

Package ‘SBMSplitMerge’

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Title Inference for a Generalised SBM with a Split Merge Sampler

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Description Inference in a Bayesian framework for a generalised stochastic block model. The generalised stochastic block model (SBM) can capture group structure in network data without requiring conjugate priors on the edge-states. Two sampling methods are provided to perform inference on edge parameters and block structure: a split-merge Markov chain Monte Carlo algorithm and a Dirichlet process sampler. Green, Richardson (2001) <doi:10.1111/1467-9469.00242>; Neal (2000) <doi:10.1080/10618600.2000.10474879>; Ludkin (2019) <doi:10.48550/arXiv.1909.09421>.

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accept	<i>accept propsbm with the acceptance probability alpha</i>
--------	---

Description

accept propsbm with the acceptance probability alpha

Usage

```
accept(currsbm, propsbm, edges, sbmmmod, logjac = 0, logu = 0, ...)
```

Arguments

currsbm	current sbm state
propsbm	proposed sbm state
edges	an edges object
sbmmod	an sbmmod model
logjac	log Jacobian of transformation of variables
logu	log density for auxiliary variables
...	additional arguments to pass to dedges

Value

updated sbm object

addblock	<i>Add a block move</i>
----------	-------------------------

Description

proposes adding an empty block labelled kappa+1 to sbm

Usage

```
addblock(sbm, edges, sbmmod, rho = 1)
```

Arguments

sbm	the current state of the sampler
edges	an edges object
sbmmod	an sbmmod model
rho	probability of choosing to add a block

Value

an updated sbm object

ARI	<i>Adjusted Rand Index</i>
-----	----------------------------

Description

Calculate the Adjusted Rand Index between two clusterings

Usage

```
ARI(z, truez)
```

Arguments

z	input vector
truez	reference vector

Value

Adjusted Rand Index of z against truez

Examples

```
ARI(c(1,1,2,2,3,3), c(2,2,1,1,3,3)) ## 1 - doesn't care for labels  
ARI(c(1,1,2,2,3,3), c(1,1,1,1,2,2)) ## 0.444
```

blockmat	<i>Block matrix</i>
----------	---------------------

Description

converts x to a matrix of block assignments

Usage

```
blockmat(x, ...)
```

Arguments

x	object for dispatch
...	additional arguments for method

Value

matrix of block assignment indicators

See Also

[blockmat.sbm](#) [blockmat.blocks](#) [blockmat.numeric](#)

blockmat.blocks	<i>Block matrix</i>
-----------------	---------------------

Description

converts block assignments of a blocks object to a matrix of block assignments

Usage

```
## S3 method for class 'blocks'
blockmat(blocks, kappa)
```

Arguments

blocks	a blocks object
kappa	number of blocks in matrix

Value

matrix with kappa rows and a 1 at (k, i) if node i is in block k under blocks

blockmat.numeric	<i>Block matrix</i>
------------------	---------------------

Description

converts a vector of block assignments to a matrix of block assignments

Usage

```
## S3 method for class 'numeric'
blockmat(x, kappa)

## S3 method for class 'factor'
blockmat(x, kappa)
```

Arguments

x	a numeric-vector of node-to-block assignments
kappa	number of blocks

Value

matrix with kappa rows and a 1 at (k, i) if node i is in block k under x

blockmat.sbm	<i>Block matrix</i>
--------------	---------------------

Description

converts block assignments of an sbm object to a matrix of block assignments

Usage

```
## S3 method for class 'sbm'
blockmat(SBM, kappa)
```

Arguments

SBM	an sbm object
kappa	number of blocks in matrix

Value

matrix with kappa rows and a 1 at (k, i) if node i is in block k under SBM

blockmod	<i>Block Model</i>
----------	--------------------

Description

create a blockmod object

Usage

```
blockmod(fixkappa, logd, dcond, r, ...)
```

Arguments

fixkappa	Logical - is kappa fixed or can it vary under the model?
logd	function(blocks) - log density for blocks
dcond	function(blocks, i) - conditional density for the block assignment i in blocks
r	function(n), sorted=FALSE - samples a blocks object from the model
...	parameters of the model for use in r, logd, dcond

Details

A block model is a probability model for a blocks object. This class creates a closure with three functions: - a random method for sampling block a structure from the model with n nodes; a - a log-density method for computing the log-density of a given block structure in a blocks object - a conditional density function that takes a blocks object and a node i

Value

a blockmod object

See Also

[multinom dma crp blocks](#)

blocks	<i>Blocks object</i>
--------	----------------------

Description

create a blocks object

Usage

blocks(z, kappa)

Arguments

z	vector of block labels for each node
kappa	maximum number of blocks

Details

stores the block allocations and total number of blocks for a stochastic block model

Value

a blocks object

Examples

```
## Assign six nodes to four blocks:
b <- blocks(c(1,1,2,3,4,4), 4)
print(b)
plot(b) ## shows id two nodes are members of the same block
```

blocktrace	<i>plot a trace of the blocks from MCMC samples</i>
------------	---

Description

plot a trace of the blocks from MCMC samples

Usage

```
blocktrace(postz, burnin)
```

Arguments

postz	output from sampler
burnin	which iterations to plot? defaults to all.

Value

‘ggplot2’ object

crp	<i>Chinese Restaurant Process</i>
-----	-----------------------------------

Description

A [blockmod](#) for the Chinese restaurant process (CRP)

Usage

```
crp(gamma)
```

Arguments

gamma	concentration parameter
-------	-------------------------

Details

The CRP posits that each node arrives in turn. The first node joins the first block. Each subsequent node starts a new block with probability ‘gamma’ or joins an existing block proportional to the block size.

Value

a block model representing a CRP(gamma) distribution

Examples

```
## simulate from a CRP(5) prior
m <- crp(5)
print(m)
m$r(10)
```

ddirichlet	<i>Dirichlet distribution</i>
------------	-------------------------------

Description

Density of Dirichlet distribution

Usage

```
ddirichlet(x, gam, log = FALSE)
```

Arguments

x	random variable in the d-dimensional simplex
gam	a length K concentration parameter
log	return the log-probability instead?

Value

the density

Examples

```
g <- rep(2,5)
p <- rdirichlet(1, g) ## a length-5 probability vector
ddirichlet(p, g)
```

dedges	<i>Density of edges</i>
--------	-------------------------

Description

Compute the probability density for an [edges](#) object

Usage

```
dedges(x, edges, edgemod, na.rm = TRUE, ...)
```

Arguments

x	an R object for dispatch
edges	an edges object
edgemod	an edgemod object
na.rm	remove NAs when calculating?
...	additional arguments

Value

matrix same size as edges\$E with density of each edge

See Also

[dedges.sbm](#) [dedges.sbm](#)

dedges.numeric	<i>likelihood of edges</i>
----------------	----------------------------

Description

likelihood of edges

Usage

```
## S3 method for class 'numeric'
dedges(x, edges, edgemod, na.rm = na.rm, ...)
```

Arguments

x	a matrix of parameters (with same size as edges\$E)
edges	an edges object
edgemod	an edgemod object
na.rm	remove NAs when calculating?
...	additional arguments passed to edgemod\$logd

Value

likelihood of edges under the [edgemod](#) using parameters in matrix pmat

dedges.sbm	<i>Density of edges</i>
------------	-------------------------

Description

Compute the probability density for an [edges](#) object under an [sbm](#) object

Usage

```
## S3 method for class 'sbm'
dedges(x, edges, edgemod, na.rm = TRUE, ...)
```

Arguments

x	an sbm object
edges	an edges object
edgemod	an edgemod object
na.rm	remove NAs when calculating?
...	additional arguments for <code>dedges.params</code>

Value

matrix same size as `edges$E` with density of each edge

Examples

```
## make an sbm model, sample data then plot and print:
model <- sbmmod(dma(2,5), param_beta(1,1,1,1), edges_bern())
s <- model$r(100)
e <- redges(s, model$edge)
dedges(s, e, model$edge)
```

delblock	<i>Delete a block move</i>
----------	----------------------------

Description

proposes deleting an empty block (chosen at random among empty Blocks)

Usage

```
delblock(sbm, edges, sbmmod, rho = 1)
```

Arguments

sbm	the current state of the sampler
edges	an edges object
sbmmod	an sbmmod model
rho	probability of choosing to add a block

Value

an updated sbm object

dma	<i>Dirichlet Multinomial Allocation</i>
-----	---

Description

A [blockmod](#) for Dirichlet Multinomial Allocation (DMA)

Usage

```
dma(gamma, delta)
```

Arguments

gamma	parameter for Dirichlet component
delta	parameter for Poisson component

Details

This model posits:

$$\begin{aligned} & \kappa - 1 \text{ Pois}(\delta) \\ & \omega | \kappa, \gamma \text{ Dirichlet}(\gamma) \\ & Z_i | \omega \text{ Multinomial}(\omega) \text{ for } i = 1..n \end{aligned}$$

Value

a block model representing a dma(gamma, delta) distribution

Examples

```
## simulate from a DMA(2, 5) prior
## This models the `number of blocks-1` as Poisson(5)
## and block assignments as Dirichlet-Multinomial(2, 2, ...)
m <- dma(2, 5)
print(m)
m$r(10)
```

drawblock.dp	<i>Draw block membership</i>
--------------	------------------------------

Description

Draw block membership in a Dirichlet process sampler

Usage

```
drawblock.dp(i, currsbm, edges, sbmmod)
```

Arguments

i	node to update
currsbm	current sbm object
edges	an edges object
sbmmod	an sbmmod object

Details

sample a new block assignment for i under a Dirichlet process. Care needs to be taken with singleton blocks to update the parameter model in currsbm.

Value

updated sbm object

See Also

For full algorithm details see <http://doi.org/10.17635/lanaster/thesis/296>

drawblock.gibbs	<i>Gibbs-like reassignment of nodes to the current set of blocks</i>
-----------------	--

Description

Reassign node 'i' to the current set of blocks given the current number of blocks and the other block assignments

Usage

```
drawblock.gibbs(i, currsbm, edges, sbmmod)
```

Arguments

i	the node to reassign
currsbm	an sbm object
edges	an edges object
sbmmod	an sbmmod object

Value

updated sbm object with new block assignment for i

drawblocks.dp	<i>Draw block memberships</i>
---------------	-------------------------------

Description

Draw block memberships in a Dirichlet process sampler

Usage

```
drawblocks.dp(currsbm, edges, sbmmod)
```

Arguments

currsbm	current sbm object
edges	an edges object
sbmmod	an sbmmod object

Details

iteratively updates the block assignment of each node using a Dirichlet process update move

Value

updated sbm object

drawblocks.gibbs	<i>Gibbs-like reassignment of nodes to the current set of blocks</i>
------------------	--

Description

Sweep through the set of nodes and reassign to the current set of blocks given the current number of blocks

Usage

```
drawblocks.gibbs(currsbm, edges, sbmmod)
```

Arguments

currsbm	an sbm object
edges	an edges object
sbmmod	an sbmmod object

Value

updated [sbm](#) object with new block assignments

drawparams	<i>Metropolis updates by drawing parameters</i>
------------	---

Description

Simulate parameters for the given model with a Metropolis-Hastings step

Usage

```
drawparams(sbm, edges, sbmmod, sigma = 0.1)
```

Arguments

sbm	current sbm object
edges	an edges
sbmmod	an sbmmod
sigma	parameter for drawparam

Details

iterate through the parameters in currsbm and update.

Value

updated sbm object

edgemo	<i>Class for edge models</i>
--------	------------------------------

Description

A class with a random and density method for edges objects

Usage

```
edgemo(logd, r, ...)
```

Arguments

logd	function(e, p) to calculate likelihood of edge an edge e given parameter array p
r	function(p) - simulate an edge given a parameter p (optional)
...	additional arguments to append to edgemo internal list

Value

an edgemo object

Note

the parameter for logd is an array of c(dimension of theta, dim(E)) e.g. from [parammat](#)

See Also

[edges_bern](#) [edges_pois](#) [edges_norm](#)

edges	<i>Class for edge data</i>
-------	----------------------------

Description

A class to hold edge data

Usage

```
edges(e, sym, loops, ...)
```

Arguments

e	a matrix or array representing the raw edge-state data
sym	is the network symmetric? (e[ji] = e[ji])
loops	does the network contain self-loops? (edges from node i to i)
...	additional arguments to append to edges internal list

Value

an edges object

Examples

```
## make an sbm model, sample data then plot and print:
model <- sbmmod(dma(2,5), param_beta(1,1,1,1), edges_bern())
s <- model$r(100)
e <- redges(s, model$edge)
plot(e)
plot(e, s)
print(e)
```

edges_bern

Bernoulli edge model

Description

Make an edgemod model with Bernoulli edge-states

Usage

```
edges_bern(...)
```

Arguments

... additional parameters to pass to rbinom

Value

an edgemod

Examples

```
eb <- edges_bern() ## makes `eb` an edgemod for Bernoulli edge-states
```

edges_nbin	<i>Negative-Binomial edge model</i>
------------	-------------------------------------

Description

Make an edgemod model with Negative-Binomial edge-states

Usage

```
edges_nbin(...)
```

Arguments

... additional parameters to pass to `rnbinom`

Value

an edgemod

Examples

```
enb <- edges_nbin() ## makes `enb` an edgemod for Negative-Binomial edge-states
```

edges_norm	<i>Normal edge model</i>
------------	--------------------------

Description

Make an edgemod model with Normal edge-states

Usage

```
edges_norm(...)
```

Arguments

... additional parameters to pass to `rnorm`

Value

an edgemod

Examples

```
en <- edges_norm() ## makes `en` an edgemod for Normal edge-states
```

edges_pois

Poisson edge model

Description

Make an edgemod model with Poisson edge-states

Usage

```
edges_pois(...)
```

Arguments

... additional parameters to pass to rpois

Value

an edgemod

Examples

```
ep <- edges_pois() ## makes `ep` an edgemod for Poisson edge-states
```

Enron

The Enron data set as extracted from igraph using the script in data-raw

Description

A data set of counts of emails between email addresses This is a non-symmetric network. Nodes represent email address. The edge-state ij between two email addresses i and j is the number of emails sent from i to j The Groups vector is the node label from the igraph attribute "notes"

Usage

```
Enron
```

Format

A list containing

Edges an edges object with each edge-state representing the number of emails between two email addresses

Groups A vector giving a group name to which the email address belong. The order matches the edges such that $Edges[i,j]$ is the edge-state between the nodes i and nodes j who are members of $Groups[i]$ and $Groups[j]$ respectively

Source

<https://cran.r-project.org/package=igraphdata>

eval_plots	<i>get a set of evaluation plots from MCMC samples</i>
------------	--

Description

get a set of evaluation plots from MCMC samples

Usage

```
eval_plots(output, burnin, theta_index)
```

Arguments

output	from sampler
burnin	burn-in period (a vector of iteration numbers to subset outputs)
theta_index	which set of thetas to plot?

Value

list of ggplot objects (with descriptive names)

is.sbm	<i>is.sbm</i>
--------	---------------

Description

Logical check if an object is an `sbm` object

Usage

```
is.sbm(x)
```

Arguments

x	an R object
---	-------------

Value

Logical indicating if x is an `sbm` object

Macaque	<i>The Macaque data set as extracted from igraph using the script in data-raw</i>
---------	---

Description

The Macaque data set as extracted from igraph using the script in data-raw

Usage

Macaque

Format

An edges object of activation counts between brain regions in a Macaque

See Also

igraph

<i>marglike_bern</i>	<i>Marginal likelihood model for Bernoulli distributed edges</i>
----------------------	--

Description

calculate the marginal likelihood for a node for samplers using conjugate models

Usage

`marglike_bern(znoi, ei, parammod)`

Arguments

- `znoi` a matrix of block assignments without node `i`
- `ei` edge-states incident to `i`
- `parammod` a `parammod` object representing the Bernoulli-Beta model

Value

log-probability of node `i` belonging to each block

marglike_norm	<i>Marginal likelihood model for Normal distributed edges</i>
---------------	---

Description

calculate the marginal likelihood for a node for samplers using conjugate models

Usage

```
marglike_norm(znoi, ei, parammod)
```

Arguments

znoi	a matrix of block assignments without node i
ei	edge-states incident to i
parammod	a parammod object

Value

log-probability of node i belonging to each block

marglike_pois	<i>Marginal likelihood model for Poisson distributed edges</i>
---------------	--

Description

calculate the marginal likelihood for a node for samplers using conjugate models

Usage

```
marglike_pois(znoi, ei, parammod)
```

Arguments

znoi	a matrix of block assignments without node i
ei	edge-states incident to i
parammod	a parammod object

Value

log-probability of node i belonging to each block

mergeavg

Merge blocks

Description

Merge-move using an average to merge parameters

Usage

```
mergeavg(sbm, edges, sbmmod, ...)
```

Arguments

sbm	the current state of the sampler
edges	an edges object
sbmmod	an sbmmod model
...	additional parameter to 'accept'

Details

the blocks are chosen at random, the nodes reassigned to the block with the smallest index, then the parameters are combined using the average on the transformed scale

Value

an updated sbm object

mergeblocks

merge move block merging

Description

merge move block merging

Usage

```
mergeblocks(currblocks, propparams, edges, sbmmod, k, l)
```

Arguments

currblocks	current blocks
propparams	proposed parameters
edges	an edges object
sbmmod	an sbmmod model
k	Blocks to merge
l	Blocks to merge

Value

list(proposed block structure, log-acceptance-prob)

mergeparams	<i>merge parameters</i>
-------------	-------------------------

Description

merge parameters

Usage

mergeparams(x, ...)

Arguments

x	an object to dispatch on
...	additional arguments for methods

Value

merged parameters from x

See Also

[mergeparams.default](#) [mergeparams.numeric](#)

mergeparams.default	<i>Merge step: parameters</i>
---------------------	-------------------------------

Description

Merge step: parameters

Usage

```
## Default S3 method:  
mergeparams(params, k, l, parammod)
```

Arguments

params	a params object
k	Blocks to merge
l	Blocks to merge
parammod	a parammod object

Value

```
list(proposed_params, log-acceptance-prob)
```

mergeparams.numeric	<i>Merge step - parameter merging</i>
---------------------	---------------------------------------

Description

Merge step - parameter merging

Usage

```
## S3 method for class 'numeric'
mergeparams(thetak, thetal, x, parammod)
```

Arguments

thetak, thetal	parameters to merge
x	auxiliary parameter
parammod	a parammod object

Value

```
list(proposed_params, log-acceptance-prob)
```

modeblocks	<i>modal block assignments from MCMC samples</i>
------------	--

Description

modal block assignments from MCMC samples

Usage

```
modeblocks(postz)
```

Arguments

postz	output from sampler
-------	---------------------

Value

a blocks object with the modal block assignments under postz

multinom	<i>Multinomial block assignment</i>
----------	-------------------------------------

Description

A `blockmod` for Multinomial allocation

Usage

```
multinom(gamma, kappa)
```

Arguments

gamma	parameter for Dirichlet component $Dirichlet(gamma, \dots, gamma)$
kappa	the number of blocks

Details

This model posits that: for $i=1:n$

$$Z_i \sim Multinomial(\omega)$$

where

$$\omega \sim Dirichlet(gamma)$$

Value

a block model representing a Multinomial(gamma) distribution

Examples

```
## A fixed number of blocks with multinomial assignment of nodes
m <- multinom(1, 4)
print(m)
m$r(10) ## simulate a blocks object with 10 nodes
```

nodelike	<i>Likelihood of node assignment</i>
----------	--------------------------------------

Description

Calculate the likelihood of a node belonging to each of block

Usage

```
nodelike(blocks, params, edges, i, sbmmmod, ...)
```

Arguments

blocks	an blocks object
params	an params object
edges	an edges object
i	the node of interest
sbmmmod	an sbmmmod object
...	additional arguments for <code>node1ike.blocks</code>

Details

the number of blocks considered is either the number of blocks in `sbm` (κ) or $\kappa+1$ when `sbmmmod` has a variable number of blocks. care is taken for data which is directed and with loops.

Value

likelihood of edges emanating from node `i`

numblockstrace	<i>plot a trace of the number of blocks from MCMC samples</i>
----------------	---

Description

plot a trace of the number of blocks from MCMC samples

Usage

```
numblockstrace(postk, burnin)
```

Arguments

postk	output from sampler
burnin	which iterations to plot? defaults to all.

Value

‘ggplot2’ object

parammat	<i>Parameter Matrix</i>
----------	-------------------------

Description

Make a matrix of parameters

Usage

```
parammat(x, ...)
```

Arguments

x	object for dispatch
...	additional arguments for method

Value

a parameter matrix object

parammat.blocks	<i>Parameter Matrix</i>
-----------------	-------------------------

Description

Make a matrix of parameters from a blocks and params object

Usage

```
## S3 method for class 'blocks'
parammat(x, params, ...)
```

Arguments

x	a blocks object
params	a params object
...	(unused)

Value

an NxN matrix P, with $P[i, j]$ = the parameter governing edge i j

parammat.matrix	<i>Parameter Matrix</i>
-----------------	-------------------------

Description

Make a matrix of parameters from a matrix of block assignments

Usage

```
## S3 method for class 'matrix'  
parammat(zleft, zright, params, ...)
```

Arguments

zleft	block assignment matrix on the left
zright	block assignment matrix on the right
params	the parameters object
...	(unused)

Value

a matrix of parameters of size |zleft| x |zright|

parammat.params	<i>Parameter Matrix</i>
-----------------	-------------------------

Description

Make a matrix of parameters from a params object

Usage

```
## S3 method for class 'params'  
parammat(x, kappa, ...)
```

Arguments

x	a params object
kappa	- number of blocks to compute for matrix (optional)
...	(unused)

Value

a matrix of parameters

parammat.sbm

Parameter Matrix

Description

Make a matrix of parameters from an sbm object

Usage

```
## S3 method for class 'sbm'
parammat(x, ...)
```

Arguments

x an sbm object
... (unused)

Value

a matrix of parameters

parammod

Parameter Model

Description

create a parammod object

Usage

```
parammod(logd, r, t, invt, loggradt, ...)
```

Arguments

logd function(params) - log-density function for parameters
r function(kappa) - random function to draw parameters
t mapping parameter space to real line
invt mapping real line to parameter space
loggradt log of the gradient of mapping t
... additional arguments to store in the parammod object

Details

A parameter model is a probability model for a params object. This class creates a closure with five functions: - a random method for sampling a params object - a log-density method for computing the log-density of a given params object - a transformation function t that maps a parameter value to the real line - the inverse of t - the log-gradient of t

Value

a parammod object

See Also

[param_beta](#) [param_gamma](#) [param_nbin](#) [param_norm](#)

params	params <i>S3 object</i>
--------	-------------------------

Description

make a params object from the between-block parameter theta0 and a vector of within block parameters thetak

Usage

params(theta0, thetak)

Arguments

theta0	between block parameters - a vector of length ‘dimension of theta’
thetak	within block parameters - a matrix with ncol=kappa and nrow=dimension of theta

Value

a params object

Examples

```
p <- params(0.1, c(0.2,0.4,0.5))
p
```

paramtrace	<i>plot a trace of parameter values from MCMC samples</i>
------------	---

Description

plot a trace of parameter values from MCMC samples

Usage

```
paramtrace(theta, range, burnin)
```

Arguments

theta	output from sampler
range	which thetas to plot? defaults to all.
burnin	which iterations to plot? defaults to all.

Value

‘ggplot2’ object

param_beta	<i>Beta parameter model</i>
------------	-----------------------------

Description

A parammod with beta-distributed parameters

Usage

```
param_beta(a0, a1, b0, b1)
```

Arguments

a0	$\theta_0 \sim \text{Beta}(a_0, a_1)$
a1	$\theta_0 \sim \text{Beta}(a_0, a_1)$
b0	$\theta_k \sim \text{Beta}(b_0, b_1)$
b1	$\theta_k \sim \text{Beta}(b_0, b_1)$

Details

This model represents a prior on theta with:

$$\theta_0 \sim \text{Beta}(a_0, a_1)$$

$$\theta_k \sim \text{Beta}(b_0, b_1)$$

for $k = 1 \dots \text{kappa}$

Value

a parammod

Examples

```
## theta0 ~ Beta(1,9); thetak ~ Beta(9,1)
pb <- param_beta(1,9,9,1)
pb$r(5) ## a draw with 5 within-block parameters
```

param_gamma	<i>Gamma parameter model</i>
-------------	------------------------------

Description

A parammod with gamma-distributed parameters

Usage

```
param_gamma(a0, a1, b0, b1)
```

Arguments

- a0 $\theta_0 \sim \text{Gamma}(a_0, a_1)$
- a1 $\theta_0 \sim \text{Gamma}(a_0, a_1)$
- b0 $\theta_k \sim \text{Gamma}(b_0, b_1)$
- b1 $\theta_k \sim \text{Gamma}(b_0, b_1)$

Details

This model represents a prior on theta with:

$$\theta_0 \sim \text{Gamma}(a_0, a_1)$$
$$\theta_k \sim \text{Gamma}(b_0, b_1)$$

for $k = 1 \dots \kappa$

Value

a parammod

Examples

```
## theta0 ~ Gamma(1,1); thetak ~ Gamma(5,5)
pg <- param_gamma(1,1,5,5)
pg$r(5) ## a draw with 5 within-block parameters
```

param_nbin	<i>Parameter model for Negative Binomial</i>
------------	--

Description

Negative Binomial parameter model: $\theta_0 = (\mu_0, \sigma_0)$ $\theta_k = (\mu_k, \sigma_k)$

Usage

```
param_nbin(a0, a1, b0, b1, c0, c1, d0, d1)
```

Arguments

a0, a1	$\mu_0 \sim \text{Gamma}(a_0, a_1)$
b0, b1	$\sigma_0 \sim \text{Beta}(b_0, b_1)$
c0, c1	$\mu_k \sim \text{Gamma}(c_0, c_1)$
d0, d1	$\sigma_k \sim \text{Beta}(d_0, d_1)$

Value

parammod representing Negative-Binomial distributed parameters

Examples

```
## theta0 = (r0, p0); r0~Gamma(1,1); p0 ~ Beta(1,1);
## thetak = (rk, pk); rk~Gamma(3,3); pk ~ Beta(5,5);
pn <- param_nbin(1,1,1,1,3,3,5,5)
pn$r(5) ## a draw with 5 within-block parameters
```

param_norm	<i>Parameter model for Normal Model</i>
------------	---

Description

Normal parameter model: $\theta_0 = (\mu_0, \sigma_0)$ $\theta_k = (\mu_k, \sigma_k)$

Usage

```
param_norm(a0, a1, b0, b1, c0, c1, d0, d1)
```

Arguments

a0, a1	$\mu_0 \sim \text{Normal}(a_0, a_1)$
b0, b1	$\sigma_0 \sim \text{Gamma}(b_0, b_1)$
c0, c1	$\mu_k \sim \text{Normal}(c_0, c_1)$
d0, d1	$\sigma_k \sim \text{Gamma}(d_0, d_1)$

Value

parammod representing Normal distributed parameters

Examples

```
## theta0 = (mu0, sigma0); mu0~Normal(0,5); sigma0 ~ Gamma(1,1);
## thetak = (muk, sigmak); muk~Normal(0,3); sigmak ~ Gamma(5,2);
pn <- param_norm(0,5,1,1,0,3,5,2)
pn$r(5) ## a draw with 5 within-block parameters
```

plot.blocks

Plot blocks

Description

plots a block object

Usage

```
## S3 method for class 'blocks'
plot(x, col, xaxt = "n", yaxt = "n", xlab = "Nodes", ylab = "Nodes", ...)

## S3 method for class 'blocks'
image(x, col, xaxt = "n", yaxt = "n", xlab = "Nodes", ylab = "Nodes", ...)
```

Arguments

x	a blocks object to plot
col	colours for the plot
xaxt	override image parameters
yaxt	override image parameters
xlab	override image parameters
ylab	override image parameters
...	additional parameters for image

Details

plot the block assignments in a blocks object as a matrix, color-coded by block membership

Examples

```
## Assign six nodes to four blocks:
b <- blocks(c(1,1,2,3,4,4), 4)
plot(b)
## note that the lower left corner has one 2x2 red square
## indicating node 1 and 2 belong to the same block
```

`plot.edges`*Plot*

Description

plots an `edges` objects

Usage

```
## S3 method for class 'edges'
plot(x, Blocks, sorted = TRUE, xlab = "Node", ylab = "Node", ...)

## S3 method for class 'edges'
image(x, Blocks, sorted = TRUE, xlab = "Node", ylab = "Node", ...)
```

Arguments

<code>x</code>	an <code>edges</code> object
<code>Blocks</code>	a blocks object or <code>sbm</code> object
<code>sorted</code>	sort by block membership in <code>sbm</code> before plotting?
<code>xlab</code>	label for x-axis
<code>ylab</code>	label for y-axis
<code>...</code>	parameters for image

Value

ggplot2 plot of edges in a raster

Examples

```
## make an sbm model, sample data then plot and print:
model <- sbmmod(dma(2,5), param_beta(1,1,1,1), edges_bern())
s <- model$r(100)
e <- redges(s, model$edge)
plot(e)
plot(e, s)
print(e)
```

plot.sbm	<i>Plot for sbm object</i>
----------	--

Description

plot an [sbm](#) object as an image

Usage

```
## S3 method for class 'sbm'  
plot(x, col, ...)
```

```
## S3 method for class 'sbm'  
image(x, col, ...)
```

Arguments

x	an sbm object
col	colours for each block - if missing, rainbow is used
...	additional arguments for plot

See Also

plot.default

plotpostpairs	<i>helper function for trace plots</i>
---------------	--

Description

helper function for trace plots

Usage

```
plotpostpairs(mat)
```

Arguments

mat	matrix to plot as an image using ggplot2
-----	--

Value

‘ggplot2’ plot objecy

postpairs	<i>mean proportion of times two nodes were in the same block under MCMC samples</i>
-----------	---

Description

mean proportion of times two nodes were in the same block under MCMC samples

Usage

```
postpairs(postz)
```

Arguments

postz	output from sampler
-------	---------------------

Value

matrix P with $P[i,j]$ = proportion of times i and j are in the same block under postz

rcat	<i>Draw draw Categorical distribution</i>
------	---

Description

Draw draw Categorical distribution

Usage

```
rcat(n, p, replace = TRUE)
```

Arguments

n	number of draws
p	a length-d probability vector
replace	should the categories be replaced? If so n < p required

Value

a draw from Categorical(p)

Examples

```
rcat(1, 1) ## returns 1 with probability 1
rcat(1, rep(1/6,6)) ## a dice roll
```

rdirichlet	<i>Dirichlet distribution</i>
------------	-------------------------------

Description

Draw from Dirichlet distribution

Usage

```
rdirichlet(n, gam)
```

Arguments

n	number of variates to draw
gam	a vector of concentration parameters of length K

Value

matrix dimension n*k of samples

Examples

```
rdirichlet(1, rep(2,5)) ## a length-5 probability vector
```

redges	<i>Simulate edges</i>
--------	-----------------------

Description

Simulate edges from an [sbm](#) object with a given [edgemod](#)

Usage

```
redges(SBM, edgemod, sym = TRUE, loops = FALSE, ...)
```

Arguments

SBM	an sbm object
edgemod	an edgemod object
sym	should the network be symmetric?
loops	should the network have self-loops?
...	additional arguments passed to <code>edgemod\$r</code>

Details

None

Value

an edges object

Examples

```
## make an sbm model, sample data then plot and print:
model <- sbmmod(dma(2,5), param_beta(1,1,1,1), edges_bern())
s <- model$r(100)
e <- redges(s, model$edge)
plot(e)
plot(e, s)
print(e)
```

rw	<i>Random Walk</i>
----	--------------------

Description

performs a random walk on a parameter value with a given parameter model

Usage

```
rw(p, pm, sigma)
```

Arguments

p	a parameter
pm	a parammod object
sigma	- scale of random walk

Value

```
ist(proposed parameter, locjacobian)
```

sampler	<i>top level sampler function</i>
---------	-----------------------------------

Description

top level sampler function

Usage

```
sampler(
  edges,
  sbmmod,
  nSteps = 1000,
  algorithm = "rj",
  sigma = 0.5,
  statusfreq,
  currsbm,
  ...
)
```

Arguments

edges	an edges object
sbmmod	an sbmmod model
nSteps	number of steps to run sampler
algorithm	choice of algorithm options are: "conjugate", "gibbs", "dp", "rj"
sigma	random walk parameter for theta
statusfreq	print the elapsed number of iterations every statusfreq iterations
currsbm	initial state for sbm object (optional - one is drawn from sbmmod if not supplied)
...	additional parameters to pass to step

Value

postz traces for block assignments z

postt traces for theta

postk traces for number of blocks kappa

postn traces for number of occupied blocks

nsteps number of iterations of chain

algorithm choice

Examples

```
## see vignette("Weibull-edges")
```

sampler.conj	<i>Conjugate model sampler</i>
--------------	--------------------------------

Description

Conjugate model sampler

Usage

```
sampler.conj(currsbm, edges, sbmmod, sigma = NULL, ...)
```

Arguments

currsbm	the current state of the sampler
edges	an edges object
sbmmod	an sbmmod model
sigma	unused
...	additional arguments for sbmmod\$marglike

Value

next state of currsbm object

Note

If using the CRP as the block model, then this is the IRM sampler of Schmidt or Morup (Schmidt, M.N. and Morup, M., 2013. Nonparametric Bayesian modeling of complex networks: An introduction. IEEE Signal Processing Magazine, 30(3), pp.110-128.)

Examples

```
model <- sbmmod(crp(3), param_beta(1,1,1,1), edges_bern(), marglike=marglike_bern)
trueSBM <- model$r(100)
Edges <- redges(trueSBM, model$edge)
out <- sampler(Edges, model, 10, "conjugate")
```

sampler.dp	<i>Dirichlet process sampler</i>
------------	----------------------------------

Description

Dirichlet process sampler

Usage

```
sampler.dp(currsbm, edges, sbmmod, sigma)
```

Arguments

currsbm	the current state of the sampler
edges	an edges object
sbmmod	an sbmmod model
sigma	random walk parameter for theta

Value

next state of currsbm object

See Also

For full algorithm details see <http://doi.org/10.17635/lancaster/thesis/296>

Examples

```
model <- sbmmod(crp(4), param_norm(0,0,1,1,3,3,1,1), edges_norm())
trueSBM <- model$r(100)
Edges <- redges(trueSBM, model$edge)
dp_out <- sampler(Edges, model, 25, "dp", sigma=0.1)
```

sampler.gibbs	<i>Gibbs sampling for node assignments</i>
---------------	--

Description

Gibbs sampling for node assignments

Usage

```
sampler.gibbs(currsbm, edges, sbmmod, sigma)
```

Arguments

currsbm	the current state of the sampler
edges	an edges object
sbmmod	an sbmmod model
sigma	random walk parameter for theta

Value

next state of currsbm object

Note

This requires a block model with a fixed kappa

Examples

```
model <- sbmmod(multinom(1, 3), param_gamma(1,1,1,1), edges_pois())
trueSBM <- model$r(10)
Edges <- redges(trueSBM, model$edge)
gibbs_out <- sampler(Edges, model, algorithm="gibbs", 10, sigma=0.1)
eval_plots(gibbs_out)
```

sampler.rj

reversible jump Markov chain Monte Carlo split-merge sampler

Description

reversible jump Markov chain Monte Carlo split-merge sampler

Usage

```
sampler.rj(currsbm, edges, sbmmod, sigma, rho = 10)
```

Arguments

currsbm	the current state of the sampler
edges	an edges object
sbmmod	an sbmmod model
sigma	random walk parameter for theta
rho	propensity to add a block

Value

next state of currsbm object

See Also

For full algorithm details see <http://doi.org/10.17635/lancaster/thesis/296>

Examples

```
model <- sbmmod(dma(1,10), param_nbin(1,1,4,4,0.5,0.5,0.5,0.5), edges_nbin())
trueSBM <- model$r(100)
Edges <- redges(trueSBM, model$edge)
rj_out <- sampler(Edges, model, 10, "rj", sigma=0.1)
```

sbm	<i>Class sbm</i>
-----	------------------

Description

Class sbm

Usage

```
sbm(blocks, params)
```

Arguments

- blocks a blocks object
- params a params object

Value

an sbm object

Examples

```
sbm(blocks(c(1,1,2,2,3,3)), params(0.1, c(0.4,0.5,0.6)))
```

sbmmod	<i>Stochastic block model object</i>
--------	--------------------------------------

Description

A wrapper for a block and parameter model

Usage

```
sbmmod(blockmod, parammod, edgemod, ...)
```

Arguments

blockmod	a blockmod object
parammod	a parammod object
edgemod	an edgemod object
...	additional arguments to store in the sbmmod object

Details

Simple wrapper for the block and parameter model for an sbm object

Value

an sbmmod object with a method 'r(n)' sampling an sbm object with n nodes from the model and a method logd(sbm) computing the log-density of sbm under the model

Author(s)

Matthew Ludkin

See Also

[blockmod](#) [parammod](#) [edgemod](#)

splitavg

split move using average to merge parameters

Description

split move using average to merge parameters

Usage

```
splitavg(sbm, edges, sbmmod, ...)
```

Arguments

sbm	the current state of the sampler
edges	an edges object
sbmmod	an sbmmod model
...	additional parameter to 'accept'

Value

an updated sbm object

splitblocks	<i>split move: blocks</i>
-------------	---------------------------

Description

split move: blocks

Usage

splitblocks(currblocks, propparams, edges, sbmmod, k)

Arguments

- currblocks current blocks
- propparams proposed parameters
- edges an edges object
- sbmmod a model list
- k block to split

Value

list(proposed block structure, log-acceptance-prob)

splitparams	<i>split move: parameters</i>
-------------	-------------------------------

Description

split move: parameters

Usage

splitparams(x, ...)

Arguments

- x object for dispatch
- ... additional arguments for method

Value

list(proposed_params, log-acceptance-prob)

splitparams.numeric	<i>split move:</i> params
---------------------	---------------------------

Description

split move: params

Usage

```
## S3 method for class 'numeric'  
splitparams(theta, u, x, parammod)
```

Arguments

theta	a parameter to split
u	auxiliary variable
x	auxiliary variable
parammod	parammod object

Value

list(proposed_params, log-acceptance-prob)

splitparams.params	<i>split move:</i> params
--------------------	---------------------------

Description

split move: params

Usage

```
## S3 method for class 'params'  
splitparams(params, k, parammod)
```

Arguments

params	a params object to split
k	block to split
parammod	parammod object

Value

list(proposed_params, log-acceptance-prob)

StackOverflow	<i>The Stack-Overflow data set as extracted from igraph using the script in data-raw</i> Extracted on 27/8/2019 from Kaggle (login required) using: <code>library(rvest)</code> <code>read_html("https://www.kaggle.com/stackoverflow/stack-overflow-tag-network/dow</code>
---------------	--

Description

The Stack-Overflow data set as extracted from igraph using the script in data-raw Extracted on 27/8/2019 from Kaggle (login required) using: `library(rvest)` `read_html("https://www.kaggle.com/stackoverflow/`

Usage

`StackOverflow`

Format

An edges object of activation counts between brain regions in a Macaque

Source

<https://www.kaggle.com/stackoverflow/stack-overflow-tag-network/>

See Also

`igraph`

updateblock	<i>Update the block assignment of a node</i>
-------------	--

Description

change the block assignment in `x` of a node to a new block

Usage

`updateblock(x, ...)`

Arguments

- `x` object for dispatch
- `...` additional arguments for method

Value

object like ‘`x`’ with updated block structure

See Also

[updateblock.blocks](#) [updateblock.sbm](#)

updateblock.blocks	<i>Update the block assignment of a node</i>
--------------------	--

Description

change the block assignment in an blocks object to a new block

Usage

```
## S3 method for class 'blocks'  
updateblock(blocks, i, newblock)
```

Arguments

- blocks a [blocks](#) object
- i the node to update
- newblock the new block for node i

Value

new blocks object

updateblock.sbm	<i>Update the block assignment of a node</i>
-----------------	--

Description

change the block assignment in an sbm object to a new block

Usage

```
## S3 method for class 'sbm'  
updateblock(currsbm, i, newblock, model)
```

Arguments

- currsbm an [sbm](#) object
- i the node to update
- newblock the new block for node i
- model an [sbmmod](#) object

Value

new sbm object

Note

If adding a new block, this draws from the prior

vmeasure	<i>V-measure</i>
----------	------------------

Description

Calculate the V-measure of two clusterings

Usage

```
vmeasure(z, truez, beta = 1)
```

Arguments

z	input vector
truez	reference vector
beta	parameter beta=1 gives equal weight to homogeneity and completeness

Details

An information based measure of similarity between two clusterings

Value

v-measure of z against truez

See Also

Rosenberg, A., & Hirschberg, J. (2007, June). V-measure: A conditional entropy-based external cluster evaluation measure. In Proceedings of the 2007 joint conference on empirical methods in natural language processing and computational natural language learning (EMNLP-CoNLL) (pp. 410-420).

Examples

```
vmeasure(c(1,1,2,2,3,3), c(2,2,1,1,3,3)) ## 1 - doesn't care for labels
vmeasure(c(1,1,2,2,3,3), c(1,1,2,2,2,2)) ## 0.7333
vmeasure(c(1,1,2,2,3,3), c(1,1,2,2,3,4)) ## 0.904
```

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