Package ‘CNPBayes’

January 21, 2017

Type Package

Title Bayesian mixture models for copy number polymorphisms

Version 1.4.0

Maintainer Jacob Carey <jcarey15@jhu.edu>

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

Date Tue Jan 20 20:41:00 EST 2015

Author Stephen Cristiano, Robert Scharpf, and Jacob Carey

Depends GenomicRanges

Imports Rcpp (>= 0.12.1), S4Vectors (>= 0.9.25), matrixStats, RColorBrewer, gtools, combinat, IRanges, GenomeInfoDb, GenomicRanges, methods, BiocGenerics, graphics, stats, coda, SummarizedExperiment

Suggests testthat, knitr, BiocStyle, VanillaICE (>= 1.31.3), BiocCheck, MASS, oligoClasses, dplyr, tidyr, ggplot2

Collate 'help.R' 'AllGenerics.R' 'AllClasses.R' 'RcppExports.R' 'data.R' 'functions.R' 'marginal_likelihood.R'

'methods-BatchModel.R' 'methods-DensityModel.R'

'methods-Hyperparameters.R' 'methods-MarginalModel.R'

'methods-McmcChains.R' 'methods-McmcParams.R'

'methods-MixtureModel.R' 'methods-SummarizedExperiment.R'

'model_initialization.R' 'relabeling.R' 'simulate_data.R'

'vesualization.R'

VignetteBuilder knitr

License Artistic-2.0

LinkingTo Rcpp

biocViews CopyNumberVariation, Bayesian

Roxygen list(wrap=FALSE)

LazyData TRUE

URL https://github.com/scristia/CNPBayes

BugReports https://github.com/scristia/CNPBayes/issues

NeedsCompilation yes

RoxygenNote 5.0.1
R topics documented:

- batch ................................................. 3
- BatchModel ........................................... 4
- BatchModel-class .................................... 4
- BatchModelExample ................................. 5
- bic ................................................. 6
- burnin .............................................. 6
- chains .............................................. 7
- chromosome ....................................... 8
- clusters ............................................ 8
- CNPBayes .......................................... 9
- collapseBatch ..................................... 9
- consensusCNP ..................................... 10
- DensityModel ...................................... 12
- DensityModel-class ................................ 12
- downsample ....................................... 14
- downSampleEachBatch ......................... 14
- eta.0 ............................................. 15
- extract ........................................... 15
- Hyperparameters .................................. 16
- Hyperparameters-class ......................... 17
- HyperparametersBatch ....................... 17
- HyperparametersBatch-class .................. 18
- HyperparametersMarginal ...................... 19
- HyperparametersMarginal-class ............. 20
- hyperParams ...................................... 20
- iter<- ............................................. 21
- k ................................................... 22
- labelSwitching .................................... 23
- logBayesFactor ................................... 23
- logPrior .......................................... 24
- log_lik .......................................... 24
- m2.0 .............................................. 25
- map ............................................... 26
- mapCnProbability ................................ 26
- marginalLikelihood ............................... 27
- MarginalModel ..................................... 28
- MarginalModel-class ............................. 28
- MarginalModelExample ......................... 29
- McmcChains-class ................................ 30
- McmcParams ....................................... 30
- mcmcParams ...................................... 31
- McmcParams-class ................................ 32
- MixtureModel-class .............................. 32
- modes ............................................. 33
- mu ............................................... 34
- muc ............................................. 34
- muMean .......................................... 35
- names,McmcChains-method .................... 35
- nStarts .......................................... 36
- nu.0 ............................................. 36
The batches are represented as a vector of integers.

**Usage**

```r
batch(object)
```

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

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

**Arguments**

- `object` see `showMethods(batch)`

**Value**

The batch of each data element.
**Description**

Create an object for running hierarchical MCMC simulations.

**Usage**

```r
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**

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

**Description**

Run hierarchical MCMC for batch model.

**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
**BatchModelExample**  

This data is a simulated example of Batch data

---

**Description**

This data is a simulated example of Batch data

**Usage**

BatchModelExample

**Value**

An example of a 'BatchModel' BatchModelExample

**Author(s)**

Jacob Carey
bic  
*Calculate BIC of a model*

**Description**

Calculate BIC of a model

**Usage**

\[
\text{bic(object)}
\]

```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**

\[
\text{bic(BatchModelExample)}
\]

---

**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**

\[
\text{burnin(object)}
\]

\[
\text{burnin(object) <- value}
\]

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

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

```r
## S4 method for signature 'MixtureModel'
burnin(object) <- value
```
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**

```r
chromosome(object, ...)
```

**Arguments**

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

**Value**

A character vector

**Examples**

```r
## 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**

```r
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)
consensusCNP

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

```r
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

```r
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 than 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))))

cnv4 <- GRanges(c("chr1", "chr5"),
               IRanges(c(10000100L, 101000999L),
                      c(10100100L, 101400999L)))

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, 10100100L))
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

Instantiates an instance of 'DensityModel' (or 'DensityBatchModel') from a MarginalModel or BatchModel object. See the corresponding class for additional details and examples.

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

```r
dm <- DensityModel(MarginalModelExample)
```

DensityModel-class

An object to store estimated mixture model densities

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.
DensityModel-class

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
nbach <- 3
means <- matrix(c(-1.2, -1.0, -0.8,
                 -0.2, 0, 0.2,
                 0.8, 1, 1.2), nbach, k, byrow=FALSE)
sds <- matrix(0.1, nbach, 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
downsampling(batch.file, plate, y, ntile = 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 little 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**

Retrieve 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'**
- **eta.0(object)**
- **## S4 method for signature 'Hyperparameters'**
- **eta.0(object)**

**Arguments**

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

**Value**

`eta.0` of a 'MixtureModel'

**Examples**

```r
eta.0(MarginalModelExample)
```

---

**extract**

extract 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**

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

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

- **## S4 method for signature 'McmcParams,ANY,ANY,ANY'**
  
  ```r
  x[i, j, ..., drop = FALSE]
  ```
Arguments

- **x**: An object of class `BatchModel`, `McmcChains`, or `McmcParams`.
- **i**: An element of the instance to be extracted.
- **j**: Not used.
- **...**: Not used.
- **drop**: Not used.

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

- **type**: specifies 'marginal' or 'batch'
- **k**: number of components
- **...**: optional parameters. See details

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 variance for the normal prior of the component means
- **alpha**: Mixture probabilities
- **beta**: Parameter for nu.0 distribution
- **a**: Shape for sigma2.0
- **b**: Rate for sigma2.0
HyperparametersBatch-class

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
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 mu.0 distribution
- a: Shape for sigma2.0
- b: Rate for sigma2.0

hyperParams(object)

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'
iter <-

Value
The Hyperparameters of a MixtureModel

Examples
### Not run:
hyperParams(MarginalModelExample)

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

iter<-

Reset number of iterations.

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

Usage
iter(object, force = FALSE) <- value
iter(object)

## S4 method for signature 'McmcParams'
iter(object)

## S4 replacement method for signature 'McmcParams'
iter(object, force = FALSE) <- value

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

## S4 replacement method for signature 'MixtureModel'
iter(object, force = FALSE) <- value

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

```r
iter(MarginalModelExample)
```

---

\( k \)

\textit{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

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

```
## 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

```r
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) 
```

## S4 method for signature 'McmcChains'  

```r  
logPrior(object) 
```

## S4 method for signature 'MixtureModel'  

```r  
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) 
```

## S4 method for signature 'McmcChains'  

```r  
log_lik(object) 
```

## S4 method for signature 'MixtureModel'  

```r  
log_lik(object) 
```

**Arguments**  

- `object`  
  see `showMethods(log_lik)`

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)
```

```r
## S4 method for signature 'MixtureModel'
m2.0(object)

## S4 method for signature 'Hyperparameters'
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.

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

Compute the marginal likelihood of a converged model.

Description

Compute the marginal likelihood of a converged model.

Usage

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

Arguments

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

marginalLikelihood(MarginalModelExample, params=list(niter=5L, root=(1/10),
MarginalModel-class


describe reject.threshold=1e-50, prop.threshold=0.5)

MarginalModel

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
probz 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`
.interim.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 sigma.2 distribution
- sigma2.0: rate parameter for sigma.2 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**

**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
```

## S4 method for signature 'MixtureModel'

```r
mcmcParams(object)
```

## S4 replacement method for signature 'MixtureModel'

```r
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 $n$ 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: \( \log(p(\sigma^2.0)p(\nu.0)p(\mu)) \)
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'
internal.constraint  Constraint on parameters. For internal use only.

Retrieve the modes from a model.

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
modes(object)
modes(object) <- value

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

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

## S4 replacement method for signature 'MixtureModel'
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
modes(MarginalModelExample)
mu

Retrieve overall mean

Description
Retrieve overall mean

Usage
mu(object)

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

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

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

Arguments
object 

Value
A vector containing 'mu'

Examples
mu(MarginalModelExample)

muc

Retrieve overall mean at each iteration of the MCMC.

Description
Retrieve overall mean at each iteration of the MCMC.

Usage
muc(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.
**muMean**

**Examples**

\[
\text{muMean(MarginalModelExample)}
\]

---

**Description**

Retrieve overall mean averaged across MCMC simulations.

**Usage**

\[
\text{muMean(object)}
\]

**Arguments**

- `object`: an object of class MarginalModel or BatchModel

**Value**

A vector of size 1 or number of batches

**Examples**

\[
\text{muMean(MarginalModelExample)}
\]

---

**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**

## S4 method for signature 'McmcChains'

\[
\text{names(x)}
\]

**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
```

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

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

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

### S4 replacement method for signature 'MixtureModel'
```r
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.
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
p

Retrieve mixture proportions.

Description
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(MarginalModelExample)

---

pic

Retrieve mixture proportions at each iteration of the MCMC.

Description
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(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.
...
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**

Starts chains are run. 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**

```r
posteriorSimulation(object, k)
```

### S4 method for signature 'MixtureModel,ANY'

```r
posteriorSimulation(object)
```

### S4 method for signature 'MixtureModel,integer'

```r
posteriorSimulation(object, k)
```

### S4 method for signature 'MixtureModel,numeric'

```r
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**

```r
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
probz

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)

# posterior cases
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
```
probz(object)
```

Arguments

- `object`
  
  see `showMethods(probz)`

Value

A matrix of size number of observations x number of components

Examples

```
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 $m_2$. Specifically, shape=$1/2*\eta_0$ and the rate=$1/2*\eta_0*m_2$. Quantiles for this distribution and the shape and rate can be obtained by specifying the hyperparameters $\eta_0$ and $m_2$, or alternatively by specifying the desired mean and standard deviation of the precisions.
Usage
qInverseTau2(eta.0 = 1800, m2.0 = 100, mn, sd)

Arguments
eta.0 hyperparameter for precision
m2.0 hyperparameter for precision
mn mean of precision
sd standard deviation of precision

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

Examples
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

Description
Save se data

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

Usage
saveBatch(se, batch.file, THR = 0.1)

Arguments
se a SummarizedExperiment object
batch.file the file name to which to save the data
THR threshold below which the null hypothesis should be rejected and batches are collapsed.

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**

```r
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**

```r
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**

```r
sigma2(object)
```

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

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

```r
## 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)
simulateBatchData

Arguments

object an object of class MarginalModel or BatchModel

Value

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

Examples

sigmac(MarginalModelExample)

simulateBatchData Create simulated batch data for testing.

Description

Create simulated batch data for testing.

Usage

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

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  

Create simulated data for testing.

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  

Retrieve overall standard deviation.

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)
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)))
tauMean

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)
**theta**  
*Accessor 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 $B \times K$, 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**

```r
theta(object)
```

## S4 method for signature 'BatchModel'

```r
theta(object)
```

## S4 method for signature 'MarginalModel'

```r
theta(object)
```

## S4 method for signature 'McmcChains'

```r
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**

```r
## 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
thin(object)

## S4 method for signature 'McmcParams'
thin(object)

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

Arguments
object see showMethods(thin)

Value
An integer of the number of thinning intervals

Examples
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
tracePlot(object, name, ...)

## S4 method for signature 'BatchModel'
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.
y

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

zFreq(MarginalModelExample)
Index

[,BatchModel,ANY,ANY,ANY-method (extract), 15
[,BatchModel,ANY,ANY-method (extract), 15
[,BatchModel,ANY-method (extract), 15
[,McmcChains,ANY,ANY,ANY-method (extract), 15
[,McmcChains,ANY-method (extract), 15
[,McmcChains-method (extract), 15
[,McmcParams,ANY,ANY,ANY-method (extract), 15
[,McmcParams,ANY-method (extract), 15
[,McmcParams-method (extract), 15
[,BatchModel-method (extract), 15
[,McmcParams-method (extract), 15
[,McmcParams-method (extract), 15
[,McmcChains-method (extract), 15
[,BatchModel,ANY-method (extract), 15
[,BatchModel,ANY,ANY,ANY-method (extract), 15
[,McmcChains,ANY,ANY,ANY-method (extract), 15
[,McmcParams,ANY,ANY,ANY-method (extract), 15
[,McmcChains-method (extract), 15
[,BatchModel-class, 4
BatchModelExample, 5
bic, 6
bic,BatchModel-method (bic), 6
bic,MarginalModel-method (bic), 6
burnin, 6
burnin,McmcParams-method (burnin), 6
burnin,MixtureModel-method (burnin), 6
burnin<-(burnin), 6
burnin<-,McmcParams-method (burnin), 6
burnin<-,MixtureModel-method (burnin), 6
chains, 7
chains,MixtureModel-method (chains), 7
clusters, 8
clusters,DensityModel-method (clusters), 8
CNPBayes, 9
CNPBayes-package (CNPBayes), 9
collapseBatch, 9
collapseBatch,BatchModel-method (collapseBatch), 9
collapseBatch,BatchModel-method (collapseBatch), 9
collapseBatch,MixtureModel-method (collapseBatch), 9
collapseBatch,SummarizedExperiment-method (collapseBatch), 9
consensusCNP, 10
DensityBatchModel-class (DensityModel-class), 12
DensityModel, 12, 13
DensityModel-class, 12
downsampling, 14
downsamplingEachBatch, 14
ing.0, 15
ing.0,MixtureModel-method (ing.0), 15
ing.0,MixtureModel-method (ing.0), 15
extract, 15
Hyperparameters, 16
Hyperparameters-class, 17
HyperparametersBatch, 17
HyperparametersBatch-class, 18
HyperparametersMarginal, 19
HyperparametersMarginal-class, 20
hyperParams, 20
hyperParams,MixtureModel-method (hyperParams), 20
hyperParams<-(hyperParams), 20
hyperParams<-,MixtureModel,Hyperparameters-method (hyperParams), 20
hyperParams<-,MixtureModel-method (hyperParams), 20
iter (iter<-), 21
iter,burnin,nStarts,McmcParams-method (McmcParams-class), 32
iter,McmcParams-method (iter<-), 21
iter,MixtureModel-method (iter<-), 21
iter<-, 21
iter<-,McmcParams-method (iter<-), 21
iter<-,MixtureModel-method (iter<-), 21
k, 22
k,DensityModel-method (k), 22
k,Hyperparameters-method (Hyperparameters-class), 17
k,MixtureModel-method (k), 22
INDEX

k <- (k), 22
k <- Hyperparameters-method (k), 22
k <- Hyperparameters-method (k), 22
k <- MixtureModel-method (k), 22
kmeans, 22

labelsSwitching, 23
labelsSwitching, MixtureModel-method (labelsSwitching), 23
log_lik, 24
log_lik, McmcChains-method (log_lik), 24
log_lik, MixtureModel-method (log_lik), 24
logBayesFactor, 23
logPrior, 24
logPrior, McmcChains-method (logPrior), 24
logPrior, MixtureModel-method (logPrior), 24

m2.0, 25
m2.0, Hyperparameters-method (m2.0), 25
m2.0, MixtureModel-method (m2.0), 25
map, 26
mapCnProbability, 26
marginalLikelihood, 27
marginalLikelihood, BatchModel, ANY-method (marginalLikelihood), 27
marginalLikelihood, BatchModel-method (marginalLikelihood), 27
marginalLikelihood, list, ANY-method (marginalLikelihood), 27
marginalLikelihood, list-method (marginalLikelihood), 27
marginalLikelihood, MarginalModel, ANY-method (marginalLikelihood), 27
marginalLikelihood, MarginalModel-method (marginalLikelihood), 27
marginalLikelihood, SingleBatchPooledVar, ANY-method (marginalLikelihood), 27
marginalLikelihood, SingleBatchPooledVar-method (marginalLikelihood), 27
MarginalModel, 28
MarginalModel-class, 28
MarginalModelExample, 29
McmcChains-class, 30
McmcParams, 30
mcmcParams, 31
mcmcParams, MixtureModel-method (mcmcParams), 31
mcmcParams-class, 32
mcmcParams <- (mcmcParams), 31

mcmcParams <- MixtureModel-method (mcmcParams), 31
MixtureModel-class, 32
modes, 33
modes, DensityModel-method (modes), 33
modes, MixtureModel-method (modes), 33
modes <- (modes), 33
modes <- MixtureModel-method (modes), 33
mu, 34
mu, BatchModel-method (mu), 34
mu, MarginalModel-method (mu), 34
mu, McmcChains-method (mu), 34
muc, 34
muMean, 35
names, McmcChains-method, 35
nStarts, 36
nStarts, McmcParams-method (nStarts), 36
nStarts, MixtureModel-method (nStarts), 36
nStarts <- (nStarts), 36
nStarts <- McmcParams-method (nStarts), 36
nStarts <- MixtureModel-method (nStarts), 36
nu.0, 36
nu.0, McmcChains-method (nu.0), 36
nu.0, MixtureModel-method (nu.0), 36
oned, 37
oned, MixtureModel-method (oned), 37

p, 38
pic, 38
plot, 39
plot, BatchModel, ANY-method (plot), 39
plot, DensityBatchModel, ANY-method (plot), 39
plot, DensityModel, ANY-method (plot), 39
plot, MixtureModel, numeric-method (plot), 39
plot, MarginalModel, ANY-method (plot), 39
posterior_cases, 40
posteriorSimulation, 40
posteriorSimulation, MixtureModel, ANY-method (posteriorSimulation), 40
posteriorSimulation, MixtureModel, integer-method (posteriorSimulation), 40
posteriorSimulation, MixtureModel, numeric-method (posteriorSimulation), 40
posteriorSimulation, MixtureModel-method (posteriorSimulation), 40
probz, 41
INDEX

probz,MixtureModel-method (probz), 41
qInverseTau2, 41
saveBatch, 42
sigma, 43
sigma2, 43
sigma2,BatchModel-method (sigma2), 43
sigma2,MarginalModel-method (sigma2), 43
sigma2,McmcChains-method (sigma2), 43
sigma2,missing-method (sigma2), 43
sigma2.0, 44
sigma2.0,McmcChains-method (sigma2.0), 44
sigma2.0,MixtureModel-method (sigma2.0), 44
sigmac, 44
simulateBatchData, 45
simulateData, 46
tau, 46
tau2, 47
tau2,BatchModel-method (tau2), 47
tau2,MarginalModel-method (tau2), 47
tau2,McmcChains-method (tau2), 47
tauc, 48
tauMean, 48
theta, 49
theta,BatchModel-method (theta), 49
theta,MarginalModel-method (theta), 49
theta,McmcChains-method (theta), 49
thin, 50
thin,McmcParams-method (thin), 50
thin,MixtureModel-method (thin), 50
tracePlot, 50
tracePlot,BatchModel-method (tracePlot), 50
y, 51
y,DensityModel-method (y), 51
y,MixtureModel-method (y), 51
z, 51
z,McmcChains-method (z), 51
z,MixtureModel-method (z), 51
zFreq, 52
zFreq,McmcChains-method (zFreq), 52
zfreq,McmcChains-method (zFreq), 52
zFreq,MixtureModel-method (zFreq), 52
zfreq,MixtureModel-method (zFreq), 52