Package ‘CNPBayes’

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Type Package

Title Bayesian mixture models for copy number polymorphisms

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Description Bayesian hierarchical mixture models for batch effects and copy number.

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    'methods-BatchModel.R' 'methods-DensityModel.R'
    'methods-Hyperparameters.R' 'methods-MarginalModel.R'
    'methods-McmcChains.R' 'methods-McmcParams.R'
    'methods-MixtureModel.R' 'methods-SummarizedExperiment.R'
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batch

Retrieve batches from object.

Description
The batches are represented as a vector of integers.

Usage
batch(object)

## S4 method for signature 'DensityModel'
batch(object)

## S4 method for signature 'MixtureModel'
batch(object)

Arguments
object see showMethods(batch)

Value
The batch of each data element.
BatchModel-class

Create an object for running hierarchical MCMC simulations.

Description
Create an object for running hierarchical MCMC simulations.

Usage
BatchModel(data = numeric(), k = 2L, batch, hypp, mcmc.params)

Arguments
- data: the data for the simulation.
- k: An integer value specifying the number of latent classes.
- batch: a vector of the different batch numbers (must be sorted)
- hypp: An object of class 'Hyperparameters' used to specify the hyperparameters of the model.
- mcmc.params: An object of class 'McmcParams'

Value
An object of class 'BatchModel'

Examples
model <- BatchModel(rnorm(10), k=1, batch=rep(1:2, each=5))

BatchModel-class
An object for running MCMC simulations.

Description
Run hierarchical MCMC for batch model.

Slots
- k: An integer value specifying the number of latent classes.
- hypparams: An object of class 'Hyperparameters' used to specify the hyperparameters of the model.
- theta: the means of each component and batch
- sigma2: the variances of each component and batch
- nu.0: the shape parameter for sigma2
- sigma2.0: the rate parameter for sigma2
pi  mixture probabilities which are assumed to be the same for all batches
mu  means from batches, averaged across batches
tau2 variances from batches, weighted by precisions
data  the data for the simulation.
data.mean the empirical means of the components
data.prec  the empirical precisions
z  latent variables
zfreq  table of latent variables
probz  n x k matrix of probabilities
logprior  log likelihood of prior: log(p(sigma2.0)p(nu.0)p(mu))
loglik  log likelihood: ∑ pk Φ(θk, σk)
mcmc.chains an object of class 'McmcChains' to store MCMC samples
batch  a vector of the different batch numbers
batchElements  a vector labeling from which batch each observation came from
modes  the values of parameters from the iteration which maximizes log likelihood and log prior
mcmc.params  An object of class 'McmcParams'
.internal.constraint  Constraint on parameters. For internal use only.
bic  

*Calculate BIC of a model*

**Description**

Calculate BIC of a model

**Usage**

```r
bic(object)
```

```r
## S4 method for signature 'BatchModel'
bic(object)
```

```r
## S4 method for signature 'MarginalModel'
bic(object)
```

**Arguments**

- `object`  
  see `showMethods(bic)`

**Value**

The BIC of the model.

**Examples**

```r
bic(BatchModelExample)
```

---

burnin  

*Number of burnin iterations.*

**Description**

This function retrieves the number of burnin simulations to be discarded.
This function changes the number of burnin simulations to be discarded.

**Usage**

```r
burnin(object)
```

```r
burnin(object) <- value
```

```r
## S4 method for signature 'McmcParams'
burnin(object)
```

```r
## S4 replacement method for signature 'McmcParams'
burnin(object) <- value
```

```r
## S4 method for signature 'MixtureModel'
```
chains

burnin(object)

## S4 replacement method for signature 'MixtureModel'

burnin(object) <- value

**Arguments**

- object see showMethods(burnin)
- value new number of burnin iterations

**Value**

The number of burnin simulations.

**Examples**

```
burnin(MarginalModelExample)
mp <- mcmcParams(MarginalModelExample)
burnin(mp)
```

---

chains

*Retrieve simulated chains from model object.*

**Description**

The method `chains` applied to a `MixtureModel`-derived class will return an object of class `McmcChains` that contains the chains for all simulated parameters. Typically, `chains` is called in conjunction with an accessor for one of these parameters.

**Usage**

```
chains(object)
```

## S4 method for signature 'MixtureModel'

chains(object)

**Arguments**

- object showMethods(chains)

**Value**

The simulated chains.

**Examples**

```
theta.chain <- theta(chains(MarginalModelExample))
dim(theta.chain)
plot.ts(theta.chain, plot.type="single",
       col=seq_len(k(MarginalModelExample)))
```
chromosome | Extract character vector of sequence names

**Description**
Short cut for `as.character(seqnames(g))` where `g` is a GRanges object.

**Usage**
```
chromosome(object, ...)
```

**Arguments**
- `object` a GRanges instance
- `...` currently ignored

**Value**
A character vector

**Examples**
```
## Not run:
g <- GRanges("chr1", IRanges(10, 15))
chromosome(g)
## End(Not run)
```

clusters | Accessor for extracting the kmeans clusters from a DensityModel instance

**Description**
Accessor for extracting the kmeans clusters from a DensityModel instance

**Usage**
```
clusters(object)
```

**Arguments**
- `object` an instance of class 'DensityModel'

**Value**
k-means clustering of the component means using the modes as centers.
See Also

DensityModel-class

Examples

```r
truth <- simulateData(N=2500, p=rep(1/3, 3),
theta=c(-1, 0, 1),
sds=rep(0.1, 3))
dm <- DensityModel(truth)
clusters(dm)
```

Description

Bayesian mixture models for copy number estimation

collapseBatch

Estimate batch from a collection of chemistry plates or some other variable that captures the time in which the arrays were processed.

Description

In high-throughput assays, low-level summaries of copy number at copy number polymorphic loci (e.g., the mean log R ratio for each sample, or a principal-component derived summary) often differ between groups of samples due to technical sources of variation such as reagents, technician, or laboratory. Technical (as opposed to biological) differences between groups of samples are referred to as batch effects. A useful surrogate for batch is the chemistry plate on which the samples were hybridized. In large studies, a Bayesian hierarchical mixture model with plate-specific means and variances is computationally prohibitive. However, chemistry plates processed at similar times may be qualitatively similar in terms of the distribution of the copy number summary statistic. Further, we have observed that some copy number polymorphic loci exhibit very little evidence of a batch effect, while other loci are more prone to technical variation. We suggest combining plates that are qualitatively similar in terms of the Kolmogorov-Smirnov two-sample test of the distribution and to implement this test independently for each candidate copy number polymorphism identified in a study. The collapseBatch function is a wrapper to the ks.test implemented in the stats package that compares all pairwise combinations of plates. The ks.test is performed recursively on the batch variables defined for a given CNP until no batches can be combined.

Usage

```r
collapseBatch(object, plate, THR = 0.1)
```

## S4 method for signature 'BatchModel'
collapseBatch(object)

## S4 method for signature 'SummarizedExperiment'
collapseBatch(object, plate, THR = 0.1)

## S4 method for signature 'numeric'
collapseBatch(object, plate, THR = 0.1)
Arguments

object see showMethods(collapseBatch)
plate a vector labelling from which batch each observation came from.
THR threshold below which the null hypothesis should be rejected and batches are collapsed.

Value
The new batch value.

Examples

bt <- collapseBatch(y(BatchModelExample), batch(BatchModelExample))
newBatchModel <- BatchModel(y(BatchModelExample), k(BatchModelExample),
                               bt, hyperParams(BatchModelExample),
                               mcmcParams(BatchModelExample))

Description
The collection of copy number variants (CNVs) identified in a study can be encapsulated in a GRangesList, where each element is a GRanges of the CNVs identified for an individual. (For a study with 1000 subjects, the GRangesList object would have length 1000 if each individual had 1 or more CNVs.) For regions in which CNVs occur in more than 2 percent of study participants, the start and end boundaries of the CNVs may differ because of biological differences in the CNV size as well as due to technical noise of the assay and the uncertainty of the breakpoints identified by a segmentation of the genomic data. Among subjects with a CNV called at a given locus, the consensusCNP function identifies the largest region that is copy number variant in half of these subjects.

Usage

consensusCNP(grl, transcripts, min.width = 2000, max.width = 2e+05,
min.prevalance = 0.02)

Arguments

grl A GRangesList of all CNVs in a study – each element is the collection of CNVs for one individual.
transcripts a GRanges object containing annotation of genes or transcripts (optional)
min.width length-one integer vector specifying the minimum width of CNVs
max.width length-one integer vector specifying the maximum width of CNVs
min.prevalance a length-one numeric vector specifying the minimum prevalence of a copy number polymorphism. Must be in the interval [0,1]. If less that 0, this function will return all CNV loci regardless of prevalence. If greater than 1, this function will return a length-zero GRanges object
Value

a GRanges object providing the intervals of all identified CNPs above a user-specified prevalence cutoff.

Examples

library(GenomicRanges)

## Simulate 2 loci at which CNVs are common
##
set.seed(100)
starts <- rpois(1000, 100) + 10e6L
ends <- rpois(1000, 100) + 10.1e6L
cnv1 <- GRanges("chr1", IRanges(starts, ends))
cnv1$id <- paste0("sample", seq_along(cnv1))

starts <- rpois(500, 1000) + 101e6L
ends <- rpois(500, 1000) + 101.4e6L
cnv2 <- GRanges("chr5", IRanges(starts, ends))
cnv2$id <- paste0("sample", seq_along(cnv2))

## Simulate a few other CNVs that are less common because they are
## very large, or because they occur in regions that in which copy
## number alterations are not common
##
cnv3 <- GRanges("chr1", IRanges(9e6L, 15e6L), id="sample1400")
starts <- seq(5e6L, 200e6L, 10e6L)
ends <- starts + rpois(length(starts), 25e3L)
cnv4 <- GRanges("chr1", IRanges(starts, ends),
                 id=paste0("sample", sample(1000:1500, length(starts))))

all_cnvs <- suppressWarnings(c(cnv1, cnv2, cnv3, cnv4))
grl <- split(all_cnvs, all_cnvs$id)
cnps <- consensusCNP(grl)

## 2nd CNP is filtered because of its size
##
truth <- GRanges("chr1", IRanges(10000100L, 10100099L),
                 IRanges(c(10000100L, 101000999L),
                         c(10100100L, 101400999L)))
seqinfo(truth) <- seqinfo(grl)
identical(cnps, truth)

## Both CNVs identified
##
cnps <- consensusCNP(grl, max.width=500e3)
truth <- GRanges(c("chr1", "chr5"),
                 IRanges(c(10000100L, 101000999L),
                         c(10100100L, 101400999L)))
seqlevels(truth, force=TRUE) <- seqlevels(grl)
seqinfo(truth) <- seqinfo(grl)
identical(cnps, truth)
DensityModel-class

Constructor for DensityModel class

Description

Instances of DensityModel store the estimated densities for each component and the overall (marginal) estimate of the density. The derived class DensityBatchModel additionally stores the density for each batch / component combination (i.e., if there are 3 components and 10 batches, there are 30 estimated densities). The intended use-case of the DensityModel class is to facilitate visualization of the estimated densities (see examples) as well as to provide an estimate of the number of modes in the overall density. If the number of estimated modes is smaller than the number of components of the best-fitting mixture model, post-hoc merging of components may be useful.

Usage

DensityModel(object, merge = FALSE)

Arguments

object see showMethods(DensityModel)
merge Logical. Whether to use kmeans clustering to cluster the component means using the estimated modes from the overall density as the centers for the kmeans function.

Value

An object of class 'DensityModel'

See Also

DensityModel-class kmeans

Examples

dm <- DensityModel(MarginalModelExample)
Slots

- **component** The component densities.
- **overall** The overall (marginal across batches and components) estimate of the density.
- **modes** A numeric vector providing the estimated modes in the overall density. The modes are defined by a crude estimate of the first derivative of the overall density (see `findModes`).
- **data** A numeric vector containing the data
- **clusters** A vector providing the k-means clustering of the component means using the modes as centers. If an object of class `DensityModel` is instantiated with `merge=FALSE`, this slot takes values 1, ..., K, where K is the number of components.

See Also

- `DensityModel`

Examples

```r
## marginal model
truth <- simulateData(N=2500, p=rep(1/3, 3),
                      theta=c(-1, 0, 1),
                      sds=rep(0.1, 3))
dm <- DensityModel(truth)
print(dm)
dm.merged <- DensityModel(truth, merge=TRUE)
print(dm.merged)
## here, because there are 3 distinct modes, specifying merge=TRUE
## does not change the resulting clusters
identical(clusters(dm), clusters(dm.merged))
## These objects can be plotted
plot(dm)
## Note that calling plot on a MixtureModel-derived object returns
## a density object as a side-effect of the plotting
dm2 <- CNPBayes::plot(truth)
identical(dm, dm2)
## batch model
k <- 3
nbatch <- 3
means <- matrix(c(-1.2, -1.0, -0.8,
                   -0.2, 0, 0.2,
                   0.8, 1, 1.2), nbatch, k, byrow=FALSE)
sds <- matrix(0.1, nbatch, k)
N <- 1500
truth <- simulateBatchData(N=N, batch=rep(letters[1:3], length.out=N),
                           theta=means,
                           sds=sds,
                           p=c(1/5, 1/3, 1-1/3-1/5))
dm <- DensityModel(truth)
dm.merged <- DensityModel(truth, merge=TRUE)
print(dm)
dm2 <- CNPBayes::plot(truth)
identical(dm, dm2)
## suppress plotting of the batch-specific densities
CNPBayes::plot(dm2, show.batch=FALSE)
```
downSampleEachBatch

Create tile labels for each observation

Description
A wrapper for function downSampleEachBatch. Batches are automatically merged as needed.

Usage
downsample(batch.file, plate, y, ntiles = 250, THR = 0.1)

Arguments
- `batch.file`: the name of a file containing RDS data to be read in.
- `plate`: a vector containing the labels from which batch each observation came from.
- `y`: in memory data
- `ntiles`: number of tiles in a batch
- `THR`: threshold above which to merge batches in Kolmogorov-Smirnov test.

Value
Tile labels for each observation

downSampleEachBatch

Create tile labels for each observation

Description
Create tile labels for each observation

Usage
downSampleEachBatch(y, nt, batch)

Arguments
- `y`: vector containing data
- `nt`: the number of tiles in a batch
- `batch`: a vector containing the labels from which batch each observation came from.

Value
Tile labels for each observation
**eta.0**

Retrieves the rate parameter for the tau2 distribution.

### Description

Retrieve the rate parameter for the tau2 distribution.

### Usage

```r
eta.0(object)
```

#### S4 method for signature 'MixtureModel'

```r
eta.0(object)
```

#### S4 method for signature 'Hyperparameters'

```r
eta.0(object)
```

### Arguments

- **object**: see `showMethods(eta.0)`

### Value

`eta.0` of a `MixtureModel`

### Examples

```r
generate
```

**extract**

extracts data, latent variable, and batch for given observation.

### Description

extract data, latent variable, and batch for given observation.

extract estimated parameters at particular iteration of simulation.

Allows a user to pass a vector for burnin, thin, and iter.

### Usage

```r
## S4 method for signature 'BatchModel,ANY,ANY,ANY'
x[i, j, ..., drop = FALSE]

## S4 method for signature 'McmcChains,ANY,ANY,ANY'
x[i, j, ..., drop = FALSE]

## S4 method for signature 'McmcParams,ANY,ANY,ANY'
x[i, j, ..., drop = FALSE]
```
Hyperparameters

Arguments

<table>
<thead>
<tr>
<th>x</th>
<th>An object of class BatchModel, McmcChains, or McmcParams</th>
</tr>
</thead>
<tbody>
<tr>
<td>i</td>
<td>An element of the instance to be extracted.</td>
</tr>
<tr>
<td>j</td>
<td>Not used.</td>
</tr>
<tr>
<td>...</td>
<td>Not used.</td>
</tr>
<tr>
<td>drop</td>
<td>Not used.</td>
</tr>
</tbody>
</table>

Value

An object of class 'BatchModel'
An object of class 'McmcChains'
An object of class 'McmcParams'

Hyperparameters

Create an object of class 'Hyperparameters'

Description

Create an object of class 'Hyperparameters'

Usage

Hyperparameters(type = "batch", k = 2L, ...)

Arguments

<table>
<thead>
<tr>
<th>type</th>
<th>specifies 'marginal' or 'batch'</th>
</tr>
</thead>
<tbody>
<tr>
<td>k</td>
<td>number of components</td>
</tr>
<tr>
<td>...</td>
<td>optional parameters. See details</td>
</tr>
</tbody>
</table>

Details

Additional hyperparameters can be passed to the HyperparametersMarginal and HyperparametersBatch models.

Value

An object of class HyperparametersMarginal or HyperparametersBatch

Examples

```r
hypp <- Hyperparameters("marginal", k=2)
```
Hyperparameters-class  An object to specify the hyperparameters of a model.

Description
An object to specify the hyperparameters of a model.

Slots

k  Number of components
mu.0  Prior mean for mu.
tau2.0  prior variance on mu
eta.0  rate parameter for tau2
m2.0  shape parameter for tau2
alpha  mixture probabilities
beta  parameter for nu.0 distribution
a  shape for sigma2.0
b  rate for sigma2.0

HyperparametersBatch  Create an object of class 'HyperparametersBatch' for the batch mixture model

Description
Create an object of class 'HyperparametersBatch' for the batch mixture model

Usage
HyperparametersBatch(k = 0L, mu.0 = 0, tau2.0 = 100, eta.0 = 1800,
m2.0 = 1/60, alpha, beta = 0.1, a = 1.8, b = 6)

Arguments

k  length-one integer vector specifying number of components (typically 1 <= k <= 4)
mu.0  length-one numeric vector of the of the normal prior for the component means.
tau2.0  length-one numeric vector of the variance for the normal prior of the component means
eta.0  length-one numeric vector of the shape parameter for the Inverse Gamma prior of the component variances, tau2_h. The shape parameter is parameterized as 1/2 * eta.0. In the batch model, tau2_h describes the inter-batch heterogeneity of means for component h.
m2.0  length-one numeric vector of the rate parameter for the Inverse Gamma prior of the component variances, tau2_h. The rate parameter is parameterized as 1/2 * eta.0 * m2.0. In the batch model, tau2_h describes the inter-batch heterogeneity of means for component h.
HyperparametersBatch-class

HyperparametersBatch

An object to specify the hyperparameters of a batch effect model.

Description

This class inherits from the Hyperparameters class. This class is for hyperparameters which are hierachical over the batches.

Slots

- k  Number of components
- mu.0 Prior mean for mu.
- tau2.0 prior variance on mu
- eta.0 rate paramater for tau2
- m2.0 shape parameter for tau2
- alpha mixture probabilities
- beta parameter for nu.0 distribution
- a  shape for sigma2.0
- b  rate for sigma2.0

Value

An object of class HyperparametersBatch

Examples

HyperparametersBatch(k=3)
Create an object of class 'HyperparametersMarginal' for the marginal mixture model

Usage

HyperparametersMarginal(k = 0L, mu.0 = 0, tau2.0 = 100, eta.0 = 1, m2.0 = 0.1, alpha, beta = 0.1, a = 1.8, b = 6)

Arguments

k  
length-one integer vector specifying number of components (typically 1 <= k <= 4)

mu.0  
length-one numeric vector of the mean for the normal prior of the component means

tau2.0  
length-one numeric vector of the variance for the normal prior of the component means

eta.0  
length-one numeric vector of the shape parameter for the Inverse Gamma prior of the component variances. The shape parameter is parameterized as 1/2 * eta.0.

m2.0  
length-one numeric vector of the rate parameter for the Inverse Gamma prior of the component variances. The rate parameter is parameterized as 1/2 * eta.0 * m2.0.

alpha  
length-k numeric vector of the shape parameters for the dirichlet prior on the mixture probabilities

beta  
length-one numeric vector for the parameter of the geometric prior for nu.0 (nu.0 is the shape parameter of the Inverse Gamma sampling distribution for the component-specific variances). beta is a probability and must be in the interval [0,1].

a  
length-one numeric vector of the shape parameter for the Gamma prior used for sigma2.0 (sigma2.0 is the shape parameter of the Inverse Gamma sampling distribution for the component-specific variances)

b  
a length-one numeric vector of the rate parameter for the Gamma prior used for sigma2.0 (sigma2.0 is the rate parameter of the Inverse Gamma sampling distribution for the component-specific variances)

Value

An object of class HyperparametersMarginal

Examples

HyperparametersMarginal(k=3)
HyperparametersMarginal-class

An object to specify the hyperparameters of a marginal model.

Description

This class inherits from the Hyperparameters class. This class is for hyperparameters which are marginal over the batches.

Slots

- k: Number of components
- mu.0: Prior mean for mu.
- tau2.0: Prior variance on mu
- eta.0: Rate parameter for tau2
- m2.0: Shape parameter for tau2
- alpha: Mixture probabilities
- beta: Parameter for nu.0 distribution
- a: Shape for sigma2.0
- b: Rate for sigma2.0

hyperParams

Accessor for Hyperparameters object for a MixtureModel-derived object

Description

Accessor for Hyperparameters object for a MixtureModel-derived object
Replace the hyperparameters for a MixtureModel-derived object

Usage

hyperParams(object)

hyperParams(object) <- value

## S4 method for signature 'MixtureModel'
hyperParams(object)

## S4 replacement method for signature 'MixtureModel,Hyperparameters'
hyperParams(object) <- value

Arguments

- object: see showMethods(hyperParams)
- value: an object of class 'Hyperparameters'
Value

The Hyperparameters of a MixtureModel

Examples

```r
## Not run:
hyperParams(MarginalModelExample)
## End(Not run)
hypp <- Hyperparameters(type="marginal",
                          k=k(MarginalModelExample),
                          alpha=c(9, 9, 10))
hyperParams(MarginalModelExample) <- hypp
```

Reset number of iterations.

Description

This function changes the number of simulations.
This function retrieves the number of iterations of an MCMC simulation.

Usage

```r
iter(object, force = FALSE) <- value
iter(object)
```

Arguments

- `object` see showMethods(iter)
- `force` Allow changing of the size of the elements?
- `value` new number of iterations

Value

The number of MCMC iterations
Examples

```
iter(MarginalModelExample)
```

---

### k

**Number of components.**

---

#### Description

This function retrieves the number of a priori components.

Updates the number of components and erases chains from a previous `posteriorSimulation` (if one was performed). Draws from prior to guess new starting values.

#### Usage

```
k(object)
k(object) <- value
```

```r
## S4 method for signature 'DensityModel'
k(object)

## S4 replacement method for signature 'Hyperparameters'
k(object) <- value

## S4 method for signature 'MixtureModel'
k(object)

## S4 replacement method for signature 'MixtureModel'
k(object) <- value
```

#### Arguments

- **object**: see `showMethods(k)`
- **value**: An integer for the new number of components.

#### Value

- The number of components

#### Examples

```
k(MarginalModelExample) <- 2
```
**labelSwitching**

*Calculate proportion of relabeling instances*

**Description**

When fitting an object of class `MixtureModel`, label switching can occur i.e. the mean of component one can be less than the mean of component two at one iteration of the MCMC sampler and at the next instance, the order is switched. Label switching should be kept at a minimum. This function returns the proportion of MCMC sample iterations where label switching has occurred.

**Usage**

```r
labelSwitching(object, merge = TRUE)
```

## S4 method for signature 'MixtureModel'

```r
labelSwitching(object, merge = TRUE)
```

**Arguments**

- `object`: An object of class `MarginalModel` or `BatchModel`
- `merge`: A logical indicating whether the components should be merged before checking for label switching

**Value**

A single proportion for a `MarginalModel` or a vector of proportions, one for each batch for a `BatchModel`

**Examples**

```r
labelSwitching(MarginalModelExample)
```

---

**logBayesFactor**

*Compute the log bayes factor between models.*

**Description**

Models of varying component sizes are compared. The log bayes factor is calculated comparing each set of two models by marginal likelihood, as computed by `marginalLikelihood`.

**Usage**

```r
logBayesFactor(x)
```

**Arguments**

- `x`: the result of a call to `computeMarginalLik`.

**Value**

Log Bayes factor comparing the two models with highest likelihood.
**logPrior**

Calculate log likelihood of prior for model

**Description**

Calculate log likelihood of prior for model

**Usage**

```r
logPrior(object)
```

```r
## S4 method for signature 'McmcChains'
logPrior(object)
```

```r
## S4 method for signature 'MixtureModel'
logPrior(object)
```

**Arguments**

- `object`  
  see `showMethods(logPrior)`

**Value**

log likelihood of the prior.

**Examples**

```r
logPrior(MarginalModelExample)
```

---

**log_lik**

Retrieve log likelihood.

**Description**

Retrieve log likelihood.

**Usage**

```r
log_lik(object)
```

```r
## S4 method for signature 'McmcChains'
log_lik(object)
```

```r
## S4 method for signature 'MixtureModel'
log_lik(object)
```

**Arguments**

- `object`  
  see `showMethods(log_lik)`
Value

The log likelihood

Examples

```r
## retrieve log likelihood at each MCMC iteration
log_lik(chains(MarginalModelExample))
## retrieve log likelihood at last MCMC iteration
log_lik(MarginalModelExample)
```

---

### m2.0

Retrieve the shape parameter for the tau2 distribution.

Description

Retrieve the shape parameter for the tau2 distribution.

Usage

```r
m2.0(object)
```

Arguments

- `object` see `showMethods(m2.0)`

Value

m2.0 for a model

Examples

```r
m2.0(MarginalModelExample)
```
map

Calculate the maximum a posteriori estimate of latent variable assignment.

Description

Calculate the maximum a posteriori estimate of latent variable assignment.

Usage

map(object)

Arguments

object an object of class MixtureModel.

Value

map estimate of latent variable assignment for each observation

Examples

map(MarginalModelExample)

mapCnProbability

Probabilistic copy number assignments.

Description

Calculate probabilistic copy number assignments using Bayes Rule applied at the MAP estimates of the cluster mean, variance, and class proportion parameters

Usage

mapCnProbability(model)

Arguments

model An object of class MixtureModel.

Value

A matrix of size N x K where N is number of observations and K is the number of components.
marginalLikelihood

**Description**

Compute the marginal likelihood of a converged model.

**Usage**

```r
marginalLikelihood(model, params = list(niter = 1000L, root = (1/10), reject.threshold = 1e-50, prop.threshold = 0.5))
```

- `model`: An object of class `MarginalModel`, or a list of `MarginalModel`'s. Can also be an object of `BatchModel` or a list of such models.
- `params`: A list containing:
  - `niter`: the number of iterations for the reduced Gibb's sampler
  - `root`: a tempering parameter. Before the log mean of the reduced Gibb's outputs are taken, the root of each iteration is taken
  - `reject.threshold`: small values for reduced Gibb's output for `theta` can indicate overfitting. Values below `reject.threshold` will be flagged
  - `prop.threshold`: If a proportion `prop.threshold` or higher of the reduced Gibb's output for `theta` are smaller than `reject.threshold`, the marginalLikelihood will not be calculated and a warning will be displayed

**Value**

A vector of the marginal likelihood of the model(s)

**Examples**

```r
marginalLikelihood(MarginalModelExample, params=list(niter=5L, root=(1/10)),
```

MarginalModel-class

Create an object for running marginal MCMC simulations.

Description
Create an object for running marginal MCMC simulations.

Usage
MarginalModel(data = numeric(), k = 2, hypp, mcmc.params)

Arguments
- **data**: the data for the simulation.
- **k**: An integer value specifying the number of latent classes.
- **hypp**: An object of class ‘Hyperparameters’ used to specify the hyperparameters of the model.
- **mcmc.params**: An object of class ‘McmcParams’

Value
An object of class 'MarginalModel'

Examples
model <- MarginalModel(data=rnorm(10), k=1)

MarginalModel-class The 'MarginalModel' class

Description
Run marginal MCMC simulation

Slots
- **k**: An integer value specifying the number of latent classes.
- **hyperparams**: An object of class ‘Hyperparameters’ used to specify the hyperparameters of the model.
- **theta**: the means of each component and batch
- **sigma2**: the variances of each component and batch
- **nu.0**: the shape parameter for sigma2
- **sigma2.0**: the rate parameter for sigma2
- **pi**: mixture probabilities which are assumed to be the same for all batches
MarginalModelExample

mu overall mean
tau2 overall variance
data the data for the simulation.
data.mean the empirical means of the components
data.prec the empirical precisions
z latent variables
zfreq table of latent variables
prozb n x k matrix of probabilities
logprior log likelihood of prior: \( \log(p(\sigma^2.0)p(\nu.0)p(\mu)) \)
loglik log likelihood: \( \sum p_k \Phi(\theta_k, \sigma_k) \)
mcmc.chains an object of class `McmcChains` to store MCMC samples
batch a vector of the different batch numbers
batchElements a vector labeling from which batch each observation came from
modes the values of parameters from the iteration which maximizes log likelihood and log prior
mcmc.params An object of class `McmcParams`.
.internai.constraint Constraint on parameters. For internal use only.

MarginalModelExample This data is a simulated example of Marginal data

Description
This data is a simulated example of Marginal data

Usage
MarginalModelExample

Value
An example of a `MarginalModel` MarginalModelExample

Author(s)
Jacob Carey
McmcChains-class

An object to hold estimated parameters.

Description

An object of this class holds estimates of each parameter at each iteration of the MCMC simulation.

Slots

- `theta`: means of each batch and component
- `sigma2`: variances of each batch and component
- `pi`: mixture probabilities
- `mu`: overall mean in a marginal. In batch model, averaged across batches
- `tau2`: overall variance in a marginal model. In a batch model, weighted average by precision across batches
- `nu.0`: shape parameter for `sigma2` distribution
- `sigma2.0`: rate parameter for `sigma2` distribution
- `logprior`: log likelihood of prior.
- `loglik`: log likelihood.
- `zfreq`: table of `z`.
- `z`: latent variables

McmcParams

Create an object of class 'McmcParams' to specify iterations, burnin, etc.

Description

Create an object of class 'McmcParams' to specify iterations, burnin, etc.

Usage

```
McmcParams(iter = 1000L, burnin = 0L, thin, nStarts = 1, 
            param_updates = .param_updates())
```

Arguments

- `iter`: number of iterations
- `burnin`: number of burnin iterations
- `thin`: thinning interval
- `nStarts`: number of chains to run
- `param_updates`: labeled vector specifying whether each parameter is to be updated (1) or not (0).

Value

An object of class 'McmcParams'
**mcmcParams**

Retrieves MCMC parameters from a model.

**Examples**

```r
mp <- McmcParams(iter=100, burnin=10)
```

**Description**

View number of iterations, burnin, etc.

Replace number of iterations, burnin, etc. Any update of the MCMC parameters will trigger an update of the chains. However, if iter (the number of MCMC iterations) is set to a nonpositive value, the chains will not be updated and kept as is.

**Usage**

```r
mcmcParams(object)
mcmcParams(object, force = FALSE) <- value
```

**Arguments**

- `object` see `showMethods(mcmcParams)`
- `force` logical value. If false (default) the update will not proceed.
- `value` an object of class `McmcParams` containing the new number of iterations, etc.

**Value**

An object of class `McmcParams`

**Examples**

```r
mcmcParams(MarginalModelExample)
```
McmcParams-class

An object to specify MCMC options for a later simulation

Description

An object to specify MCMC options for a later simulation

Slots

- **thin**: A one length numeric to specify thinning. A value of n indicates that every nth sample should be saved. Thinning helps to reduce autocorrelation.
- **iter**: A one length numeric to specify how many MCMC iterations should be sampled.
- **burnin**: A one length numeric to specify burnin. The first Sn samples will be discarded.
- **nstarts**: A one length numeric to specify the number of chains in a simulation.
- **param_updates**: Indicates whether each parameter should be updated (1) or fixed (0).

Examples

```r
McmcParams()
McmcParams(iter=1000)
mp <- McmcParams()
iter(mp)
```

MixtureModel-class

An object for running MCMC simulations.

Description

BatchModel and MarginalModel both inherit from this class.

Slots

- **k**: An integer value specifying the number of latent classes.
- **hyperparams**: An object of class 'Hyperparameters' used to specify the hyperparameters of the model.
- **theta**: The means of each component and batch.
- **sigma2**: The variances of each component and batch.
- **nu.0**: The shape parameter for sigma2.
- **sigma2.0**: The rate parameter for sigma2.
- **pi**: Mixture probabilities which are assumed to be the same for all batches.
- **mu**: Overall mean.
- **tau2**: Overall variance.
- **data**: The data for the simulation.
- **data.mean**: The empirical means of the components.
- **data.prec**: The empirical precisions.
modes

z latent variables
zfreq table of latent variables
prozb n x k matrix of probabilities
logprior log likelihood of prior: log(p(sigma2.0)p(nu.0)p(mu))
loglik log likelihood: \sum p_k \Phi(\theta_k, \sigma_k)
mcmc.chains an object of class 'McmcChains' to store MCMC samples
batch a vector of the different batch numbers
batchElements a vector labeling from which batch each observation came from
modes the values of parameters from the iteration which maximizes log likelihood and log prior
mcmc.params An object of class 'McmcParams'
.internal.constraint Constraint on parameters. For internal use only.

### Description

The iteration which maximizes log likelihood and log prior is found. The estimates for each parameter at this iteration are retrieved.

For a mixture model with K components, there are K! possible modes. One can permute the ordering of the modes and assign the permuted order to a MixtureModel derived class by this method.

### Usage

```r
modes(object)
modes(object) <- value
```

### Arguments

- **object**
  - a MixtureModel-derived class
- **value**
  - a list of the modes. See `mode(object)` to obtain the correct format of the list.

### Value

A list of the modes of each parameter

### Examples

```r
modes(MarginalModelExample)
```
**mu**

*Retrieve overall mean*

### Description

Retrieve overall mean

### Usage

```r
mu(object)
```

```r
## S4 method for signature 'BatchModel'
mu(object)
```

```r
## S4 method for signature 'MarginalModel'
mu(object)
```

```r
## S4 method for signature 'McmcChains'
mu(object)
```

### Arguments

- **object**

### Value

A vector containing 'mu'

### Examples

```r
mu(MarginalModelExample)
```

---

**muc**

*Retrieve overall mean at each iteration of the MCMC.*

### Description

Retrieve overall mean at each iteration of the MCMC.

### Usage

```r
muc(object)
```

### Arguments

- **object**

### Value

A vector of length N or matrix of size N x B, where N is the number of observations and B is the number of unique batches.
**muMean**

*Examples*

```r
cum(MarginalModelExample)
```

---

**muMean**

*Retrieve overall mean averaged across MCMC simulations.*

**Description**

Retrieve overall mean averaged across MCMC simulations.

**Usage**

```r
muMean(object)
```

**Arguments**

- `object` an object of class MarginalModel or BatchModel

**Value**

A vector of size 1 or number of batches

**Examples**

```r
muMean(MarginalModelExample)
```

---

**names,McmcChains-method**

*Retrieve the names of the parameters estimated in the MCMC chain.*

**Description**

Retrieve the names of the parameters estimated in the MCMC chain.

**Usage**

```r
## S4 method for signature 'McmcChains'
names(x)
```

**Arguments**

- `x` an object of class `McmcChains`

**Value**

A vector of strings containing the names of each parameter
nStarts

**Number of MCMC chains.**

**Description**
This function retrieves the number of chains used for an MCMC simulation. This function changes the number of chains used for an MCMC simulation.

**Usage**

```r
nStarts(object)

nStarts(object) <- value
```

```r
## S4 method for signature 'McmcParams'
nStarts(object)

## S4 replacement method for signature 'McmcParams'
nStarts(object) <- value

## S4 method for signature 'MixtureModel'
nStarts(object)

## S4 replacement method for signature 'MixtureModel'
nStarts(object) <- value
```

**Arguments**

- `object` see `showMethods(nStarts)`
- `value` new number of chains

**Value**
An integer of the number of different starts.

**Examples**

```r
number_of_chains <- nStarts(MarginalModelExample)
number_of_chains <- 3
nStarts(MarginalModelExample) <- number_of_chains
```

nu.0

**Retrieve the shape parameter for the sigma.2 distribution.**

**Description**
Retrieve the shape parameter for the sigma.2 distribution.
oned

Usage

nu.0(object)

## S4 method for signature 'McmcChains'
nu.0(object)

## S4 method for signature 'MixtureModel'
nu.0(object)

Arguments

object see showMethods(nu.0)

Value

An integer

Examples

nu.0(MarginalModelExample)

oned

Retrieve data.

Description

Retrieve data.

Usage

oned(object)

## S4 method for signature 'MixtureModel'
oned(object)

Arguments

object see showMethods(oned)

Value

A vector the length of the data
Retrieve mixture proportions.

Usage

\( p(object) \)

Arguments

object

an object of class MarginalModel or BatchModel

Value

A vector of length the number of components

Examples

\( p(\text{MarginalModelExample}) \)

Retrieve mixture proportions at each iteration of the MCMC.

Usage

\( pic(object) \)

Arguments

object

an object of class MarginalModel or BatchModel

Value

A matrix of size MCMC iterations x Number of components

Examples

\( pic(\text{MarginalModelExample}) \)
plot

Plot the densities estimated from a mixture model for a copy number polymorphism

Description

Plot estimates of the posterior density for each component and the overall, marginal density. For batch models, one can additionally plot batch-specific density estimates.

Usage

plot(x, y, ...)

## S4 method for signature 'DensityModel,ANY'
plot(x, y, ...)

## S4 method for signature 'MarginalModel,ANY'
plot(x, y, ...)

## S4 method for signature 'BatchModel,ANY'
plot(x, y, show.batch = TRUE, ...)

## S4 method for signature 'DensityBatchModel,ANY'
plot(x, show.batch = TRUE, ...)

Arguments

x

a DensityModel-derived object, or a MixtureModel-derived object.

y

If x is a DensityModel, y is a numeric vector of the one-dimensional summaries for a given copy number polymorphism. If x is a MixtureModel, y is ignored.

... Additional arguments passed to hist.

show.batch a logical. If true, batch specific densities will be plotted.

Value

A plot showing the density estimate

Examples

set.seed(100)
truth <- simulateData(N=2500,
  theta=c(-2, -0.4, 0),
  sds=c(0.3, 0.15, 0.15),
  p=c(0.05, 0.1, 0.8))
mcmcp <- McmcParams(iter=500, burnin=500, thin=2)
model <- MarginalModel(y(truth), k=3, mcmc.params=mcmcp)
model <- CNPBayes:::startAtTrueValues(model, truth)
model <- posteriorSimulation(model)
par(mfrow=c(1,2), las=1)
plot(truth)
plot(model)
posteriorSimulation Run the MCMC simulation.

Description

*n*Starts chains are run. *b* burnin iterations are run and then discarded. Next, *s* iterations are run in each train. The user can also specify an alternative number of components. The mode of the MCMC simulation is also calculated.

Usage

posteriorSimulation(object, k)

## S4 method for signature 'MixtureModel,ANY'
posteriorSimulation(object)

## S4 method for signature 'MixtureModel,integer'
posteriorSimulation(object, k)

## S4 method for signature 'MixtureModel,numeric'
posteriorSimulation(object, k)

Arguments

object see showMethods(posteriorSimulation)

k The number of a priori components. This is optional and if not specified, the stored k model components are used. This parameters is useful for running multiple models of varying components.

Value

An object of class 'MarginalModel' or 'BatchModel'

posterior_cases Calculate posterior proportion of cases by component

Description

Calculate posterior proportion of cases by component

Usage

posterior_cases(model, case_control, alpha = 1, beta = 1)

Arguments

model An instance of a MixtureModel-derived class.

case_control A vector of 1’s and 0’s where a 1 indicates a case and a 0 a control

alpha prior alpha for the beta

beta prior beta for the beta
Value

A matrix of dimension S (MCMC iterations) by K (number of components) where each element i,j indicates the posterior proportion of cases at an iteration and component.

Examples

```r
# generate random case control status
case_control <- rbinom(length(y(MarginalModelExample)), 1, 0.5)
case_control_posterior <- posterior_cases(MarginalModelExample, case_control)
```

---

**probz**  
Retrieve the probability of latent variable membership by observation.

**Description**

Retrieve the probability of latent variable membership by observation.

**Usage**

```r
probz(object)
```

## S4 method for signature 'MixtureModel'

```r
probz(object)
```

**Arguments**

- `object`  
  see showMethods(probz)

**Value**

A matrix of size number of observations x number of components.

**Examples**

```r
probz(MarginalModelExample)
```

---

**qInverseTau2**  
Quantiles, shape, and rate of the prior for the inverse of tau2 (the precision)

**Description**

The precision prior for tau2 in the hierarchical model is given by gamma(shape, rate). The shape and rate are a function of the hyperparameters eta.0 and m2.0. Specifically, shape=1/2*eta.0 and the rate=1/2*eta.0*m2.0. Quantiles for this distribution and the shape and rate can be obtained by specifying the hyperparameters eta.0 and m2.0, or alternatively by specifying the desired mean and standard deviation of the precisions.
Usage

\texttt{qInverseTau2(eta.0 = 1800, m2.0 = 100, mn, sd)}

Arguments

\begin{itemize}
  \item \texttt{eta.0} \hspace{1cm} hyperparameter for precision
  \item \texttt{m2.0} \hspace{1cm} hyperparameter for precision
  \item \texttt{mn} \hspace{1cm} mean of precision
  \item \texttt{sd} \hspace{1cm} standard deviation of precision
\end{itemize}

Value

a list with elements 'quantiles', 'eta.0', 'm2.0', 'mean', and 'sd'

Examples

\begin{verbatim}
results <- qInverseTau2(mn=100, sd=1)
precision.quantiles <- results$quantiles
sd.quantiles <- sqrt(1/precision.quantiles)
results$mean
results$sd
results$eta.0
results$m2.0

results2 <- qInverseTau2(eta.0=1800, m2.0=100)

## Find quantiles from the default set of hyperparameters
hypp <- Hyperparameters(type="batch")
results3 <- qInverseTau2(eta.0(hypp), m2.0(hypp))
default.precision.quantiles <- results3$quantiles
\end{verbatim}

Description

Batches drawn from the same distribution as identified by Kolmogorov-Smirnov test are combined.

Usage

\texttt{saveBatch(se, batch.file, THR = 0.1)}

Arguments

\begin{itemize}
  \item \texttt{se} \hspace{1cm} a SummarizedExperiment object
  \item \texttt{batch.file} \hspace{1cm} the file name to which to save the data
  \item \texttt{THR} \hspace{1cm} threshold below which the null hypothesis should be rejected and batches are collapsed.
\end{itemize}

Value

A vector of collapsed batch labels
sigma

Retrieve standard deviations of each component/batch mean.

Description
Retrieve standard deviations of each component/batch mean.

Usage
sigma(object)

Arguments
object an object of class MarginalModel or BatchModel

Value
A vector of length K, or a matrix of size B x K, where K is the number of components and B is the number of batches

Examples
sigma(MarginalModelExample)

sigma2

Retrieve the variances of each component and batch distribution

Description
For a MarginalModel, this function returns a vector of variances. For a BatchModel, returns a matrix of size number of batches by number of components.

Usage
sigma2(object)

## S4 method for signature 'BatchModel'
sigma2(object)

## S4 method for signature 'MarginalModel'
sigma2(object)

## S4 method for signature 'McmcChains'
sigma2(object)

Arguments
object see showMethods(sigma2)
Value
A vector of length number of components or a matrix of size number of batches x number of components

Examples

`sigma2(MarginalModelExample)`

---

`sigma2.0`  
Retrieve the rate parameter for the sigma.2 distribution.

Description
Retrieve the rate parameter for the sigma.2 distribution.

Usage

`sigma2.0(object)`

## S4 method for signature 'McmcChains'
`sigma2.0(object)`

## S4 method for signature 'MixtureModel'
`sigma2.0(object)`

Arguments

object see `showMethods(sigma2.0)`

Value
A length 1 numeric

Examples

`sigma2.0(MarginalModelExample)`

---

`sigmac`  
Retrieve standard deviation of each component/batch mean at each iteration of the MCMC.

Description
Retrieve standard deviation of each component/batch mean at each iteration of the MCMC.

Usage

`sigmac(object)`
The `simulateBatchData` function is used to create simulated batch data for testing.

**Description**

Create simulated batch data for testing.

**Usage**

```r
simulateBatchData(N = 2500, p, theta, sds, batch, zz)
```

**Arguments**

- `N`: number of observations
- `p`: a vector indicating probability of membership to each component
- `theta`: a vector of means, one per component/batch
- `sds`: a vector of standard deviations, one per component/batch
- `batch`: a vector of labels indication from which batch each simulation should come from
- `zz`: a vector indicating latent variable membership. Can be omitted.

**Value**

An object of class 'BatchModel'

**Examples**

```r
k <- 3
nbatch <- 3
means <- matrix(c(-1.2, -1.0, -0.8,
                  -0.2, 0, 0.2,
                  0.8, 1, 1.2), nbatch, k, byrow=FALSE)
sds <- matrix(0.1, nbatch, k)
N <- 1500
truth <- simulateBatchData(N=N,
                          batch=rep(letters[1:3], length.out=N),
                          theta=means,
                          sds=sds,
                          p=c(1/5, 1/3, 1-1/3-1/5))
```
simulateData

Description

Create simulated data for testing.

Usage

simulateData(N, p, theta, sds)

Arguments

N  number of observations
p  a vector indicating probability of membership to each component
theta a vector of means, one per component
sds  a vector of standard deviations, one per component

Value

An object of class 'MarginalModel'

Examples

truth <- simulateData(N=2500, p=rep(1/3, 3),
                      theta=c(-1, 0, 1),
                      sds=rep(0.1, 3))

tau

Description

Retrieve overall standard deviation.

Usage

tau(object)

Arguments

object an object of class MarginalModel or BatchModel

Value

A vector of standard deviations

Examples

tau(MarginalModelExample)
tau2

Accessor for the tau2 parameter in the hierarchical mixture model

Description

The interpretation of tau2 depends on whether object is a MarginalModel or a BatchModel. For BatchModel, tau2 is a vector with length equal to the number of components. Each element of the tau2 vector can be interpreted as the within-component variance of the batch means (theta). For objects of class MarginalModel (assumes no batch effect), tau2 is a length-one vector that describes the variance of the component means between batches. The hyperparameters of tau2 are eta.0 and m2.0. See the following examples for setting the hyperparameters, accessing the current value of tau2 from a MixtureModel-derived object, and for plotting the chain of tau2 values.

Usage

tau2(object)

## S4 method for signature 'BatchModel'
tau2(object)

## S4 method for signature 'MarginalModel'
tau2(object)

## S4 method for signature 'McmcChains'
tau2(object)

Arguments

object see showMethods(tau2)

Value

A vector of variances

See Also

Hyperparameters

Examples

k(BatchModelExample)
tau2(BatchModelExample)
plot.ts(tau2(chains(BatchModelExample)))
tauc

Retrieve overall standard deviation at each iteration of the MCMC.

Description
Retrieve overall standard deviation at each iteration of the MCMC.

Usage
tauc(object)

Arguments

object an object of class MarginalModel or BatchModel

Value
A vector of length N or matrix of size N x B, where N is the number of observations and B is the number of unique batches.

Examples
tauc(MarginalModelExample)

tauMean

Retrieve overall standard deviation averaged across MCMC simulations.

Description
Retrieve overall standard deviation averaged across MCMC simulations.

Usage
tauMean(object)

Arguments

object an object of class MarginalModel or BatchModel

Value
A vector of size 1 or number of batches

Examples
tauMean(MarginalModelExample)
Access for the theta parameter in the hierarchical mixture model

Description

The interpretation of theta depends on whether object is a MarginalModel or a BatchModel. For BatchModel, theta is a matrix of size B x K, where B is the number of batches and K is the number of components. Each column of the theta matrix can be interpreted as the batch means for a particular component. For objects of class MarginalModel (assumes no batch effect), theta is a vector of length K. Each element of theta can be interpreted as the mean for a component. See the following examples for accessing the current value of theta from a MixtureModel-derived object, and for plotting the chain of theta values.

Usage

theta(object)

## S4 method for signature 'BatchModel'
theta(object)

## S4 method for signature 'MarginalModel'
theta(object)

## S4 method for signature 'McmcChains'
theta(object)

Arguments

object  see showMethods(theta)

Value

A vector of length number of components or a matrix of size number of batches x number of components

Examples

## MarginalModel
k(MarginalModelExample)
theta(MarginalModelExample)
plot.ts(theta(chains(MarginalModelExample)))

## BatchModel
k(BatchModelExample)
length(unique(batch(BatchModelExample)))
theta(BatchModelExample)

## Plot means for batches in one component
plot.ts(theta(chains(BatchModelExample))[, 1:3])
**thin**

Number of thinning intervals.

**Description**

This function retrieves the number of thinning intervals used for an MCMC simulation.

**Usage**

```r
thin(object)
```

## S4 method for signature 'McmcParams'

```r
thin(object)
```

## S4 method for signature 'MixtureModel'

```r
thin(object)
```

**Arguments**

- **object**: see `showMethods(thin)`

**Value**

An integer of the number of thinning intervals

**Examples**

```r
thin(MarginalModelExample)
```

---

**tracePlot**

Create a trace plot of a parameter estimated by MCMC.

**Description**

Create a trace plot of a parameter estimated by MCMC.

**Usage**

```r
tracePlot(object, name, ...)
```

## S4 method for signature 'BatchModel'

```r
tracePlot(object, name, ...)
```

**Arguments**

- **object**: see `showMethods(tracePlot)`
- **name**: the name of the parameter for which to plot values. Can be ‘theta’, ‘sigma’, ‘p’, ‘mu’, or ‘tau’.
- **...**: Other argument to pass to plot.
Value

A traceplot of a parameter value

Examples

tracePlot(BatchModelExample, "theta")
tracePlot(BatchModelExample, "sigma")

---

y

Retrieve data.

Description

Retrieve data.

Usage

y(object)

## S4 method for signature 'DensityModel'
y(object)

## S4 method for signature 'MixtureModel'
y(object)

Arguments

object see showMethods(y)

Value

A vector containing the data

Examples

y(MarginalModelExample)

---

z

Retrieve latent variable assignments.

Description

Retrieves the simulated latent variable assignments of each observation at each MCMC simulation.
Usage

z(object)

## S4 method for signature 'McmcChains'
z(object)

## S4 method for signature 'MixtureModel'
z(object)

Arguments

object see showMethods(z)

Value

A vector the length of the data

Examples

z(MarginalModelExample)

zFreq

Calculates a frequency table of latent variable assignments by observation.

Description

Calculates a frequency table of latent variable assignments by observation.

Usage

zFreq(object)

## S4 method for signature 'McmcChains'
zFreq(object)

## S4 method for signature 'MixtureModel'
zFreq(object)

Arguments

object see showMethods(zFreq)

Value

An integer vector of length the number of components

Examples

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