

Package ‘AntMAN’

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Author Priscilla Ong [aut, edt],
Raffaele Argiento [aut],
Bruno Bodin [aut, cre],
Maria De Iorio [aut]

Maintainer Bruno Bodin <bruno.bodin@yale-nus.edu.sg>

Description Fits finite Bayesian mixture models with a random number of components. The MCMC algorithm implemented is based on point processes as proposed by Argiento and De Iorio (2019) <doi:10.48550/arXiv.1904.09733> and offers a more computationally efficient alternative to reversible jump. Different mixture kernels can be specified: univariate Gaussian, multivariate Gaussian, univariate Poisson, and multivariate Bernoulli (latent class analysis). For the parameters characterising the mixture kernel, we specify conjugate priors, with possibly user specified hyper-parameters. We allow for different choices for the prior on the number of components: shifted Poisson, negative binomial, and point masses (i.e. mixtures with fixed number of components).

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URL <https://github.com/bbodin/AntMAN>

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AM_clustering	<i>Return the clustering matrix</i>
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Description

Given an [AM_mcmc_output](#) object, this function returns the clustering matrix.

Usage

AM_clustering(fit)

Arguments

fit an [AM_mcmc_output](#) object.

Details

The clustering matrix is an M by n matrix. Each of the M rows represents a clustering of n items using cluster labels. Items i and j are in the same cluster if fit[m,i] == fit[m,j] for the mth clustering.

Value

A numeric clustering matrix

See Also

[AM_coclustering](#)

Examples

```
fit = AM_demo_uvp_poi()$fit
ccm <- AM_clustering(fit)
```

AM_coclustering	<i>Return the co-clustering matrix</i>
-----------------	--

Description

Given an [AM_mcmc_output](#) object, this function returns the co-clustering matrix.

Usage

```
AM_coclustering(fit)
```

Arguments

`fit` an [AM_mcmc_output](#) object.

Details

The co-clustering matrix is produced by the simultaneous clustering of the rows and columns. Each entry denotes the (posterior) probability that items i and j are together. This technique is also known as bi-clustering and block clustering (Govaert and Nadif 2013), and is useful for understanding the number of clusters in the dataset.

Value

A numeric co-clustering matrix

See Also

[AM_clustering](#)

Examples

```
fit = AM_demo_uvp_poi()$fit
ccm <- AM_coclustering(fit)
```

AM_demo_mvb_poi	<i>Returns an example of AM_mcmc_fit output produced by the multi-variate bernoulli model</i>
-----------------	---

Description

This function allows us to generate a sample output of fitting the multivariate Bernoulli model. No arguments are needed to be passed. The purpose of this function is to serve as a demo for users to understand the model's output, without diving too deep into details. By default, this demo generates a sample dataset of dimension 500x4, where the MCMC sampler is specified to run for 2000 iterations, with a burn-in of 1000, and a thinning interval of 10. All possible outputs that can be produced by [AM_mcmc_fit](#) are returned (see return value below).

Usage

```
AM_demo_mvb_poi()
```

Value

A list containing the following items:

- the vector (or matrix) containing the synthetic data used to fit the model.
- the vector containing the final cluster assignment of each observation.
- an [AM_mcmc_output](#) object, which is the typical output of [AM_mcmc_fit](#).

Examples

```
mvb_output <- AM_demo_mvb_poi()
```

AM_demo_mvn_poi	Returns an example of AM_mcmc_fit output produced by the multi-variate gaussian model
-----------------	---

Description

This function allows us to generate a sample output of fitting the multivariate Gaussian model. No arguments are needed to be passed. The purpose of this function is to serve as a demo for users to understand the model's output, without diving too deep into details. By default, this demo generates a sample dataset of dimension 500x2, where the MCMC sampler is specified to run for 2000 iterations, with a burn-in of 1000, and a thinning interval of 10. All possible outputs that can be produced by [AM_mcmc_fit](#) are returned (see return value below).

Usage

```
AM_demo_mvn_poi()
```

Value

A list containing the following items:

- the vector (or matrix) containing the synthetic data used to fit the model.
- the vector containing the final cluster assignment of each observation.
- an [AM_mcmc_output](#) object, which is the typical output of [AM_mcmc_fit](#).

Examples

```
mvn_output <- AM_demo_mvn_poi()
```

AM_demo_uvn_poi	Returns an example of AM_mcmc_fit output produced by the univariate Gaussian model
-----------------	--

Description

This function allows us to generate a sample output of fitting the univariate gaussian model. No arguments are needed to be passed. The purpose of this function is to serve as a demo for users to understand the model's output, without diving too deep into details. By default, this demo generates a sample dataset of dimension 500x1, where the MCMC sampler is specified to run for 2000 iterations, with a burn-in of 1000, and a thinning interval of 10. All possible outputs that can be produced by [AM_mcmc_fit](#) are returned (see return value below).

Usage

```
AM_demo_uvn_poi()
```

Value

A list containing the following items:

- the vector (or matrix) containing the synthetic data used to fit the model.
- the vector containing the final cluster assignment of each observation.
- an [AM_mcmc_output](#) object, which is the typical output of [AM_mcmc_fit](#).

Examples

```
mvn_output <- AM_demo_uvn_poi()
```

AM_demo_uvp_poi	Returns an example of AM_mcmc_fit output produced by the univariate Poisson model
-----------------	---

Description

This function allows us to generate a sample output of fitting the univariate poisson model. No arguments are needed to be passed. The purpose of this function is to serve as a demo for users to understand the model's output, without diving too deep into details. By default, this demo generates a sample dataset of dimension 500x1, where the MCMC sampler is specified to run for 2000 iterations, with a burn-in of 1000, and a thinning interval of 10. All possible outputs that can be produced by [AM_mcmc_fit](#) are returned (see return value below).

Usage

```
AM_demo_uvp_poi()
```

Value

A list containing the following items:

- the vector (or matrix) containing the synthetic data used to fit the model.
- the vector containing the final cluster assignment of each observation.
- an [AM_mcmc_output](#) object, which is the typical output of [AM_mcmc_fit](#).

Examples

```
mvn_output <- AM_demo_uvn_poi()
```

AM_emp_bayes_uninorm	<i>compute the hyperparameters of an Normal-Inverse-Gamma distribution using an empirical Bayes approach</i>
----------------------	--

Description

This function computes the hyperparameters of a Normal Inverse-Gamma distribution using an empirical Bayes approach. More information about how these hyperparameters are determined can be found here: *Bayes and empirical Bayes: do they merge?* (Petrone et al. 2012).

Usage

```
AM_emp_bayes_uninorm(y, scEmu = 1, scEsig2 = 3, CVsig2 = 3)
```

Arguments

y	The data y. If y is univariate, a vector is expected. Otherwise, y should be a matrix.
scEmu	a positive value (default=1) such that marginally $E(\mu) = s^2 * \text{scEmu}$, where s^2 is the sample variance.
scEsig2	a positive value (default=3) such that marginally $E(\sigma^2) = s^2 * \text{scEsig2}$, where s^2 is the sample variance.
CVsig2	The coefficient of variation of σ^2 (default=3).

Value

an object of class [AM_mix_hyperparams](#), in which hyperparameters $m0$, $k0$, $nu0$ and $sig02$ are specified. To understand the usage of these hyperparameters, please refer to [AM_mix_hyperparams_uninorm](#).

AM_extract	<i>Extract values within a <code>AM_mcmc_output</code> object</i>
------------	---

Description

Given an `AM_mcmc_output` object, as well as the target variable names, `AM_extract` will return a list of the variables of interest.

Usage

```
AM_extract(object, targets, iterations = NULL, debug = FALSE)
```

Arguments

<code>object</code>	an <code>AM_mcmc_output</code> object.
<code>targets</code>	List of variables to extract (ie. K, M, mu).
<code>iterations</code>	Can specify particular iterations to extracts, NULL for all.
<code>debug</code>	Activate log to.

Details

Due to the complexity of AntMAN outputs, `AM_mcmc_output` object can be difficult to handle. The `AM_extract` function eases access of particular variables within the `AM_mcmc_output` object. Variables of varying dimension are expected to result from the transdimensional moves. When considering such variables, the extracted list would correspond to an $n \times 1$ list, where n refers to the number of extracted iterations. Each of these $n \times 1$ entries consists of another list of dimension $m \times 1$, where m specifies the number of components inferred for that iteration.

Value

a list of variables specified in `targets`.

AM_find_gamma_Delta	<i>Given that the prior on M is a dirac delta, find the γ hyperparameter of the weights prior to match $E(K) = K^*$, where K^* is user-specified</i>
---------------------	---

Description

Once a fixed value of the number of components M^* is specified, this function adopts a *bisection method* to find the value of γ such that the induced distribution on the number of clusters is centered around a user specified value K^* , i.e. the function uses a bisection method to solve for γ (Argiento and Iorio 2019). The user can provide a lower γ_l and an upper γ_u bound for the possible values of γ . The default values are $\gamma_l = 10^{-3}$ and $\gamma_u = 10$. A default value for the tolerance is $\epsilon = 0.1$. Moreover, after a maximum number of iteration (default is 31), the function stops warning that convergence has not been reached.

Usage

```
AM_find_gamma_Delta(
  n,
  Mstar,
  Kstar = 6,
  gam_min = 1e-04,
  gam_max = 10,
  tolerance = 0.1
)
```

Arguments

n	sample size.
Mstar	number of components of the mixture.
Kstar	mean number of clusters the user wants to specify.
gam_min	lower bound of the interval in which gamma should lie (default 1e-4).
gam_max	upper bound of the interval in which gamma should lie (default 10).
tolerance	Level of tolerance for the method.

Value

A value of gamma such that $E(K) = K^*$

Examples

```
n <- 82
Mstar <- 12
gam_de <- AM_find_gamma_Delta(n,Mstar,Kstar=6, gam_min=1e-4,gam_max=10, tolerance=0.1)
prior_K_de <- AM_prior_K_Delta(n,gam_de,Mstar)
prior_K_de%%1:n
```

AM_find_gamma_NegBin	<i>Given that the prior on M is a Negative Binomial, find the γ hyper-parameter of the weights prior to match $E(K) = K^*$, where K^* is user-specified</i>
----------------------	---

Description

Once the prior on the number of mixture components M is assumed to be a Negative Binomial with parameter $r > 0$ and $0 < p < 1$, with mean is $1 + r \cdot p / (1 - p)$, this function adopts a *bisection method* to find the value of gamma such that the induced distribution on the number of clusters is centered around a user specified value K^* , i.e. the function uses a bisection method to solve for γ (Argiento and Iorio 2019). The user can provide a lower γ_l and an upper γ_u bound for the possible values of γ . The default values are $\gamma_l = 10^{-3}$ and $\gamma_u = 10$. A default value for the tolerance is $\epsilon = 0.1$. Moreover, after a maximum number of iteration (default is 31), the function stops warning that convergence has not been reached.

Usage

```
AM_find_gamma_NegBin(
  n,
  r,
  p,
  Kstar = 6,
  gam_min = 0.001,
  gam_max = 10000,
  tolerance = 0.1
)
```

Arguments

n	The sample size.
r	The dispersion parameter r of the Negative Binomial.
p	The probability of failure parameter p of the Negative Binomial.
Kstar	The mean number of clusters the user wants to specify.
gam_min	The lower bound of the interval in which gamma should lie.
gam_max	The upper bound of the interval in which gamma should lie.
tolerance	Level of tolerance of the method.

Value

A value of gamma such that $E(K) = K^*$

Examples

```
n <- 82
r <- 1
p <- 0.8571
gam_nb= AM_find_gamma_NegBin(n,r,p,Kstar=6, gam_min=0.001,gam_max=10000, tolerance=0.1)
prior_K_nb= AM_prior_K_NegBin(n,gam_nb, r, p)
prior_K_nb%%1:n
```

AM_find_gamma_Pois	<i>Given that the prior on M is a shifted Poisson, find the γ hyperparameter of the weights prior to match $E(K) = K^*$, where K^* is user-specified</i>
--------------------	--

Description

Once the prior on the number of mixture components M is assumed to be a Shifted Poisson of parameter Lambda, this function adopts a *bisection method* to find the value of γ such that the induced distribution on the number of clusters is centered around a user specified value K^* , i.e. the function uses a bisection method to solve for γ (Argiento and Iorio 2019). The user can provide a lower γ_l and an upper γ_u bound for the possible values of γ . The default values are $\gamma_l = 10^{-3}$ and $\gamma_u = 10$. A default value for the tolerance is $\epsilon = 0.1$. Moreover, after a maximum number of iteration (default is 31), the function stops warning that convergence has not been reached.

Usage

```
AM_find_gamma_Pois(
  n,
  Lambda,
  Kstar = 6,
  gam_min = 1e-04,
  gam_max = 10,
  tolerance = 0.1
)
```

Arguments

n	The sample size.
Lambda	The parameter of the Shifted Poisson for the number of components of the mixture.
Kstar	The mean number of clusters the user wants to specify.
gam_min	The lower bound of the interval in which gamma should lie.
gam_max	The upper bound of the interval in which gamma should lie.
tolerance	Level of tolerance of the method.

Value

A value of gamma such that $E(K) = K^*$

Examples

```
n <- 82
Lam <- 11
gam_po <- AM_find_gamma_Pois(n,Lam,Kstar=6, gam_min=0.0001,gam_max=10, tolerance=0.1)
prior_K_po <- AM_prior_K_Pois(n,gam_po,Lam)
prior_K_po%%1:n
```

AM_mcmc_configuration *S3 class AM_mcmc_configuration*

Description

Output type of return values from [AM_mcmc_parameters](#).

Value

[AM_mcmc_configuration](#)

See Also

[AM_mcmc_fit](#)

AM_mcmc_fit

Performs a Gibbs sampling

Description

The `AM_mcmc_fit` function performs a Gibbs sampling in order to estimate the mixture comprising the sample data `y`. The mixture selected must be of a predefined type `mix_kernel_hyperparams` (defined with `AM_mix_hyperparams_*` functions, where star `*` denotes the chosen kernel). Additionally, a prior distribution on the number of mixture components must be specified through `mix_components_prior` (generated with `AM_mix_components_prior_*` functions, where `*` denotes the chosen prior). Similarly, a prior on the weights of the mixture should be specified through `mix_weight_prior` (defined with `AM_mix_weights_prior_*` functions). Finally, with `mcmc_parameters`, the user sets the MCMC parameters for the Gibbs sampler (defined with [AM_mcmc_parameters](#) functions).

Usage

```
AM_mcmc_fit(
  y,
  mix_kernel_hyperparams,
  initial_clustering = NULL,
  init_K = NULL,
  fixed_clustering = NULL,
  mix_components_prior = AM_mix_components_prior_pois(),
  mix_weight_prior = AM_mix_weights_prior_gamma(),
  mcmc_parameters = AM_mcmc_parameters()
)
```

Arguments

<code>y</code>	input data, can be a vector or a matrix.
<code>mix_kernel_hyperparams</code>	is a configuration list, defined by <code>*_mix_hyperparams</code> functions, where <code>*</code> denotes the chosen kernel. See AM_mix_hyperparams_multiber , AM_mix_hyperparams_multinorm , AM_mix_hyperparams_uninorm , AM_mix_hyperparams_unipois for more details.
<code>initial_clustering</code>	is a vector CI of initial cluster assignement. If no clustering is specified (either as <code>init_K</code> or <code>init_clustering</code>), then every observation is assigned to its own cluster.
<code>init_K</code>	initial value for the number of cluster. When this is specified, AntMAN initialises the clustering assign usng K-means.
<code>fixed_clustering</code>	if specified, this is the vector CI containing the cluster assignments. This will remain unchanged for every iteration.

- `mix_components_prior`
 is a configuration list defined by `AM_mix_components_prior_*` functions, where * denotes the chosen prior. See [AM_mix_components_prior_dirac](#), [AM_mix_components_prior_negbin](#), [AM_mix_components_prior_pois](#) for more details.
- `mix_weight_prior`
 is a configuration list defined by `AM_weight_prior_*` functions, where * denotes the chosen prior specification. See [AM_mix_weights_prior_gamma](#) for more details.
- `mcmc_parameters`
 is a configuration list defined by `AM_mcmc_parameters`. See [AM_mcmc_parameters](#) for more details.

Details

If no initial clustering is specified (either as `init_K` or `init_clustering`), then every observation is allocated to a different cluster. If `init_K` is specified then AntMAN initialises the clustering through K-means.

Warning: if the user does not specify `init_K` or `initial_cluster`, the first steps can be time-consuming because of default setting of the initial clustering.

Value

The return value is an [AM_mcmc_output](#) object.

Examples

```
AM_mcmc_fit( AM_sample_unipois()$y,
             AM_mix_hyperparams_unipois (alpha0=2, beta0=0.2),
             mcmc_parameters = AM_mcmc_parameters(niter=50, burnin=0, thin=1, verbose=0))
```

AM_mcmc_output	<i>S3 class AM_mcmc_output</i>
----------------	--------------------------------

Description

Output type of return values from [AM_mcmc_fit](#).

Value

[AM_mcmc_output](#)

See Also

[AM_mcmc_fit](#)

AM_mcmc_parameters	<i>MCMC Parameters</i>
--------------------	------------------------

Description

This function generates an MCMC parameters list to be used as `mcmc_parameters` argument within [AM_mcmc_fit](#).

Usage

```
AM_mcmc_parameters(
  niter = 5000,
  burnin = 2500,
  thin = 1,
  verbose = 1,
  output = c("CI", "K"),
  parallel = TRUE,
  output_dir = NULL
)
```

Arguments

<code>niter</code>	Total number of MCMC iterations to be carried out.
<code>burnin</code>	Number of iterations to be considered as burn-in. Samples from this burn-in period are discarded.
<code>thin</code>	Thinning rate. This argument specifies how often a draw from the posterior distribution is stored after burnin, i.e. one every -th samples is saved. Therefore, the total number of MCMC samples saved is $(niter - burnin)/thin$. If <code>thin = 1</code> , then AntMAN stores every iteration.
<code>verbose</code>	A value from 0 to 4, that specifies the desired level of verbosity (0:None, 1:Warnings, 2:Debug, 3:Extras).
<code>output</code>	A list of parameters output to return.
<code>parallel</code>	Some of the algorithms can be run in parallel using OpenMP. When set to True, this parameter triggers the parallelism.
<code>output_dir</code>	Path to an output dir, where to store all the outputs.

Value

An [AM_mcmc_configuration](#) Object. This is a list to be used as `mcmc_parameters` argument with [AM_mcmc_fit](#).

Examples

```
AM_mcmc_parameters (niter=1000, burnin=10000, thin=50)
AM_mcmc_parameters (niter=1000, burnin=10000, thin=50, output=c("CI", "W", "TAU"))
```

AM_mcmc_refit

*Performs a Gibbs sampling reusing previous configuration***Description**

Similar to [AM_mcmc_fit](#), the `AM_mcmc_refit` function performs a Gibbs sampling in order to estimate a mixture. However parameters will be reused from a previous result from [AM_mcmc_fit](#).

Usage

```
AM_mcmc_refit(y, fit, fixed_clustering, mcmc_parameters = AM_mcmc_parameters())
```

Arguments

`y` input data, can be a vector or a matrix.

`fit` previous output from [AM_mcmc_fit](#) that is used to setup kernel and priors.

`fixed_clustering` is a vector CI of cluster assignment that will remain unchanged for every iterations.

`mcmc_parameters` is a configuration list defined by [AM_mcmc_parameters](#).

Details

In practice this function will call `AM_mcmc_fit(y, fixed_clustering = fixed_clustering, ...)`; with the same parameters as previously specified.

Value

The return value is an [AM_mcmc_output](#) object.

Examples

```
y = AM_sample_unipois()$y
fit = AM_mcmc_fit( y ,
  AM_mix_hyperparams_unipois (alpha0=2, beta0=0.2),
  mcmc_parameters = AM_mcmc_parameters(niter=20, burnin=0, thin=1, verbose=0))
eam = AM_coclustering(fit)
cluster = AM_salso(eam, "binder")
refit = AM_mcmc_refit(y , fit, cluster,
  mcmc_parameters = AM_mcmc_parameters(niter=20, burnin=0, thin=1, verbose=0));
```

AM_mix_components_prior

S3 class AM_mix_components_prior

Description

Object returned by AM_mix_components_prior_*.

Value

[AM_mix_components_prior](#)

See Also

[AM_mix_components_prior_dirac](#), [AM_mix_components_prior_negbin](#), [AM_mix_components_prior_pois](#)

AM_mix_components_prior_dirac

Generate a configuration object that contains a Point mass prior

Description

Generate a configuration object that assigns a Point mass prior to the number of mixture components. This is the simplest option and it requires users to specify a value M^* such that $Pr(M = M^*) = 1$.

Usage

```
AM_mix_components_prior_dirac(Mstar)
```

Arguments

Mstar Fixed value M^* for the number of components.

Value

An [AM_mix_components_prior](#) object. This is a configuration list to be used as mix_components_prior argument for [AM_mcmc_fit](#).

See Also

[AM_mcmc_fit](#)

Examples

```
AM_mix_components_prior_dirac (Mstar=3)
```

AM_mix_components_prior_negbin

Generate a configuration object for a Shifted Negative Binomial prior on the number of mixture components

Description

This generates a configuration object for a Shifted Negative Binomial prior on the number of mixture components such that

$$q_M(m) = Pr(M = m) = \frac{\Gamma(r + m - 1)}{(m - 1)! \Gamma(r)} p^{m-1} (1 - p)^r, \quad m = 1, 2, 3, \dots$$

The hyperparameters $p \in (0, 1)$ (probability of success) and $r > 0$ (size) can either be fixed using `r` and `p` or assigned appropriate prior distributions. In the latter case, we assume $p \sim \text{Beta}(a_P, b_P)$ and $r \sim \text{Gamma}(a_R, b_R)$. In AntMAN we assume the following parametrization of the Gamma density:

$$p(x \mid a, b) = \frac{b^a x^{a-1}}{\Gamma(a)} \exp\{-bx\}, \quad x > 0.$$

Usage

```
AM_mix_components_prior_negbin(
  a_R = NULL,
  b_R = NULL,
  a_P = NULL,
  b_P = NULL,
  R = NULL,
  P = NULL,
  init_R = NULL,
  init_P = NULL
)
```

Arguments

<code>a_R</code>	The shape parameter a of the $\text{Gamma}(a, b)$ prior distribution for r .
<code>b_R</code>	The rate parameter b of the $\text{Gamma}(a, b)$ prior distribution for r .
<code>a_P</code>	The parameter a of the $\text{Beta}(a, b)$ prior distribution for p .
<code>b_P</code>	The parameter b of the $\text{Beta}(a, b)$ prior distribution for p .
<code>R</code>	It allows to fix r to a specific value.
<code>P</code>	It allows to fix p to a specific value.
<code>init_R</code>	The initial value of r , when specifying <code>a_R</code> and <code>b_R</code> .
<code>init_P</code>	The initial value of p , when specifying <code>a_P</code> and <code>b_P</code> .

Details

If no arguments are provided, the default is $r = 1, a_P = 1, b_P = 1$.

Additionally, when `init_R` and `init_P` are not specified, there are default values: $init_R = 1$ and $init_P = 0.5$.

Value

An `AM_mix_components_prior` object. This is a configuration list to be used as `mix_components_prior` argument for `AM_mcmc_fit`.

See Also

`AM_mcmc_fit`

Examples

```
AM_mix_components_prior_negbin (R=1, P=1)
AM_mix_components_prior_negbin ()
```

```
AM_mix_components_prior_pois
```

Generate a configuration object for a Poisson prior on the number of mixture components

Description

This function generates a configuration object for a Shifted Poisson prior on the number of mixture components such that

$$q_M(m) = \Pr(M = m) = \frac{e^{-\Lambda} \Lambda^{m-1}}{(m-1)!}, \quad m = 1, 2, 3, \dots$$

The hyperparameter Λ can either be fixed using `Lambda` or assigned a $\text{Gamma}(a, b)$ prior distribution with `a` and `b`. In AntMAN we assume the following parametrization of the Gamma density:

$$p(x \mid a, b) = \frac{b^a x^{a-1}}{\Gamma(a)} \exp\{-bx\}, \quad x > 0.$$

Usage

```
AM_mix_components_prior_pois(a = NULL, b = NULL, Lambda = NULL, init = NULL)
```

Arguments

<code>a</code>	The shape parameter a of the $\text{Gamma}(a, b)$ prior distribution.
<code>b</code>	The rate parameter b of the $\text{Gamma}(a, b)$ prior distribution.
<code>Lambda</code>	It allows to set the hyperparameter Λ to be assigned a fixed value.
<code>init</code>	The initial value for Λ , when specifying <code>a</code> and <code>b</code> .

Details

If no arguments are provided, the default is a prior distribution with $a = 1$ and $b = 1$.

Value

An `AM_mix_components_prior` object. This is a configuration list to be used as `mix_components_prior` argument for `AM_mcmc_fit`.

See Also

`AM_mcmc_fit`

Examples

```
components_prior = AM_mix_components_prior_pois (init=3, a=1, b=1)
```

AM_mix_hyperparams	<i>S3 class AM_mix_hyperparams</i>
--------------------	------------------------------------

Description

Object type returned by `AM_mix_hyperparams_*` commands.

Value

`AM_mix_hyperparams`

See Also

`AM_mix_hyperparams_unipois`, `AM_mix_hyperparams_uninorm`, `AM_mix_hyperparams_multiber`, `AM_mix_hyperparams_multinorm`

AM_mix_hyperparams_multiber	<i>multivariate Bernoulli mixture hyperparameters (Latent Class Analysis)</i>
-----------------------------	---

Description

Generate a configuration object that defines the prior hyperparameters for a mixture of multivariate Bernoulli. If the dimension of the data is P , then the prior is a product of P independent Beta distributions, $\text{Beta}(a_{0i}, b_{0i})$. Therefore, the vectors of hyperparameters, a_0 and b_0 , are P -dimensional. Default is $(a_0 = c(1, \dots, 1), b_0 = c(1, \dots, 1))$.

Usage

```
AM_mix_hyperparams_multiber(a0, b0)
```

Arguments

a0 The a0 hyperparameters.
b0 The b0 hyperparameters.

Value

An [AM_mix_hyperparams](#) object. This is a configuration list to be used as `mix_kernel_hyperparams` argument for [AM_mcmc_fit](#).

Examples

```
AM_mix_hyperparams_multiber (a0= c(1,1,1,1),b0= c(1,1,1,1))
```

AM_mix_hyperparams_multinorm

multivariate Normal mixture hyperparameters

Description

Generate a configuration object that specifies a multivariate Normal mixture kernel, where users can specify the hyperparameters for the conjugate prior of the multivariate Normal mixture. We assume that the data are d-dimensional vectors $\mathbf{y}_i$, where $\mathbf{y}_i$ are i.i.d Normal random variables with mean $\boldsymbol{\mu}$ and covariance matrix $\boldsymbol{\Sigma}$. The conjugate prior is

$$\pi(\boldsymbol{\mu}, \boldsymbol{\Sigma} \mid \mathbf{m}_0, \kappa_0, \nu_0, \boldsymbol{\Lambda}_0) = \pi_{\boldsymbol{\mu}}(\boldsymbol{\mu} \mid \boldsymbol{\Sigma}, \mathbf{m}_0, \kappa_0) \pi_{\boldsymbol{\Sigma}}(\boldsymbol{\Sigma} \mid \nu_0, \boldsymbol{\Lambda}_0),$$

$$\pi_{\boldsymbol{\mu}}(\boldsymbol{\mu} \mid \boldsymbol{\Sigma}, \mathbf{m}_0, \kappa_0) = \frac{\sqrt{\kappa_0^d}}{\sqrt{(2\pi)^d |\boldsymbol{\Sigma}|}} \exp\left(-\frac{\kappa_0}{2}(\boldsymbol{\mu} - \mathbf{m}_0)^T \boldsymbol{\Sigma}^{-1}(\boldsymbol{\mu} - \mathbf{m}_0)\right), \quad \boldsymbol{\mu} \in \mathcal{R}^d,$$

$$\pi_{\boldsymbol{\Sigma}}(\boldsymbol{\Sigma} \mid \nu_0, \boldsymbol{\Lambda}_0) = \frac{|\boldsymbol{\Lambda}_0|^{\nu_0/2}}{2^{\nu_0 d/2} \Gamma_d(\frac{\nu_0}{2})} |\boldsymbol{\Sigma}|^{-(\nu_0+d+1)/2} e^{-\frac{1}{2} \text{tr}(\boldsymbol{\Lambda}_0 \boldsymbol{\Sigma}^{-1})}, \quad \boldsymbol{\Sigma}^2 > 0,$$

where `mu0` corresponds to $\mathbf{m}_0$, `ka0` corresponds to κ_0 , `nu0` to ν_0 , and `Lam0` to $\boldsymbol{\Lambda}_0$.

Usage

```
AM_mix_hyperparams_multinorm(mu0 = NULL, ka0 = NULL, nu0 = NULL, Lam0 = NULL)
```

Arguments

mu0 The hyperparameter $\mathbf{m}_0$.
ka0 The hyperparameter κ_0 .
nu0 The hyperparameter ν_0 .
Lam0 The hyperparameter $\boldsymbol{\Lambda}_0$.

Details

Default is $(\mu_0=c(0, \dots, 0), \kappa_0=1, \nu_0=\text{Dim}+2, \text{Lam}_0=\text{diag}(\text{Dim}))$ with Dim is the dimension of the data y. We advise the user to set ν_0 equal to at least the dimension of the data, Dim, plus 2.

Value

An [AM_mix_hyperparams](#) object. This is a configuration list to be used as `mix_kernel_hyperparams` argument for [AM_mcmc_fit](#).

Examples

```
AM_mix_hyperparams_multinorm ()
```

AM_mix_hyperparams_uninorm
univariate Normal mixture hyperparameters

Description

Generate a configuration object that specifies a univariate Normal mixture kernel, where users can specify the hyperparameters of the Normal-InverseGamma conjugate prior. As such, the kernel is a Gaussian distribution with mean μ and variance σ^2 . The prior on (μ, σ^2) the Normal-InverseGamma:

$$\begin{aligned}\pi(\mu, \sigma^2 \mid m_0, \kappa_0, \nu_0, \sigma_0^2) &= \pi_\mu(\mu \mid \sigma^2, m_0, \kappa_0) \pi_{\sigma^2}(\sigma^2 \mid \nu_0, \sigma_0^2), \\ \pi_\mu(\mu \mid \sigma^2, m_0, \kappa_0) &= \frac{\sqrt{\kappa_0}}{\sqrt{2\pi\sigma^2}} \exp^{-\frac{\kappa_0}{2\sigma^2}(\mu - m_0)^2}, \quad \mu \in \mathcal{R}, \\ \pi_{\sigma^2}(\sigma^2 \mid \nu_0, \sigma_0^2) &= \frac{\sigma_0^{2\nu_0}}{\Gamma(\nu_0)} (1/\sigma^2)^{\nu_0+1} \exp\left(-\frac{\sigma_0^2}{\sigma^2}\right), \quad \sigma^2 > 0.\end{aligned}$$

Usage

```
AM_mix_hyperparams_uninorm(m0, k0, nu0, sig02)
```

Arguments

<code>m0</code>	The m_0 hyperparameter.
<code>k0</code>	The κ_0 hyperparameter.
<code>nu0</code>	The ν_0 hyperparameter.
<code>sig02</code>	The σ_0^2 hyperparameter.

Details

m_0 corresponds `m0`, κ_0 corresponds `k0`, ν_0 corresponds `nu0`, and σ_0^2 corresponds `sig02`.

If hyperparameters are not specified, the default is `m0=0`, `k0=1`, `nu0=3`, `sig02=1`.

Value

An `AM_mix_hyperparams` object. This is a configuration list to be used as `mix_kernel_hyperparams` argument for `AM_mcmc_fit`.

Examples

```
#### This example ...

data(galaxy)
y_uvn = galaxy
mixture_uvn_params = AM_mix_hyperparams_uninorm (m0=20.83146, k0=0.3333333,
                                                  nu0=4.222222, sig02=3.661027)

mcmc_params      = AM_mcmc_parameters(niter=2000, burnin=500, thin=10, verbose=0)
components_prior = AM_mix_components_prior_pois (init=3, a=1, b=1)
weights_prior    = AM_mix_weights_prior_gamma (init=2, a=1, b=1)

fit <- AM_mcmc_fit(
  y = y_uvn,
  mix_kernel_hyperparams = mixture_uvn_params,
  mix_components_prior = components_prior,
  mix_weight_prior = weights_prior,
  mcmc_parameters = mcmc_params)

summary (fit)
plot (fit)
```

AM_mix_hyperparams_unipois

univariate Poisson mixture hyperparameters

Description

Generate a configuration object that specifies a univariate Poisson mixture kernel, where users can specify the hyperparameters of the conjugate Gamma prior, i.e. the kernel is a $Poisson(\tau)$ and $\tau \sim Gamma(\alpha_0, \beta_0)$. In AntMAN we assume the following parametrization of the Gamma density:

$$p(x \mid a, b) = \frac{b^a x^{a-1}}{\Gamma(a)} \exp\{-bx\}, \quad x > 0.$$

Usage

```
AM_mix_hyperparams_unipois(alpha0, beta0)
```

Arguments

<code>alpha0</code>	The shape hyperparameter α_0 .
<code>beta0</code>	The rate hyperparameter β_0 .

Details

Note that by default, $\alpha_0=1$ and $\beta_0=1$.

Value

An [AM_mix_hyperparams](#) object. This is a configuration list to be used as `mix_kernel_hyperparams` argument for [AM_mcmc_fit](#).

Examples

```
AM_mix_hyperparams_unipois (alpha0=2, beta0=0.2)
```

AM_mix_weights_prior *S3 class AM_mix_weights_prior*

Description

Object type returned by `AM_mix_weights_prior_*` commands.

Value

[AM_mix_weights_prior](#)

See Also

[AM_mix_weights_prior_gamma](#)

AM_mix_weights_prior_gamma
specify a prior on the hyperparameter γ for the Dirichlet mixture weights prior

Description

Generate a configuration object to specify a prior on the hyperparameter γ for the Dirichlet prior on the mixture weights. We assume $\gamma \sim \text{Gamma}(a, b)$. Alternatively, we can fix γ to a specific value. Default is $\gamma = 1/N$, where N is the number of observations. In AntMAN we assume the following parametrization of the Gamma density:

$$p(x \mid a, b) = \frac{b^a x^{a-1}}{\Gamma(a)} \exp\{-bx\}, \quad x > 0.$$

Usage

```
AM_mix_weights_prior_gamma(a = NULL, b = NULL, gamma = NULL, init = NULL)
```

Arguments

a	The shape parameter a of the Gamma prior.
b	The rate parameter b of the Gamma prior.
gamma	It allows to fix γ to a specific value.
init	The init value for γ , when we assume γ random.

Value

A [AM_mix_weights_prior](#) object. This is a configuration list to be used as mix_weight_prior argument for [AM_mcmc_fit](#).

Examples

```
AM_mix_weights_prior_gamma (a=1, b=1)
AM_mix_weights_prior_gamma (a=1, b=1, init=1)
AM_mix_weights_prior_gamma (gamma = 3)
AM_mix_weights_prior_gamma ()
```

AM_plot_chaincor	<i>Plot the Autocorrelation function</i>
------------------	--

Description

Given an [AM_mcmc_output](#) object, this function produces the autocorrelation function bars describing the MCMC results. AM_plot_chaincor makes use of bayesplot's plotting function mcmc_acf_bar (Gabry et al. 2019).

Usage

```
AM_plot_chaincor(x, tags = NULL, lags = NULL, title = "MCMC Results")
```

Arguments

x	An AM_mcmc_output object, produced by calling AM_mcmc_fit .
tags	A list of variables to consider. This function only produces meaningful plots for variables that have fixed dimension across the draws. If not specified, plots pertaining to M and K will be produced. This function is built upon bayesplot's mcmc_acf_bar.
lags	An integer specifying the number of lags to plot. If no value is specified, the default number of lags shown is half the total number of iterations.
title	Title for the plot.

Value

A ggplot object.

AM_plot_density	<i>Plot the density of variables from AM_mcmc_output object</i>
-----------------	---

Description

Given an [AM_mcmc_output](#) object, `AM_plot_density` plots the posterior density of the specified variables of interest. `AM_plot_density` makes use of `bayesplot`'s plotting function `mcmc_areas` (Gabry et al. 2019).

Usage

```
AM_plot_density(x, tags = NULL, title = "MCMC Results")
```

Arguments

<code>x</code>	An AM_mcmc_output fit object, produced by calling AM_mcmc_fit .
<code>tags</code>	A list of variables to consider. This function only produces meaningful plots for variables that have fixed dimension across the draws.
<code>title</code>	Title for the plot.

Value

a `ggplot` object visualising the posterior density of the specified variables.

AM_plot_mvb_cluster_frequency	<i>Visualise the cluster frequency plot for the multivariate bernoulli model</i>
-------------------------------	--

Description

Given an [AM_mcmc_output](#) object, and the data the model was fit on, this function will produce a cluster frequency plot for the multivariate bernoulli model.

Usage

```
AM_plot_mvb_cluster_frequency(
  fit,
  y,
  x_lim_param = c(0.8, 7.2),
  y_lim_param = c(0, 1)
)
```

Arguments

<code>fit</code>	An AM_mcmc_output fit object, produced by calling <code>AM_mcmc_fit</code> .
<code>y</code>	A matrix containing the y observations which produced fit.
<code>x_lim_param</code>	A vector with two elements describing the plot's x_axis scale, e.g. <code>c(0.8, 7.2)</code> .
<code>y_lim_param</code>	A vector with two elements describing the plot's y_axis scale, e.g. <code>c(0, 1)</code> .

Value

No return value. Called for side effects.

<code>AM_plot_pairs</code>	<i>Plot AM_mcmc_output scatterplot matrix</i>
----------------------------	---

Description

visualise a matrix of plots describing the MCMC results. This function is built upon GGally's plotting function `ggpairs` (Schloerke et al. 2021).

Usage

```
AM_plot_pairs(x, tags = NULL, title = "MCMC Results")
```

Arguments

<code>x</code>	an AM_mcmc_output object, produced by calling <code>AM_mcmc_fit</code> .
<code>tags</code>	A list of variables to consider for plotting. This function only produces meaningful plots for variables that have fixed dimension across the draws. If not specified, plots pertaining to M and K will be produced.
<code>title</code>	Title for the plot.

Value

Same as `ggpairs` function, a `ggmatrix` object that if called, will print.

AM_plot_pmf	<i>Plot the probability mass function of variables from AM_mcmc_output object</i>
-------------	---

Description

Given an [AM_mcmc_output](#) object, AM_plot_pmf plots the posterior probability mass function of the specified variables.

Usage

```
AM_plot_pmf(x, tags = NULL, title = "MCMC Results")
```

Arguments

x	An AM_mcmc_output object, produced by calling AM_mcmc_fit .
tags	A list of variables to consider. If not specified, the pmf of both M and K will be plotted.
title	Title for the plot.

Value

No return value. Called for side effects.

AM_plot_similarity_matrix	<i>Plot the Similarity Matrix</i>
---------------------------	-----------------------------------

Description

Given an [AM_mcmc_output](#) object, this function will produce an image of the Similarity Matrix.

Usage

```
AM_plot_similarity_matrix(x, loss, ...)
```

Arguments

x	An AM_mcmc_output fit object, produced by calling AM_mcmc_fit .
loss	Loss function to minimise. Specify either "VI" or "binder". If not specified, the default loss to minimise is "binder".
...	All additional parameters will be pass to the image command.

Value

No return value. Called for side effects.

AM_plot_traces	<i>Plot traces of variables from an AM_mcmc_output object</i>
----------------	---

Description

Given an [AM_mcmc_output](#) object, [AM_plot_traces](#) visualises the traceplots of the specified variables involved in the MCMC inference. [AM_plot_traces](#) is built upon bayesplot's `mcmc_trace` (Gabry et al. 2019).

Usage

```
AM_plot_traces(x, tags = NULL, title = "MCMC Results")
```

Arguments

<code>x</code>	An AM_mcmc_output fit object, produced by calling AM_mcmc_fit .
<code>tags</code>	A list of variables to consider. This function only produces meaningful plots for variables that have fixed dimension across the draws. If not specified, plots pertaining to M and K will be produced.
<code>title</code>	Title for the plot

Value

No return value. Called for side effects.

AM_plot_values	<i>Plot posterior interval estimates obtained from MCMC draws</i>
----------------	---

Description

Given an object of class [AM_mcmc_fit](#), [AM_plot_values](#) visualises the interval estimates of the specified variables involved in the MCMC inference. [AM_plot_values](#) is built upon bayesplot's `mcmc_intervals` (Gabry et al. 2019).

Usage

```
AM_plot_values(x, tags = NULL, title = "MCMC Results")
```

Arguments

<code>x</code>	An AM_mcmc_output fit object, produced by calling AM_mcmc_fit .
<code>tags</code>	A list of variables to consider. This function only produces meaningful plots for variables that have fixed dimension across the draws. If not specified, plots pertaining to M and K will be produced.
<code>title</code>	Title for the plot.

Value

No return value. Called for side effects.

AM_prior	<i>S3 class AM_prior</i>
----------	--------------------------

Description

Object type returned by AM_prior_* commands.

Value

[AM_prior](#)

See Also

[AM_prior_K_Delta](#), [AM_prior_K_Pois](#), [AM_prior_K_NegBin](#)

AM_prior_K_Delta	<i>Computes the prior on the number of clusters</i>
------------------	---

Description

This function computes the prior on the number of clusters, i.e. occupied components of the mixture for a Finite Dirichlet process when the prior on the component-weights of the mixture is a Dirichlet with parameter gamma (i.e. when unnormalised weights are distributed as $\text{Gamma}(\gamma, 1)$). This function can be used when the number of components is fixed to M^* , i.e. a Dirac prior assigning mass only to M^* is assumed. See (Argiento and Iorio 2019) There are no default values.

Usage

```
AM_prior_K_Delta(n, gamma, Mstar)
```

Arguments

n	The sample size.
gamma	The gamma parameter of the Dirichlet distribution.
Mstar	The number of component of the mixture.

Value

an [AM_prior](#) object, that is a vector of length n, reporting the values $V(n, k)$ for $k=1, \dots, n$.

Examples

```
n <- 82
gam_de <- 0.1743555
Mstar <- 12
prior_K_de <- AM_prior_K_Delta(n,gam_de, Mstar)
plot(prior_K_de)
```

AM_prior_K_NegBin	<i>computes the prior number of clusters</i>
-------------------	--

Description

This function computes the prior on the number of clusters, i.e. occupied component of the mixture for a Finite Dirichlet process when the prior on the component-weights of the mixture is a Dirichlet with parameter γ (i.e. when unnormalized weights are distributed as $\text{Gamma}(\gamma, 1)$). This function can be used when the prior on the number of components is Negative Binomial with parameter $r > 0$ and $0 < p < 1$, with mean $\mu = 1 + r * p / (1 - p)$. See (Argiento and Iorio 2019) for more details.

Usage

```
AM_prior_K_NegBin(n, gamma, r, p)
```

Arguments

n	The sample size.
gamma	The gamma parameter of the Dirichlet distribution.
r	The dispersion parameter r of the Negative Binomial.
p	The probability of failure parameter p of the Negative Binomial.

Details

There are no default values.

Value

an [AM_prior](#) object, that is a vector of length n , reporting the values $V(n, k)$ for $k=1, \dots, n$.

Examples

```
n <- 50
gamma <- 1
r <- 0.1
p <- 0.91
gam_nb <- 0.2381641
prior_K_nb <- AM_prior_K_NegBin(n,gam_nb,r,p)
plot(prior_K_nb)
```

AM_prior_K_Pois	<i>Computes the prior number of clusters</i>
-----------------	--

Description

This function computes the prior on the number of clusters, i.e. occupied components of the mixture for a Finite Dirichlet process when the prior on the component-weights of the mixture is a Dirichlet with parameter γ (i.e. when unnormalized weights are distributed as $\text{Gamma}(\gamma, 1)$). This function can be used when the prior on the number of components is Shifted Poisson of parameter Λ . See (Argiento and Iorio 2019) for more details.

Usage

```
AM_prior_K_Pois(n, gamma, Lambda)
```

Arguments

n	The sample size.
gamma	The gamma parameter of the Dirichlet distribution.
Lambda	The Lambda parameter of the Poisson.

Details

There are no default values.

Value

an [AM_prior](#) object, that is a vector of length n, reporting the values of the prior on the number of clusters induced by the prior on M and w , i.e. p^*_k for $k=1, \dots, n$. See (Argiento and Iorio 2019) for more details.

Examples

```
n <- 82
Lambda <- 10
gam_po <- 0.1550195
prior_K_po <- AM_prior_K_Pois(n, gam_po, Lambda)
plot(prior_K_po)
```

Description

Heuristic partitioning to minimise the expected loss function with respect to a given expected adjacency matrix. This function is built upon R-package `salso`'s implementation of the `salso` function. See `salso` (Dahl et al. 2021) for more details.

Usage

```
AM_salso(
  eam,
  loss,
  maxNClusters = 0,
  nRuns = 16,
  maxZealousAttempts = 10,
  probSequentialAllocation = 0.5,
  nCores = 0
)
```

Arguments

<code>eam</code>	a co-clustering/ clustering matrix. See <code>salso</code> for more information on which matrix to use.
<code>loss</code>	the recommended loss functions to be used are the "binder" or "VI". However, other loss functions that are supported can be found in the R-package <code>salso</code> 's <code>salso</code> function.
<code>maxNClusters</code>	Maximum number of clusters to be considered. The actual number of clusters searched may be lower. Default is 0.
<code>nRuns</code>	Number of runs to try.
<code>maxZealousAttempts</code>	Maximum number of tries for zealous updates. See <code>salso</code> for more information.
<code>probSequentialAllocation</code>	The probability of using sequential allocation instead of random sampling via <code>sample(1:K,ncol(x),TRUE)</code> , where <code>K</code> is <code>maxNClusters</code> . Default is 0.5. See <code>salso</code> for more information. argument.
<code>nCores</code>	Number of CPU cores to engage. Default is 0.

Value

A numeric vector describing the estimated partition. The integer values represent the cluster labels of each item respectively.

Source

David B. Dahl and Devin J. Johnson and Peter Müller (2021). *salso: Search Algorithms and Loss Functions for Bayesian Clustering*. R package version 0.2.15.

AntMAN

AntMAN: A package for fitting finite Bayesian Mixture models with a random number of components

Description

AntMAN: Anthology of Mixture ANalysis tools AntMan is an R package fitting Finite Bayesian Mixture models with a random number of components. The MCMC algorithm behind AntMAN is based on point processes and offers a more computationally efficient alternative to the Reversible Jump. Different mixture kernels can be specified: univariate Gaussian, multivariate Gaussian, univariate Poisson, and multivariate Bernoulli (Latent Class Analysis). For the parameters characterising the mixture kernel, we specify conjugate priors, with possibly user specified hyper-parameters. We allow for different choices on the prior on the number of components: Shifted Poisson, Negative Binomial, and Point Masses (i.e. mixtures with fixed number of components).

Package Philosophy

The main function of the AntMAN package is [AM_mcmc_fit](#). AntMAN performs a Gibbs sampling in order to fit, in a Bayesian framework, a mixture model of a predefined type `mix_kernel_hyperparams` given a sample y . Additionally AntMAN allows the user to specify a prior on the number of components `mix_components_prior` and on the weights `mix_weight_prior` of the mixture. MCMC parameters `mcmc_parameters` need to be given as argument for the Gibbs sampler (number of iterations, burn-in, ...). Initial values for the number of clusters (`init_K`) or a specific clustering allocation (`init_clustering`) can also be user-specified. Otherwise, by default, we initialise each element of the sample y to a different cluster allocation. This choice can be computationally inefficient.

For example, in order to identify clusters over a population of patients given a set of medical assumptions:

```
mcmc = AM_mcmc_parameters(niter=20000)
mix = AM_mix_hyperparams_multiber ()
fit = AM_mcmc_fit (mix, mcmc)
summary (fit)
```

In this example `AM_mix_hyperparams_multiber` is one of the possible mixtures to use.

AntMAN currently support four different mixtures :

```
AM_mix_hyperparams_unipois(alpha0, beta0)
AM_mix_hyperparams_uninorm(m0, k0, nu0, sig02)
AM_mix_hyperparams_multiber(a0, b0)
AM_mix_hyperparams_multinorm(mu0, ka0, nu0, Lam0)
```

Additionally, three types of kernels on the prior number of components are available:

```
AM_mix_components_prior_pois()
AM_mix_components_prior_negbin()
AM_mix_components_prior_dirac()
```

For example, in the context of image segmentation, if we know that there are 10 colours present, a prior dirac can be used :

```
mcmc = AM_mcmc_parameters(niter=20000)
mix = AM_mix_hyperparams_multinorm ()
prior_component = AM_mix_components_prior_dirac(10) # 10 colours present
fit = AM_mcmc_fit (mix, prior_component, mcmc)
summary (fit)
```

brain

Teen Brain Images from the National Institutes of Health, U.S.

Description

Picture of brain activities from a teenager consuming drugs.

Usage

```
brain
```

Format

A list that contains `dim` a (W:width,H:height) pair, and `pic` a data frame (W*H pixels image in RGB format).

Source

<https://www.flickr.com/photos/nida-nih/29741916012>

References

Crowley TJ, Dalwani MS, Mikulich-Gilbertson SK, Young SE, Sakai JT, Raymond KM, et al. (2015) Adolescents' Neural Processing of Risky Decisions: Effects of Sex and Behavioral Disinhibition. PLoS ONE 10(7): e0132322. doi:10.1371/journal.pone.0132322

Examples

```
data(brain)
```

`carcinoma`*Carcinoma dataset*

Description

The carcinoma data from Agresti (2002, 542) consist of seven dichotomous variables representing the ratings by seven pathologists of 118 slides on the presence or absence of carcinoma. The purpose of studying this data is to model "interobserver agreement" by examining how subjects might be divided into groups depending upon the consistency of their diagnoses.

Usage

```
carcinoma
```

Format

A data frame with 118 rows and 7 variables (from A to G).

References

Agresti A (2002). Categorical Data Analysis. John Wiley & Sons, Hoboken.

Examples

```
data(carcinoma)
```

`galaxy`*Galaxy velocities dataset*

Description

This data set considers the physical information of velocities (10^3 km/second) for 82 galaxies reported by Roeder (1990). These are drawn from six well-separated conic sections of the Corona Borealis region.

Usage

```
galaxy
```

Format

A data frame with X rows and Y variables.

A numeric vector giving the speed of galaxies ($1000 \times (\text{km/second})$)

Source

Roeder, K. (1990). Density estimation with confidence sets exemplified by superclusters and voids in the galaxies, Journal of the American Statistical Association, 85: 617-624.

Examples

```
data(galaxy)
```

```
plot.AM_mcmc_output      plot AM_mcmc_output
```

Description

Given an [AM_mcmc_output](#) object, this function plots some useful information about the MCMC results regarding M and K . Besides the PMFs, some of the diagnostic plots of the MCMC chain are visualised.

Usage

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

Arguments

`x` an [AM_mcmc_output](#) object.
`...` all additional parameters are ignored.

Value

NULL. Called for side effects.

```
plot.AM_prior            plot AM_prior
```

Description

plot the prior on the number of clusters for a given [AM_prior](#) object.

Usage

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

Arguments

- x an [AM_prior](#) object. See [AM_prior_K_Delta](#), [AM_prior_K_NegBin](#), [AM_prior_K_Pois](#) for more details.
- ... all additional parameters are ignored.

Value

NULL. Called for side effects.

said	<i>Usage frequency of the word "said" in the Brown corpus</i>
------	---

Description

Usage frequency of the word "said" in the Brown corpus

Usage

said

Format

A list with 500 observations on the frequency of said in different texts.

Source

<https://www.kaggle.com/nltkdata/brown-corpus>

References

Francis, W., and Kucera, H. (1982) Frequency Analysis of English Usage, Houghton Mifflin Company, Boston.

Examples

```
data(said)
```

`summary.AM_mcmc_configuration`*summary information of the AM_mcmc_configuration object*

Description

Given an [AM_mcmc_configuration](#) object, this function prints the summary information of the specified mcmc configuration.

Usage

```
## S3 method for class 'AM_mcmc_configuration'
summary(object, ...)
```

Arguments

<code>object</code>	an AM_mcmc_configuration object.
<code>...</code>	all additional parameters are ignored

Value

NULL. Called for side effects.

See Also

[AM_mcmc_parameters](#)

`summary.AM_mcmc_output`*summary information of the AM_mcmc_output object*

Description

Given an [AM_mcmc_output](#) object, this function prints the summary information pertaining to the given model output.

Usage

```
## S3 method for class 'AM_mcmc_output'
summary(object, ...)
```

Arguments

<code>object</code>	a AM_mcmc_output object
<code>...</code>	all additional parameters are ignored

Value

NULL. Called for side effects.

See Also

[AM_mcmc_fit](#), [AM_mcmc_refit](#)

summary.AM_mix_components_prior

summary information of the AM_mix_components_prior object

Description

Given an [AM_mix_components_prior](#) object, this function prints the summary information of the specified prior on the number of components.

Usage

```
## S3 method for class 'AM_mix_components_prior'
summary(object, ...)
```

Arguments

object	an AM_mix_components_prior object.
...	all additional parameters are ignored.

Value

NULL. Called for side effects.

See Also

[AM_mix_components_prior](#)

`summary.AM_mix_hyperparams`*summary information of the AM_mix_hyperparams object*

Description

Given an [AM_mix_hyperparams](#) object, this function prints the summary information of the specified mixture hyperparameters.

Usage

```
## S3 method for class 'AM_mix_hyperparams'
summary(object, ...)
```

Arguments

<code>object</code>	an AM_mix_hyperparams object.
<code>...</code>	all additional parameters are ignored.

Value

NULL. Called for side effects.

See Also

[AM_mix_hyperparams](#)

`summary.AM_mix_weights_prior`*summary information of the AM_mix_weights_prior object*

Description

Given an [AM_mix_weights_prior](#) object, this function prints the summary information of the specified mixture weights prior.

Usage

```
## S3 method for class 'AM_mix_weights_prior'
summary(object, ...)
```

Arguments

<code>object</code>	an AM_mix_weights_prior object.
<code>...</code>	all additional parameters are ignored.

Value

NULL. Called for side effects.

See Also

[AM_mix_weights_prior](#)

summary.AM_prior	<i>summary information of the AM_prior object</i>
------------------	---

Description

Given an [AM_prior](#) object, this function prints the summary information of the specified prior on the number of clusters.

Usage

```
## S3 method for class 'AM_prior'  
summary(object, ...)
```

Arguments

object	an AM_prior object. See AM_prior_K_Delta , AM_prior_K_NegBin , AM_prior_K_Pois for more details.
...	all additional parameters are ignored.

Value

NULL. Called for side effects.

See Also

[AM_prior](#)

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