–703. <https://doi.org/10.1137/070710111>.

**See Also**

[patchdistr\\_sews](#), [xmin\\_estim](#)

**Examples**

```
# Fit an exponential model to patch size distribution
exp_fit(patchsizes(forestgap[[8]]))

# Use the estimated parameters as an indicator function
## Not run:

get_truncation <- function(mat) {
  c(exp_cutoff = exp_fit(patchsizes(mat))$cutoff)
}
trunc_indic <- compute_indicator(forestgap, get_truncation)
plot(trunc_indic)
plot(indicest(trunc_indic, nulln = 19))

## End(Not run)
```

---

raw_cg_moran	<i>Moran's Index at lag of 1</i>
--------------	----------------------------------

---

### Description

This functions computes the Moran's spatial correlation index (with lag one) on a matrix.

### Usage

```
raw_cg_moran(mat, subsize = 1)
```

### Arguments

mat	A matrix
subsize	logical. Dimension of the submatrix used to coarse-grain the original matrix (set to 1 for no coarse-graining).

### Value

The Moran's I index measuring autocorrelation at lag 1 as a named vector

### References

Dakos, V., van Nes, E. H., Donangelo, R., Fort, H., & Scheffer, M. (2010). Spatial correlation as leading indicator of catastrophic shifts. *Theoretical Ecology*, 3(3), 163-174.

Legendre, P., & Legendre, L. F. J. (2012). *Numerical Ecology*. Elsevier Science.

### See Also

[generic\\_sews](#)

### Examples

```
## Not run:  
data(serengeti)  
raw_cg_moran(serengeti[[1]], subsize = 1)  
  
## End(Not run)
```

---

raw_cg_skewness	<i>Skewness indicator</i>
-----------------	---------------------------

---

### Description

Compute the spatial skewness of spatial data (a matrix).

### Usage

```
raw_cg_skewness(mat, subsize = 5, absolute = TRUE)
```

### Arguments

mat	A matrix. The matrix values can be logical, with FALSE (empty) or TRUE (occupied) values. The entries can also be continuous (like NDVI or EVI data).
subsize	Dimension of the submatrix used to coarse-grain the original matrix. This must be an integer less than size of the full matrix. Coarse-graining reduces the size of the matrix by a factor subsize in each dimension of the matrix. Skewness is calculated on the coarse-grained matrix.
absolute	Should the function return the absolute value or raw value of skewness ?

### Details

Spatial skewness is a measure of fluctuations in space; specifically, it measures if fluctuations are getting biased (skewed) in one direction. Based on the theory of critical slowing down, when systems approach critical points they are expected to show increased fluctuations in space. Thus, increasing spatial skewness is proposed as an early warning signal of impending critical transitions.

Computing spatial skewness is straightforward. However, detecting trends of skewness that correspond to critical slowing down can be tricky, especially if data come from discrete classification of state variable.

Many high resolution spatial data are classified as FALSE (empty) or TRUE (occupied by plant). In such cases, spatial skewness captures just the skewness in data, but not that of spatial structure. To resolve the issue, this function employs a method called coarse-graining, proposed in Kefi et al (2014), and described in detail in Sankaran et al. (2017). One must specify a subsize above one for binary valued data sets to obtain meaningful values.

subsize has to be an integer. It has to be less than or equal to half of matrix size (N). subsize must also be preferably a divisor of N. If it is not a divisor of N, the remainder rows and columns are discarded when computing coarse-graining matrices.

Null model evaluations are also done on coarse-grained matrices.

### Value

The spatial skewness of the matrix as a named vector



## References

- Guttal, V., and Jayaprakash, C. (2009). Spatial variance and spatial skewness: leading indicators of regime shifts in spatial ecological systems. *Theoretical Ecology*, 2(1), 3-12.
- Kefi, S., Guttal, V., Brock, W.A., Carpenter, S.R., Ellison, A.M., Livina, V.N., et al. (2014). Early Warning Signals of Ecological Transitions: Methods for Spatial Patterns. *PLoS ONE*, 9, e92097.
- Sankaran, S., Majumder, S., Kefi, S., and Guttal, V. (2017). Implication of being discrete and spatial in detecting early warning signals of regime shifts. *Ecological indicators*.

## See Also

[generic\\_sews](#)

## Examples

```
data(serengeti)
## Not run:
raw_cg_skewness(serengeti[[1]])
compute_indicator(serengeti, fun = raw_cg_skewness, subsize = 5)

## End(Not run)
```

---

raw_cg_variance	<i>Spatial variance indicator</i>
-----------------	-----------------------------------

---

## Description

This functions computes the spatial variance of a matrix.

## Usage

```
raw_cg_variance(mat, subsize = 5)
```

## Arguments

- |         |  |
|---------|--|
| mat     | A matrix. Its values can be logical, with FALSE (empty) or TRUE (occupied) values. The entries can also be continuous (like NDVI or EVI data).   |
| subsize | Dimension of the submatrix used to coarse-grain the original matrix. This must be an integer less than size of the full matrix. Coarse-graining reduces the size of the matrix by a factor subsize in each dimension of the matrix. Variance is calculated on the coarse-grained matrix. |

## Details

Spatial variance is a measure of fluctuations in space. Based on the theory of critical slowing down, when systems approach critical points they are expected to show increased fluctuations in space. Thus, increasing spatial variance is proposed as an early warning signal of impending critical transitions.

Many high resolution spatial data are classified as FALSE (empty) or TRUE (occupied). In such cases, spatial variance captures just the variance in data, but not that of spatial structure. To resolve the issue, this function employs a method called coarse-graining, proposed in Kefi et al (2014), and described in detail in Sankaran et al. (2017). One must specify a subsize above one for binary valued data sets to obtain meaningful values.

subsize has to be an integer. It has to be less than or equal to half of matrix size (N). subsize must also be preferably a divisor of N. If it is not a divisor of N, the remainder rows and columns are discarded when computing coarse-graining matrices.

Null model evaluations are also done on coarse-grained matrices.

## Value

The variance of the coarse-grained matrix as a named vector

## References

Guttal, V., and Jayaprakash, C. (2009). Spatial variance and spatial skewness: leading indicators of regime shifts in spatial ecological systems. *Theoretical Ecology*, 2(1), 3-12.

Kefi, S., Guttal, V., Brock, W.A., Carpenter, S.R., Ellison, A.M., Livina, V.N., et al. (2014). Early Warning Signals of Ecological Transitions: Methods for Spatial Patterns. *PLoS ONE*, 9, e92097.

Sankaran, S., Majumder, S., Kefi, S., and Guttal, V. (2017). Implication of being discrete and spatial in detecting early warning signals of regime shifts. *Ecological Indicators*.

## See Also

[generic\\_sews](#)

## Examples

```
## Not run:
data(serengeti)
raw_cg_variance(serengeti[[1]])
compute_indicator(serengeti, fun = raw_cg_variance, subsize = 5)

## End(Not run)
```

---

`raw_flowlength_uniform`*Flow length (uniform slope)*

---

### Description

Compute a simple approximation of the flow length assuming a constant slope

### Usage

```
raw_flowlength_uniform(mat, slope, cell_size)
```

### Arguments

<code>mat</code>	The input matrix (must be a logical matrix)
<code>slope</code>	The slope of the area documented by the matrix (in degrees).
<code>cell_size</code>	The horizontal size of a cell in the matrix (as viewed from above).

### Details

This function computes the Flowlength of a given matrix, using a uniform approximation (the slope is constant across the whole matrix, with maximum slope being from the top of the matrix to its bottom), as per Rodriguez et al. (2017). See [flowlength\\_sews](#) for more details.

### Value

A named vector of length 1 containing the flow length numerical value

### References

Rodriguez, F., A. G. Mayor, M. Rietkerk, and S. Bautista. 2017. A null model for assessing the cover-independent role of bare soil connectivity as indicator of dryland functioning and dynamics. *Ecological Indicators*.

### See Also

[flowlength\\_sews](#)

[indicetest](#), to test the significance of indicator values.

### Examples

```
## Not run:  
raw_flowlength_uniform(arizona[[1]], slope = 20, cell_size = 1)  
  
## End(Not run)
```

---

`raw_kbdm`*Kolmogorov complexity of a matrix*

---

**Description**

Compute the Kolmogorov complexity of a matrix using the Block Decomposition Method (requires the `acss` package).

**Usage**

```
raw_kbdm(mat, subsize)
```

**Arguments**

<code>mat</code>	A logical matrix (with TRUE/FALSE values)
<code>subsize</code>	A submatrix size to carry out the Block Decomposition Method (must be between 1 and 3)

**Details**

The Kolmogorov complexity cannot be computed directly for large strings (i.e. matrices). However, the complexity of smaller submatrices can be estimated, then combined to obtain an approximation of the complexity of the whole matrix. This method, the Block Decomposition Method is implemented in this function. See also [kbdm\\_sews](#) for more details.

**Value**

The KBDM numeric value as a named vector

**See Also**

[kbdm\\_sews](#), [acss](#)

**Examples**

```
## Not run:  
raw_kbdm(forestgap[[1]], subsize = 3)  
  
## End(Not run)
```

---

`raw_moran`*Spatial correlation at lag 1*

---

## Description

This function computes the Moran's I index of spatial correlation at lag 1.

## Usage

```
raw_moran(mat)
```

## Arguments

`mat`            A matrix

## Details

This function returns the spatial correlation as measured by the Moran's I index. If the variance of the matrix is zero, then NaN is returned. This function assumes a 4-way neighborhood, and does not wrap around at the sides of the matrix.

## Value

The Moran's I numeric value as a numeric number.

## See Also

[indicator\\_moran](#), [generic\\_sews](#)

## Examples

```
# Spatial correlation of white noise is close to zero
rmat <- matrix(runif(1000) > .5, ncol = 100)
raw_moran(rmat)

# Spatial correlation of a half-ones / half-zeros matrix is close to one.
# This would produce close but inaccurate results in version <3.0.2
m <- cbind(matrix(1, nrow = 100, ncol = 50),
           matrix(0, nrow = 100, ncol = 50))

raw_moran(m)
```

---

raw_plrange	<i>Power-law range indicator</i>
-------------	----------------------------------

---

**Description**

Compute the power-law range of a matrix

**Usage**

```
raw_plrange(mat, xmin_bounds = NULL)
```

**Arguments**

mat	A logical matrix, or a list of logical matrices
xmin_bounds	A vector of two integer values, defining a range in which to search for the best xmin (see Details).

**Details**

Some ecosystems show typical changes in their patch-size distribution as they become more and more degraded. In particular, an increase in the truncation of the patch-size distribution (PSD) is expected to occur. The power-law range (PLR) measures the truncation of the PSD in a single value (see also [patchdistr\\_sews](#) for more details).

To compute the PLR, power-laws are fitted with a variable minimum patch size (xmin) and the one with the lowest Kolmogorov-Smirnov distance to the empirical distribution is retained. PLR is then computed using this best-fitting xmin:

$$\frac{\log(x_{max}) - \log(x_{min})}{\log(x_{max}) - \log(x_{smallest})}$$

where  $x_{max}$  is the maximum observed patch size, and  $x_{smallest}$  is the minimum observed patch size.

**Value**

A named vector containing the power-law range value

**References**

Clauset, A., Shalizi, C. R., & Newman, M. E. (2009). Power-law distributions in empirical data. *SIAM review*, 51(4), 661-703.

Berdugo, M., Kefi, S., Soliveres, S. & Maestre, F.T. (2017). Plant spatial patterns identify alternative ecosystem multifunctionality states in global drylands. *Nature in Ecology and Evolution*.

**See Also**

[patchdistr\\_sews](#)

**Examples**

```
## Not run:
forestgap.plr <- raw_plrange(forestgap[[2]])

# Restrict to small xmins
forestgap.plr2 <- indicator_plrange(forestgap[[2]], xmin_bounds = c(1, 10))

## End(Not run)
```

raw\_sdr

*Spectral Density Ratio (SDR) indicator***Description**

Compute the ratio of low frequencies over high frequencies of the r-spectrum.

**Usage**

```
raw_sdr(mat, sdr_low_range = NULL, sdr_high_range = NULL)
```

**Arguments**

mat	A matrix with continuous values, or a logical matrix (TRUE/FALSE).
sdr_low_range	The range of values (in proportion) to use for the computation of the spectral density ratio. For example, for the lowest 20% (default value), set sdr_low_range to c(0, .2).
sdr_high_range	The range of values (in proportion) to use for the computation of the spectral density ratio. For example, for the highest 20% (default value), set sdr_high_range to c(.8, 1).

**Details**

SDR measures the increase in long-range correlations before a critical point. It is the ratio of the average low frequency value over high frequency values. In this implementation, an increase in SDR implies a "reddening" of the *r-spectrum*. See also [spectral\\_sews](#) for a more complete description.

Low and high frequencies are averaged in order to compute the SDR. The parameters sdr\_low\_range and sdr\_high\_range control which frequencies are selected for averaging. For example sdr\_low\_range = c(0, .2) (default) uses the lower 20 the average of low frequencies. sdr\_high\_range = c(.8, 1) uses the higher 20

**Value**

The SDR values computed on the matrix as a named vector

**References**

Carpenter, S.R. & Brock, W.A. (2010). Early warnings of regime shifts in spatial dynamics using the discrete Fourier transform. *Ecosphere*

**See Also**

[indicest](#), [rspectrum](#), [plot\\_spectrum](#), [spectral\\_sews](#), [extract\\_spectrum](#)

**Examples**

```
## Not run:
data(serengeti)
serengeti.sdr <- raw_sdr(serengeti[[1]],
                        sdr_low_range = c(0, 0.2),
                        sdr_high_range = c(0.8, 1))
compute_indicator(serengeti, raw_sdr)

## End(Not run)
```

---

raw\_structvar

*Structural variance*


---

**Description**

Compute the structural variance on a matrix.

**Usage**

```
raw_structvar(mat, model = "sph", nmax = 100000L, nbins = 32, cutoff = NULL)
```

**Arguments**

mat	A matrix
model	The variogram model to use, either "sph" (for a spherical model) or "exp" (for an exponential model)
nmax	The maximum number of pairs of cells to use when computing the variogram
nbins	Number of distance bins to use to compute the variogram
cutoff	Maximum distance to consider in the variogram. If NULL, then a distance equal to one third of the diagonal of the matrix is used

**See Also**

[raw\\_variogram\\_metrics](#), [variogram\\_sews](#)

**Examples**

```
raw_structvar(serengeti[[5]])
```



---

raw\_variogram\_metrics *Variogram parameters*

---

## Description

Compute the nugget, partial sill, correlation range and structural variance on a matrix.

## Usage

```
raw_variogram_metrics(  
  mat,  
  model = "sph",  
  nmax = 100000L,  
  nbins = 32,  
  cutoff = NULL  
)
```

## Arguments

mat	A matrix
model	The variogram model to use, either "sph" (for a spherical model) or "exp" (for an exponential model)
nmax	The maximum number of pairs of cells to use when computing the variogram
nbins	Number of distance bins to use to compute the variogram
cutoff	Maximum distance to consider in the variogram. If NULL, then a distance equal to one third of the diagonal of the matrix is used

## See Also

variogram\_sews, raw\_structvar

## Examples

```
raw_variogram_metrics(serengeti[[5]])
```

---

rspectrum	<i>r-spectrum</i>
-----------	-------------------

---

### Description

Compute the r-spectrum of a matrix

### Usage

```
rspectrum(mat)
```

### Arguments

mat                    A matrix with logical or numeric values

### Details

This functions returns a data.frame with NAs in the rspec column if the input matrix has zero variance. Note that if the matrix is not square, then only the largest square matrix fitting in the upper right corner is used.

### Value

A data.frame with two columns: dist, the wave number and rspec, the normalized value of the r-spectrum

### See Also

[spectral\\_sews](#)

### Examples

```
# Spectrum of white noise
rmat <- matrix(runif(100*100) > .5, ncol = 100)
spec <- rspectrum(rmat)
plot(spec, type = "l")

# Add some spatial correlation and compare the two spectra
rmat.cor <- rmat
for (i in seq(1, nrow(rmat)-1)) {
  for (j in seq(1, nrow(rmat)-1)) {
    rmat.cor[i,j] <- mean(rmat[(i-1):(i+1), (j-1):(j+1)])
  }
}
spec.cor <- rspectrum(rmat.cor)
plot(spec.cor, type = "n")
lines(spec, col = "black")
lines(spec.cor, col = "blue")
```

---

serengeti

*Serengeti dataset*

---

### **Description**

Vegetation data along a rainfall gradient in Serengeti national park.

### **Usage**

serengeti

serengeti.rain

### **Format**

A list of logical matrices

The annual rainfall corresponding to the matrices in the serengeti dataset, in the corresponding order.

### **Details**

The data-set consists of a rectangular area of size 7.5 km x 90 km. These data are represented as a list of matrices. Each matrix is a moving window of 7.5 km x 7.5 km which moves my 2.5 km along the length of the rectangular data-set. Each entry in the matrix is vegetation data at a resolution of 30m as classified into binary units with 0 (grass) and 1 (forest). The rainfall data provided here is the average rainfall (mm/yr) of a moving window of dimension 7.5km which moves my 2.5 km along the length of the rectangular data-set.

### **Source**

Extracted from Eby's et al (2017) supplementary material <https://github.com/tee-lab/spacetime-csd/>

### **References**

Eby, S., Agrawal, A., Majumder, S., Dobson, A.P. & Guttal, V. (2017). Alternative stable states and spatial indicators of critical slowing down along a spatial gradient in a savanna ecosystem: *Global Ecology and Biogeography*, 26, 638-649

Reed, D. N., Anderson, T. M., Dempewolf, J., Metzger, K., & Serneels, S. (2009). The spatial distribution of vegetation types in the Serengeti ecosystem: the influence of rainfall and topographic relief on vegetation patch characteristics. *Journal of Biogeography*, 36(4), 770-782.

---

 simple\_sews

 simple\_sews *objects*


---

## Description

This help page describes the structure of `simple_sews_*` objects, such as those defined by the classes `simple_sews_single`, `simple_sews_list`

## Details

The `spatialwarnings` uses S3 objects (lists) internally to store indicator values, along with the necessary data to plot and display results. It is not recommended to extract data directly from these objects, as they are subject to change with different releases of the package. The preferred method is to use dedicated generic functions such as `plot()` or `as.data.frame()` to display or export the results. Nonetheless, we document the structure of these objects here for reference.

`simple_sews` objects are returned by all indicator functions that return numeric values. This includes for example `generic_sews`, `flowlength_sews`, `compute_indicator` but *not* `patchdistr_sews` or `spectral_sews`, which provide indicators that depend on non-numeric values (e.g. patch-size distribution type), or need to store more information than just a single numerical value (e.g. the spectrum of the input matrix).

`simple_sews` objects come in multiple variants: `simple_sews_single` is the result of an indicator function applied to a single matrix, and `simple_sews_test_single` is the result of `indictest` applied to a `simple_sews_single` object. Both these objects have list equivalents, `simple_sews_list` and `simple_sews_test_list` which are simply a collection of their 'single' equivalent. These 'list' objects are used to store the results of computations when working with multiple matrices.

A `simple_sews_single` object is a list with the following components

- `value`: the indicator values. A vector of length one if there is only one numeric value returned by the indicator function (e.g. `flowlength_sews`, or with a length above one otherwise)
- `orig_data`: the original matrix on which the indicator was computed
- `fun.args`: the argument used in the call to the indicator function (the function that given a matrix, returns the spatial metrics of interest)
- `taskname`: a character string describing the current indicator(s) being computed
- `indicf`: the indicator function, which given the matrix, returns the spatial metric(s) of interest

`simple_sews_test_single` have all of the above components, plus the following:

- `nulldistr`: the null distribution of values, with `nulln` rows and as many columns as the number of values returned by the indicator function
- `null_mean`: the mean indicator values in the null distribution
- `null_sd`: the standard deviation of the null distribution
- `null_qsup`: the upper quantile of the null distribution, by default the 95 adjust this
- `null_qinf`: the upper quantile of the null distribution, by default the 05 adjust this

- `z_score`: the `z_score` of the observed value relative to the null distribution, i.e.  $(\text{value} - \text{null\_mean}) / \text{null\_sd}$
- `pval`: the p-value of the indicator, i.e. the proportion of values of the null distribution that fall below the observed indicator value
- `null_method`: the method used to produce the null matrices. See [indictest](#) for details
- `nulln`: the number of null matrices used
- `get_nullmat`: a function that can be called to obtain a randomized matrix
- `matrixn`: the number of the matrix, can be above one if the computations have been run on a list of matrices, or non-existent if only one matrix was used

### See Also

[custom\\_indicator](#)

---

spatialwarnings

*Early Spatial-Warnings of Ecosystem Degradation*

---

### Description

Many dynamical systems such as ecosystems exhibit non-linear responses to changes in their external drivers, resulting in possible wide state shifts with strong ecological or economical consequences. This often happens when a system exhibit a change in its stability properties as a threshold is crossed, *e.g.* going from multiple stable states to a single stable state. For a few decades, much research has been dedicated to finding a way to anticipate these tipping points in ecological systems. This has led to the development of several indicators, i.e. metrics based on spatial structure, that could reflect the proximity of an ecosystem to a tipping point.

This package implements the computation of these indicators, or *early-warning signals* (EWS), on spatial raster data. High-level functions and methods provide familiar workflows to compute the indicators and display their variations along environmental gradients or time-series. Lower-level functions are also available to integrate early-warning signals into different workflows.

Main functions provided by this package:

"Workflow" functions, which may compute several indicators at once:

- `generic_sews`: Generic spatial EWS
- `spectral_sews`: Spectrum-based EWS
- `patchdistr_sews`: EWS based on patch-size distributions
- `kbdm_sews`: Kolmogorov complexity
- `flowlength_sews`: Flow length
- `variogram_sews`: Variogram-based indicators

Individual indicators, which may be used to compute raw indicator values on a single matrix:

- `raw_cg_moran`: lag-1 spatial autocorrelation

- `raw_cg_variance`: Spatial variance
- `raw_cg_skewness`: Spatial skewness
- `raw_sdr`: Spectral density ratio (SDR)
- `indicator_psdtype`: Patch-size distribution shape
- `indicator_plrange`, `raw_plrange` : Power-law range
- `raw_kbdm`: Kolmogorov complexity
- `raw_flowlength_uniform`: Flow Length
- `raw_variogram_metrics`: Variogram-based metrics

The package homepage is available at [Github](#) and a [user guide](#) is also available.

---

spectral\_sews

*Spectrum-based spatial early-warning signals.*

---

## Description

Computation of spatial early warning signals based on spectral properties.

## Usage

```
spectral_sews(mat, sdr_low_range = NULL, sdr_high_range = NULL, quiet = FALSE)
```

## Arguments

<code>mat</code>	The input matrix or a list of matrices.
<code>sdr_low_range</code>	The range of values (in proportion) to use for the computation of the spectral density ratio. For example, for the lowest 20 <code>c(0, .2)</code> . See also the Details section.
<code>sdr_high_range</code>	The range of values (in proportion) to use for the computation of the spectral density ratio. For example, for the higher 20 <code>c(.8, 1)</code> . See also the Details section.
<code>quiet</code>	Do not display some warnings

## Details

Spectral early warning signals are based on the fact that some dynamical systems can exhibit an change in some characteristics of their spatial structure when approaching a transition. In particular, long-range correlations are expected to have an increased importance.

This is expected to be reflected in the spectrum of the spatial structure by an increase of the relative importance of lower frequencies over higher frequencies ("reddening" of the spectrum).

This task allows computing the radial-spectrum which gives the relative importance of each space scale as a function of distance, from 1 to  $N/2$  ( $N$  being the minimum between the number of rows and columns). If the matrix is not square, then it is cropped to biggest square that fits within the left side of the matrix.

Additionally, it summarizes this spectrum into a Spectral Density Ratio (SDR), which is the ratio of low frequencies over high frequencies of the r-spectrum. The SDR value is expected to increase before a transition point.

The significance of spectral early-warning signals can be estimated by reshuffling the original matrix (function `indicest`). Indicators are then recomputed on the shuffled matrices and the values obtained are used as a null distribution. P-values are obtained based on the rank of the observed value in the null distribution.

The trend of SDR values can be plotted using the `plot()` method. Alternatively, the spectrum itself can be plotted (with facets if multiple input matrices were used) using the `plot_spectrum` method.

## Value

Function `spectral_sews` object of class `spectral_sews_list` or `spectral_sews_single` depending on whether the input was a list of matrices or a single matrix.

Function `indicest`

The `plot` methods returns a `ggplot` object (usually displayed immediately when called interactively).

## References

Kefi, S., Guttal, V., Brock, W.A., Carpenter, S.R., Ellison, A.M., Livina, V.N., et al. (2014). Early Warning Signals of Ecological Transitions: Methods for Spatial Patterns. *PLoS ONE*, 9, e92097.

## See Also

[rspectrum](#), [plot\\_spectrum](#), [raw\\_sdr](#), [extract\\_spectrum](#)  
[indicest](#), to test the significance of indicator values.

## Examples

```
## Not run:

data(serengeti)
data(serengeti.rain)

spec_indic <- spectral_sews(serengeti,
                           sdr_low_range = c(0, .2),
                           sdr_high_range = c(.8, 1))

summary(spec_indic)

# Display trends along the varying model parameter
plot(spec_indic, along = serengeti.rain)

# Computing spectra many times is expensive, consider setting parallel
# computing using: options(mc.cores = n)

# Assess significance
```

```

spec_test <- indictest(spec_indic, nulln = 199)
summary(spec_test)

# Display the SDR trend, now with a grey ribbon representing 5%-95%
# quantiles of the null distribution
plot(spec_test, along = serengeti.rain)

# Add a line highlighting the shift
if (require(ggplot2)) {
  plot(spec_test, along = serengeti.rain) +
    geom_vline(xintercept = 590, color = "red", linetype = "dashed")
}

# Display radial-spectra
plot_spectrum(spec_indic, along = serengeti.rain)

# Graphics can be modified using ggplot2 functions
if (require(ggplot2)) {
  plot_spectrum(spec_indic, along = serengeti.rain) +
    scale_y_log10()
}

## End(Not run)

```

---

spectral\_spews

*(DEFUNCT) Spectrum-based spatial early-warning signals.*


---

### Description

Computation of spatial early warning signals based on spectral properties.

### Usage

```
spectral_spews(mat, sdr_low_range = NULL, sdr_high_range = NULL, quiet = FALSE)
```

### Arguments

mat	The input matrix or a list of matrices.
sdr_low_range	The range of values (in proportion) to use for the computation of the spectral density ratio. For example, for the lowest 20 c(0, .2). See also the Details section.
sdr_high_range	The range of values (in proportion) to use for the computation of the spectral density ratio. For example, for the higher 20 c(.8, 1). See also the Details section.
quiet	Do not display some warnings



## Details

spectral\_spews has been renamed, please use [spectral\\_sews](#) instead.

---

variogram_sews	<i>Early-Warning signals based on variograms (EXPERIMENTAL)</i>
----------------	---

---

## Description

Compute Early-warning signals based on metrics derived from semi-variograms.

## Usage

```
variogram_sews(mat, model = "sph", nmax = 1e+05, nbins = 32, cutoff = NULL)
```

## Arguments

mat	A matrix (TRUE/FALSE values) or a list of matrices
model	The variogram model to use, either "sph" (for a spherical model) or "exp" (for an exponential model)
nmax	The maximum number of pairs of cells to use when computing the variogram
nbins	Number of distance bins to use to compute the variogram
cutoff	Maximum distance to consider in the variogram. If NULL, then a distance equal to one third of the diagonal of the matrix is used

## Details

During ecosystem degradation and especially before a regime shift occurs in some ecosystems, spatial autocorrelation is expected to increase in a landscape. This increase can be measured based on variograms, which represent how the difference (variance) between two points in a landscape varies as a function of distance.

The approach used to derive variogram-based EWS is to compute the empirical variogram of a landscape (represented passed as a matrix of values), then fit a variogram model to it. Three parameters are then extracted from the variogram model (see Nijp et al. 2019 for a visual description of these parameters):

1. The *nugget* (intercept)
2. The *partial sill*, i.e. the reduction in semivariance at distance zero
3. The *correlation range*, i.e. the distance at which the relationship between semivariance and distance flattens

Additionally, the *structural variance* is computed as (partial sill)/(nugget + partial sill), which quantifies whether the data are spatially structured (structural variance of one), or completely unstructured (value of zero). Theoretical work suggests that partial sill, correlation range and structural variance should increase before a regime shift occurs in an ecosystem (Nijp et al. 2019).

This function offers to fit a spherical model or an exponential model. The best-fitting model depends on your data, you should try different options and review the fits using [plot\\_variogram](#).

Please note that this part of the package is still experimental and deserves more testing.

**Value**

A list object of class "variogram\_sews", that can be displayed using `summary()`, `plot()`, etc. Significance of values can be tested using `indicest`.

**References**

Nijp, Jelmer J., Arnaud J.A.M. Temme, George A.K. Voorn, Lammert Kooistra, Geerten M. Hengeveld, Merel B. Soons, Adriaan J. Teuling, and Jakob Wallinga. (2019) Spatial Early Warning Signals for Impending Regime Shifts: A Practical Framework for Application in Real-world Landscapes. *Global Change Biology* 25 (6): 1905-21. doi: [10.1111/gcb.14591](https://doi.org/10.1111/gcb.14591)

**See Also**

`raw_structvar`, `plot_variogram`, `extract_variogram`, `predict`  
`indicest`, to test the significance of indicator values.

**Examples**

```
## Not run:
serengeti_ews <- variogram_sews(serengeti,
                               model = "exp")
plot(serengeti_ews, along = serengeti.rain)
summary(serengeti_ews)

plot_variogram(serengeti_ews)

# nulln should be set to a higher values for meaningful results
serengeti_test <- indicest(serengeti_ews, nulln = 9)
plot(serengeti_test) # gray ribbons indicate the null indicator values
summary(serengeti_test)

## End(Not run)
```

---

variogram\_sews\_plot    *Early-warning signals based on variograms*

---

**Description**

Plot trends of indicators based on variograms

**Usage**

```
## S3 method for class 'variogram_sews'
plot(x, along = NULL, ...)

plot_variogram(x, along = NULL, ...)
```

```
## S3 method for class 'variogram_sews'
plot_variogram(x, along = NULL, ...)

## S3 method for class 'variogram_sews_test'
plot(x, along = NULL, what = "value", display_null = TRUE, ...)

## S3 method for class 'variogram_sews_test'
plot_variogram(x, along = NULL, what = "value", display_null = TRUE, ...)
```

### Arguments

x	An object produced by <a href="#">variogram_sews</a> , or the result of applying <code>indictest</code> on such object.
along	A vector providing values along which the indicator trends will be plotted. If NULL then the indicator values are plotted sequentially in their original order.
...	Other arguments are ignored.
what	The trendline to be displayed. Defaults to the indicator's values ("value") but other metrics can be displayed. Accepted values are "value", "pval" or "z_score".
display_null	Chooses whether a grey ribbon should be added to reflect the null distribution. Note that it can not be displayed when the trend line reflects something else than the indicator values (when what is not set to "value").

### Details

The `plot()` function will display how the estimated variogram parameters change along a set of values (passed with argument `along`). If the object passed has been processed through `indictest`, then the null values are also displayed. `plot_variogram()` can be used to display the individual variograms that have been fit to the data.

### See Also

[variogram\\_sews](#), [indictest](#), [plot\\_variogram](#)

### Examples

```
## Not run:
serengeti_ews <- variogram_sews(serengeti, model = "exp")

# Display the change in variogram parameters
plot(serengeti_ews, along = serengeti.rain) +
  ggplot2::labs(x = "Rainfall (mm)")

# Visualize the fitted variograms
plot_variogram(serengeti_ews, along = serengeti.rain)

# Test the trends (nulln should be set to a higher value to obtain
# meaningful results
```

```
serengeti_test <- indictest(serengeti_ews, nulln = 19)
plot(serengeti_test, along = serengeti.rain)
plot_variogram(serengeti_test, along = serengeti.rain)

## End(Not run)
```

---

variogram\_sews\_predict

*predict() method for variogram\_sews objects*

---

### Description

Export the fitted variogram(s)

### Usage

```
## S3 method for class 'variogram_sews_list'
predict(object, newdist = NULL, ...)
```

### Arguments

object	An object produced by <code>variogram_sews</code>
newdist	A vector of distances at which to return the variogram fit values (defaults to 128 regularly-spaced values).
...	Additional arguments (ignored)

### Value

A data.frame with the distances (column `dist`), the fitted values (`gamma`), and if `object` contains more than one matrix, a column `matrixn`.

### See Also

[variogram\\_sews](#)

### Examples

```
## Not run:
vario_indics <- variogram_sews(serengeti)
predict(vario_indics)
vario_test <- indictest(vario_indics, nulln = 19)
predict(vario_test) # same result

## End(Not run)
```

---

`xmin_estim`*Estimate the minimum patch size of a power-law distribution*

---

### Description

When fitting a power-law to a discrete distribution, it might be worth discarding points below a certain threshold (`xmin`) to improve the fit. This function estimates the optimal `xmin` based on the Kolmogorov-Smirnoff distance between the fit and the empirical distribution, as suggested by Clauset et al. (2009).

### Usage

```
xmin_estim(dat, bounds = range(dat))
```

### Arguments

<code>dat</code>	A vector of integer values
<code>bounds</code>	A vector of two values representing the bounds in which the best <code>xmin</code> is searched

### Details

The function returns NA if `dat` has only three unique values or if the power-law fit failed.

### Value

The estimated `xmin` as an integer value

### References

Clauset, A., Shalizi, C. R., & Newman, M. E. (2009). Power-law distributions in empirical data. *SIAM review*, 51(4), 661-703.

### See Also

[patchdistr\\_sews](#)

### Examples

```
## Not run:  
psd <- patchsizes(forestgap[[5]])  
xmin_estim(psd)  
  
## End(Not run)
```

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