

Package ‘nullcat’

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Description Provides null model algorithms for categorical and quantitative community ecology data. Extends classic binary null models (e.g., 'curveball', 'swap') to work with categorical data. Provides a stratified randomization framework for continuous data.

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c0cat	<i>Column-constrained categorical randomization (c0cat)</i>
-------	---

Description

c0cat() preserves the multiset of categories within each column but randomizes their positions across rows, leaving row margins free. This is the categorical analog to vegan's c0 algorithm. It is a non-sequential method.

Usage

```
c0cat(x, n_iter = 1L, output = c("category", "index"), seed = NULL)
```

Arguments

x	A matrix of categorical data, encoded as integers. Values should represent category or stratum membership for each cell.
n_iter	Number of iterations. Default is 1000. Larger values yield more thorough mixing. Ignored for non-sequential methods. Minimum burn-in times can be estimated with suggest_n_iter().
output	Character indicating type of result to return: <ul style="list-style-type: none"> • "category" (default) returns randomized matrix • "index" returns an index matrix describing where original entries (a.k.a. "tokens") moved. Useful mainly for testing, and for applications like quantize() that care about token tracking in addition to generic integer categories.
seed	Integer used to seed random number generator, for reproducibility.

Value

A matrix of the same dimensions as `x`, either randomized categorical values (when `output = "category"`) or an integer index matrix describing the permutation of entries (when `output = "index"`).

Examples

```
set.seed(123)
x <- matrix(sample(1:4, 100, replace = TRUE), nrow = 10)

# Randomize within columns (column margins fixed, row margins free)
x_rand <- c0cat(x)

# Verify columns are preserved but rows are not
all.equal(sort(x[, 1]), sort(x_rand[, 1]))
any(sort(x[1, ]) != sort(x_rand[1, ]))
```

curvecat	<i>Categorical curveball randomization (curvecat)</i>
----------	---

Description

Categorical generalization of the binary curveball algorithm (Strona et al. 2014) to matrices of categorical data. This function is a convenience wrapper around `nullcat()` with `method = "curvecat"`.

Usage

```
curvecat(
  x,
  n_iter = 1000L,
  output = "category",
  swaps = "auto",
  wt_row = NULL,
  wt_col = NULL,
  seed = NULL
)
```

Arguments

<code>x</code>	A matrix of categorical data, encoded as integers. Values should represent category or stratum membership for each cell.
<code>n_iter</code>	Number of iterations. Default is 1000. Larger values yield more thorough mixing. Ignored for non-sequential methods. Minimum burn-in times can be estimated with <code>suggest_n_iter()</code> .
<code>output</code>	Character indicating type of result to return: <ul style="list-style-type: none"> • "category" (default) returns randomized matrix

	<ul style="list-style-type: none"> • "index" returns an index matrix describing where original entries (a.k.a. "tokens") moved. Useful mainly for testing, and for applications like <code>quantize()</code> that care about token tracking in addition to generic integer categories.
swaps	<p>Character string controlling the direction of token movement. Only used when method is "curvecat", "swapcat", or "tswapcat". Affects the result only when output = "index", otherwise it only affects computation speed. Options include:</p> <ul style="list-style-type: none"> • "vertical": Tokens move between rows (stay within columns). • "horizontal": Tokens move between columns (stay within rows). • "alternating": Tokens move in both dimensions, alternating between vertical and horizontal swaps. Provides full 2D mixing without preserving either row or column token sets. • "auto" (default): For output = "category", automatically selects the fastest option based on matrix dimensions. For output = "index", defaults to "alternating" for full mixing. When <code>wt_row</code> or <code>wt_col</code> is supplied, defaults to the appropriate direction, or "alternating" if both are supplied.
wt_row	<p>An optional square numeric matrix of non-negative weights controlling which pairs of rows are likely to exchange tokens during randomization. Must be <code>nrow(x)</code> by <code>nrow(x)</code>. This enables spatially or trait-constrained null models where nearby or similar sites exchange tokens more frequently.</p> <p>Values are treated as relative weights (not probabilities) and are normalized internally. The diagonal is ignored. The matrix should be symmetric. Only supported for sequential methods (curvecat, swapcat, tswapcat).</p> <p>When both <code>wt_row</code> and <code>wt_col</code> are supplied, <code>swaps</code> is forced to "alternating", producing a Gibbs-like sweep that applies each weight matrix on its respective margin in alternation.</p>
wt_col	<p>An optional square numeric matrix of non-negative weights controlling which pairs of columns are likely to exchange tokens during randomization. Must be <code>ncol(x)</code> by <code>ncol(x)</code>. See <code>wt_row</code> for details on weight interpretation.</p>
seed	<p>Integer used to seed random number generator, for reproducibility.</p>

Details

The curvecat algorithm randomizes a categorical matrix while keeping the category multisets of each row and column fixed. In other words, the permuted matrix has the same set of integer values in every row and every column as the original matrix, but they are permuted. It operates on pairs of rows at a time, grouping differing entries by unordered category pairs and redistributing the orientation of those pairs while preserving the multiset of categories within each row. When there are only two categories, `curvecat()` reduces to the behavior of the original binary curveball algorithm (Strona et al. 2014) applied to a 0/1 matrix.

Value

A matrix of the same dimensions as `x`, either randomized categorical values (when output = "category") or an integer index matrix describing the permutation of entries (when output = "index").

References

Strona, G., Nappo, D., Boccacci, F., Fattorini, S., & San-Miguel-Ayanz, J. (2014). A fast and unbiased procedure to randomize ecological binary matrices with fixed row and column totals. *Nature Communications*, 5, 4114.

See Also

[nullcat\(\)](#), [nullcat_methods\(\)](#)

Examples

```
# Create a categorical matrix
set.seed(123)
x <- matrix(sample(1:4, 100, replace = TRUE), nrow = 10)

# Randomize preserving row and column category multisets
x_rand <- curvecat(x, n_iter = 1000)

# Verify margins are preserved
all.equal(sort(x[1, ]), sort(x_rand[1, ])) # row multisets preserved
all.equal(sort(x[, 1]), sort(x_rand[, 1])) # column multisets preserved
```

nullcat

Categorical matrix randomization

Description

Randomize binary or categorical community matrices using categorical generalizations of binary community null model algorithms. Optionally constrain mixing using spatial (row) and taxonomic (column) weights.

Usage

```
nullcat(
  x,
  method = nullcat_methods(),
  n_iter = 1000L,
  output = c("category", "index"),
  swaps = c("auto", "vertical", "horizontal", "alternating"),
  wt_row = NULL,
  wt_col = NULL,
  seed = NULL
)
```

Arguments

x	A matrix of categorical data, encoded as integers. Values should represent category or stratum membership for each cell.
method	Character specifying the randomization algorithm to use. Options include the following; see details and linked functions for more info. <ul style="list-style-type: none"> • "curvecat": categorical analog to curveball; see <code>curvecat()</code> for details. • "swapcat": categorical analog to swap; see <code>swapcat()</code> for details. • "tswapcat": categorical analog to tswap; see <code>tswapcat()</code> for details. • "r0cat": categorical analog to r0; see <code>r0cat()</code> for details. • "c0cat": categorical analog to c0; see <code>c0cat()</code> for details.
n_iter	Number of iterations. Default is 1000. Larger values yield more thorough mixing. Ignored for non-sequential methods. Minimum burn-in times can be estimated with <code>suggest_n_iter()</code> .
output	Character indicating type of result to return: <ul style="list-style-type: none"> • "category" (default) returns randomized matrix • "index" returns an index matrix describing where original entries (a.k.a. "tokens") moved. Useful mainly for testing, and for applications like <code>quantize()</code> that care about token tracking in addition to generic integer categories.
swaps	Character string controlling the direction of token movement. Only used when method is "curvecat", "swapcat", or "tswapcat". Affects the result only when output = "index", otherwise it only affects computation speed. Options include: <ul style="list-style-type: none"> • "vertical": Tokens move between rows (stay within columns). • "horizontal": Tokens move between columns (stay within rows). • "alternating": Tokens move in both dimensions, alternating between vertical and horizontal swaps. Provides full 2D mixing without preserving either row or column token sets. • "auto" (default): For output = "category", automatically selects the fastest option based on matrix dimensions. For output = "index", defaults to "alternating" for full mixing. When <code>wt_row</code> or <code>wt_col</code> is supplied, defaults to the appropriate direction, or "alternating" if both are supplied.
wt_row	An optional square numeric matrix of non-negative weights controlling which pairs of rows are likely to exchange tokens during randomization. Must be <code>nrow(x)</code> by <code>nrow(x)</code> . This enables spatially or trait-constrained null models where nearby or similar sites exchange tokens more frequently. Values are treated as relative weights (not probabilities) and are normalized internally. The diagonal is ignored. The matrix should be symmetric. Only supported for sequential methods (curvecat, swapcat, tswapcat). When both <code>wt_row</code> and <code>wt_col</code> are supplied, <code>swaps</code> is forced to "alternating", producing a Gibbs-like sweep that applies each weight matrix on its respective margin in alternation.
wt_col	An optional square numeric matrix of non-negative weights controlling which pairs of columns are likely to exchange tokens during randomization. Must be <code>ncol(x)</code> by <code>ncol(x)</code> . See <code>wt_row</code> for details on weight interpretation.
seed	Integer used to seed random number generator, for reproducibility.

Details

curvecat, swapcat, and tswapcat are sequential algorithms that hold category multisets fixed in every row and column. These three algorithms typically reach the same stationary distribution. They differ primarily in efficiency, with curvecat being the most efficient (i.e. fewest steps to become fully mixed); swapcat and tswapcat are thus useful mainly for methodological comparison.

The r0cat algorithm holds category multisets fixed in rows but not columns, while c0cat does the opposite.

Note that categorical null models are for cell-level categorical data. Site-level attributes (e.g., land cover) or species-level attributes (e.g., functional traits) should be analyzed using different approaches. See vignette for details.

Value

A matrix of the same dimensions as `x`, either randomized categorical values (when `output = "category"`) or an integer index matrix describing the permutation of entries (when `output = "index"`).

See Also

[nullcat_batch\(\)](#) for efficient generation of multiple randomized matrices; [nullcat_commsim\(\)](#) for integration with `vegan`.

Examples

```
# Create a categorical matrix
set.seed(123)
x <- matrix(sample(1:4, 100, replace = TRUE), nrow = 10)

# Randomize using curvecat method (preserves row & column margins)
x_rand <- nullcat(x, method = "curvecat", n_iter = 1000)

# Check that row multisets are preserved
all.equal(sort(x[1, ]), sort(x_rand[1, ]))

# Spatially constrained randomization using row weights
coords <- cbind(runif(10), runif(10))
d <- as.matrix(dist(coords))
W <- exp(-d / 0.3) # Gaussian distance decay
x_spatial <- nullcat(x, method = "curvecat", n_iter = 1000, wt_row = W)

# Dual-margin weighting (Gibbs-like alternating)
W_row <- exp(-as.matrix(dist(cbind(runif(10), runif(10)))) / 0.3)
W_col <- exp(-as.matrix(dist(cbind(runif(10), runif(10)))) / 0.3)
x_dual <- nullcat(x, method = "curvecat", n_iter = 1000,
                 wt_row = W_row, wt_col = W_col)
```

nullcat_batch	<i>Generate a batch of null matrices using nullcat()</i>
---------------	--

Description

Runs the categorical null model implemented in `nullcat()` repeatedly, generating a batch of randomized matrices or, optionally, a batch of summary statistics computed from those matrices. This is the categorical analog of `quantize_batch()`.

Usage

```
nullcat_batch(x, n_reps = 999L, stat = NULL, n_cores = 1L, seed = NULL, ...)
```

Arguments

<code>x</code>	Community matrix (sites \times species) or any categorical matrix of integers.
<code>n_reps</code>	Number of randomizations to generate. Default is 999.
<code>stat</code>	Optional summary function taking a matrix and returning a numeric statistic. If NULL (default), the function returns the full set of randomized matrices.
<code>n_cores</code>	Number of compute cores to use for parallel processing. Default is 1.
<code>seed</code>	Integer used to seed random number generator, for reproducibility.
<code>...</code>	Additional arguments passed to <code>nullcat()</code> (e.g. <code>method</code> , <code>n_iter</code> , <code>output</code>).

Value

If `stat` is NULL, returns a 3D array (rows \times cols \times `n_reps`). If `stat` is not NULL, returns a numeric array of statistic values (dimensionality depends on `stat`).

Examples

```
set.seed(123)
x <- matrix(sample(1:4, 100, replace = TRUE), nrow = 10)

# Generate 99 randomized matrices
nulls <- nullcat_batch(x, n_reps = 99, method = "curvecat", n_iter = 100)

# Or compute a statistic on each
row_sums <- nullcat_batch(x, n_reps = 99, stat = rowSums,
                        method = "curvecat", n_iter = 100)

# Specify multiple cores for parallel processing
nulls <- nullcat_batch(x, n_reps = 99, n_iter = 100, n_cores = 2)
```

nullcat_commsim	<i>Nullcat-based commsim (non-sequential)</i>
-----------------	---

Description

Construct a `vegan::commsim()` object that uses `nullcat()` as a non-sequential null model for categorical / integer matrices. Each simulated matrix is generated independently by applying `nullcat()` with `n_iter` trades starting from the original matrix.

Usage

```

nullcat_commsim(
  n_iter = 10000,
  method = nullcat_methods(),
  output = c("category", "index")
)

```

Arguments

<code>n_iter</code>	Integer, number of iterations (trades) per simulated matrix. Must be a positive integer. Default is 1e4.
<code>method</code>	Character specifying which nullcat randomization algorithm to use. See <code>nullcat()</code> and <code>nullcat_methods()</code> for details.
<code>output</code>	Character, passed to <code>nullcat(output = ...)</code> . Typically "category" (default) or "index".

Value

An object of class "commsim" suitable for use with `vegan::nullmodel()` and `vegan::oecosimu()`.

Details

This generates a `commsim` object that is **non-sequential**: each simulated matrix starts from the original matrix and is randomized independently using `n_iter` trades of the chosen method.

When used via `vegan::simulate.nullmodel()`, the arguments behave as:

- `nsim`: number of simulated matrices to generate.
- `n_iter` (here, in `nullcat_commsim()`): number of trades per simulated matrix (controls how strongly each replicate is shuffled).
- `burnin` and `thin`: are **ignored** for this `commsim`, because `isSeq = FALSE` (the simulations are not a Markov chain).

In other words, treat `n_iter` as the tuning parameter for how thoroughly each independent null matrix is randomized.

See Also

[nullcat_batch\(\)](#) if you just want a batch of null matrices without going through **vegan**.

Examples

```
library(vegan)

x <- matrix(sample(1:5, 50, replace = TRUE), 10, 5)
cs <- nullcat_commsim(n_iter = 1e4, method = "curvecat")

nm <- nullmodel(x, cs)
sims <- simulate(nm, nsim = 999)
```

nullcat_commsim_seq *Nullcat-based commsim (sequential / Markov chain)*

Description

Construct a `vegan::commsim()` object that uses [nullcat\(\)](#) as a *sequential* null model: successive simulated matrices form a Markov chain. Internally, each simulation "step" advances the chain by thin trades of the chosen method (e.g. "curvecat"), where *thin* is supplied via `vegan::simulate.nullmodel()` arguments. This is analogous to how sequential swap / curveball null models are used in **vegan**, but extended to categorical data via [nullcat\(\)](#).

Usage

```
nullcat_commsim_seq(
  method = nullcat_methods(),
  output = c("category", "index")
)
```

Arguments

method	Character specifying which nullcat randomization algorithm to use. See nullcat() and nullcat_methods() for details.
output	Character, passed to <code>nullcat(output = ...)</code> . Typically "category" (default) or "index".

Value

An object of class "commsim" suitable for use with `vegan::nullmodel()` and `vegan::oecosimu()`.

Details

This model is **sequential**: simulated matrices form a Markov chain. The current matrix is updated in-place by repeated calls to the randomization model, and successive matrices are obtained by advancing the chain.

In `vegan::simulate.nullmodel()`, the control arguments behave as:

- `nsim`: number of matrices to *store* from the chain.
- `thin`: number of trades per step. Each "step" of the chain applies `thin` trades of the chosen method to the current state before possibly storing it.
- `burnin`: number of initial steps to perform (each with `thin` trades) before storing any matrices, i.e. the Markov chain burn-in.

There is no `n_iter` argument here: mixing is controlled entirely by `thin` (trades per step) and `burnin` (number of initial steps discarded), in the same spirit as sequential swap / curveball models in **vegan**.

Examples

```
library(vegan)

x <- matrix(sample(1:5, 50, replace = TRUE), 10, 5)
cs <- nullcat_commsim_seq(method = "curvecat")

nm <- nullmodel(x, cs)

# control the chain with 'thin' and 'burnin'
sims <- simulate(nm, nsim = 999, thin = 100, burnin = 1000)
```

nullcat_methods

Supported nullcat methods

Description

Return the character vector of supported categorical randomization methods.

Usage

```
nullcat_methods()
```

```
nullcat_methods()
```

Value

A character vector of method names.

Character vector of available method names.

Examples

```
nullcat_methods()
```

 quantize

Stratified quantitative null models via quantize

Description

quantize() implements a stratified randomization framework for continuous ecological data. It discretizes quantitative values into strata, randomizes the strata assignments using a categorical null model algorithm (via [nullcat\(\)](#)), and then reassigns the original quantitative values according to the new stratum layout.

Usage

```
quantize(
  x = NULL,
  prep = NULL,
  method = nullcat_methods(),
  fixed = c("cell", "stratum", "row", "col"),
  breaks = NULL,
  n_strata = 5,
  transform = identity,
  offset = 0,
  zero_stratum = FALSE,
  n_iter = 1000,
  wt_row = NULL,
  wt_col = NULL,
  seed = NULL
)
```

Arguments

- | | |
|--------|--|
| x | Community matrix with sites in rows, species in columns, and nonnegative quantitative values in cells. Can be NULL when prep is provided. |
| prep | A "quantize_prep" object (from quantize_prep()). If provided, x and all stratification arguments are ignored and the precomputed overhead is used directly for fast repeated draws. |
| method | Character specifying the randomization algorithm to use. Options include the following; see details and linked functions for more info. <ul style="list-style-type: none"> • "curvecat": categorical analog to curveball; see curvecat() for details. • "swapcat": categorical analog to swap; see swapcat() for details. • "tswapcat": categorical analog to tswap; see tswapcat() for details. • "r0cat": categorical analog to r0; see r0cat() for details. |

	<ul style="list-style-type: none"> • "c0cat": categorical analog to c0; see <code>c0cat()</code> for details.
fixed	<p>Character string specifying the level at which quantitative values are held fixed during randomization. One of:</p> <ul style="list-style-type: none"> • "cell" (the default; only available when <code>method = "curvecat"</code>): values remain attached to their original cells and move with them during the categorical randomization. Row and column value distributions are not preserved, but the mapping between each original cell and its randomized destination is fixed. • "stratum": values are shuffled globally within each stratum, holding only the overall stratum-level value distribution fixed. • "row": values are shuffled within strata separately for each row, holding each row's value multiset fixed. Not compatible with all methods. • "col": values are shuffled within strata separately for each column, holding each column's value multiset fixed. <p>Note that this interacts with <code>method</code>: different null models fix different margins in the underlying binary representation.</p>
breaks	Numeric vector of stratum breakpoints.
n_strata	Integer giving the number of strata to split the data into. Must be 2 or greater. Larger values yield randomizations with less mixing but higher fidelity to the original marginal distributions. Default is 5. Ignored unless <code>breaks = NULL</code> .
transform	A function used to transform the values in <code>x</code> before assigning them to <code>n_strata</code> equal-width intervals. Examples include <code>sqrt</code> , <code>log</code> , <code>rank</code> (for equal-occupancy strata), etc.; the default is identity. If <code>zero_stratum = TRUE</code> , the transformation is only applied on nonzero values. The function should pass NA values. This argument is ignored unless <code>breaks = NULL</code> .
offset	Numeric value between -1 and 1 (default 0) indicating how much to shift stratum breakpoints relative to the binwidth (applied during quantization as: <code>breaks <- breaks + offset * bw</code>). To assess sensitivity to stratum boundaries, run <code>quantize()</code> multiple times with different offset values. Ignored unless <code>breaks = NULL</code> .
zero_stratum	Logical indicating whether to segregate zeros into their own stratum. If <code>FALSE</code> (the default), zeros will likely be combined into a stratum that also includes small positive numbers. If <code>breaks</code> is specified, zero simply gets added as an additional break; if not, one of the <code>n_strata</code> will represent zeros and the others will be nonzero ranges.
n_iter	Number of iterations. Default is 1000. Larger values yield more thorough mixing. Ignored for non-sequential methods. Minimum burn-in times can be estimated with <code>suggest_n_iter()</code> .
wt_row	<p>An optional square numeric matrix of non-negative weights controlling which pairs of rows are likely to exchange tokens during randomization. Must be <code>nrow(x)</code> by <code>nrow(x)</code>. This enables spatially or trait-constrained null models where nearby or similar sites exchange tokens more frequently.</p> <p>Values are treated as relative weights (not probabilities) and are normalized internally. The diagonal is ignored. The matrix should be symmetric. Only supported for sequential methods (<code>curvecat</code>, <code>swapcat</code>, <code>tswapcat</code>).</p>

	When both <code>wt_row</code> and <code>wt_col</code> are supplied, <code>swaps</code> is forced to "alternating", producing a Gibbs-like sweep that applies each weight matrix on its respective margin in alternation.
<code>wt_col</code>	An optional square numeric matrix of non-negative weights controlling which pairs of columns are likely to exchange tokens during randomization. Must be <code>ncol(x)</code> by <code>ncol(x)</code> . See <code>wt_row</code> for details on weight interpretation.
<code>seed</code>	Integer used to seed random number generator, for reproducibility.

Value

A randomized version of `x`, with the same dimensions and dimnames. For `method = "curvecat"`, the quantitative values are reassigned within strata while preserving row and column stratum multisets. For binary methods, the result corresponds to applying the chosen binary null model to each stratum and recombining.

See Also

[quantize_batch\(\)](#) for efficient generation of multiple randomized matrices; [quantize_commsim\(\)](#) for integration with `vegan`.

Examples

```
# toy quantitative community matrix
set.seed(1)
comm <- matrix(rexp(50 * 40), nrow = 50,
              dimnames = list(paste0("site", 1:50),
                             paste0("sp", 1:40)))

# default: curvecat-backed stratified randomization
rand1 <- quantize(comm)

# change stratification and preservation mode
rand2 <- quantize(comm, n_strata = 4,
                 transform = sqrt,
                 fixed = "row",
                 n_iter = 2000)

# use a different randomization algorithm
rand3 <- quantize(comm, method = "swapcat", n_iter = 10000)

# precompute overhead and reuse for many randomizations
prep <- quantize_prep(comm, method = "curvecat",
                    n_strata = 5, fixed = "row")
rand4 <- quantize(prepare = prep)
rand5 <- quantize(prepare = prep)
```

quantize_batch	<i>Generate a batch of null matrices using quantize()</i>
----------------	---

Description

Runs the stratified null model implemented in `quantize()` repeatedly, generating a batch of randomized matrices or, optionally, a batch of summary statistics computed from those matrices.

Usage

```
quantize_batch(x, n_reps = 999L, stat = NULL, n_cores = 1L, seed = NULL, ...)
```

Arguments

<code>x</code>	Community matrix (species \times sites, or any numeric matrix).
<code>n_reps</code>	Number of randomizations to generate. Default is 999.
<code>stat</code>	Optional summary function taking a matrix and returning a numeric statistic (e.g. <code>rowSums</code> with abundance data would give total abundance per site). If <code>NULL</code> (default), the function returns the full set of randomized matrices.
<code>n_cores</code>	Number of compute cores to use for parallel processing. Default is 1.
<code>seed</code>	Integer used to seed random number generator, for reproducibility.
<code>...</code>	Additional arguments passed to <code>quantize()</code> , (e.g. <code>method</code> , <code>breaks</code> , <code>n_strata</code> , <code>transform</code> , <code>offset</code> , <code>zero_stratum</code> , <code>fixed</code> , <code>n_iter</code> , etc.).

Value

If `stat` is `NULL`, returns a 3D array (rows \times cols \times `n_reps`). If `stat` is not `NULL`, returns a numeric array of statistic values (dimensionality depends on `stat`).

Examples

```
set.seed(123)
x <- matrix(runif(100), nrow = 10)

# Generate 99 randomized matrices
nulls <- quantize_batch(x, n_reps = 99, method = "curvecat", n_iter = 100)

# Or compute a statistic on each
row_sums <- nullcat_batch(x, n_reps = 99, stat = rowSums,
                        method = "curvecat", n_iter = 100)

# Specify multiple cores for parallel processing
nulls <- quantize_batch(x, n_reps = 99, n_iter = 100, n_cores = 2)
```

quantize_commsim *Quantize-based commsim (non-sequential)*

Description

Construct a `vegan::commsim()` object that uses `quantize()` as a non-sequential null model for numeric community matrices. Each simulated matrix is generated independently by applying `quantize()` with `n_iter` trades (via its internal call to `nullcat()`) starting from the original matrix.

Usage

```
quantize_commsim(n_iter = 10000, ...)
```

Arguments

<code>n_iter</code>	Integer, number of iterations (trades) per simulated matrix. Must be a positive integer. Default is 1e4.
<code>...</code>	Arguments passed to <code>quantize()</code> , such as <code>breaks</code> , <code>n_strata</code> , <code>transform</code> , <code>offset</code> , <code>zero_stratum</code> , <code>fixed</code> , <code>method</code> , etc. Do not supply <code>x</code> or <code>n_iter</code> here; these are set internally by <code>quantize_commsim()</code> . See <code>quantize()</code> for details.

Value

An object of class "commsim" suitable for `vegan::nullmodel()` and `vegan::oecosimu()`.

Details

This generates a `commsim` object that is **non-sequential**: each simulated matrix starts from the original matrix and is randomized independently using `n_iter` trades of the chosen method.

When used via `vegan::simulate.nullmodel()`, the arguments behave as:

- `nsim`: number of simulated matrices to generate.
- `n_iter` (here, in `nullcat_commsim()`): number of trades per simulated matrix (controls how strongly each replicate is shuffled).
- `burnin` and `thin`: are **ignored** for this `commsim`, because `isSeq = FALSE` (the simulations are not a Markov chain).

In other words, treat `n_iter` as the tuning parameter for how thoroughly each independent null matrix is randomized.

See Also

`quantize_batch()` if you just want a batch of null matrices without going through **vegan**.

Examples

```

library(vegan)

x <- matrix(rexp(50), 10, 5)

cs <- quantize_commsim(
  n_strata = 10,
  method   = "curvecat",
  n_iter   = 1000L
)

nm <- nullmodel(x, cs)
sims <- simulate(nm, nsim = 999)

```

quantize_commsim_seq *Quantile-based quantize commsim (sequential / Markov chain)*

Description

Construct a `vegan::commsim()` object that uses `quantize()` as a *sequential* null model: successive simulated matrices form a Markov chain in the space of numeric community matrices. Internally, each simulation "step" advances the chain by re-applying `quantize()` to the current matrix using the settings provided via `...`

Usage

```
quantize_commsim_seq(...)
```

Arguments

`...` Arguments passed to `quantize()`, such as `breaks`, `n_strata`, `transform`, `offset`, `zero_stratum`, `fixed`, `method`, `n_iter`, etc. Do **not** supply `x` or `n_iter` here; `x` is provided by `vegan` and `n_iter` is set internally from `thin`. See `quantize()` for details.

Value

An object of class "commsim" suitable for `vegan::nullmodel()` and `vegan::oecosimu()`.

Details

This model is **sequential**: simulated matrices form a Markov chain. The current matrix is updated in-place by repeated calls to the randomization model, and successive matrices are obtained by advancing the chain.

In `vegan::simulate.nullmodel()`, the control arguments behave as:

- `nsim`: number of matrices to *store* from the chain.
- `thin`: number of trades per step. Each "step" of the chain applies `thin` trades of the chosen method to the current state before possibly storing it.
- `burnin`: number of initial steps to perform (each with `thin` trades) before storing any matrices, i.e. the Markov chain burn-in.

There is no `n_iter` argument here: mixing is controlled entirely by `thin` (trades per step) and `burnin` (number of initial steps discarded), in the same spirit as sequential swap / curveball models in **vegan**.

Examples

```
library(vegan)

x <- matrix(rexp(50), 10, 5)

cs <- quantize_commsim_seq(
  n_strata = 5,
  method   = "curvecat"
)

nm <- nullmodel(x, cs)

sims <- simulate(
  nm,
  nsim  = 999,
  thin  = 10,    # 10 quantize updates between stored states
  burnin = 100  # 100 initial steps discarded
)
```

quantize_prep

Prepare stratified null model overhead for quantize()

Description

`quantize_prep()` precomputes all of the stratification and bookkeeping needed by `quantize()` for a given quantitative community matrix. This is useful when you want to generate many randomizations of the same dataset: the expensive steps (strata assignment, value pools, and arguments for the underlying null model) are computed once, and the resulting object can be passed to `quantize(prepare = ...)` for fast repeated draws.

Usage

```
quantize_prep(
  x,
  method = nullcat_methods(),
```

```

fixed = c("cell", "stratum", "row", "col"),
breaks = NULL,
n_strata = 5,
transform = identity,
offset = 0,
zero_stratum = FALSE,
n_iter = 1000,
wt_row = NULL,
wt_col = NULL
)

```

Arguments

x	Community matrix with sites in rows, species in columns, and nonnegative quantitative values in cells. This is the dataset for which stratification and null model overhead should be prepared.
method	Character specifying the randomization algorithm to use. Options include the following; see details and linked functions for more info. <ul style="list-style-type: none"> "curvecat": categorical analog to curveball; see curvecat() for details. "swapcat": categorical analog to swap; see swapcat() for details. "tswapcat": categorical analog to tswap; see tswapcat() for details. "r0cat": categorical analog to r0; see r0cat() for details. "c0cat": categorical analog to c0; see c0cat() for details.
fixed	Character string specifying the level at which quantitative values are held fixed during randomization. One of: <ul style="list-style-type: none"> "cell" (the default; only available when method = "curvecat"): values remain attached to their original cells and move with them during the categorical randomization. Row and column value distributions are not preserved, but the mapping between each original cell and its randomized destination is fixed. "stratum": values are shuffled globally within each stratum, holding only the overall stratum-level value distribution fixed. "row": values are shuffled within strata separately for each row, holding each row's value multiset fixed. Not compatible with all methods. "col": values are shuffled within strata separately for each column, holding each column's value multiset fixed. <p>Note that this interacts with method: different null models fix different margins in the underlying binary representation.</p>
breaks	Numeric vector of stratum breakpoints.
n_strata	Integer giving the number of strata to split the data into. Must be 2 or greater. Larger values yield randomizations with less mixing but higher fidelity to the original marginal distributions. Default is 5. Ignored unless breaks = NULL.
transform	A function used to transform the values in x before assigning them to n_strata equal-width intervals. Examples include sqrt, log, rank (for equal-occupancy

	strata), etc.; the default is identity. If <code>zero_stratum = TRUE</code> , the transformation is only applied on nonzero values. The function should pass NA values. This argument is ignored unless <code>breaks = NULL</code> .
<code>offset</code>	Numeric value between -1 and 1 (default 0) indicating how much to shift stratum breakpoints relative to the binwidth (applied during quantization as: <code>breaks <- breaks + offset * bw</code>). To assess sensitivity to stratum boundaries, run <code>quantize()</code> multiple times with different offset values. Ignored unless <code>breaks = NULL</code> .
<code>zero_stratum</code>	Logical indicating whether to segregate zeros into their own stratum. If <code>FALSE</code> (the default), zeros will likely be combined into a stratum that also includes small positive numbers. If <code>breaks</code> is specified, zero simply gets added as an additional break; if not, one of the <code>n_strata</code> will represent zeros and the others will be nonzero ranges.
<code>n_iter</code>	Number of iterations. Default is 1000. Larger values yield more thorough mixing. Ignored for non-sequential methods. Minimum burn-in times can be estimated with <code>suggest_n_iter()</code> .
<code>wt_row</code>	An optional square numeric matrix of non-negative weights controlling which pairs of rows are likely to exchange tokens during randomization. Must be <code>nrow(x)</code> by <code>nrow(x)</code> . This enables spatially or trait-constrained null models where nearby or similar sites exchange tokens more frequently. Values are treated as relative weights (not probabilities) and are normalized internally. The diagonal is ignored. The matrix should be symmetric. Only supported for sequential methods (<code>curvecat</code> , <code>swapcat</code> , <code>tswapcat</code>). When both <code>wt_row</code> and <code>wt_col</code> are supplied, <code>swaps</code> is forced to "alternating", producing a Gibbs-like sweep that applies each weight matrix on its respective margin in alternation.
<code>wt_col</code>	An optional square numeric matrix of non-negative weights controlling which pairs of columns are likely to exchange tokens during randomization. Must be <code>ncol(x)</code> by <code>ncol(x)</code> . See <code>wt_row</code> for details on weight interpretation.

Details

Internally, `quantize_prep()`:

- transforms and stratifies `x` into `n_strata` numeric intervals (via `stratify()`),
- constructs the appropriate value pools given `fixed`, and
- assembles arguments for the underlying null model call to `nullcat()`.

The returned object can be reused across calls to `quantize()`, `quantize_batch()`, or other helpers that accept a `prep` argument.

Value

A list with class "quantize_prep" (if you want to set it) containing the components needed by `quantize()`:

- `x`: original quantitative matrix `x`,
- `strata`: integer matrix of the same dimension as `x`, giving the stratum index (`1:n_strata`) for each cell.

- `pool`: data structure encoding the quantitative value pools used during reassignment.
- `method`: the null model method used (as in the `method` argument).
- `n_strata`, `transform`, `offset`, `fixed`: the stratification and reassignment settings used to construct `strata` and `pool`.
- `sim_args`: named list of arguments passed to `nullcat()` (e.g. `n_iter`).
- `wt_row`, `wt_col`: the row and column weight matrices (or `NULL`).

This object is intended to be passed unchanged to the `prep` argument of `quantize()` or `quantize_batch()`.

See Also

[quantize\(\)](#), [quantize_batch\(\)](#)

Examples

```
set.seed(1)
comm <- matrix(rexp(50 * 40), nrow = 50,
              dimnames = list(paste0("site", 1:50),
                             paste0("sp", 1:40)))

# prepare overhead for a curvecat-backed stratified null model
prep <- quantize_prep(comm, method = "curvecat",
                    n_strata = 5,
                    fixed = "row",
                    n_iter = 2000)

# fast repeated randomizations using the same prep
rand1 <- quantize(prepare = prep)
rand2 <- quantize(prepare = prep)
```

r0cat

Row-constrained categorical randomization (r0cat)

Description

`r0cat()` preserves the multiset of categories within each row but randomizes their positions across columns, leaving column margins free. This is the categorical analog to `vegan`'s `r0` algorithm. It is a non-sequential method.

Usage

```
r0cat(x, n_iter = 1L, output = c("category", "index"), seed = NULL)
```

Arguments

<code>x</code>	A matrix of categorical data, encoded as integers. Values should represent category or stratum membership for each cell.
<code>n_iter</code>	Number of iterations. Default is 1000. Larger values yield more thorough mixing. Ignored for non-sequential methods. Minimum burn-in times can be estimated with <code>suggest_n_iter()</code> .
<code>output</code>	Character indicating type of result to return: <ul style="list-style-type: none"> • "category" (default) returns randomized matrix • "index" returns an index matrix describing where original entries (a.k.a. "tokens") moved. Useful mainly for testing, and for applications like <code>quantize()</code> that care about token tracking in addition to generic integer categories.
<code>seed</code>	Integer used to seed random number generator, for reproducibility.

Value

A matrix of the same dimensions as `x`, either randomized categorical values (when `output = "category"`) or an integer index matrix describing the permutation of entries (when `output = "index"`).

Examples

```
set.seed(123)
x <- matrix(sample(1:4, 100, replace = TRUE), nrow = 10)

# Randomize within rows (row margins fixed, column margins free)
x_rand <- r0cat(x)

# Verify rows are preserved but columns are not
all.equal(sort(x[1, ]), sort(x_rand[1, ]))
any(sort(x[, 1]) != sort(x_rand[, 1]))
```

stratify

Bin quantitative data into strata

Description

Bin quantitative data into strata

Usage

```
stratify(
  x,
  breaks = NULL,
  n_strata = 5,
  transform = identity,
  offset = 0,
  zero_stratum = FALSE
)
```

Arguments

x	A matrix or vector containing non-negative values.
breaks	Numeric vector of stratum breakpoints.
n_strata	Integer giving the number of strata to split the data into. Must be 2 or greater. Larger values yield randomizations with less mixing but higher fidelity to the original marginal distributions. Default is 5. Ignored unless breaks = NULL.
transform	A function used to transform the values in x before assigning them to n_strata equal-width intervals. Examples include sqrt, log, rank (for equal-occupancy strata), etc.; the default is identity. If zero_stratum = TRUE, the transformation is only applied on nonzero values. The function should pass NA values. This argument is ignored unless breaks = NULL.
offset	Numeric value between -1 and 1 (default 0) indicating how much to shift stratum breakpoints relative to the binwidth (applied during quantization as: breaks <- breaks + offset * bw). To assess sensitivity to stratum boundaries, run <code>quantize()</code> multiple times with different offset values. Ignored unless breaks = NULL.
zero_stratum	Logical indicating whether to segregate zeros into their own stratum. If FALSE (the default), zeros will likely be combined into a stratum that also includes small positive numbers. If breaks is specified, zero simply gets added as an additional break; if not, one of the n_strata will represent zeros and the others will be nonzero ranges.

Value

An object the same size as x, with integer values representing stratum classifications.

Examples

```
# Stratify a numeric vector
x <- c(0, 0, 0.1, 0.5, 1.2, 3.4, 5.6, 10.2)
stratify(x, n_strata = 3)

# With transformation
stratify(x, n_strata = 3, transform = log1p)

# Separate zero stratum
stratify(x, n_strata = 3, zero_stratum = TRUE)
```

suggest_n_iter

Suggest a reasonable n_iter for a randomization

Description

Uses trace diagnostics to estimate how many burn-in iterations are needed for a nullcat or quantize randomization to reach its apparent stationary distribution, given a dataset and randomization method. Uses a "first pre-tail sign-crossing" rule per chain, then returns the maximum across chains. Can be called on a community matrix or a cat_trace object.

Usage

```
suggest_n_iter(trace = NULL, tail_frac = 0.3, plot = FALSE, ...)
```

Arguments

trace	Either a <code>cat_trace</code> object (as returned by <code>trace_cat()</code>), or <code>NULL</code> . If <code>NULL</code> , arguments to <code>trace_cat()</code> , including <code>x</code> and any other relevant parameters must be supplied via <code>...</code>
tail_frac	Fraction of the trace (at the end) used as the tail window (default 0.3).
plot	If <code>TRUE</code> , plot the trace, with a vertical line at the suggested value.
...	Arguments passed to <code>trace_cat()</code> including arguments it passes to the <code>nullcat()</code> or <code>quantize()</code> function. Ignored if <code>trace</code> is non- <code>NULL</code> .

Details

This function uses a “first pre-tail sign-crossing” heuristic to identify burn-in cutoff. This is a simple variant of standard mean-stability tests used in MCMC convergence diagnostics (e.g., Heidelberg & Welch 1983; Geweke 1992; Geyer 1992). It computes the long-run mean based on the “tail window” of the chain, and detects the first iteration at which the trace statistic crosses this long-run mean, indicating that the chain has begun to oscillate around its stationary value. If the chain does not reach the long-run mean before the start of the tail window, the chain is determined not to have reached stationarity, and the function returns `NA` with attribute `converged = FALSE`.

Value

An integer of class “`nullcat_n_iter`” with attributes: `n_iter` (numeric or `NA`), `trace` (matrix), `steps` (vector), `tail_mean` (per-chain), `per_chain` (data.frame), `converged` (logical).

References

Heidelberg, P. & Welch, P.D. (1983). Simulation run length control in the presence of an initial transient. *Operations Research*, 31(6): 1109–1144.

Geweke, J. (1992). Evaluating the accuracy of sampling-based approaches to the calculation of posterior moments. In *Bayesian Statistics 4*, pp. 169–193.

Geyer, C.J. (1992). Practical Markov Chain Monte Carlo. *Statistical Science*, 7(4): 473–483.

Feller, W. (1968). *An Introduction to Probability Theory and Its Applications*, Vol. I. Wiley.

Examples

```
set.seed(1234)
x <- matrix(sample(1:5, 2500, replace = TRUE), 50)

# call `trace_cat`, then pass result to `suggest_n_iter`:
trace <- trace_cat(x = x, fun = "nullcat", n_iter = 1000,
                  n_chains = 5, method = "curvecat")
suggest_n_iter(trace, tail_frac = 0.3, plot = TRUE)

# alternatively, supply `trace_cat` arguments directly to `suggest_n_iter`:
```

```
x <- matrix(runif(2500), 50)
n_iter <- suggest_n_iter(
  x = x, n_chains = 5, n_iter = 1000, tail_frac = 0.3,
  fun = "quantize", n_strata = 4, fixed = "stratum",
  method = "curvecat", plot = TRUE)
```

 swapcat

Categorical swap randomization (swapcat)

Description

Categorical generalization of the binary 2x2 swap algorithm to matrices of categorical data. This function is a convenience wrapper around `nullcat()` with `method = "swapcat"`.

Usage

```
swapcat(
  x,
  n_iter = 1000L,
  output = c("category", "index"),
  swaps = "auto",
  wt_row = NULL,
  wt_col = NULL,
  seed = NULL
)
```

Arguments

- | | |
|--------|--|
| x | A matrix of categorical data, encoded as integers. Values should represent category or stratum membership for each cell. |
| n_iter | Number of iterations. Default is 1000. Larger values yield more thorough mixing. Ignored for non-sequential methods. Minimum burn-in times can be estimated with <code>suggest_n_iter()</code> . |
| output | Character indicating type of result to return: <ul style="list-style-type: none"> • "category" (default) returns randomized matrix • "index" returns an index matrix describing where original entries (a.k.a. "tokens") moved. Useful mainly for testing, and for applications like <code>quantize()</code> that care about token tracking in addition to generic integer categories. |
| swaps | Character string controlling the direction of token movement. Only used when method is "curvecat", "swapcat", or "tswapcat". Affects the result only when <code>output = "index"</code> , otherwise it only affects computation speed. Options include: <ul style="list-style-type: none"> • "vertical": Tokens move between rows (stay within columns). • "horizontal": Tokens move between columns (stay within rows). |

- "alternating": Tokens move in both dimensions, alternating between vertical and horizontal swaps. Provides full 2D mixing without preserving either row or column token sets.
- "auto" (default): For output = "category", automatically selects the fastest option based on matrix dimensions. For output = "index", defaults to "alternating" for full mixing. When wt_row or wt_col is supplied, defaults to the appropriate direction, or "alternating" if both are supplied.

wt_row	An optional square numeric matrix of non-negative weights controlling which pairs of rows are likely to exchange tokens during randomization. Must be $nrow(x)$ by $nrow(x)$. This enables spatially or trait-constrained null models where nearby or similar sites exchange tokens more frequently. Values are treated as relative weights (not probabilities) and are normalized internally. The diagonal is ignored. The matrix should be symmetric. Only supported for sequential methods (curvecat, swapcat, tswapcat). When both wt_row and wt_col are supplied, swaps is forced to "alternating", producing a Gibbs-like sweep that applies each weight matrix on its respective margin in alternation.
wt_col	An optional square numeric matrix of non-negative weights controlling which pairs of columns are likely to exchange tokens during randomization. Must be $ncol(x)$ by $ncol(x)$. See wt_row for details on weight interpretation.
seed	Integer used to seed random number generator, for reproducibility.

Details

The swapcat algorithm attempts random 2x2 swaps of the form:

```
a b      b a
b a  <->  a b
```

where a and b are distinct categories. These swaps preserve the multiset of categories in each row and column. With only two categories present, swapcat() reduces to the behavior of the standard binary swap algorithm.

Value

A matrix of the same dimensions as x , either randomized categorical values (when output = "category") or an integer index matrix describing the permutation of entries (when output = "index").

References

Gotelli, N. J. (2000). Null model analysis of species co-occurrence patterns. *Ecology*, 81(9), 2606–2621.

See Also

[curvecat\(\)](#) for an algorithm that produces equivalent results with better computational efficiency.

Examples

```
set.seed(123)
x <- matrix(sample(1:4, 100, replace = TRUE), nrow = 10)
x_rand <- swapcat(x, n_iter = 1000)
```

trace_cat

*Trace diagnostics for categorical randomizations***Description**

Applies `nullcat()` or `quantize()` to a community matrix, recording a summary statistic at each iteration to help assess mixing on a given dataset.

Usage

```
trace_cat(
  x,
  fun = c("nullcat", "quantize"),
  n_iter = 1000L,
  thin = NULL,
  n_chains = 5L,
  n_cores = 1L,
  stat = NULL,
  seed = NULL,
  plot = FALSE,
  ...
)
```

Arguments

<code>x</code>	Matrix of categorical data (integers) or quantitative values.
<code>fun</code>	Which function to trace: "nullcat" or "quantize".
<code>n_iter</code>	Total number of update iterations to simulate. Default is 1000.
<code>thin</code>	Thinning interval (updates per recorded point). Default $\sim n_iter/100$. Smaller values increase resolution but increase run time.
<code>n_chains</code>	Number of independent chains to run, to assess consistency (default 5).
<code>n_cores</code>	Parallel chains (default 1).
<code>stat</code>	Function that compares <code>x</code> to a permuted <code>x_rand</code> to quantify their similarity. Either a function <code>f(x, x_rand)</code> returning a scalar, or NULL. If NULL (the default), traces use Cohen's kappa for <code>nullcat()</code> or Pearson's correlation for <code>quantize()</code> .
<code>seed</code>	Optional integer seed for reproducible traces.
<code>plot</code>	If TRUE, plot the traces.
<code>...</code>	Arguments to the chosen <code>fun</code> (<code>nullcat()</code> or <code>quantize()</code>), such as <code>method</code> , <code>n_strata</code> , <code>fixed</code> , etc.

Value

An object of class "cat_trace" with elements:

- traces: matrix of size (n_steps+1) x n_chains, including iteration 0
- steps: integer vector of iteration numbers (starting at 0)
- fun, n_iter, thin, n_chains, n_cores, stat_name, call
- fun_args: list of the ... used (for reproducibility)

Plotting is available via `plot(cat_trace)`.

Examples

```
# nullcat trace
set.seed(123)
x <- matrix(sample(1:5, 2500, replace = TRUE), 50)
tr <- trace_cat(x, n_iter = 1000, n_chains = 5, fun = "nullcat",
               method = "curvecat")
plot(tr)

# quantize trace
x <- matrix(runif(2500), 50)
tr <- trace_cat(x, n_iter = 1000, n_chains = 5, fun = "quantize",
               method = "curvecat", n_strata = 3, fixed = "cell")
plot(tr)
```

tswapcat

Trial-swap categorical randomization (tswapcat)

Description

The trial-swap ("tswap") algorithm is a fixed-fixed randomization that repeatedly attempts random 2x2 swaps until a valid one is found in each iteration, reducing the number of wasted draws compared to the simple swap. `tswapcat()` extends this logic to categorical matrices.

Usage

```
tswapcat(
  x,
  n_iter = 1000L,
  output = c("category", "index"),
  swaps = "auto",
  wt_row = NULL,
  wt_col = NULL,
  seed = NULL
)
```

Arguments

x	A matrix of categorical data, encoded as integers. Values should represent category or stratum membership for each cell.
n_iter	Number of iterations. Default is 1000. Larger values yield more thorough mixing. Ignored for non-sequential methods. Minimum burn-in times can be estimated with <code>suggest_n_iter()</code> .
output	Character indicating type of result to return: <ul style="list-style-type: none"> • "category" (default) returns randomized matrix • "index" returns an index matrix describing where original entries (a.k.a. "tokens") moved. Useful mainly for testing, and for applications like <code>quantize()</code> that care about token tracking in addition to generic integer categories.
swaps	Character string controlling the direction of token movement. Only used when method is "curvecat", "swapcat", or "tswapcat". Affects the result only when output = "index", otherwise it only affects computation speed. Options include: <ul style="list-style-type: none"> • "vertical": Tokens move between rows (stay within columns). • "horizontal": Tokens move between columns (stay within rows). • "alternating": Tokens move in both dimensions, alternating between vertical and horizontal swaps. Provides full 2D mixing without preserving either row or column token sets. • "auto" (default): For output = "category", automatically selects the fastest option based on matrix dimensions. For output = "index", defaults to "alternating" for full mixing. When <code>wt_row</code> or <code>wt_col</code> is supplied, defaults to the appropriate direction, or "alternating" if both are supplied.
wt_row	An optional square numeric matrix of non-negative weights controlling which pairs of rows are likely to exchange tokens during randomization. Must be <code>nrow(x)</code> by <code>nrow(x)</code> . This enables spatially or trait-constrained null models where nearby or similar sites exchange tokens more frequently. Values are treated as relative weights (not probabilities) and are normalized internally. The diagonal is ignored. The matrix should be symmetric. Only supported for sequential methods (curvecat, swapcat, tswapcat). When both <code>wt_row</code> and <code>wt_col</code> are supplied, <code>swaps</code> is forced to "alternating", producing a Gibbs-like sweep that applies each weight matrix on its respective margin in alternation.
wt_col	An optional square numeric matrix of non-negative weights controlling which pairs of columns are likely to exchange tokens during randomization. Must be <code>ncol(x)</code> by <code>ncol(x)</code> . See <code>wt_row</code> for details on weight interpretation.
seed	Integer used to seed random number generator, for reproducibility.

Value

A matrix of the same dimensions as `x`, either randomized categorical values (when output = "category") or an integer index matrix describing the permutation of entries (when output = "index").

References

- Gotelli, N. J. (2000). Null model analysis of species co-occurrence patterns. *Ecology*, 81(9), 2606-2621.
- Miklos, I. & Podani, J. (2004). Randomization of presence-absence matrices: comments and new algorithms. *Ecology*, 85(1), 86-92.

See Also

[curvecat\(\)](#) for an algorithm that produces equivalent results with better computational efficiency.

Examples

```
set.seed(123)
x <- matrix(sample(1:4, 100, replace = TRUE), nrow = 10)
x_rand <- tswapcat(x, n_iter = 1000)
```

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