Package ‘robber’

October 14, 2022

Title Using Block Model to Estimate the Robustness of Ecological Network

Version 0.2.2

Description Implementation of a variety of methods to compute the robustness of ecological interaction networks with binary interactions as described in <arXiv:1910.10512>. In particular, using the Stochastic Block Model and its bipartite counterpart, the Latent Block Model to put a parametric model on the network, allows the comparison of the robustness of networks differing in species richness and number of interactions. It also deals with networks that are partially sampled and/or with missing values.

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URL `https://github.com/Chabert-Liddell/robber`

BugReports `https://github.com/Chabert-Liddell/robber/issues`

Depends R (>= 3.5)

Imports blockmodels (>= 1.1.2), ggplot2, GREMLINS, igraph, magrittr, pammtools, partitions, purrr, stats

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R topics documented:

`auc_robustness_lbm` *Fast computation of the LBM robustness statistic for uniform extinctions*

Description

This function provides much faster computation than `robustness_lbm` for the case where `ext_seq = "uniform"`, when just the AUC statistic is needed and the robustness function is not needed. This is particularly useful if `nr` gets large.

Usage

```
auc_robustness_lbm(con, pi, rho, nr, nc)
```

Arguments

`con`	A matrix, the connectivity parameter
`pi`	A vector of length `nrow(con)`, the proportion of row blocks
`rho`	A vector of length `ncol(con)`, the proportion of column blocks
`nr`	An integer, the number of row (primary) species
`nc`	An integer, the number of column (secondary) species

Value

The AUC of the LBM Robustness function for uniform primary extinctions sequences.

Examples

```
con <- matrix(c(.5,.3,.3,.1), 2, 2)
pi  <- c(.25,.75)
rho <- c(1/3, 2/3)
nr <- 50
nc <- 30
auc_robustness_lbm(con, pi, rho, nr, nc)
```

`compare_robustness` *Compare the robustness for different LBM parameters*

Description

This function is designed to be used with a list of parameters as the one given by the function `get_lbm_param()`. The default parameters are designed such that the return value for a uniform extinction sequence is bounded above by 0.5.

Usage

```
compare_robustness(
  list_param,
  dens = 0.0156,
  new_nr = 100,
  new_nc = 100,
  ext_seq = "uniform"
)
```

Arguments

`list_param`	A list of list of LBM parameters, each list must contain at list `con`, `pi` and `rho` entries, such as the one returned by the function `get_lbm_param()`. The size of the network is optional.
`dens`	The density (connectance) used to compare the network. The `com` parameters of `list_param` will be normalized so that the average probability of interaction in the network is equal to `dens`. Default to 0.0156.
`new_nr`	The number of rows of the normalized networks. Default to 100.
`new_nc`	The number of columns of the normalized networks. Default to 100.
`ext_seq`	The distribution of the primary extinction sequence used to compare the networks. One of `c("uniform", "decreasing", "increasing")`. Default to `"uniform"`.

Value

A list of the sames length as `list_param`, the robustness (AUC) after normalization for all set of parameters.

Examples

```
par1 <- list(con = matrix(c(.5,.3,.3,.1), 2, 2),
             pi  = c(.25,.75),
             rho = c(1/3, 2/3))
par2 <- list(con = matrix(c(.4,.1,.1,.4), 2, 2),
             pi  = c(.25,.75),
             rho = c(1/2, 1/2))
compare_robustness(list_param = list(par1, par2), ext_seq = "decreasing")
compare_robustness(list_param = list(par1, par2), ext_seq = "increasing")
```

`get_lbm_param` *Estimate the parameters of a LBM*

Description

Estimate the parameters of a LBM

Usage

```
get_lbm_param(A, model_size = NULL, ...)
```

Arguments

`A`	A matrix, the incident matrix of the network
`model_size`	A vector of size 2, the size of the model parameters. If `NULL`, the default, model will be chosen as the one with the highest ICL criterion among all fitted models during the inference.
`...`	Additional arguments pass to the inference function of package `GREMLIN` if there are missing value and `blockmodels` if none.

Value

A list of the LBM parameters. The list is set

Examples

```
# When the size of the model is unknown:
data("seeddispersal")
param <- get_lbm_param(seeddispersal, ncores = 1L)
do.call(auc_robustness_lbm, param)

# For a fixed number of blocks (useful for comparison)
param <- get_lbm_param(seeddispersal, model_size = c(1, 3), ncores = 1L)
do.call(auc_robustness_lbm, param)

# For data with missing observations

A <- seeddispersal
```

```
A[sample(seq_len(nrow(A)), 5),
  sample(seq_len(ncol(A)), 10)] <- NA
param <- get_lbm_param(A, nbCores = 1L)
do.call(auc_robustness_lbm, param)
```

`hostparasite` *A binarized host-parasite network*

Description

Locality: Tomsk-Tumen Reference:Hadfield JD, Krasnov BR, Poulin R, Shinichi N (2013) A tale of two phylogenies: comparative analyses of ecological interactions. The American Naturalist 183(2): 174-187

Usage

```
hostparasite
```

Format

A matrix of binary entries with 27 rows and 26 columns

Source

`http://www.web-of-life.es/`

`https://datadryad.org/stash/dataset/doi:10.5061/dryad.jf3tj`

`plot.robber` *Plot function pour robber class*

Description

Plot function pour robber class

Usage

```
## S3 method for class 'robber'
plot(x, type = "function", add = FALSE, ...)
```

Arguments

`x`	An object of class robber
`type`	Type of the plot, just function
`add`	Whether it should be added to a previous ggplot
`...`	`lty`, `col`, ... to be passed to `geom_step()` in `ggplot2`

Value

A `ggplot2` object

Examples

```
data("hostparasite", package = "robber")
rob <- robustness_emp(hostparasite)
plot(rob)
```

`pollination` *A plant-pollinator network*

Description

Locality: Tenerife, Canary Islands Stald L (2003). Struktur og dynamik i rum og tid af et bestøvningsnetværk på Tenerife, De Kanariske Øer. Msc thesis (Univ of Aarhus, Aarhus, Denmark)

Usage

```
pollination
```

Format

A matrix of binary entries with 17 rows and 51 columns

Source

`http://www.web-of-life.es/`

`robustness_emp` *Empirical Robustness of a Network*

Description

Compute the robustness of an ecological network by averaging over a great number of randomly generated primary extinctions sequences

Usage

```
robustness_emp(
  A,
  ext_seq = "uniform",
  nb_iter = 300,
  net_type = "bipartite",
  method = "ordered",
  power = 1,
  block = NULL
)
```

Arguments

`A`	A binary incident matrix
`ext_seq`	A string, the rule for the primary extinctions sequences, one of `"uniform"`, the default for uniform extinctions sequences, `"decreasing"` and `"increasing"` for primary extinctions sequences by increasing and decreasing degree order sequence on the row species
`nb_iter`	An integer, the number of generated sequences. Default to `300`.
`net_type`	A string, the type of network. For now, only "bipartite" is available.
`method`	A string used when `ext_seq = "decreasing"` or `ext_seq = "increasing"`: • `"linear"` (default) set an extinction probability for each row species that is linear in its degree. It is a shortcut for `method = "power"` and `power = 1`. • `"ordered"` strictly follow the degree order, i.e. the most connected species will always goes last for `ext_seq = "increasing"` or first for `ext_seq = "decreasing"`.
`power`	An integer (default to 1). Only used when `method = "power"`, the power to which the degree are elevated to compute the primary extinctions sequences for `"increasing"` and `"decreasing"` ext_seq. For 1, it is equivalent to `method = "linear"`, for 0, it is the same as `ext_seq = "uniform"`. The largest the number the closest it will be to `method = "ordered"`.
`block`	A vector of row species memberships for `method = "block"`

Value

A list (robber object) with the following fields:

- `$model`, `$ext_seq`, `$method`, `power`
- `$fun` is the robustness function, a vector of size `(nrow(A) +1)`
- `$sd` Standard deviation of the secondary extinctions
- `$auc` the area under the curve of the robustness function

Examples

```
A <- matrix(c(1, 0, 0,
             0, 1, 0,
             0, 0, 1,
             1, 1, 1), nrow = 4, ncol = 3, byrow = TRUE)
my_rob <- robustness_emp(A, ext_seq = "increasing")
my_rob$fun
my_rob$auc
```

`robustness_lbm` *Robustness for LBM*

Description

Compute the robustness for a given set of Latent Block Model parameters.

Usage

```
robustness_lbm(
  con = NULL,
  pi = NULL,
  rho = NULL,
  nr = NULL,
  nc = NULL,
  ext_seq = "uniform",
  method = "exact",
  approx_threshold = 10000,
  net = NULL,
  ...
)
```

Arguments

`con`	A matrix, the connectivity parameter
`pi`	A vector of length `nrow(con)`, the proportion of row blocks
`rho`	A vector of length `ncol(con)`, the proportion of column blocks
`nr`	An integer, the number of row (primary) species
`nc`	An integer, the number of column (secondary) species
`ext_seq`	A string, the rule for the primary extinctions sequences, one of: • `"uniform"`, the default for uniform extinctions sequences, • `"decreasing"` and `"increasing"` for primary extinctions sequences by increasing and decreasing row blocks connection probability, • `"natural"` primary extinctions sequences with the block ordering given in the function parameter. • `"blocks"` primary extinctions sequences for all blocks permutation.
`method`	A string, the method used to compute the robustness by block. One of: • `"exact"` (the default), average on all possible networks • `"no_empty_block"` restricts the networks space to the ones with no empty block of primary species • `"expected"` restricts the networks space to the ones that have approximately the same number of species per block than the expected one. Do not do anything for `ext_seq = "uniform"`.

`approx_threshold`	A numeric, the maximum size of the possible block partition allowed for exact robustness by block calculation. Higher threshold gives more precise results at the cost of computation times and possibly memory problem. Do not do anything for `ext_seq` = `"uniform"`. When the threshold is exceeded the robustness is computed by a Monte Carlo approximation with `approx_threshold` number of samples.
`net`	A network, if given, the function will fit a LBM to obtain the parameters of the network and then compute the robustness.
`...`	Option to be passed to get_`lbm_param` function.

Value

A list and a robber type object:

- `$fun` the robustness function, a vector of size `nr` `+1`
- `$auc` the area under the curve of the robustness function
- `$block` a vector of size `length(pi)`, the block ordering for primary extinctions sequence by blocks. `NULL` if `ext_seq` = `"uniform"`.
- `$model`, `$method`, `$ext_seq`, `$param`.

Examples

```
con <- matrix(c(.5,.3,.3,.1), 2, 2)
pi  <- c(.25,.75)
rho <- c(1/3, 2/3)
nr <- 50
nc <- 30
my_rob <- robustness_lbm(con, pi, rho, nr, nc, ext_seq = "natural")
my_rob$fun
my_rob$auc
# A easier alternative way, if you don't know the parameters of the network:
data(hostparasite)
(robustness_lbm(net = hostparasite, ncores = 1L))
```

`seeddispersal` *A seed-dispersal network*

Description

Locality: North Negros Forest Reserve, Central Philippi Hammann, A. & Curio, B. (1999) Interactions among frugivores and fleshy fruit trees in a Philippine submontane rainforest.

Usage

```
seeddispersal
```

Format

A matrix of binary entries with 36 rows and 19 columns

Source

`http://www.web-of-life.es/`

`https://conbio.org/publications/conservation-biology`

`simulate_lbm` *Simulate a bipartite interaction network using block model*

Description

Simulate a bipartite interaction network using block model

Usage

```
simulate_lbm(con, pi, rho, nr, nc, method = "gnp")
```

Arguments

`con`	A matrix, the connectivity between blocks. If `method = "gnp"` then each entry is the probability of interactions given 2 blocks. If `method = "gnm"` then each entry is the number of interactions between 2 blocks.
`pi`	A vector of the same length as `nrow(con)`, the block mixture for the row species. If `method = "gnp"`, then `pi` is a probability vector, if `method = "gnm"`, then `pi` is the number of species per block, must sum to `nr`.
`rho`	A vector of the same length as `ncol(con)`, the block mixture for the column species. If `method = "gnm"`, then `rho` is a probability vector, if `method = "gnm"`, then `rho` is the number of species per block, must sum to `nc`.
`nr`	The number of row Species
`nc`	The number of column Species
`method`	One of `"gnp"` (the default) where the blocks size and number of interactions is random and `"gnm"` where the blocks size and number of interactions are fixed.

Value

A list of 3 elements:

- `A` The incident matrix of size `nrxnc`
- `Z` A vector of length `nr`, the block assignment of the row species
- `W` A vector of length `nc`, the block assignment of the column species

Examples

```
# For a random number of interactions and blocks sizes
con <- matrix(c(.5,.3,.3,.1), 2, 2)
pi  <- c(.25,.75)
rho <- c(1/3, 2/3)
nr <- 50
nc <- 30
simulate_lbm(con, pi, rho, nr, nc, method = "gnp")

# For a fixed number of ineractions and blocks sizes
con <- matrix(c(50, 120, 60, 80), 2, 2)
pi  <- c(10, 40)
rho <- c(10, 20)
nr <- 50
nc <- 30
simulate_lbm(con, pi, rho, nr, nc, method = "gnm")
```

`var_auc_unif_lbm` *Compute the Conditional variance of the AUC of the LBM Robustness*

Description

Compute the Conditional variance of the AUC of the LBM Robustness

Usage

```
var_auc_unif_lbm(con, pi, rho, nr, nc)
```

Arguments

`con`	A matrix, the connectivity parameter
`pi`	A vector of length `nrow(con)`, the proportion of row blocks
`rho`	A vector of length `ncol(con)`, the proportion of column blocks
`nr`	An integer, the number of row (primary) species
`nc`	An integer, the number of column (secondary) species

Value

A numeric, the variance

Examples

```
con <- matrix(c(.5,.3,.3,.1), 2, 2)
pi  <- c(.25,.75)
rho <- c(1/3, 2/3)
nr <- 50
nc <- 30
var_auc_unif_lbm(con, pi, rho, nr, nc)
```

`var_fun_unif_lbm` *Compute the Conditional variance of the LBM Robustness term by term*

Description

Compute the Conditional variance of the LBM Robustness term by term

Usage

```
var_fun_unif_lbm(con, pi, rho, nr, nc)
```

Arguments

`con`	A matrix, the connectivity parameter
`pi`	A vector of length `nrow(con)`, the proportion of row blocks
`rho`	A vector of length `ncol(con)`, the proportion of column blocks
`nr`	An integer, the number of row (primary) species
`nc`	An integer, the number of column (secondary) species

Value

A vector, the variance after m extinctions

Examples

```
con <- matrix(c(.5,.3,.3,.1), 2, 2)
pi  <- c(.25,.75)
rho <- c(1/3, 2/3)
nr <- 50
nc <- 30
var_fun_unif_lbm(con, pi, rho, nr, nc)
```

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