Package ‘MLVSBM’

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**Type** Package

**Title** A Stochastic Block Model for Multilevel Networks

**Version** 0.2.3


A multilevel network is defined as the junction of two interaction networks, the upper level or inter-organizational level and the lower level or inter-individual level. The inter-level represents an affiliation relationship.

**License** GPL-3

**Encoding** UTF-8

**URL** [https://github.com/Chabert-Liddell/MLVSBM](https://github.com/Chabert-Liddell/MLVSBM)

**BugReports** [https://github.com/Chabert-Liddell/MLVSBM/issues](https://github.com/Chabert-Liddell/MLVSBM/issues)

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\begin{itemize}
  \item ARI \quad \textit{Compare two clustering with the Adjusted Rand Index}
\end{itemize}

\section*{Description}

Compare two clustering with the Adjusted Rand Index

\section*{Usage}

\texttt{ARI(x, y)}

\section*{Arguments}

\begin{itemize}
  \item \textbf{x} \quad A vector of integers, the clusters labels
  \item \textbf{y} \quad A vector of integers of the same length as \texttt{x}, the clusters labels
\end{itemize}

\section*{Value}

A number between 0 (random clustering) and 1 (identical clustering)

\section*{Examples}

\texttt{ARI(x = c(1, 2, 1), y = c(2, 2, 1))}
**build_fold_matrix**

---

**build_fold_matrix**

**Title**

**Description**

Title

**Usage**

`build_fold_matrix(X, K)`

**Arguments**

- `X`: An adjacency matrix
- `K`: An integer, the number of folds

**Value**

A matrix of the same size than `X` with class integer as coefficient

---

**coef.FitMLVSBM**

**Extract model coefficients**

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**Description**

Extracts model coefficients from objects with class `FitMLVSBM`

**Usage**

```r
## S3 method for class 'FitMLVSBM'
coef(object, ...)
```

**Arguments**

- `object`: an R6 object of class `FitMLVSBM`
- `...`: additional parameters for S3 compatibility. Not used

**Value**

List of parameters.
FitMLVSBM

An R6 Class object, a fitted multilevel network once $dovem()$ is done

Description

An R6 Class object, a fitted multilevel network once $dovem()$ is done

Public fields

vbound  The vector of variational bound for monitoring convergence

Active bindings

affiliation_matrix  Get the affiliation matrix
adjacency_matrix  Get the list of adjacency matrices
nb_nodes  Get the list of the number of nodes
nb_clusters  Get the list of the number of blocks
parameters  Get the list of the model parameters
membership  Get the list of the variational parameters
independent  Are the levels independent?
distribution  Emission distribution of each level
directed  Are the levels directed?
density  Get the entropy of the model
bound  Get the variational bound of the model
df_mixture  Get the degrees of freedom of the mixture parameters
df_connect  Get the degrees of freedom of the connection parameters
connect  Get the number of possible observed connections
ICL  Get the ICL model selection criterion of the model
full_penalty  Get the penalty used to compute the ICL
Z  Get the list of block memberships (vector form)
X_hat  Get the list of the matrices of probability connection predictions
map  Get the list of block memberships (matrix form)
penalty  Get the ICL penalty
likelihood  Compute the likelihood of both levels
complete_likelihood  Get the complete likelihood of the model
Methods

Public methods:
- \texttt{FitMLVSBM$new()}
- \texttt{FitMLVSBM$update_alpha()}
- \texttt{FitMLVSBM$update_pi()}
- \texttt{FitMLVSBM$update_gamma()}
- \texttt{FitMLVSBM$init_clustering()}
- \texttt{FitMLVSBM$clear()}
- \texttt{FitMLVSBM$m_step()}
- \texttt{FitMLVSBM$ve_step()}
- \texttt{FitMLVSBM$do_vem()}
- \texttt{FitMLVSBM$permute_empty_class()}
- \texttt{FitMLVSBM$plot()}
- \texttt{FitMLVSBM$show()}
- \texttt{FitMLVSBM$print()}
- \texttt{FitMLVSBM$clone()}

Method \texttt{new()}: Constructor for the FitMLVSBM class

\textit{Usage}:
\begin{verbatim}
FitMLVSBM$new(Q = list(I = 1, O = 1),
A = NA,
X = NA,
M = list(I = NA, O = NA),
directed = NA,
distribution = list("bernoulli", "bernoulli"),
independent = FALSE)
\end{verbatim}

\textit{Arguments}:
- \texttt{Q} List of number of blocks
- \texttt{A} Affiliation matrix
- \texttt{X} List of adjacency matrices
- \texttt{M} List of Mask matrices
- \texttt{directed} List of boolean
- \texttt{distribution} List of string
- \texttt{independent} Boolean

\textit{Returns}: A FitMLVSBM object

Method \texttt{update_alpha()}: Update the connection parameters for the M step

\textit{Usage}:
\begin{verbatim}
FitMLVSBM$update_alpha(safeguard = 2 * .Machine$double.eps)
\end{verbatim}

\textit{Arguments}:
- \texttt{safeguard} Parameter live in a compact \([safeguard, 1-safeguard]\)
Method `update_pi()`: Update the upper level mixture parameter for the M step

Usage:
```
FitMLVSBM$update_pi(safeguard = 0.001)
```
Arguments:
safeguard Parameter live in a compact [safeguard, 1-safeguard]

Method `update_gamma()`: Update the lower level mixture parameter for the M step

Usage:
```
FitMLVSBM$update_gamma(safeguard = 1e-06)
```
Arguments:
safeguard Parameter live in a compact [safeguard, 1-safeguard]

Method `init_clustering()`: `init_clustering` Initial clustering for VEM algorithm

Usage:
```
FitMLVSBM$init_clustering(
  safeguard = 2 * .Machine$double.eps,
  method = "hierarchical",
  Z = NULL
)
```
Arguments:
safeguard Parameter live in a compact [safeguard, 1-safeguard]
method Algorithm used to initiate the clustering, either "spectral", "hierarchical" or "merge_split"
  (if `Z` is provided)
Z Initial clustering if provided

Method `clear()`: Reset all parameters

Usage:
```
FitMLVSBM$clear()
```

Method `m_step()`: `m_step` Compute the M step of the VEM algorithm

Usage:
```
FitMLVSBM$m_step(safeguard = 1e-06)
```
Arguments:
safeguard Parameter live in a compact [safeguard, 1-safeguard]

Method `ve_step()`: Compute the VE step of the VEM algorithm

Usage:
```
FitMLVSBM$ve_step(threshold = 1e-06, fixPointIter = 10, safeguard = 1e-06)
```
Arguments:
threshold The convergence threshold
fixPointIter The maximum number of fixed point iterations
safeguard Parameter live in a compact [safeguard, 1-safeguard]
**Method** do_vem(): Launch a Variational EM algorithm

*Usage:*

```r
do_vem(
    init = "hierarchical",
    threshold = 1e-06,
    maxIter = 1000,
    fixPointIter = 100,
    safeguard = 1e-06,
    Z = NULL
)
```

*Arguments:*

- `init`: The method for `self$init_clustering`
- `threshold`: The convergence threshold
- `maxIter`: The max number of VEM iterations
- `fixPointIter`: The max number of fixed point iterations for VE step
- `safeguard`: Parameter live in a compact $[\text{safeguard}, 1-\text{safeguard}]$
- `Z`: Initial clustering if provided

**Method** permute_empty_class(): permute_empty_class Put empty blocks numbers at the end

*Usage:*

```r
permute_empty_class()
```

**Method** plot(): Plot of FitMLVSBM objects

*Usage:*

```r
plot(type = c("matrix"), ...)
```

*Arguments:*

- `type`: A string for the type of plot, just "matrix" for now

*Returns:*

a `ggplot2` object

**Method** show(): print method

*Usage:*

```r
show(type = "Multilevel Stochastic Block Model")
```

*Arguments:*

- `type`: character to tune the displayed name

**Method** print(): print method

*Usage:*

```r
print()
```

**Method** clone(): The objects of this class are cloneable with this method.

*Usage:*

```r
clone(deep = FALSE)
```

*Arguments:*

- `deep`: Whether to make a deep clone.
**Description**

a fitted level of a unilevel network once `do_vem()` is done

**Public fields**

- `vbound` vector of variational bound for convergence monitoring

**Active bindings**

- `adjacency` Get the adjacency matrix
- `mask` Get the mask matrix for dealing with NA
- `nb_nodes` Get the number of nodes of the level
- `nb_clusters` Get the number of blocks
- `distribution` Get the distribution used for the connections
- `directed` Get if the level is directed or not
- `mixture_parameter` Access the block proportions
- `connectivity_parameter` Access the connectivity matrix
- `membership` Access the variational parameters
- `entropy` Get the entropy of the model
- `bound` Get the variational bound of the model
- `df_mixture` Get the degree of freedom of the block proportion
- `df_connect` Get the degree of freedom of the connection parameters
- `connect` Get the number of observed dyads
- `ICL` Get the ICL model selection criterion
- `penalty` Get the penalty used for computing the ICL
- `Z` Access the vector of block membership (clustering)
- `X_hat` Get the connection probability matrix
- `X_likelihood` adjacency part of the log likelihood
- `Z_likelihood` block part of the log likelihood
- `likelihood` complete log likelihood
Methods

Public methods:

- `FitSBM$new()`
- `FitSBM$update_alpha()`
- `FitSBM$update_pi()`
- `FitSBM$init_clustering()`
- `FitSBM$m_step()`
- `FitSBM$ve_step()`
- `FitSBM$do_vem()`
- `FitSBM$permute_empty_class()`
- `FitSBM$clear()`
- `FitSBM$clone()`

**Method new():** Constructor for FitSBM R6 class

*Usage:*

```r
FitSBM$new(Q = 1, X = NULL, M = NULL, directed = FALSE, distribution = "bernoulli")
```

*Arguments:*
- `Q`: Number of blocks
- `X`: Adjacency matrix
- `M`: Mask matrix
- `directed`: boolean
- `distribution`: string (only "bernoulli")

*Returns:* A new FitSBM object

**Method update_alpha():** Update the connection parameter for the M step

*Usage:*

```r
FitSBM$update_alpha(safeguard = 1e-06)
```

*Arguments:*
- `safeguard`: Parameter live in a compact [safeguard, 1-safeguard]

**Method update_pi():** Update the upper level mixture parameter for the M step

*Usage:*

```r
FitSBM$update_pi(safeguard = 1e-06)
```

*Arguments:*
- `safeguard`: Parameter live in a compact [safeguard, 1-safeguard]

**Method init_clustering():** `init_clustering` Initial clustering for VEM algorithm
Usage:
`FitSBM$init_clustering(safeguard = 1e-06, method = "hierarchical", Z = NULL)`

Arguments:
- `safeguard` Parameter live in a compact $[\text{safeguard}, 1-\text{safeguard}]$
- `method` Algorithm used to initiate the clustering, either "spectral", "hierarchical" or "merge_split" (if Z is provided)
- `Z` Initial clustering if provided

Method `m_step()`: Compute the M step of the VEM algorithm

Usage:
`FitSBM$m_step(safeguard = 1e-06)`

Arguments:
- `safeguard` Parameter live in a compact $[\text{safeguard}, 1-\text{safeguard}]$

Method `ve_step()`: Compute the VE step of the VEM algorithm

Usage:
`FitSBM$ve_step(threshold = 1e-06, fixPointIter = 100, safeguard = 1e-06)`

Arguments:
- `threshold` The convergence threshold
- `fixPointIter` The maximum number of fixed point iterations
- `safeguard` Parameter live in a compact $[\text{safeguard}, 1-\text{safeguard}]$

Method `do_vem()`: Launch a Variational EM algorithm

Usage:
`FitSBM$do_vem(
    init = "hierarchical",
    threshold = 1e-06,
    maxIter = 1000,
    fixPointIter = 100,
    safeguard = 1e-06,
    Z = NULL
)`

Arguments:
- `init` The method for `self$init_clustering`
- `threshold` The convergence threshold
- `maxIter` The max number of VEM iterations
- `fixPointIter` The max number of fixed point iterations for VE step
- `safeguard` Parameter live in a compact $[\text{safeguard}, 1-\text{safeguard}]$
- `Z` Initial clustering if provided

Method `permute_empty_class()`: permute_empty_class Put empty blocks numbers at the end

Usage:
`FitSBM$permute_empty_class()`
### hierarClust

**Method** clear(): Reset all parameters

**Usage:**

```r
FitSBM$clear()
```

**Method** clone(): The objects of this class are cloneable with this method.

**Usage:**

```r
FitSBM$clone(deep = FALSE)
```

**Arguments:**
- deep Whether to make a deep clone.

---

**hierarClust**  
*Perform a Hierarchical Clustering*

**Description**

Perform a Hierarchical Clustering

**Usage**

```r
hierarClust(X, K)
```

**Arguments**

- **X**  
  An Adjacency Matrix

- **K**  
  the number of wanted clusters

**Value**

A vector: The clusters labels

---

**merge_clust**  
*Merge a list of clusters*

**Description**

Merge a list of clusters

**Usage**

```r
merge_clust(Z, Q)
```

**Arguments**

- **Z**  
  a vector of cluster memberships

- **Q**  
  the number of original clusters
Value
A list of $Q(Q-1)/2$ clustering of $Q-1$ clusters

Description
Store all simulation parameters and list of fitted models. Methods for global inference and model selection are included.

Active bindings
- `nb_nodes` List of the number of nodes for each levels
- `simulation_parameters` List of parameters of the MLVSBM
- `affiliation_matrix` Access the affiliation matrix
- `adjacency_matrix` Access the list of adjacency matrix
- `memberships` Access the list of the clusterings
- `fittedmodels` Get the list of selected fitted FitMLVSBM objects
- `ICL` A summary table of selected fitted models and ICL model selection criterion
- `ICL_sbm` Summary table of ICL by levels
- `tmp_fittedmodels` A list of all fitted FitMLVSBM objects
- `fittedmodels_sbm` A list of selected fitted FitSBM objects of each levels
- `max_clusters` Access the list of maximum model size
- `min_clusters` Access the list of minimum model size
- `directed` Access the list of boolean for levels direction
- `directed` Access the list of the distribution used for each levels

Methods
Public methods:
- `MLVSBM$estimate_level()`
- `MLVSBM$estimate_sbm_neighbours()`
- `MLVSBM$estimate_sbm_from_neighbours()`
- `MLVSBM$estimate_sbm()`
- `MLVSBM$mcestimate()`
- `MLVSBM$estimate_from_neighbours()`
- `MLVSBM$estimate_neighbours()`
- `MLVSBM$merge_split_membership()`
- `MLVSBM$mc_ms_estimate()`
- `MLVSBM$estimate_one()`
• MLVSBM$estimate_all_bm()
• MLVSBM$new()
• MLVSBM$findmodel()
• MLVSBM$clearmodels()
• MLVSBM$addmodel()
• MLVSBM$simulate()
• MLVSBM$clone()

Method estimate_level():
Usage:
MLVSBM$estimate_level(
  level = "lower",
  Q_min = 1,
  Q_max = 10,
  Z = NULL,
  init = "hierarchical",
  depth = 1,
  nb_cores = NULL
)

Method estimate_sbm_neighbours():
Usage:
MLVSBM$estimate_sbm_neighbours(
  level = "lower",
  Q = NULL,
  Q_min = 1,
  Q_max = 10,
  fit = NULL,
  nb_cores = NULL,
  init = NULL
)

Method estimate_sbm_from_neighbours():
Usage:
MLVSBM$estimate_sbm_from_neighbours(
  level = "lower",
  Q = NULL,
  fits = NULL,
  nb_cores = NULL
)

Method estimate_sbm():
Usage:
MLVSBM$estimate_sbm(level = "lower", Q = Q, Z = NULL, init = "hierarchical")

Method mcestimate():
Usage:
MLVSBM$mestimate(Q, Z = NULL, init = "hierarchical", independent = FALSE)

Method estimate_from_neighbours():
  Usage:
  MLVSBM$estimate_from_neighbours(
    Q,
    models = NULL,
    independent = FALSE,
    nb_cores = nb_cores
  )

Method estimate_neighbours():
  Usage:
  MLVSBM$estimate_neighbours(
    Q,
    fit = NULL,
    independent = independent,
    nb_cores = NULL
  )

Method merge_split_membership():
  Usage:
  MLVSBM$merge_split_membership(
    fitted = private$fitted[[length(private$fitted)]]
  )

Method mc_ms_estimate():
  Usage:
  MLVSBM$mc_ms_estimate(Z = NA, independent = FALSE, nb_cores = NULL)

Method estimate_one():
  Usage:
  MLVSBM$estimate_one(
    Q,
    Z = NULL,
    independent = FALSE,
    init = "hierarchical",
    nb_cores = NULL
  )

Method estimate_all_bm():
  Usage:
  MLVSBM$estimate_all_bm(
    Q = NULL,
    Z = NULL,
    independent = FALSE,
    clear = TRUE,
    nb_cores = NULL
  )
Method `new()`: Constructor for R6 class MLVSBM

*Usage:*

```r
MLVSBM$new(  
n = NULL,  
X = NULL,  
A = NULL,  
Z = NULL,  
directed = NULL,  
sim_param = NULL,  
distribution = list("bernoulli", "bernoulli")
)
```

*Arguments:*

- `n`: A list of size 2, the number of nodes
- `X`: A list of 2 adjacency matrices
- `A`: The affiliation matrix
- `Z`: A list of 2 vectors, the blocks membership
- `directed`: A list of 2 booleans
- `sim_param`: A list of MLVSBM parameters for simulating networks
- `distribution`: The distributions of the interactions ("bernoulli")

*Returns:* A MLVSBM object

Method `findmodel()`: Find a fitted model of a given size

*Usage:*

```r
MLVSBM$findmodel(nb_clusters = NA, fit = NA)
```

*Arguments:*

- `nb_clusters`: A list of the size of the model
- `fit`: if `fit = "best"` return the best model according to the ICL

*Returns:* A FitMLVSBM object

Method `clearmodels()`: delete all fitted models

*Usage:*

```r
MLVSBM$clearmodels()
```

Method `addmodel()`: Added a FitMLVSBM object to the list of fitted model

*Usage:*

```r
MLVSBM$addmodel(fit)
```

*Arguments:*

- `fit`: The FitMLVSBM object to be added

Method `simulate()`:

*Usage:*

```r
MLVSBM$simulate()
```

Method `clone()`: The objects of this class are cloneable with this method.
Usage:
MLVSBM$clone(deep = FALSE)

Arguments:
deep Whether to make a deep clone.

Description
Create a MLVSBM object from observed data

Usage
mlvsbm_create_network(
  X,
  A,
  directed = NULL,
  distribution = list("bernoulli", "bernoulli")
)

Arguments

X A list of 2 squares binary matrices, the first one being the individual or lower level the second one being the organizational or upper level

A A matrix the affiliation matrix with individuals in rows and organizations in columns

directed A list of 2 boolean are the upper and lower level directed or not. Default will check if the matrix are symmetric or not.

distribution A list for the distribution of X, only "bernoulli" is implemented

Value
An unfitted MLVSBM object corresponding to the multilevel network

Examples
ind_adj <- matrix(stats::rbinom(n = 10**2, size = 1, prob = .2),
  nrow = 10, ncol = 10)
org_adj <- matrix(stats::rbinom(n = 10**2, size = 1, prob = .3),
  nrow = 10, ncol = 10)
affiliation <- diag(1, 10)
my_mlvsbm <- mlvsbm_create_network(X = list(I = ind_adj, O = org_adj),
  directed = list(I = FALSE, O = FALSE),
  A = affiliation)
Infer a multilevel network (MLVSBM object), the original object is modified

Description

The inference use a greedy algorithm to navigate between model size. For a given model size, the inference is done via a variational EM algorithm. The returned model is the one with the highest ICL criterion among all visited models.

By default the algorithm fits a single level SBM for each level, before inferring the multilevel network. This step can be skipped by specifying an initial clustering with the init_clustering. Also, a given model size can be force by setting the parameters nb_clusters to a given value.

Usage

```r
mlvsbm_estimate_network(
  mlv,
  nb_clusters = NULL,
  init_clustering = NULL,
  nb_cores = NULL,
  init_method = "hierarchical"
)
```

Arguments

- **mlv**: A MLVSBM object, the network to be inferred.
- **nb_clusters**: A list of 2 integers, the model size. If left to NULL, the algorithm will navigate freely. Otherwise it will navigate between the specified model size and its neighbors.
- **init_clustering**: A list of 2 vectors of integers of the same length as the number of node of each level. If specified, the algorithm will start from this clustering, then navigate freely.
- **nb_cores**: An integer, the number of cores to use. Default to 1 for Windows and detectCores()\(\)/2 for Linux and MacOS
- **init_method**: One of "hierarchical" (the default) or "spectral", "spectral" might be more efficient but can lead to some numeric errors. Not used when init_clustering is given.

Value

A FitMLVSBM object, the best inference of the network
Examples

```r
my_mlvsbm <- MLVSBM::mlvsbm_simulate_network(
  n = list(I = 10, O = 20), # Number of nodes for the lower level and the upper level
  Q = list(I = 2, O = 2), # Number of blocks for the lower level and the upper level
  pi = c(.3, .7), # Block proportion for the upper level, must sum to one
  gamma = matrix(c(.9, .2, # Block proportion for the lower level,
                   .1, .8), # each column must sum to one
                 nrow = 2, ncol = 2, byrow = TRUE),
  alpha = list(I = matrix(c(.8, .2,
                           .2, .1),
                        nrow = 2, ncol = 2, byrow = TRUE), # Connection matrix
                O = matrix(c(.99, .3,
                             .3, .1),
                           nrow = 2, ncol = 2, byrow = TRUE)), # between blocks
  directed = list(I = FALSE, O = FALSE), # Are the upper and lower level directed or not ?
  affiliation = "preferential") # How the affiliation matrix is generated
fit <- MLVSBM::mlvsbm_estimate_network(mlv = my_mlvsbm, nb_cores = 1)
```

### mlvsbm_log_likelihood

Compute the complete log likelihood of a multilevel network for a given clustering of the nodes.

#### Description

This function is useful to compute the likelihood for clusters obtained by different methods.

#### Usage

```r
mlvsbm_log_likelihood(mlv, clustering)
```

#### Arguments

- **mlv**: A MLVSBM object, the network data
- **clustering**: A list of 2 vectors of integers of the same length as the number of node of each level.

#### Value

A numeric, the log likelihood of the multilevel network for the given clustering.

#### Examples

```r
my_mlvsbm <- MLVSBM::mlvsbm_simulate_network(
  n = list(I = 40, O = 20), # Number of nodes for the lower level and the upper level
  Q = list(I = 2, O = 2), # Number of blocks for the lower level and the upper level
  pi = c(.3, .7), # Block proportion for the upper level, must sum to one
  gamma = matrix(c(.9, .2, # Block proportion for the lower level,
                   .1, .8), # each column must sum to one
                 nrow = 2, ncol = 2, byrow = TRUE),
```
Create a simulated multilevel network (MLVSBM object)

Description
Create a simulated multilevel network (MLVSBM object)

Usage
mlvsbm_simulate_network(
  n,
  Q,
  pi,
  gamma,
  alpha,
  directed,
  affiliation = "uniform",
  distribution = list("bernoulli", "bernoulli"),
  no_empty_org = FALSE,
  no_isolated_node = FALSE
)

Arguments

n A list of 2 positive integers, the number of individuals and organizations.
Q A list of 2 positive integers, the number of clusters of individuals and organizations.
pi A vector of probabilities of length Q_O, the mixture parameter for the organizations.
gamma A Q_I × Q_O matrix with each column summing to one, the mixture parameters for the individuals
alpha A list of 2 matrices, a Q_I × Q_I matrix giving the connectivity probabilities of the individuals and a Q_O × Q_O matrix giving the connectivity probabilities of the organizations.
directed A list of 2 logical. Is the individual level a directed network? Is the inter-organizational level a directed network?
affiliation
The distribution under which the affiliation matrix is simulated in c("uniform", "preferential").
distribution
A list for the distribution of X, only "bernoulli" is implemented.
no_empty_org
A logical with FALSE as default, should every organizations have at least one affiliated individual? Needs to have $n_I \geq n_O$.
no_isolated_node
A logical, if TRUE then the network is simulated again until all nodes are connected.

Value
An MLVSBM object, a simulated multilevel network with levels, affiliations and memberships.

Examples

```r
my_mlvsbm <- MLVSBM::mlvsbm_simulate_network(
  n = list(I = 10, O = 20), # Number of nodes for the lower level and the upper level
  Q = list(I = 2, O = 2), # Number of blocks for the lower level and the upper level
  pi = c(.3, .7), # Block proportion for the upper level, must sum to one
  gamma = matrix(c(.9, .2, .1, .8), # Block proportion for the lower level,
                  nrow = 2, ncol = 2, byrow = TRUE), # each column must sum to one
  alpha = list(I = matrix(c(.8, .2,
                           .2, .1),
                      nrow = 2, ncol = 2, byrow = TRUE), # Connection matrix
               O = matrix(c(.99, .3,
                            .3, .1),
                      nrow = 2, ncol = 2, byrow = TRUE)), # between blocks
  directed = list(I = FALSE, O = FALSE)) # Are the upper and lower level directed
```

plot.FitMLVSBM

**Multilevel SBM Plot**

**Description**

basic matrix plot method for a FitMLVSBM object

**Usage**

```r
## S3 method for class 'FitMLVSBM'
plot(x, type = c("matrix"), ...)
```

**Arguments**

- **x**
  an R6 object of class `FitMLVSBM`
- **type**
  A string for the type of plot, just "matrix" for now
- **...**
  additional parameters. block ordering with order = c("affiliation", "degree", "natural")
Details

Basic matrix plot method for a FitMLVSBM object

Value

a ggplot2 object

Description

Make predictions from an SBM.

Usage

## S3 method for class 'FitMLVSBM'
predict(object, ...)  

Arguments

object an R6 object of class FitMLVSBM  
... additional parameters for S3 compatibility. Not used

Value

A list with the following entries:

dyads A list of matrix with the probability of each dyads  

nodes A list of vectors with the clustering of each nodes

Description

Simulation an adjacency matrix

Usage

simulate_adjacency(  
  Z,  
n,  
alpha,  
directed,  
distribution = "bernoulli",  
no_isolated_node = FALSE  
)
**simulate_affiliation**

**Arguments**

- \( Z \): A vector of integer of size \( n \), the label
- \( n \): An integer, the number of rows or columns of the matrix
- \( \alpha \): A \( \max(Z) \times \max(Z) \) matrix, the connectivity parameters
- \( \text{directed} \): A boolean, Is the network directed or not?
- \( \text{distribution} \): The distribution of the indices: only "bernoulli"
- \( \text{no_isolated_node} \): A boolean, may row and column of adjacency matrices sum to 0

**Value**

A \( nxn \) adjacency matrix

**Description**

Simulate of matrix of affiliation

**Usage**

\[
\text{simulate_affiliation}(n, m, \text{affiliation} = \"uniform\", \text{no_empty_org} = \text{FALSE})
\]

**Arguments**

- \( n \): An integer, the number of individuals
- \( m \): An integer, the number of organizations
- \( \text{affiliation} \): The type of affiliation between c("uniform", "preferential")
- \( \text{no_empty_org} \): A Boolean. Force all columns to have at least a 1. Must have \( n > m \).

**Value**

A \( n \times m \) affiliation matrix, with a unique 1 on each rows
**spcClust**  
*Perform a spectral clustering*

**Description**
Perform a spectral clustering

**Usage**
spcClust(X, K)

**Arguments**
- **X**: an Adjacency matrix
- **K**: the number of clusters

**Value**
A vector: The clusters labels

---

**split_clust**  
*Merge a list of clusters*

**Description**
Merge a list of clusters

**Usage**
split_clust(X, Z, Q)

**Arguments**
- **X**: an adjacency matrix
- **Z**: a vector of cluster memberships
- **Q**: The number of maximal clusters

**Value**
A list of Q clustering of Q+1 clusters
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