

Package ‘shar’

March 8, 2022

Type Package

Title Species-Habitat Associations

Version 1.3.2

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Description Analyse species-habitat associations in R. Therefore, information about the location of the species (as a point pattern) is needed together with environmental conditions (as a categorical raster). To test for significance habitat associations, one of the two components is randomized. Methods are mainly based on Plotkin et al. (2000) <doi:10.1006/jtbi.2000.2158> and Harms et al. (2001) <doi:10.1111/j.1365-2745.2001.00615.x>.

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URL <https://r-spatialecology.github.io/shar/>

BugReports <https://github.com/r-spatialecology/shar/issues/>

Depends R (>= 3.1.0)

Imports classInt, graphics, grDevices, methods, raster, spatstat.core, spatstat.geom, spatstat.random, stats, utils

RoxygenNote 7.1.2

Suggests covr, dplyr, future, future.apply, knitr, rmarkdown, spatstat (>= 2.0.0), testthat (>= 2.1.0)

VignetteBuilder knitr

Encoding UTF-8

LazyData true

NeedsCompilation no

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Repository CRAN

Date/Publication 2022-03-08 13:40:02 UTC

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calculate_energy	<i>calculate_energy</i>
------------------	-------------------------

Description

Calculate mean energy

Usage

```
calculate_energy(
  pattern,
  weights = c(0.5, 0.5),
  return_mean = FALSE,
  comp_fast = 1000,
  verbose = TRUE
)
```

Arguments

pattern	List with reconstructed patterns.
weights	Vector with weights used to calculate energy. The first number refers to Gest(r), the second number to pcf(r).
return_mean	Logical if the mean energy is returned.
comp_fast	Integer with threshold at which summary functions are estimated in a computational fast way.
verbose	Logical if progress report is printed.

Details

The function calculates the mean energy (or deviation) between the observed pattern and all reconstructed patterns (for more information see Tscheschel & Stoyan (2006) or Wiegand & Moloney (2014)). The pair correlation function and the nearest neighbour distance function are used to describe the patterns. For large patterns `comp_fast = TRUE` decreases the computational demand, because no edge correction is used and the pair correlation function is estimated based on Ripley's K-function. For more information see [estimate_pcf_fast](#).

Value

vector

References

- Kirkpatrick, S., Gelatt, C.D.Jr., Vecchi, M.P., 1983. Optimization by simulated annealing. *Science* 220, 671–680. <<https://doi.org/10.1126/science.220.4598.671>>
- Tscheschel, A., Stoyan, D., 2006. Statistical reconstruction of random point patterns. *Computational Statistics and Data Analysis* 51, 859–871. <<https://doi.org/10.1016/j.csda.2005.09.007>>
- Wiegand, T., Moloney, K.A., 2014. Handbook of spatial point-pattern analysis in ecology. Chapman and Hall/CRC Press, Boca Raton. ISBN 978-1-4200-8254-8

See Also

[plot_energy](#)
[reconstruct_pattern](#)
[fit_point_process](#)

Examples

```
pattern_random <- fit_point_process(species_a, n_random = 19)
calculate_energy(pattern_random)
calculate_energy(pattern_random, return_mean = TRUE)

## Not run:
marks_sub <- spatstat.geom::subset.ppp(species_a, select = dbh)
marks_recon <- reconstruct_pattern_marks(pattern_random$randomized[[1]], marks_sub,
n_random = 19, max_runs = 1000)
calculate_energy(marks_recon, return_mean = FALSE)
```

```
## End(Not run)
```

classify_habitats	<i>classify_habitats</i>
-------------------	--------------------------

Description

Classify habitats

Usage

```
classify_habitats(raster, return_breaks = FALSE, ...)
```

Arguments

raster	RasterLayer with continuous environmental values.
return_breaks	Logical if breaks should be returned as well.
...	Arguments passed on to <code>classIntervals</code> .

Details

Classifies a RasterLayer from the raster packages with continuous values into n discrete classes. The cut function used to classify the raster, uses `include.lowest = TRUE`.

For more information about the classification methods, see `classIntervals` from the `classInt` package and/or the provided References. The help page of `classIntervals` also includes further possible arguments to find breaks (e.g., different styles, number of classes, fixed breaks, etc.).

Value

RasterLayer

References

Armstrong, M.P., Xiao, N., Bennett, D.A., 2003. Using genetic algorithms to create multicriteria class intervals for choropleth maps. *Annals of the Association of American Geographers* 93, 595–623. <<https://doi.org/10.1111/1467-8306.9303005>>

Dent, B.D., 1999. *Cartography: Thematic map design*, 5th ed. WCB/McGraw-Hill, Boston, USA. ISBN 978-0-697-38495-9

Fisher, W.D., 1958. On grouping for maximum homogeneity. *Journal of the American Statistical Association* 53, 789–798. <<https://doi.org/10.1080/01621459.1958.10501479>>

Jenks, G.F., Caspall, F.C., 1971. Error in choroplethic maps: Definition, measurement, reduction. *Annals of the Association of American Geographers* 61, 217–244. <<https://doi.org/10.1111/j.1467-8306.1971.tb00779.x>>

Jiang, B., 2013. Head/tail breaks: A new classification scheme for data with a heavy-tailed distribution. *The Professional Geographer* 65, 482-494. <<https://doi.org/10.1080/00330124.2012.700499>>

Slocum, T.A., McMaster, R.B., Kessler, F.C., Howard, H.H., 2009. *Thematic cartography and geovisualization*, 3rd ed. ed, Prentice Hall Series in Geographic Information Science. Pearson Prentice Hall, Upper Saddle River, USA. ISBN 978-0-13-229834-6

Wand, M. P., 1995. Data-based choice of histogram binwidth. *The American Statistician* 51, 59-64. <<https://doi.org/10.1080/00031305.1997.10473591>>

See Also

[classIntervals](#)

Examples

```
landscape_classified <- classify_habitats(landscape, n = 5, style = "fisher")
```

```
landscape_classified <- classify_habitats(landscape, style = "fixed",  
fixedBreaks = c(0, 0.25, 0.75, 1.0), return_breaks = TRUE)
```

estimate_pcf_fast *estimate_pcf_fast*

Description

Fast estimation of the pair correlation function

Usage

```
estimate_pcf_fast(pattern, ...)
```

Arguments

pattern	ppp object with point pattern.
...	Arguments passed down to <code>link{Kest}</code> or <code>pcf.fv</code> .

Details

The functions estimates the pair correlation functions based on an estimation of Ripley's K-function. This makes it computationally faster than estimating the pair correlation function directly. It is a wrapper around `Kest` and `pcf.fv`.

Value

fv.object

References

Chiu, S.N., Stoyan, D., Kendall, W.S., Mecke, J., 2013. Stochastic geometry and its applications, 3rd ed, Wiley Series in Probability and Statistics. John Wiley & Sons Inc, Chichester, UK. ISBN 978-0-470-66481-0

Ripley, B.D., 1977. Modelling spatial patterns. Journal of the Royal Statistical Society. Series B (Methodological) 39, 172–192. <<https://doi.org/10.1111/j.2517-6161.1977.tb01615.x>>

Stoyan, D., Stoyan, H., 1994. Fractals, random shapes and point fields. John Wiley & Sons, Chichester. ISBN 978-0-471-93757-9

See Also

[Kest](#)
[pcf.fv](#)

Examples

```
pcf_species_b <- estimate_pcf_fast(species_a)
```

`fit_point_process` *fit_point_process*

Description

Fit point process to randomize data

Usage

```
fit_point_process(  
  pattern,  
  n_random = 1,  
  process = "poisson",  
  return_input = TRUE,  
  simplify = FALSE,  
  verbose = TRUE  
)
```

Arguments

<code>pattern</code>	ppp object with point pattern
<code>n_random</code>	Integer with number of randomizations.
<code>process</code>	Character specifying which point process model to use. Either "poisson" or "cluster".
<code>return_input</code>	Logical if the original input data is returned.
<code>simplify</code>	Logical if only pattern will be returned if <code>n_random = 1</code> and <code>return_input = FALSE</code> .
<code>verbose</code>	Logical if progress report is printed.

Details

The functions randomizes the observed point pattern by fitting a point process to the data and simulating `n_random` patterns using the fitted point process. It is possible to choose between a Poisson process or a Thomas cluster process model. For more information about the point process models, see e.g. Wiegand & Moloney (2014).

Value

`rd_pat`

References

Plotkin, J.B., Potts, M.D., Leslie, N., Manokaran, N., LaFrankie, J.V., Ashton, P.S., 2000. Species-area curves, spatial aggregation, and habitat specialization in tropical forests. *Journal of Theoretical Biology* 207, 81–99. <<https://doi.org/10.1006/jtbi.2000.2158>>

Wiegand, T., Moloney, K.A., 2014. *Handbook of spatial point-pattern analysis in ecology*. Chapman and Hall/CRC Press, Boca Raton. ISBN 978-1-4200-8254-8

Examples

```
pattern_fitted <- fit_point_process(pattern = species_a, n_random = 39)
```

gamma_test

Gamma test

Description

Randomized data for species b using the gamma test.

Usage

```
gamma_test
```

Format

`rd_pat` object.

landscape	<i>Example landscape (random cluster neutral landscape model).</i>
-----------	--

Description

An example map to show landscapetools functionality generated with the NLMR: :nlm_fbm() algorithm.

Usage

```
landscape
```

Format

A RasterLayer object.

Source

Simulated neutral landscape model with R. <https://github.com/ropensci/NLMR/>

list_to_randomized	<i>list_to_randomized</i>
--------------------	---------------------------

Description

Convert list to rd_* object.

Usage

```
list_to_randomized(list, observed = NULL)
```

Arguments

list	List
observed	Observed

Details

Convert list of randomized point pattern or raster layer to a rd_* object that can be used with all functions of the package. The main purpose of this utility function is to allow an easy parallelization of the randomization approach.

For more information, please see the "Parallelization" article.

Value

rd_pat, rd_ras

See Also

[randomize_raster](#)
[translate_raster](#)
[reconstruct_pattern](#)

Examples

```

## Not run:
fit_list <- lapply(X = 1:39, FUN = function(i) {fit_point_process(pattern = species_a,
n_random = 1, simplify = TRUE, return_input = FALSE, verbose = FALSE)})

list_to_randomized(list = fit_list, observed = species_a)

## End(Not run)

```

plot.rd_mar

plot.rd_mar

Description

Plot method for rd_pat object

Usage

```

## S3 method for class 'rd_mar'
plot(
  x,
  what = "sf",
  n = NULL,
  probs = c(0.025, 0.975),
  comp_fast = 1000,
  ask = TRUE,
  verbose = TRUE,
  ...
)

```

Arguments

x	rd_mar object with randomized patterns.
what	Character specifying to plot summary functions of point patterns (what = "sf") or actual patterns (what = "pp").
n	Integer with number or vector of ids of randomized pattern to plot. See Details section for more information.
probs	Vector with quantiles of randomized data used for envelope construction.
comp_fast	Integer with threshold at which summary functions are estimated in a computational fast way.

ask	Logical if the user is asked to press <RETURN> before second summary function is plotted (only used if what = "sf").
verbose	Logical if progress report is printed.
...	Not used.

Details

The function plots the pair correlation function and the nearest neighbour function of the observed pattern and the reconstructed patterns (as "simulation envelopes"). For large patterns `comp_fast = TRUE` decreases the computational demand because no edge correction is used and the pair correlation function is estimated based on Ripley's K-function. For more information see [estimate_pcf_fast](#).

It is also possible to plot `n` randomized patterns and the observed pattern using `what = "pp"`. If `n` is a single number, `n` randomized patterns will be sampled to plot. If `n` is a vector, the corresponding patterns will be plotted.

Value

void

See Also

[reconstruct_pattern](#)
[fit_point_process](#)

Examples

```
## Not run:
pattern_recon <- reconstruct_pattern(species_a, n_random = 1, max_runs = 1000,
simplify = TRUE, return_input = FALSE)
marks_sub <- spatstat.geom::subset.ppp(species_a, select = dbh)
marks_recon <- reconstruct_pattern_marks(pattern_recon, marks_sub,
n_random = 19, max_runs = 1000)
plot(marks_recon)

## End(Not run)
```

plot.rd_pat

plot.rd_pat

Description

Plot method for `rd_pat` object

Usage

```
## S3 method for class 'rd_pat'
plot(
  x,
  what = "sf",
  n = NULL,
  probs = c(0.025, 0.975),
  comp_fast = 1000,
  ask = TRUE,
  verbose = TRUE,
  ...
)
```

Arguments

x	rd_pat bject with randomized patterns.
what	Character specifying to plot summary functions of point patterns (what = "sf") or actual patterns (what = "pp").
n	Integer with number or vector of ids of randomized pattern to plot. See Details section for more information.
probs	Vector with quantiles of randomized data used for envelope construction.
comp_fast	Integer with threshold at which summary functions are estimated in a computational fast way.
ask	Logical if the user is asked to press <RETURN> before second summary function is plotted (only used if what = "sf").
verbose	Logical if progress report is printed.
...	Not used.

Details

The function plots the pair correlation function and the nearest neighbour function of the observed pattern and the reconstructed patterns (as "simulation envelopes"). For large patterns `comp_fast = TRUE` decreases the computational demand because no edge correction is used and the pair correlation function is estimated based on Ripley's K-function. For more information see [estimate_pcf_fast](#).

It is also possible to plot `n` randomized patterns and the observed pattern using `what = "pp"`. If `n` is a single number, `n` randomized patterns will be sampled to plot. If `n` is a vector, the corresponding patterns will be plotted.

Value

void

See Also

[reconstruct_pattern](#)
[fit_point_process](#)

Examples

```
## Not run:
pattern_random <- fit_point_process(species_a, n_random = 39)
plot(pattern_random)

pattern_recon <- reconstruct_pattern(species_b, n_random = 19,
max_runs = 1000, method = "hetero")
plot(pattern_recon)

## End(Not run)
```

plot.rd_ras

plot.rd_ras

Description

Plot method for rd_ras object

Usage

```
## S3 method for class 'rd_ras'
plot(x, n = NULL, col, verbose = TRUE, nrow, ncol, ...)
```

Arguments

x	rd_ras object with randomized raster.
n	Integer with number or vector of ids of randomized raster to plot. See Details section for more information.
col	Vector with color palette used for plotting.
verbose	Logical if messages are printed.
nrow, ncol	Integer with number of rows and columns of plot grid.
...	Not used.

Details

Function to plot randomized raster. If n is a single number, n randomized raster will be sampled to plot. If n is a vector, the corresponding raster will be plotted. col, nrow, ncol are passed to plot.

Value

void

See Also

[randomize_raster](#)
[translate_raster](#)

Examples

```
## Not run:
landscape_classified <- classify_habitats(landscape, n = 5, style = "fisher")
landscape_random <- randomize_raster(landscape_classified, n_random = 19)
plot(landscape_random)

## End(Not run)
```

plot_energy	<i>plot_energy</i>
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Description

Plot energy of pattern reconstruction

Usage

```
plot_energy(pattern, col = NULL)
```

Arguments

pattern	rd_pat or rd_mar object with randomized patterns.
col	Vector with colors. Must be the same length as n_random.

Details

The function plots the decrease of the energy over time, i.e. the iterations. This can help to identify if the chosen max_runs for the reconstruction were sufficient. The pattern object must have been created using reconstruct_pattern_* .

Value

void

See Also

[reconstruct_pattern](#)
[fit_point_process](#)

Examples

```
## Not run:
pattern_recon <- reconstruct_pattern(species_a, n_random = 3, max_runs = 1000)
plot_energy(pattern_recon)

marks_sub <- spatstat.geom::subset.ppp(species_a, select = dbh)
marks_recon <- reconstruct_pattern_marks(pattern_recon$randomized[[1]], marks_sub,
```

```
n_random = 1, max_runs = 1000)
plot_energy(marks_recon)

## End(Not run)
```

print.rd_mar	<i>print.rd_mar</i>
--------------	---------------------

Description

Print method for rd_mar object

Usage

```
## S3 method for class 'rd_mar'
print(x, digits = 4, ...)
```

Arguments

x	rd_mar object with randomized patterns.
digits	Integer with number of decimal places (round) to be printed.
...	Arguments passed to cat.

Details

Printing method for random patterns created with [reconstruct_pattern_marks](#).

Value

void

See Also

[reconstruct_pattern_marks](#)

Examples

```
## Not run:
pattern_recon <- reconstruct_pattern(species_a, n_random = 1, max_runs = 1000,
simplify = TRUE, return_input = FALSE)
marks_sub <- spatstat.geom::subset.ppp(species_a, select = dbh)
marks_recon <- reconstruct_pattern_marks(pattern_recon, marks_sub,
n_random = 19, max_runs = 1000)
print(marks_recon)

## End(Not run)
```

print.rd_pat	<i>print.rd_pat</i>
--------------	---------------------

Description

Print method for rd_pat object

Usage

```
## S3 method for class 'rd_pat'  
print(x, digits = 4, ...)
```

Arguments

x	rd_pat object with randomized patterns.
digits	Integer with number of decimal places (round).
...	Arguments passed to cat.

Details

Printing method for random patterns created with reconstruct_pattern*.

Value

void

See Also

[reconstruct_pattern](#)
[fit_point_process](#)

Examples

```
pattern_random <- fit_point_process(species_a, n_random = 199)  
print(pattern_random)  
  
## Not run:  
pattern_recon <- reconstruct_pattern(species_b, n_random = 19, max_runs = 1000,  
method = "hetero")  
print(pattern_recon)  
  
## End(Not run)
```

print.rd_ras	<i>print.rd_ras</i>
--------------	---------------------

Description

Print method for rd_ras object

Usage

```
## S3 method for class 'rd_ras'  
print(x, ...)
```

Arguments

x	rd_ras object with randomized raster.
...	Arguments passed to cat.

Details

Printing method for random patterns created with [randomize_raster](#) or [translate_raster](#).

Value

void

See Also

[randomize_raster](#)
[translate_raster](#)

Examples

```
## Not run:  
landscape_classified <- classify_habitats(landscape, n = 5, style = "fisher")  
landscape_random <- randomize_raster(landscape_classified, n_random = 19)  
  
print(landscape_random)  
  
## End(Not run)
```

randomize_raster	<i>randomize_raster</i>
------------------	-------------------------

Description

Randomized-habitats procedure

Usage

```
randomize_raster(
  raster,
  n_random = 1,
  directions = 4,
  return_input = TRUE,
  simplify = FALSE,
  verbose = TRUE
)
```

Arguments

raster	RasterLayer with discrete habitat classes.
n_random	Integer with number of randomizations.
directions	Integer with cells neighbourhood rule: 4 (rook's case), 8 (queen's case).
return_input	Logical if the original input data is returned.
simplify	Logical if only the raster will be returned if n_random = 1 and return_input = FALSE.
verbose	Logical if progress report is printed.

Details

The function randomizes a habitat map with discrete classes (as RasterLayer) as proposed by Harms et al. (2001) as “randomized-habitats procedure”. The algorithm starts with an empty habitat map and starts to assign random neighbouring cells to each habitat (in increasing order of abundance in observed map). We modified the procedure slightly by increasing a probability to jump to a non-neighbouring cell as the current patch becomes larger.

In case the RasterLayer contains NA cells, this needs to be reflected in the observation window of the point pattern as well (i.e., no point locations possible in these areas).

Value

rd_ras

References

Harms, K.E., Condit, R., Hubbell, S.P., Foster, R.B., 2001. Habitat associations of trees and shrubs in a 50-ha neotropical forest plot. *Journal of Ecology* 89, 947–959. <<https://doi.org/10.1111/j.1365-2745.2001.00615.x>>

See Also[translate_raster](#)**Examples**

```
## Not run:  
landscape_classified <- classify_habitats(landscape, n = 5, style = "fisher")  
landscape_random <- randomize_raster(landscape_classified, n_random = 19)  
  
## End(Not run)
```

random_walk	<i>Random walk</i>
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Description

Randomization of the landscape using the habitat randomization algorithm.

Usage

```
random_walk
```

Format

rd_ras object.

reconstruction	<i>Reconstruction</i>
----------------	-----------------------

Description

Randomized data for species b using pattern reconstruction.

Usage

```
reconstruction
```

Format

rd_pat object.

reconstruct_pattern *reconstruct_pattern*

Description

Pattern reconstruction

Usage

```
reconstruct_pattern(
  pattern,
  method = "homo",
  n_random = 1,
  e_threshold = 0.01,
  max_runs = 1000,
  no_change = Inf,
  annealing = 0.01,
  comp_fast = 1000,
  n_points = NULL,
  window = NULL,
  weights = c(0.5, 0.5),
  r_length = 250,
  return_input = TRUE,
  simplify = FALSE,
  verbose = TRUE,
  plot = FALSE
)
```

Arguments

pattern	ppp object with pattern.
method	Character with specifying the method. Either "homo", "cluster" or "hetero".
n_random	Integer with number of randomizations.
e_threshold	Double with minimum energy to stop reconstruction.
max_runs	Integer with maximum number of iterations if e_threshold is not reached.
no_change	Integer with number of iterations at which the reconstruction will stop if the energy does not decrease.
annealing	Double with probability to keep relocated point even if energy did not decrease.
comp_fast	Integer with threshold at which summary functions are estimated in a computational fast way.
n_points	Integer with number of points to be simulated.
window	owin object with window of simulated pattern.
weights	Vector with weights used to calculate energy. The first number refers to Gest(r), the second number to pcf(r).

<code>r_length</code>	Integer with number of intervals from $r=0$ to $r=r_{\max}$ for which the summary functions are evaluated.
<code>return_input</code>	Logical if the original input data is returned.
<code>simplify</code>	Logical if only pattern will be returned if <code>n_random=1</code> and <code>return_input=FALSE</code> .
<code>verbose</code>	Logical if progress report is printed.
<code>plot</code>	Logical if <code>pcf(r)</code> function is plotted and updated during optimization.

Details

The functions randomizes the observed pattern by using pattern reconstruction as described in Tscheschel & Stoyan (2006) and Wiegand & Moloney (2014). The algorithm shifts a point to a new location and keeps the change only, if the deviation between the observed and the reconstructed pattern decreases. The pair correlation function and the nearest neighbour distance function are used to describe the patterns.

For large patterns ($n > \text{comp_fast}$) the pair correlation function can be estimated from Ripley's K-function without edge correction. This decreases the computational time. For more information see [estimate_pcf_fast](#).

The reconstruction can be stopped automatically if for n steps the energy does not decrease. The number of steps can be controlled by `no_change` and is set to `no_change = Inf` as default to never stop automatically.

The weights must be $0 < \text{sum}(\text{weights}) \leq 1$. To weight both summary functions identical, use `weights = c(0.5, 0.5)`.

`spatstat` sets `r_length` to 513 by default. However, a lower value decreases the computational time, while increasing the "bumpiness" of the summary function.

The arguments `n_points` and `window` are used for `method="homo"` only.

`method="homo"`:: The algorithm starts with a random pattern.

`method="cluster"`:: The algorithm starts with a random but clustered pattern.

`method="hetero"`:: The algorithm starts with a random but heterogeneous pattern.

Value

`rd_pat`

References

Kirkpatrick, S., Gelatt, C.D.Jr., Vecchi, M.P., 1983. Optimization by simulated annealing. *Science* 220, 671–680. <<https://doi.org/10.1126/science.220.4598.671>>

Tscheschel, A., Stoyan, D., 2006. Statistical reconstruction of random point patterns. *Computational Statistics and Data Analysis* 51, 859–871. <<https://doi.org/10.1016/j.csda.2005.09.007>>

Wiegand, T., Moloney, K.A., 2014. Handbook of spatial point-pattern analysis in ecology. Chapman and Hall/CRC Press, Boca Raton. ISBN 978-1-4200-8254-8

See Also

[calculate_energy](#)
[reconstruct_pattern_marks](#)

Examples

```
## Not run:  
pattern_recon <- reconstruct_pattern(species_b, n_random = 19, max_runs = 1000)  
  
## End(Not run)
```

```
reconstruct_pattern_marks  
      reconstruct_pattern_marks
```

Description

Pattern reconstruction of marked pattern

Usage

```
reconstruct_pattern_marks(  
  pattern,  
  marked_pattern,  
  n_random = 1,  
  e_threshold = 0.01,  
  max_runs = 10000,  
  no_change = Inf,  
  annealing = 0.01,  
  r_length = 250,  
  return_input = TRUE,  
  simplify = FALSE,  
  verbose = TRUE,  
  plot = FALSE  
)
```

Arguments

pattern	ppp object with pattern.
marked_pattern	ppp object with marked pattern. See Details section for more information.
n_random	Integer with number of randomizations.
e_threshold	Double with minimum energy to stop reconstruction.
max_runs	Integer with maximum number of iterations if e_threshold is not reached.
no_change	Integer with number of iterations at which the reconstruction will stop if the energy does not decrease.

annealing	Double with probability to keep relocated point even if energy did not decrease.
r_length	Integer with number of intervals from $r = 0$ to $r = r_{\max}$ for which the summary functions are evaluated.
return_input	Logical if the original input data is returned.
simplify	Logical if only pattern will be returned if <code>n_random = 1</code> and <code>return_input = FALSE</code> .
verbose	Logical if progress report is printed.
plot	Logical if <code>pcf(r)</code> function is plotted and updated during optimization.

Details

The function randomizes the numeric marks of a point pattern using pattern reconstruction as described in Tscheschel & Stoyan (2006) and Wiegand & Moloney (2014). Therefore, an unmarked as well as a marked pattern must be provided. The unmarked pattern must have the spatial characteristics and the same observation window and number of points as the marked one (see `reconstruct_pattern_*` or `fit_point_process`). Marks must be numeric because the mark-correlation function is used as summary function. Two randomly chosen marks are switch each iterations and changes only kept if the deviation between the observed and the reconstructed pattern decreases.

`spatstat` sets `r_length` to 513 by default. However, a lower value decreases the computational time while increasing the "bumpiness" of the summary function.

Value

`rd_mar`

References

Kirkpatrick, S., Gelatt, C.D.Jr., Vecchi, M.P., 1983. Optimization by simulated annealing. *Science* 220, 671–680. <<https://doi.org/10.1126/science.220.4598.671>>

Tscheschel, A., Stoyan, D., 2006. Statistical reconstruction of random point patterns. *Computational Statistics and Data Analysis* 51, 859–871. <<https://doi.org/10.1016/j.csda.2005.09.007>>

Wiegand, T., Moloney, K.A., 2014. Handbook of spatial point-pattern analysis in ecology. Chapman and Hall/CRC Press, Boca Raton. ISBN 978-1-4200-8254-8

See Also

[fit_point_process](#)
[reconstruct_pattern](#)

Examples

```
## Not run:
pattern_recon <- reconstruct_pattern(species_a, n_random = 1, max_runs = 1000,
simplify = TRUE, return_input = FALSE)
marks_sub <- spatstat.geom::subset.ppp(species_a, select = dbh)
marks_recon <- reconstruct_pattern_marks(pattern_recon, marks_sub,
n_random = 19, max_runs = 1000)
```

```
## End(Not run)
```

```
results_habitat_association  
  results_habitat_association
```

Description

Results habitat association

Usage

```
results_habitat_association(  
  pattern,  
  raster,  
  significance_level = 0.05,  
  breaks = NULL,  
  digits = NULL,  
  verbose = TRUE  
)
```

Arguments

pattern	ppp object with original point pattern data or rd_pat or rd_mar object with randomized point pattern.
raster	RasterLayer with original discrete habitat data or rd_ras object with randomized environmental data.
significance_level	Double with significance level.
breaks	Vector with breaks of habitat classes.
digits	Integer with digits used during rounding.
verbose	Logical if messages should be printed.

Details

The functions shows significant habitat associations by comparing the number of points within a habitat between the observed data and randomized data as described in Plotkin et al. (2000) and Harms et al. (2001). Significant positive or associations are present if the observed count in a habitat is above or below a certain threshold of the randomized count, respectively.

In case the RasterLayer contains NA cells, this needs to be reflected in the observation window of the point pattern as well (i.e., no point locations possible in these areas).

If breaks = NULL (default), only habitat labels (but not breaks) will be returned. If a vector with breaks is provided (same order as increasing habitat values), the breaks will be included as well.

Value

data.frame

References

Harms, K.E., Condit, R., Hubbell, S.P., Foster, R.B., 2001. Habitat associations of trees and shrubs in a 50-ha neotropical forest plot. *Journal of Ecology* 89, 947–959. <<https://doi.org/10.1111/j.1365-2745.2001.00615.x>>

Plotkin, J.B., Potts, M.D., Leslie, N., Manokaran, N., LaFrankie, J.V., Ashton, P.S., 2000. Species-area curves, spatial aggregation, and habitat specialization in tropical forests. *Journal of Theoretical Biology* 207, 81–99. <<https://doi.org/10.1006/jtbi.2000.2158>>

See Also

[reconstruct_pattern](#)
[fit_point_process](#)

Examples

```
landscape_classified <- classify_habitats(landscape, n = 5, style = "fisher")
species_a_random <- fit_point_process(species_a, n_random = 199)
results_habitat_association(pattern = species_a_random, raster = landscape_classified)
```

species_a

Species a

Description

A species with negative associations to habitat 4 of landscape. Please be aware that a negative association to one habitat will inevitable lead to positive associations to other habitats (Yamada et al. 2006).

Usage

species_a

Format

A spatstat ppp object.

References

Yamada, T., Tomita, A., Itoh, A., Yamakura, T., Ohkubo, T., Kanzaki, M., Tan, S., Ashton, P.S., 2006. Habitat associations of Sterculiaceae trees in a Bornean rain forest plot. *Journal of Vegetation Science* 17, 559–566.

species_b

Species b

Description

A species with positive associations to habitat 5 of landscape. Please be aware that a positive association to one habitat will inevitable lead to negative associations to other habitats (Yamada et al. 2006)

Usage

species_b

Format

A spatstat ppp object.

References

Yamada, T., Tomita, A., Itoh, A., Yamakura, T., Ohkubo, T., Kanzaki, M., Tan, S., Ashton, P.S., 2006. Habitat associations of Sterculiaceae trees in a Bornean rain forest plot. *Journal of Vegetation Science* 17, 559–566.

torus_trans

Torus trans

Description

Torus translation of the classified landscape.

Usage

torus_trans

Format

rd_ras object.

translate_raster	<i>translate_raster</i>
------------------	-------------------------

Description

Torus translation

Usage

```
translate_raster(
  raster,
  steps_x = NULL,
  steps_y = NULL,
  return_input = TRUE,
  simplify = FALSE,
  verbose = TRUE
)
```

Arguments

raster	RasterLayer with discrete habitat classes.
steps_x, steps_y	Integer with number of steps (cells) the raster is translated into the corresponding direction. If both are null, all possible combinations are used resulting in $n = ((50 + 1) * (50 + 1)) - 4$ rasters.
return_input	Logical if the original input data is returned.
simplify	Logical if only the raster will be returned if <code>n_random = 1</code> and <code>return_input = FALSE</code> .
verbose	Logical if progress report is printed.

Details

Torus translation test as described in Harms et al. (2001). The raster is shifted in all four cardinal directions by steps equal to the raster resolution. If a cell exits the extent on one side, it enters the extent on the opposite side.

The method does not allow any NA values to be present in the RasterLayer.

Value

rd_ras

References

Harms, K.E., Condit, R., Hubbell, S.P., Foster, R.B., 2001. Habitat associations of trees and shrubs in a 50-ha neotropical forest plot. *Journal of Ecology* 89, 947–959. <<https://doi.org/10.1111/j.1365-2745.2001.00615.x>>

See Also

[randomize_raster](#)

Examples

```
## Not run:  
landscape_classified <- classify_habitats(landscape, n = 5, style = "fisher")  
  
landscape_random <- translate_raster(landscape_classified)  
landscape_random_sub <- translate_raster(landscape_classified,  
steps_x = 1:10, steps_y = 1:5)  
  
## End(Not run)
```

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