

# Package ‘spatialwarnings’

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**Type** Package

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

**Version** 1.3.1

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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)

**Imports** Rcpp, ggplot2 (>= 1.0.0), plyr, VGAM, reshape2, tidyr, stats,  
utils, parallel

**Suggests** moments, powerLaw, testthat, covr, acss

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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	<i>Matrix coarse-graining</i>
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## 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')
```

---

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, indicname = as.character(substitute(fun)))

custom_indicator(mat, fun, indicname = as.character(substitute(fun)),
                ...)
```

**Arguments**

fun	A function that takes a real-valued matrix as input and returns a single, numerical value.
indicname	The indicator name. Optional, used for plots and textual summaries, but mandatory if fun is an anonymous function.
mat	A matrix or a list of matrices.
...	Additional arguments that are passed to the function fun

**Details**

Spatial Early-warning signals (EWS) are metrics that are based on the spatial structure of a system and measure the degradation of an ecological system. The package `spatialwarnings` provides generic indicators ([generic\\_sews](#)), spectrum-based indicators ([spectral\\_sews](#)) and indicators based on patch size distributions ([patchdistr\\_sews](#)).

`create_indicator` extends the package to any arbitrary function. It takes a function ‘fun’ and returns another function that can be used as an indicator similar to the `*_sews` function family. The results of this function can be assessed for significance using `indictest` and trends can be displayed using `plot`, `summary`, etc. (see Examples). `custom_indicator` does the same but without creating an intermediate indicator function.

fun should be a function that takes as input a matrix and possibly more arguments, and return a single numeric value. Note that the matrix is converted internally to numeric values, as a side effect of using c++ code when assessing significance.

## Value

create\_indicator returns a function that can be used in the same way than the other \*\_sews functions (e.g. generic\_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, nperm = 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 custom_indicator
cv_indic2 <- custom_indicator(serengeti, spatial_cv, subsize = 3)
plot(cv_indic2, along = serengeti.rain)
```

```
## Not run:
indictest(cv_indic, nperm = 99)

## 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,
  method = "uniform topography")
```

### 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).
method	The method to use to compute the flow length (for now only the method "uniform", using a single slope approximation, is implemented)

### 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.

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

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*.
- 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. *Landsc. 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.

## 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, nperm = 19)
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).

**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. <http://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)
```

```
## S3 method for class 'generic_sews'
indicest(x, nperm = 999, ...)
```

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

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



**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 ?
x	A generic_sews object (as provided by the generic_sews function).
nperm	The number of replicates to use to compute a null distribution
...	Additional arguments passed onto methods
along	A vector providing values over which the indicator trend will be plotted. If NULL 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. Correct 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 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.

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

**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.

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

plot methods return `ggplot` objects, usually immediately displayed when 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

[indicator\\_moran](#), [indicator\\_variance](#) and [indicator\\_skewness](#) for individual indicators.

## 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 <- indicest(gen_indic, nperm = 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	<i>(DEPRECATED) Generic Spatial Early-Warning signals</i>
---------------	---

---

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

---

### 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, nreplicates = 999)
```

**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).
nreplicates	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 nreplicates 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 xmin's
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 xmin's 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
- 'expo', 'rate', 'meanlog', 'sdlog' the estimates for distribution parameters.
- '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

*Spectral 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,
  nreplicates = 999)

```

**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 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).
nreplicates	The number of replicates 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 `nreplicates` 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, nreplicates = 499)
do.call(rbind, serengeti.sdr) # convert results to data.frame

## End(Not run)
```

---

indicator\_skewness      *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,
  nreplicates = 999)
```

### 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 ?
nreplicates	Number of replicates to produce to estimate null distribution of index.

### 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 nreplicates 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**

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

## End(Not run)
```

---

indicator\_variance      *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, nreplicates = 999)
```

**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.
nreplicates	Number of replicates to produce to estimate null distribution of index.

**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 nreplicates 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, nreplicates = 499)

## End(Not run)
```

---

indictest

*Significance-assessment of spatial early-warning signals*

---

### Description

Assess the significance of spatial early-warning values

### Usage

```
indictest(x, nperm = 999, ...)
```

### Arguments

x	A spatial warning object such as one produced by the *_sews function family
nperm	The number of permutations to carry out to produce the null distribution
...	Additional arguments passed to methods

### Details

The significance of many early-warning signals can be estimated by reshuffling the original matrix. 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.

### Value

An object of class ending in \*\_sews\_test, whose exact class depends on the input object (in reality a data.frame)

### 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`*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](#)

## Examples

```
## Not run:

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

kbdm_test <- indictest(kbdm_result, nperm = 99)
plot(kbdm_test, along = serengeti.rain)

# Plot deviation to a random matrix
plot(kbdm_test, along = serengeti.rain, what = "z_score")

## End(Not run)
```

---

label	<i>Labelling of unique patches and detection of percolation.</i>
-------	--

---

## 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 "labels" 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 labeled 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](#)

**Examples**

```
data(forestgap)

par(mfrow=c(1, 2))
rmat <- matrix(rnorm(100) > .1, ncol = 10)
image(rmat)
image(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)
image(label(rmat, nbmask8, wrap = FALSE))
```

---

patchdistr\_sews

*Early-warning signals based on patch size distributions*

---

**Description**

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

**Usage**

```
patchdistr_sews(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

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, expo refers to the power-law exponent  $\lambda$  in the previous equations and rate 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.

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

## See Also

[indicator\\_psdtype](#), [patchsizes](#), [plot](#), [plot\\_distr](#), [predict](#)

## 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 <a href="#">spectral_sews</a>
along	A vector providing values over which the indicator trend will be plotted. If NULL then the values are plotted sequentially in their original order.
...	Further arguments passed to methods
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 complex figure summarizing the change 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_spectrum` 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. This mode of representation can be cumbersome when working with a high number of matrices but displays the full shape of the distributions.

**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"])
```

```
## 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)
```

## Arguments

object	An <a href="#">patchdistr_sews</a> 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.

## 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](#), [plot](#), [plot\\_distr](#),

**Examples**

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

predict(patch_indics)

## End(Not run)
```

---

patchdistr_spews	<i>(DEPRECATED) Early-warning signals based on patch size distributions</i>
------------------	---

---

**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 of 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 these 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)
```

---

raw_cg_skewness	<i>Skewness of a coarse-grained matrix</i>
-----------------	--

---

**Description**

Compute the skewness of a given matrix after coarse-graining

**Usage**

```
raw_cg_skewness(mat, subsize, absolute)
```

**Arguments**

mat	A matrix that can contain logical (with TRUE/FALSE values)
subsize	The size of the submatrices used for coarse-graining
absolute	Whether to return the unmodified skewness, or its absolute value

---

raw_flowlength_uniform	<i>Flow length (uniform slope)</i>
------------------------	------------------------------------

---

**Description**

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

**Usage**

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

**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 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**

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](#)

**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 = 3)
```

**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**

A numeric value

**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.

**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)
```

---

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 (TRUE/FALSE values)
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**

The power-law range value of the matrix, a single number

**See Also**

[indicator\\_plrange](#), [patchdistr\\_sews](#)

**Examples**

```
raw_plrange(serengeti[[1]])
```

---

rspectrum

*r-spectrum*

---

**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](#), [indicator\\_sdr](#)

**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

### 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.

## 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 exhibits 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 suggestion of several indicators 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 in a different workflow.

Main functions provided by this package

"Workflow" functions:

- `generic_sews`: Generic spatial EWS
- `spectral_sews`: Spectrum-based EWS
- `patchdistr_sews`: EWS based on patch-size distributions

Individual indicators:

- `indicator_moran`: lag-1 spatial autocorrelation (Moran's I)
- `indicator_variance`: Spatial variance
- `indicator_skewness`: Spatial skewness
- `indicator_sdr`: Spectral density ratio (SDR)
- `indicator_psdtype`: Patch-size distribution shape
- `indicator_plrange`: Power-law range

The package home page is available at [Github]<https://github.com/spatial-ews/spatialwarnings> and a [FAQ covering technical issues](<https://alex.lecairn.org/spatialwarnings-faq.html>) 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)

## S3 method for class 'spectral_sews'
indicest(x, nperm = 999, ...)

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

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

### 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
x	A spectral_sews_test object as produced by <a href="#">indicest</a>
nperm	The number of replicates to use to compute use in the null distribution
...	Ignored
along	An optional vector of values along which the trend is to be displayed. The length of the vector must be equal to the number of indicator values provided in the object x.
what	What the trend-line to be displayed should represent about the indicator. Defaults to the indicator's values ("value") but other metrics can be displayed. Correct values are "value", "pval" or "z_score".
display_null	Sets 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

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 `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.

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 `indictest`

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.

## 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 <- indicitest(spec_indic, nperm = 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

*(DEPRECATED) 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.

---

xmin_estim	<i>Estimate the minimum patch size of a power-law distribution</i>
------------	--

---

### 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

dat	A vector of integer values
bounds	A bounds

### 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](#), [patchsizes](#), [indicator\\_psdtype](#)

**Examples**

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

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