Package ‘sbm’

July 17, 2020

Title Stochastic Blockmodels

Version 0.2.1

Description A collection of tools and function to adjust a variety of stochastic blockmodels (SBM).
Support at the moment Simple and Bipartite SBM (undirected and directed) for Bernoulli, Poisson and
Gaussian emission laws of the edges as described in Léger, 2016 <arxiv:1602.07587>.

URL https://grosssbm.github.io/sbm/

BugReports https://github.com/GrossSBM/sbm/issues

License GPL (>= 3)

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

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'R6Class-BipartiteSBM_fit.R' 'R6Class-SBM_sampler.R'
'R6Class-BipartiteSBM_sampler.R' 'R6Class-SimpleSBM_fit.R'
'R6Class-SimpleSBM_sampler.R' 'RcppExports.R' 'estimate.R'
'fungus_tree_network.R' 'plotMyMatrix.R' 'sample.R'
'sbm-package.R' 'utils.pipe.R' 'utils.R'

LinkingTo Rcpp, RcppArmadillo

VignetteBuilder knitr

Depends R (>= 3.5.0)

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BipartiteSBM_fit

Description

R6 Class definition of an Bipartite SBM fit

Details

This class is designed to give a representation and adjust an LBM fitted with blockmodels.

Super classes

`sbm::SBM -> sbm::SBM_fit -> BipartiteSBM_fit`
BipartiteSBM_fit

Active bindings

nbNodes  vector of size 2: number of nodes (rows, columns)
nbBlocks  vector of size 2: number of blocks (rows, columns)
nbDyads  number of dyads (potential edges in the network)
memberships  list of size 2: vector of memberships in row, in column.
storedModels  data.frame of all models fitted (and stored) during the optimization

Methods

Public methods:

• BipartiteSBM_fit$new()
• BipartiteSBM_fit$optimize()
• BipartiteSBM_fit$predict()
• BipartiteSBM_fit$reorder()
• BipartiteSBM_fit$show()
• BipartiteSBM_fit$clone()

Method new(): constructor for a Bipartite SBM fit

Usage:
BipartiteSBM_fit$new(incidenceMatrix, model, covarList = list())

Arguments:
incidenceMatrix  rectangular (weighted) matrix
model  character ("bernoulli", "poisson", "gaussian")
covarList  and optional list of covariates, each of whom must have the same dimension as incidenceMatrix

Method optimize(): function to perform optimization

Usage:
BipartiteSBM_fit$optimize(
  verbosity = 3,
  plot = FALSE,
  explorFactor = 1.5,
  nbBlocksRange = c(4, Inf),
  nbCores = 2,
  fast = TRUE
)

Arguments:
verbositiy  integer, the level of verbosity. Default to 3
plot  logical, if TRUE plotting is done dynamically on the screen. Default to TRUE
explorFactor  double factor for exploring successive model
nbBlocksRange  2-size vector: range of exploration
nbCores  integer, the number of cores to use. Default is 2.
BipartiteSBM_sampler

R6 class for Bipartite SBM sampler

Description
R6 class for Bipartite SBM sampler
R6 class for Bipartite SBM sampler

Super classes

```
sbm::SBM -> sbm::SBM_sampler -> BipartiteSBM_sampler
```

Active bindings

```
nbNodes  vector of size 2: number of nodes (rows, columns)
nbBlocks vector of size 2: number of blocks (rows, columns)
nbDyads  number of dyads (potential edges in the network)
memberships list of size 2: vector of memberships in row, in column.
indMemberships list of 2 matrix for clustering memberships
expectation  expected values of connection under the current model
```
Methods

Public methods:

- BipartiteSBM_sampler$new()
- BipartiteSBM_sampler$rMemberships()
- BipartiteSBM_sampler$rIncidence()
- BipartiteSBM_sampler$show()
- BipartiteSBM_sampler$clone()

Method new(): constructor for SBM

Usage:
BipartiteSBM_sampler$new(model, nbNodes, blockProp, connectParam, covarParam = numeric(0), covarList = list())

Arguments:
model character describing the type of model
nbNodes number of nodes in the network
blockProp parameters for block proportions (vector of list of vectors)
connectParam list of parameters for connectivity with a matrix of means 'mean' and an optional scalar for the variance 'var'. The dimensions of mu must match blockProp lengths
covarParam optional vector of covariates effect
covarList optional list of covariates data

Method rMemberships(): a method to generate a vector of block indicators

Usage:
BipartiteSBM_sampler$rMemberships()

Method rIncidence(): a method to sample an adjacency matrix for the current SBM

Usage:
BipartiteSBM_sampler$rIncidence()

Returns: nothing (sampled matrix is store in the current object, accessible via $netMatrix)

Method show(): show method

Usage:
BipartiteSBM_sampler$show(type = "Sampler for a Bipartite Stochastic Block Model")

Arguments:
type character used to specify the type of SBM
**Method clone():** The objects of this class are cloneable with this method.

*Usage:*

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

*Arguments:*

depth Whether to make a deep clone.

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<table>
<thead>
<tr>
<th>coef.SBM</th>
<th>Extract model coefficients</th>
</tr>
</thead>
</table>

**Description**

Extracts model coefficients from objects with class SBM and children (`SimpleSBM_fit`, `BipartiteSBM_fit`)

**Usage**

```r
## S3 method for class 'SBM'
coef(object, type = c("connectivity", "block", "covariates"), ...)
```

**Arguments**

- `object` an R6 object inheriting from class SBM_fit (like SimpleSBM_fit or BipartiteSBM_fit)
- `type` type of parameter that should be extracted. Either 'block' for
  
  \[ \pi \]

  , 'connectivity' for

  \[ \theta \]

  , or "covariates" for

  \[ \beta \]

  . Default is 'connectivity'.

  ...

  additional parameters for S3 compatibility. Not used

**Value**

- vector or list of parameters.
estimateBipartiteSBM

Estimation of Bipartite SBMs

Description

This function performs variational inference of bipartite Stochastic Block Models, with various model for the distribution of the edges: Bernoulli, Poisson, or Gaussian models.

Usage

```r
estimateBipartiteSBM(
  netMat,
  model = "bernoulli",
  covariates = list(),
  estimOptions = list()
)
```

Arguments

- `netMat`: a matrix describing the network: either an adjacency (square) or incidence matrix with possibly weighted entries.
- `model`: character describing the model for the relation between nodes ('bernoulli', 'poisson', 'gaussian', ...). Default is 'bernoulli'.
- `covariates`: a list of matrices with same dimension as mat describing covariates at the edge level. No covariate per Default.
- `estimOptions`: a list of parameters controlling the inference algorithm and model selection. See details.

Details

The list of parameters `estimOptions` essentially tunes the optimization process and the variational EM algorithm, with the following parameters:

- "nbCores": integer for number of cores used. Default is 2
- "verbosity": integer for verbosity (0, 1). Default is 1
- "plot": boolean, should the ICL by dynamically plotted or not. Default is TRUE
- "exploreFactor": control the exploration of the number of groups
- "nbBlocksRange": minimal and maximal number or blocks explored

Value

a list with the estimated parameters. See details...
Examples

### BIPARTITE BINARY SBM (Bernoulli model)

```r
### Graph parameters and Sampling
nbNodes <- c(60, 80)
blockProp <- list(c(.5, .5), c(1/3, 1/3, 1/3)) # group proportions
means <- matrix(runif(6), 2, 3) # connectivity matrix
# In Bernoulli SBM, parameters is a list with a
# matrix of means 'mean' which are probabilities of connection
connectParam <- list(mean = means)
mySampler <- sampleBipartiteSBM(nbNodes, blockProp, connectParam, model = 'bernoulli')

### Estimation
myBipartiteSBM <- estimateBipartiteSBM(mySampler$netMatrix, estimOptions = list(plot = FALSE))
plot(myBipartiteSBM, 'expected')
```

### BIPARTITE POISSON SBM

```r
### Graph parameters & Sampling
nbNodes <- c(60, 80)
blockProp <- list(c(.5, .5), c(1/3, 1/3, 1/3)) # group proportions
means <- matrix(rbinom(6, 30, 0.25), 2, 3) # connectivity matrix
connectParam <- list(mean = means)
mySampler <- sampleBipartiteSBM(nbNodes, blockProp, connectParam, model = 'poisson')

### Estimation
myBipartiteSBM <-
    estimateBipartiteSBM(mySampler$netMatrix, 'poisson', estimOptions = list(plot = FALSE))
plot(myBipartiteSBM, 'expected')
```

### BIPARTITE GAUSSIAN SBM

```r
### Graph parameters & sampling
nbNodes <- c(60, 80)
blockProp <- list(c(.5, .5), c(1/3, 1/3, 1/3)) # group proportions
means <- 20 * matrix(runif(6), 2, 3) # connectivity matrix
connectParam <- list(mean = means, var = 1)
mySampler <- sampleBipartiteSBM(nbNodes, blockProp, connectParam, model = 'gaussian')

### Estimation
myBipartiteSBM <-
    estimateBipartiteSBM(mySampler$netMatrix, 'gaussian', estimOptions = list(plot = FALSE))
plot(myBipartiteSBM, 'expected')
```
**estimateSimpleSBM**

**Description**

This function performs variational inference of simple Stochastic Block Models, with various model for the distribution of the edges: Bernoulli, Poisson, or Gaussian models.

**Usage**

```r
estimateSimpleSBM(
  netMat,
  model = "bernoulli",
  directed = !isSymmetric(netMat),
  covariates = list(),
  estimOptions = list()
)
```

**Arguments**

- `netMat`: a matrix describing the network: either an adjacency (square) or incidence matrix with possibly weighted entries.
- `model`: character describing the model for the relation between nodes ('bernoulli', 'poisson', 'gaussian', ...). Default is 'bernoulli'.
- `directed`: logical: is the network directed or not? Only relevant when type is 'Simple'. Default is TRUE if netMat is symmetric, FALSE otherwise.
- `covariates`: a list of matrices with same dimension as mat describing covariates at the edge level. No covariate per Default.
- `estimOptions`: a list of parameters controlling the inference algorithm and model selection. See details.

**Details**

The list of parameters `estimOptions` essentially tunes the optimization process and the variational EM algorithm, with the following parameters:

- "nbCores" integer for number of cores used. Default is 2
- "verbosity" integer for verbosity (0, 1). Default is 1
- "plot" boolean, should the ICL by dynamically plotted or not. Default is TRUE
- "exploreFactor" control the exploration of the number of groups
- "nbBlocksRange" minimal and maximal number or blocks explored

**Value**

a list with the estimated parameters. See details...
Examples

### SIMPLE BINARY SBM (Bernoulli model)

```r
## Graph parameters & Sampling
nbNodes <- 90
deletedèmes <- c(.5, .25, .25) # group proportions
deletedèmes <- diag(.4, 3) + 0.05 # connectivity matrix: affiliation network
deletedèmes <- list(mean = deletedèmes)
deletedèmes <- sampleSimpleSBM(nbNodes, blockProp, connectParam)
adjacencyMatrix <- deletedèmes$netMatrix

## Estimation
mySimpleSBM <-
  estimateSimpleSBM(adjacencyMatrix, 'bernoulli', estimOptions = list(plot = FALSE))
plot(mySimpleSBM, 'data', ordered = FALSE)
plot(mySimpleSBM, 'expected', ordered = FALSE)
plot(mySimpleSBM, 'expected')
```

### SIMPLE POISSON SBM

```r
## Graph parameters & Sampling
nbNodes <- 90
deletedèmes <- c(.5, .25, .25) # group proportions
deletedèmes <- diag(15., 3) + 5 # connectivity matrix: affiliation network
deletedèmes <- list(mean = deletedèmes)
deletedèmes <- sampleSimpleSBM(nbNodes, blockProp, list(mean = deletedèmes), model = "poisson")
adjacencyMatrix <- deletedèmes$netMatrix

## Estimation
mySimpleSBM <-
  estimateSimpleSBM(adjacencyMatrix, 'poisson', estimOptions = list(plot = FALSE))
plot(mySimpleSBM, 'data', ordered = FALSE)
plot(mySimpleSBM, 'expected', ordered = FALSE)
plot(mySimpleSBM, 'expected')
```

### SIMPLE GAUSSIAN SBM

```r
## Graph parameters & Sampling
nbNodes <- 90
deletedèmes <- c(.5, .25, .25) # group proportions
deletedèmes <- diag(15., 3) + 5 # connectivity matrix: affiliation network
deletedèmes <- list(mean = deletedèmes, var = 2)
deletedèmes <- sampleSimpleSBM(nbNodes, blockProp, connectParam, model = "gaussian")

## Estimation
mySimpleSBM <-
  estimateSimpleSBM(mySimpleSBM$netMatrix, 'gaussian', estimOptions = list(plot = FALSE))
plot(mySimpleSBM, 'data', ordered = FALSE)
plot(mySimpleSBM, 'data')
```
fitted.SBM_fit

plot(mySimpleSBM, 'expected', ordered = FALSE)
plot(mySimpleSBM, 'expected')

fitted.SBM_fit

Extract model fitted values
Extracts fitted values for object with class SBM_fit and children (SimpleSBM_fit, BipartiteSBM_fit)

Description

Extract model fitted values Extracts fitted values for object with class SBM_fit and children (SimpleSBM_fit, BipartiteSBM_fit)

Usage

## S3 method for class 'SBM_fit'
fitted(object, ...)

Arguments

object an R6 object inheriting from class SBM_fit (like SimpleSBM_fit or BipartiteSBM_fit)
...
additional parameters for S3 compatibility. Not used

Value

a matrix of expected fitted values for each dyad

fungus_tree_network

fungus-tree interaction network

Description

This data set provides information about $154$ fungi sampled on $51$ tree species.

Usage

fungus_tree_network

Format

A list with the following entries:

fungi_list list of the fungus species names
tree_list list of the tree species names
fungus_tree binary fungus-tree interactions
tree_tree weighted tree-tree interactions (number of common fungal species two tree species host)
covar_tree covariates associated to pairs of trees (namely genetic, taxonomic and geographic distances)

---

**Description**

basic matrix plot method for SBM object

**Usage**

```r
## S3 method for class 'SBM'
plot(
x, 
type = c("data", "expected"),
ordered = TRUE,
rowLabel = NULL,
colLabel = NULL,
...
)
```

**Arguments**

- `x` a object inheriting from class SBM
- `type` character for the type of plot: either 'data' (true connection) or 'expected' (fitted connection). Default to 'data'.
- `ordered` logical: should the rows and columns be reordered according to the clustering? Default to TRUE.
- `rowLabel` character : type of the individual in row. Default to NULL.
- `colLabel` character : type of the individual in col. Default to NULL.
- `...` additional parameters for S3 compatibility. Not used

**Details**

Basic matrix plot method for SBM object

**Value**

a ggplot2 object
plotMyMatrix

Plot an adjacency or incidence Matrix

Description

Plot an adjacency or incidence Matrix

Usage

plotMyMatrix(Mat, rowLabel = NULL, collLabel = NULL)

Arguments

Mat : a matrix representing the network
rowLabel character : type of nodes in rows (functional group) (Default is NULL)
collLabel character : type of nodes in columns (functional group) (Default is NULL)

Value

a ggplot object corresponding to the plot

Examples

M <- matrix(sample(c(0,1),900,replace=TRUE),30,30)
plotMyMatrix(M)
M2 <- matrix(rpois(800,10),40,20)
plotMyMatrix(M2,rowLabel='ind',collLabel = 'book')

predict.SBM

Model Predictions

Description

Make predictions from an SBM.

Usage

## S3 method for class 'SBM'
predict(object, covarList = object$covarList, ...)

Arguments

object an R6 object inheriting from class SBM_fit (like SimpleSBM_fit or BipartiteSBM_fit)
covarList a list of covariates. By default, we use the covariates associated with the model.
... additional parameters for S3 compatibility. Not used
Description

This function samples a simple Stochastic Block Models, with various model for the distribution of the edges: Bernoulli, Poisson, or Gaussian models, and possibly with covariates.

Usage

```r
sampleBipartiteSBM(
  nbNodes,
  blockProp,
  connectParam,
  model = "bernoulli",
  covariates = list(),
  covariatesParam = numeric(0)
)
```

Arguments

- `nbNodes`: number of nodes in the network
- `blockProp`: parameters for block proportions: list of size two with row and column block proportions
- `connectParam`: list of parameters for connectivity with a matrix of means 'mean' and an optional matrix of variances 'var', the sizes of which must match `blockProp` length (in row, respectively in column)
- `model`: character describing the model for the relation between nodes ('bernoulli', 'poisson', 'gaussian', ...). Default is 'bernoulli'.
- `covariates`: a list of matrices with same dimension as `mat` describing covariates at the edge level. No covariate per Default.

Value

an object with class `BipartiteSBM_sampler`
Examples

### BIPARTITE BERNOULLI SBM

```
## Graph parameters
nbNodes <- c(100, 120)
blockProp <- list(c(.5, .5), c(1/3, 1/3, 1/3)) # group proportions
means <- matrix(runif(6), 2, 3) # connectivity matrix
# In Bernoulli SBM, parameters is a list with
# a matrix of means 'mean' which are probabilities of connection
connectParam <- list(mean = means)

## Graph Sampling
mySampler <- sampleBipartiteSBM(nbNodes, blockProp, connectParam, model = 'bernoulli')
plot(mySampler)
mySampler$rMemberships() # sample new memberships
mySampler$rIncidence() # sample new incidence matrix
plot(mySampler)
hist(mySampler$netMatrix)
```

### BIPARTITE POISSON SBM

```
## Graph parameters
nbNodes <- c(100, 120)
blockProp <- list(c(.5, .5), c(1/3, 1/3, 1/3)) # group proportions
means <- matrix(rbinom(6, 30, 0.25), 2, 3) # connectivity matrix
# In Poisson SBM, parameters is a list with a matrix of
# means 'mean' which are a mean integer value taken by edges
connectParam <- list(mean = means)

## Graph Sampling
mySampler <- sampleBipartiteSBM(nbNodes, blockProp, connectParam, model = 'poisson')
plot(mySampler)
hist(mySampler$netMatrix)
```

### BIPARTITE GAUSSIAN SBM

```
## Graph parameters
nbNodes <- c(100, 120)
blockProp <- list(c(.5, .5), c(1/3, 1/3, 1/3)) # group proportions
means <- 20 * matrix(runif(6), 2, 3) # connectivity matrix
# In Gaussian SBM, parameters is a list with a matrix
# of means 'mean' and a matrix of variances 'var'
connectParam <- list(mean = means, var = 1)

## Graph Sampling
mySampler <- sampleBipartiteSBM(nbNodes, blockProp, connectParam, model = 'gaussian')
plot(mySampler)
hist(mySampler$netMatrix)
```
sampleSimpleSBM

Sampling of Simple SBMs

Description
This function samples a simple Stochastic Block Models, with various model for the distribution of the edges: Bernoulli, Poisson, or Gaussian models, and possibly with covariates.

Usage
sampleSimpleSBM(
  nbNodes,
  blockProp,
  connectParam,
  model = "bernoulli",
  directed = FALSE,
  covariates = list(),
  covariatesParam = numeric(0)
)

Arguments

nbNodes number of nodes in the network
blockProp parameters for block proportions
connectParam list of parameters for connectivity with a matrix of means 'mean' and an optional matrix of variances 'var', the sizes of which must match blockProp length
model character describing the model for the relation between nodes ('bernoulli', 'poisson', 'gaussian', ...). Default is 'bernoulli'.
directed logical, directed network or not. Default is FALSE.
covariates a list of matrices with same dimension as mat describing covariates at the edge level. No covariate per Default.
covariatesParam optional vector of covariates effect. A zero length numeric vector by default.

Value
an object with class SimpleSBM_sampler

Examples

### =======================================
### SIMPLE BINARY SBM (Bernoulli model)
## Graph parameters
nbNodes <- 90
blockProp <- c(.5, .25, .25) # group proportions
means <- diag(.4, 3) + 0.05 # connectivity matrix: affiliation network
# In Bernoulli SBM, parameters is a list with a
# matrix of means 'mean' which are probabilities of connection
connectParam <- list(mean = means)

## Graph Sampling
mySampler <- sampleSimpleSBM(nbNodes, blockProp, connectParam, model = 'bernoulli')
plot(mySampler)
mySampler$rMemberships() # sample new memberships
mySampler$rAdjacency()  # sample new adjacency matrix
plot(mySampler)
hist(mySampler$netMatrix)

### SIMPLE POISSON SBM
## Graph parameters
nbNodes <- 90
blockProp <- c(.5, .25, .25) # group proportions
means <- diag(15., 3) + 5  # connectivity matrix: affiliation network
# In Poisson SBM, parameters is a list with
# a matrix of means 'mean' which are a mean integer value taken by edges
connectParam <- list(mean = means)

## Graph Sampling
mySampler <- sampleSimpleSBM(nbNodes, blockProp, list(mean = means), model = "poisson")
plot(mySampler)
hist(mySampler$netMatrix)

### SIMPLE GAUSSIAN SBM
## Graph parameters
nbNodes <- 90
blockProp <- c(.5, .25, .25) # group proportions
means <- diag(15., 3) + 5  # connectivity matrix: affiliation network
# In Gaussian SBM, parameters is a list with
# a matrix of means 'mean' and a matrix of variances 'var'
connectParam <- list(mean = means, var = 2)

## Graph Sampling
mySampler <- sampleSimpleSBM(nbNodes, blockProp, connectParam, model = "gaussian")
plot(mySampler)
hist(mySampler$netMatrix)

---

**SBM**

*R6 virtual class for SBM representation (mother class of Simple and Bipartite SBM fit and sampler)*

---

**Description**

R6 virtual class for SBM representation (mother class of Simple and Bipartite SBM fit and sampler)
R6 virtual class for SBM representation (mother class of Simple and Bipartite SBM fit and sampler)
Active bindings

- **dimension**: size-2 vector: dimension of the network
- **modelName**: character, the family of model for the distribution of the edges
- **nbCovariates**: integer, the number of covariates
- **blockProp**: vector of block proportions (aka prior probabilities of each block)
- **connectParam**: parameters associated to the connectivity of the SBM, e.g. matrix of inter/inter block probabilities when model is Bernoulli
- **covarParam**: vector of regression parameters associated with the covariates.
- **covarList**: list of matrices of covariates
- **covarEffect**: effect of covariates
- **netMatrix**: the matrix (adjacency or incidence) encoding the network

Methods

**Public methods:**

- **SBM$new()**
- **SBM$plot()**
- **SBM$show()**
- **SBM$print()**
- **SBM$clone()**

**Method new()**: constructor for SBM

*Usage:*

```r
SBM$new(
  model = "",
  dimension = numeric(2),
  blockProp = numeric(0),
  connectParam = list(mean = matrix()),
  covarParam = numeric(length(covarList)),
  covarList = list()
)
```

*Arguments:*

- **model**: character describing the type of model
- **dimension**: dimension of the network matrix
- **blockProp**: parameters for block proportions (vector of list of vectors)
- **connectParam**: list of parameters for connectivity
- **covarParam**: optional vector of covariates effect
- **covarList**: optional list of covariates data

**Method plot()**: basic matrix plot method for SBM object

*Usage:*
SBM$plot(
    type = c("data", "expected"),
    ordered = TRUE,
    rowLabel = NULL,
    colLabel = NULL
)

Arguments:
- **type** character for the type of plot: either 'data' (true connection) or 'expected' (fitted connection). Default to 'data'.
- **ordered** logical: should the rows and columns be reordered according to the clustering? Default to TRUE.
- **rowLabel** character: type of the individual in row. Default to NULL.
- **colLabel** character: type of the individual in col. Default to NULL.

Returns: a ggplot2 object

**Method** `show()`: print method

*Usage:*
SBM$show(type = "Stochastic Block Model")

**Arguments:**
- **type** character to tune the displayed name

**Method** `print()`: print method

*Usage:*
SBM$print()

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

*Usage:*
SBM$clone(deep = FALSE)

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

---

**SBM_fit**

*R6 virtual class for SBM fit (mother class of Simple and Bipartite SBM fit)*

---

**Description**

R6 virtual class for SBM fit (mother class of Simple and Bipartite SBM fit)

R6 virtual class for SBM fit (mother class of Simple and Bipartite SBM fit)

**Super class**

`sbm::SBM` -> `SBM_fit`
Active bindings

- probMemberships: matrix – or list of 2 matrices for Bipartite network – of estimated probabilities for block memberships for all nodes
- loglik: double: approximation of the log-likelihood (variational lower bound) reached
- ICL: double: value of the integrated classification log-likelihood
- expectation: expected values of connection under the currently adjusted model
- fitted: matrix of predicted value of the network

Methods

Public methods:

- `SBM_fit$new()`
- `SBM_fit$show()`
- `SBM_fit$setModel()`
- `SBM_fit$clone()`

Method `new()`: constructor for SBM fit

Usage:
```
SBM_fit$new(data, model, covarList)
```

Arguments:
- `data`: the data matrix of the network
- `model`: character describing the type of model
- `covarList`: optional list of matrices for covariates

Method `show()`: print/show method

Usage:
```
SBM_fit$show(type = "Fit of a Stochastic Block Model")
```

Arguments:
- `type`: character to tune the displayed name

Method `setModel()`: method to select a specific model among the ones fitted during the optimization. Fields of the current SBM_fit will be updated accordingly.

Usage:
```
SBM_fit$setModel(index)
```

Arguments:
- `index`: integer, the index of the model to be selected (row number in storedModels)

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

Usage:
```
SBM_fit$clone(deep = FALSE)
```

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

R6 class for SBM sampler

R6 class for SBM sampler

**Super class**

`sbm::SBM -> SBM_sampler`

**Active bindings**

- `variance` variance of each dyad under the current model

**Methods**

**Public methods:**

- `SBM_sampler$new()`
- `SBM_sampler$show()`
- `SBM_sampler$clone()`

**Method new(): constructor for SBM**

*Usage:*

```r
SBM_sampler$new(
  model,
  nbNodes,
  blockProp,
  connectParam,
  covarParam = numeric(0),
  covarList = list()
)
```

*Arguments:*

- `model` character describing the type of model
- `nbNodes` number of nodes in the network
- `blockProp` parameters for block proportions (vector of list of vectors)
- `connectParam` list of parameters for connectivity with a matrix of means 'mean' and an optional scalar for the variance 'var'. The dimensions of mu must match blockProp lengths
- `covarParam` optional vector of covariates effect
- `covarList` optional list of covariates data

**Method show(): print/show method**

*Usage:*

```r
```
SBM_sampler$show(type = "Sampler for a Stochastic Block Model")

**Arguments:**
- `type` character to tune the displayed name

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

**Usage:**
SBM_sampler$clone(deep = FALSE)

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

---

### SimpleSBM_fit

**R6 Class definition of an Simple SBM fit**

#### Description

R6 Class definition of an Simple SBM fit

R6 Class definition of an Simple SBM fit

#### Details

This class is designed to give a representation and adjust an SBM fitted with blockmodels.

#### Super classes

`sbm::SBM` $-> `sbm::SBM_fit` $-> `SimpleSBM_fit`

#### Active bindings

- `nbNodes` number of nodes
- `nbBlocks` number of blocks
- `nbDyads` number of dyads (potential edges in the network)
- `memberships` vector of clustering
- `directed` is the network directed or not
- `storedModels` data.frame of all models fitted (and stored) during the optimization

#### Methods

**Public methods:**
- `SimpleSBM_fit$new()`
- `SimpleSBM_fit$optimize()
- `SimpleSBM_fit$predict()
- `SimpleSBM_fit$reorder()
- `SimpleSBM_fit$show()`
SimpleSBM_fit$clone()

**Method** `new()`: constructor for a Simple SBM fit

*Usage:*

```
SimpleSBM_fit$new(adjacencyMatrix, model, directed, covarList = list())
```

*Arguments:*

- `adjacencyMatrix`: square (weighted) matrix
- `model`: character (`'bernoulli'`, `'poisson'`, `'gaussian'`)
- `directed`: logical, directed network or not. In not, `adjacencyMatrix` must be symmetric.
- `covarList`: and optional list of covariates, each of whom must have the same dimension as `adjacencyMatrix`

**Method** `optimize()`: function to perform optimization

*Usage:*

```
SimpleSBM_fit$optimize(
  verbosity = 3,
  plot = FALSE,
  explorFactor = 1.5,
  nbBlocksRange = c(4, Inf),
  nbCores = 2,
  fast = TRUE
)
```

*Arguments:*

- `verbosity`: integer, the level of verbosity. Default to 3
- `plot`: logical, if TRUE plotting is done dynamically on the screen. Default to TRUE
- `explorFactor`: double factor for exploring successive model
- `nbBlocksRange`: 2-size vector: range of exploration
- `nbCores`: integer, the number of cores to use. Default is 2.
- `fast`: logical: should approximation be used for Bernoulli model with covariates. Default to TRUE

**Method** `predict()`: prediction under the currently estimated model

*Usage:*

```
SimpleSBM_fit$predict(covarList = self$covarList)
```

*Arguments:*

- `covarList`: a list of covariates. By default, we use the covariates with which the model was estimated

*Returns: a matrix of expected values for each dyad*

**Method** `reorder()`: permute group labels by order of decreasing probability

*Usage:*

```
SimpleSBM_fit$reorder()
```

**Method** `show()`: show method
Usage:
SimpleSBM_fit$show(type = "Fit of a Simple Stochastic Block Model")

Arguments:
type character used to specify the type of SBM

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

Arguments:
depth Whether to make a deep clone.

---

SimpleSBM_sampler R6 class for Simple SBM sampler

Description
R6 class for Simple SBM sampler
R6 class for Simple SBM sampler

Super classes

  sbm::SBM -> sbm::SBM_sampler -> SimpleSBM_sampler

Active bindings

  nbNodes number of nodes
  nbBlocks number of blocks
  nbDyads number of dyads (potential edges in the network)
  memberships vector of clustering
  indMemberships matrix for clustering memberships
  expectation expected values of connection under the current model
  directed is the network directed or not

Methods

Public methods:

  * SimpleSBM_sampler$new()
  * SimpleSBM_sampler$rMemberships()
  * SimpleSBM_sampler$rAdjacency()
  * SimpleSBM_sampler$show()
  * SimpleSBM_sampler$clone()

Method new(): constructor for SBM
Usage:
SimpleSBM_sampler$new(
  model,
  nbNodes,
  directed,
  blockProp,
  connectParam,
  covarParam = numeric(0),
  covarList = list()
)

Arguments:
model character describing the type of model
nbNodes number of nodes in the network
directed logical, directed network or not.
blockProp parameters for block proportions (vector of list of vectors)
connectParam list of parameters for connectivity with a matrix of means 'mean' and an optional scalar for the variance 'var'. The size of mu must match blockProp length
covarParam optional vector of covariates effect
covarList optional list of covariates data

Method rMemberships(): a method to generate a vector of block indicators
  Usage:
  SimpleSBM_sampler$rMemberships()
  Returns: nothing (sampled memberships is stored in the current object)

Method rAdjacency(): a method to sample an adjacency matrix for the current SBM
  Usage:
  SimpleSBM_sampler$rAdjacency()
  Returns: nothing (sampled adjacency matrix is stored in the current object)

Method show(): show method
  Usage:
  SimpleSBM_sampler$show(type = "Sampler for a Simple Stochastic Block Model")
  Arguments:
  type character used to specify the type of SBM

Method clone(): The objects of this class are cloneable with this method.
  Usage:
  SimpleSBM_sampler$clone(deep = FALSE)
  Arguments:
  deep Whether to make a deep clone.
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