Package ‘XDE’

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Title XDE: a Bayesian hierarchical model for cross-study analysis of differential gene expression

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Description Multi-level model for cross-study detection of differential gene expression.

Depends R (>= 2.10.0), Biobase (>= 2.5.5), methods, graphics

Imports Biobase, BiocGenerics, genefilter, graphics, grDevices, gtools, MergeMaid, methods, stats, utils, mvtnorm

Suggests siggenes, genefilter, MASS, RColorBrewer, GeneMeta, RUnit

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Enhances coda

License LGPL-2

Collate functions.R AllClasses.R AllGenerics.R RUpdates.R
  methods-ExpressionSet.R methods-ExpressionSetList.R
  methods-mergeExpressionSet.R methods-Parameters.R

LazyLoad yes

biocViews Microarray, DifferentialExpression

NeedsCompilation yes

R topics documented:

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burnin

Indicator for running a MCMC burnin

Description

When TRUE, log files from MCMC chains are not written to file. When FALSE, log files are written for every parameter by default.

Usage

burnin(object)

Arguments

object An object of class XdeParameter

Value

logical

Author(s)

R. Scharpf

See Also

XdeParameter-class
calculatePosteriorAvg

Examples

```r
## Not run:
data(expressionSetList)
params <- new("XdeParameter", phenotypeLabel="adenoVsquamous",
esetList=expressionSetList)
##the replacement method for burnin is called for its side effect of
##providing default values of storing MCMC chains
output(params)[2:22]
burnin(params) <- FALSE
output(params)[2:22]
burnin(params) <- TRUE
output(params)[2:22]
## End(Not run)
```

calculatePosteriorAvg  
*Calculate the posterior average for indicators of concordant and discordant differential expression*

Description

This function calculates the posterior average for indicators of concordant and discordant differential expression from the saved log files. See details.

Usage

```r
calculatePosteriorAvg(object, NCONC=2, NDIFF=1, burnin=0)
```

Arguments

- **object**: Object of class XdeMcmc
- **NCONC**: Integer: number of studies for which the gene must be differentially expressed (in the same direction) to be classified as concordant differential expression
- **NDIFF**: Integer: number of studies for which a gene must be up- or down-regulated to be classified as differentially expressed. It is the union of concordant and discordant differential expression.
- **burnin**: Integer: number of MCMC iterations for the burnin. Posterior means are computed from the MCMC samples following burnin.

Details

For each iteration,
1. calculate the sign of delta * Delta
2. For each gene, compute the number of positive signs (P) and the number of negative signs (N) (a G x 2 matrix, where G is the number of genes in common across all studies). P + N is <= S, where S is the number of studies.
3. for a given gene, the discordant indicator is simply when P * N is nonzero.
4. The concordant indicator requires P * N = 0 AND P + N >= NCONC, where NCONC is specified by the user.
5. differential expression is simply $|P| + |N| \geq NDIFF$. By default, NDIFF is 1 but can be user-specified. The posterior average is then computed from the mean over all MCMC iterations.

**Value**

A $G \times 3$ matrix.

**Author(s)**

RS

**See Also**

posteriorAvg

---

**empiricalStart**  
*Empirical starting values for the MCMC*

**Description**

Empirical starting values for the MCMC are based on data in objects of class ExpressionSetList.

**Usage**

`empiricalStart(object, zeroNu = FALSE, phenotypeLabel, one.delta=FALSE, T_THRESH=4)`

**Arguments**

- **object**: An object of class ExpressionSetList
- **zeroNu**: Logical: if TRUE, the nu in the Bayesian model are not modeled – set to zero and not updated in the MCMC. Setting zeroNu to TRUE should be regarded as experimental
- **phenotypeLabel**: character: binary phenotype. phenotypeLabel must be in the varLabels of each ExpressionSet object
- **one.delta**: delta in the Bayesian model is a gene-specific indicator for differential expression. If one.delta is FALSE, we assume that a gene can be differentially expressed in a subset of studies. When TRUE, we assume that a gene is differentially expressed in all studies or in none.
- **T_THRESH**: A threshold of t-statistics (calculated row-wise for each study) for determining starting values of the differential expression indicator, delta.

**Value**

A list containing starting values for the MCMC that are derived from empirical estimates of the data.

**Author(s)**

R. Scharpf
expressionSetList

See Also
zeroNu, XdeParameter-class, ExpressionSetList-class

Examples
library(XDE)
data(expressionSetList)
elist <- studyCenter(expressionSetList)
empirical <- empiricalStart(elist, phenotypeLabel="adenoVsquamous", T_THRESH=3)
##By default, initial values for the MCMC are sampled from the prior
##when initializing an object of class XdeParameter
params <- new("XdeParameter", esetList=elist,

phenotypeLabel="adenoVsquamous", one.delta=FALSE, burnin=TRUE)
##The initial values can be replaced by empirical values as follows:
firstMcmc(params) <- empirical

expressionSetList Example of ExpressionSetList

Description
Object of class ExpressionSetList containing three studies. Each element in the list is an ExpressionSet

Usage
data(expressionSetList)

Details
Parmigiani et al. (2004) performed a cross-study analysis of three lung cancer studies. The studies used in this analysis were merged by UniGene identifiers to obtain a set of 3,171 gene. The R experiment data package lungExpression that was developed to facilitate the reproducibility of this analysis contains the three studies as ExpressionSets. Here, we take a random sample of 500 features from one study (the "stanford" study), and split this study into three artificial studies that each contain 4 squamous carcinomas and 3 adenocarcinomas. The three artificial studies are then used to create an instance of the ExpressionSetList class.
See Garber et al. (2001) for the raw data and description of the stanford study.

Source
The experiment data package lungExpression (www.bioconductor.org)

References

Examples
data(expressionSetList)
ExpressionSetList-class

A class for containing a list of ExpressionSets

Description

Each element in the list must be a valid ExpressionSet. The featureNames must be identical for each ExpressionSet.

Objects from the Class

Objects can be created by calls of the form new("ExpressionSetList", ...).

Slots

.Data: Object of class "list"

Extends

Class "list", from data part. Class "vector", by class "list", distance 2. Class class.AssayData, by class "list", distance 2.

Methods

.integrativeCorrelationFilter signature(object = "ExpressionSetList") Experimental function for filtering an arbitrary list of ExpressionSets by integrative correlation. Genes are excluded that do not exceed the fdr threshold in at least 1 of the studies.

"[" signature(x = "ExpressionSetList") Subsets each ExpressionSet element in the list.

coerce signature(from = "list", to = "ExpressionSetList") Coerces a list of ExpressionSet objects to an object of class ExpressionSetList. The validityMethod for the ExpressionSetList class will return an error if the featureNames for each ExpressionSet are not identical.

dim signature(x="ExpressionSetList") applies dim to each element of the list.

featureNames signature(object = "ExpressionSetList") Accessor for the featureNames

geneCenter signature(object = "ExpressionSetList") See geneCenter

lapply signature(object="ExpressionSetList") Coerces instance of ExpressionSetList to a list and does lapply on the list. Returns an object of class ExpressionSetList

nSamples signature(x = "ExpressionSetList") Numerical vector giving the number of samples in each ExpressionSet

nrow signature(x = "ExpressionSetList") Numerical: number of features or genes

pData signature(object = "ExpressionSetList") returns a list of data.frames. The elements of the list correspond to the studies in the ExpressionSetList object.

phenotype signature(object="ExpressionSetList", varLabel="character") Accessor for the clinical variable. Assumes that the clinical variable has the same name in each study.

standardizeSamples signature(object = "ExpressionSetList") See standardizeSamples

studyCenter signature(object = "ExpressionSetList") See studyCenter

zeroNu signature(object = "ExpressionSetList") See zeroNu.
**ExpressionSetList-methods**

**Author(s)**
R. Scharpf

**See Also**
- `XdeMcmc-class`
- `XdeParameter-class`

**Examples**
```
showClass("ExpressionSetList")
data(expressionSetList)
```

---

**Description**
Methods for objects of class `ExpressionSetList`.

**Usage**
```r
phenotype(object, varLabel)
```

**Arguments**
- `object` A `ExpressionSetList`.
- `varLabel` character. Name of the clinical variable.

**Value**
`phenotype` returns a matrix of the clinical variable where each column is a study. We require that the clinical variable have the same name in each study (each element of the `ExpressionSetList` object) and that the clinical variable is binary with values 1 or 0.

---

**firstMcmc**

**Values for the first MCMC iteration**

**Description**
Accessor method for the values of the first MCMC iteration

**Usage**
```r
firstMcmc(object)
```

**Arguments**
- `object` An object of class `XdeParameter`
geneCenter

Value

Returns a list of the values to be used in the first iteration of the MCMC.

Author(s)

R. Scharpf

See Also

XdeParameter-class, lastMcmc

Examples

data(expressionSetList)
params <- new("XdeParameter", phenotypeLabel="adenovsquamous",
            esetList=expressionSetList)
str(firstMcmc(params))

geneCenter

Center the expression values for each gene in a study to zero

Description

Mean centers the genes for each study in a list

Usage

geneCenter(object)

Arguments

object Object of class ExpressionSetList

Value

Object of class ExpressionSetList

Author(s)

R. Scharpf

See Also

studyCenter, ExpressionSetList-class

Examples

data(expressionSetList)
centered <- geneCenter(expressionSetList)
**hyperparameters**  

*Accessor for hyperparameters of the Bayesian model*

### Description

Accessor and replacement methods for hyperparameters of the Bayesian model are provided.

### Usage

```r
hyperparameters(object)
```

### Arguments

- `object`  
  An object of class `XdeParameter`.

### Details

See the `XdeParameterClass` vignette for a more detailed discussion. The default values provided when initializing an object of class `XdeParameter` works well in most instances.

### Value

A numerical vector.

### Author(s)

R. Scharpf

### References

R. Scharpf et al., A Bayesian Model for Cross-Study Differential Gene Expression, Technical Report 158, Johns Hopkins University, Department of Biostatistics, 2007

### Examples

```r
data(expressionSetList)
xlist <- new("XdeParameter", esetList=expressionSetList, phenotypeLabel="adenosquamous")
hyperparameters(xlist)
```
iterations | Number of MCMC iterations

## Description
Number of MCMC iterations

## Usage
```r
erations(object)
```

## Arguments
- `object` | An object of class `XdeParameter` or `XdeMcmc`.

## Details
For an object of class `XdeParameter`, `iterations` specifies the total number of MCMC iterations. Note that by setting the `thin` parameter to a value greater than 1, the number of MCMC iterations will be greater than the number of saved MCMC iterations (saved iterations = iterations / thin).

For an object of class `XdeMcmc` (a class that stores output from the MCMC), `iterations` specifies the number of iterations that were saved.

The replacement method is only defined for the `XdeParameter` class. The class `XdeMcmc` is meant to reflect the information in an already run chain, whereas `XdeParameter` is a class for parameterizing the Bayesian model that has not yet been fit.

## Value
An integer

## Author(s)
R. Scharpf

## See Also
- `XdeParameter-class`, `XdeMcmc-class`

---

lastMcmc | MCMC values for the last iteration

## Description
MCMC values for the last iteration. Useful if more iterations are needed.

## Usage
```r
lastMcmc(object)
```
output

Arguments

object Object of class XdeMcmc

Value
An environment.

Author(s)
R. Scharpf

See Also
firstMcmc

Examples

## Not run:
data(expressionSetList)
xparam <- new("XdeParameter", phenotypeLabel="adenoVsquamous", esetList=expressionSetList)
iterations(xparam) <- 10
fit <- xde(xparam, esetList=expressionSetList)
#Do more iterations and use a different seed
firstMcmc(xparam) <- lastMcmc(fit)
seed(xparam) <- 97814
fit2 <- xde(xparam, esetList=expressionSetList)

#Or
fit2 <- xde(xparam, esetList=expressionSetList, outputMcmc=fit)

## End(Not run)

Description
A numeric vector indicating which chains to write to file and, for those parameters that are written to file, how often the chains should be written to file.

Usage
output(object)

Arguments

object An object of class XdeParameter or XdeMcmc

Details
Replacement methods are only available for objects of class XdeParameter. Accessor methods are available for objects of class XdeParameter and XdeMcmc.
Parameters-class

Value

A named numerical vector. The first element (thin) specifies how often to write chains to file. For instance, if output[1]=2 the chains will be written to file every other iteration. Elements 2 - 22 of the vector are indicators for whether to write the chains of the Bayesian parameters to file.

Note

Parameters indexed by gene and study (Delta, Phi, Nu, and sigma2) grow very large quickly.

Author(s)

R. Scharpf

See Also

burnin, XdeParameter-class, XdeMcmc-class

Examples

data(xmcmc)
output(xmcmc)

pairs-methods

pairs function for high-throughput data

Description

A convenient wrapper for pairs that uses smoothScatter to plot the density of the points and displays the spearman correlation coefficient of the pairwise scatterplots.

Methods

x = "matrix" Typically a matrix of effect size estimates obtained in each study. Rows are genes, columns are studies.

x = "data.frame" Typically a data.frame of effect size estimates obtained in each study. Rows are genes, columns are studies.

Parameters-class

Container for XDE parameters

Description

Container for XDE parameters

Objects from the Class

Objects can be created by calls of the form new("Parameters", ...).
Parameters-class

Slots

seed: Object of class "integer" ~~
data: Object of class "numeric" ~~
phenodata: Object of class "integer" ~~
G: Object of class "integer" ~~
Q: Object of class "integer" ~~
S: Object of class "integer" ~~
alphaA: Object of class "numeric" ~~
alphaB: Object of class "numeric" ~~
betaA: Object of class "numeric" ~~
betaB: Object of class "numeric" ~~
pA0: Object of class "numeric" ~~
pA1: Object of class "numeric" ~~
pB0: Object of class "numeric" ~~
pB1: Object of class "numeric" ~~
uR: Object of class "numeric" ~~
uRho: Object of class "numeric" ~~
alphaXi: Object of class "numeric" ~~
betaXi: Object of class "numeric" ~~
c2Max: Object of class "numeric" ~~
alphaEta: Object of class "numeric" ~~
betaEta: Object of class "numeric" ~~
pOmega0: Object of class "numeric" ~~
lambdaOmega: Object of class "numeric" ~~
lambdaKappa: Object of class "numeric" ~~
gamma2: Object of class "numeric" ~~
c2: Object of class "numeric" ~~
tau2Rho: Object of class "numeric" ~~
tau2R: Object of class "numeric" ~~
a: Object of class "numeric" ~~
b: Object of class "numeric" ~~
l: Object of class "numeric" ~~
t: Object of class "numeric" ~~
lambda: Object of class "numeric" ~~
theta: Object of class "numeric" ~~
phi: Object of class "numeric" ~~
sigma2: Object of class "numeric" ~~
r: Object of class "numeric" ~~
rho: Object of class "numeric" ~~
nu: Object of class "numeric" ~~
delta: Object of class "numeric" ~~
Delta: Object of class "numeric" ~~
xi: Object of class "numeric" ~
posteriorAvg

Methods

"[[<-" signature(x = "Parameters"):
"[[" signature(x = "Parameters"):
"$<-" signature(x = "Parameters"):
$ signature(x = "Parameters"):
coerce signature(from = "XdeParameter", to = "Parameters"):
show signature(object = "Parameters"):

Examples

showClass("Parameters")

| posteriorAvg | Accessor and replacement methods for posterior averages of differential expression |

Description

Accessor and replacement methods for objects of class XdeMcmc for posterior averages of differential expression

Usage

posteriorAvg(object)
posteriorAvg(object) <- value

Arguments

object Object of class XdeMcmc
value A matrix of dimension G x 3, where G is the number of genes and 3 are different ways of quantifying differential expression in the context of multiple studies (concordant, discordant, or the union).

Value

A matrix of dimension G x 3, where G is the number of genes and 3 are different ways of quantifying differential expression in the context of multiple studies (concordant, discordant, or the union).

Author(s)

RS

See Also

calculatePosteriorAvg
seed

Seed for the MCMC

Description
Setting a seed is useful for reproducing MCMC chains

Usage

seed(object)
seed(object) <- value

Arguments

object An object of XdeParameter or XdeMcmc
value Numeric or integer

Details
The seed stored in the slot of an object of class XdeParameter and an object of class XdeMcmc are useful in different ways. For the XdeParameter class, the seed indicates what seed was used to initialize an MCMC chain. By contrast, an object of class XdeMcmc contains a seed that would be useful for running additional iterations – the seed here is guaranteed to be different from the seed that was used to initiate the MCMC.

Value
An integer

Author(s)
R. Scharpf

ssStatistic Calculate single study estimates of effect size

Description
Calculate single study estimates of effect size for lists of ExpressionSets

Usage

ssStatistic(statistic = c("t", "sam", "z")[1], phenotypeLabel, esetList, ...)

Arguments

statistic Character string indicating Welch t-statistic (t), SAM (sam), or a z-statistic (z)
phenotypeLabel Character string indicating the name of the binary covariate
esetList An object of class ExpressionSetList
...

Not implemented. Potentially additional arguments to the above methods that are implemented in other packages
Details

This function is a wrapper that provides an estimate of effect size for each study (element) in an ExpressionSetList object.

For Welch t-statistic, this function is a wrapper for mt.teststat in the multtest package.

For SAM, this function is a wrapper for the sam function in the siggenes package.

The "z" statistic is a standardized unbiased estimate of effect size (Hedges and Olkin, 1985) – implementation is in the zScores function in the R package GeneMeta.

See the complete references below.

Value

A matrix: rows are genes and columns are studies

Author(s)

R. Scharpf

References

J.K. Choi, U. Yu, S. Kim, and O.J. Yoo (2003), Combining multiple microarray studies and modeling interstudy variation, Bioinformatics, 19(1) I84-I90.

Y. Ge, S. Dudoit & T. P. Speed (2003), Resampling-based multiple testing for microarray data hypothesis Test 12(1): 1-44 (with discussions on 44-77).

L. Lusa R. Gentleman, and M. Ruschhaupt, GeneMeta: MetaAnalysis for High Throughput Experiments


Examples

```r
data(expressionSetList)
if(require(siggenes)){
  sam <- ssStatistic("sam", esetList=expressionSetList, phenotypeLabel="adenovsquamous")
}
```

standardizeSamples  
Centers the genes at zero and standardizes the samples to have variance 1

Description

For each study (element) in an ExpressionSetList object, this function centers the genes to have mean zero (rows) and scales the variance of the samples to 1.

Usage

```r
standardizeSamples(object, ...)
```
studyCenter

Arguments

  object  Object of class ExpressionSetList
  ...    Additional arguments not implemented

Value

  An object of class ExpressionSetList

Note

  Requires genefilter package

Author(s)

  R. Scharpf

Description

  Centers each study in a list so that the average expression value of each study is zero

Usage

  studyCenter(object)

Arguments

  object  An object of class ExpressionSetList

Value

  An object of class ExpressionSetList

Author(s)

  R. Scharpf

See Also

  geneCenter, ExpressionSetList-class

Examples

  data(expressionSetList)
  centered <- studyCenter(expressionSetList)
  lapply(centered, function(object) round(mean(exprs(object)), 4))
symbolsInteresting

Useful for changing the look of pairs plots to emphasize concordant or discordant genes

Description

This function can be used to order genes in a matrix by the rank of a statistic and provide different plotting symbols and colors for genes that exceed a certain threshold of the ranking statistic.

Usage

symbolsInteresting(rankingStatistic, percentile = 0.9, colors = c("grey50", "royalblue"), symbols = c(".", "o"), size = c(3, 1), background = c("white", "grey70"))

Arguments

- **rankingStatistic**: Any numerical vector
- **percentile**: A percentile of the rankingStatistic – above which a gene would be classified as ‘interesting’
- **colors**: character string of length 2: a color for genes not exceeding the percentile and a color for genes exceeding the threshold
- **symbols**: two plotting symbols (numeric or character): symbol for genes not exceeding percentile and symbol for genes exceeding percentile
- **size**: numeric vector of length 2: size of plotting symbol for genes not exceeding percentile and size of plotting symbol for genes exceeding percentile
- **background**: character vector of length 2: background color of plotting symbols for gene not exceeding percentile and for genes exceeding the percentile

Value

- **order**: the order of the rankingStatistic
- **pch**: plotting symbols (same length as rankingStatistic)
- **col**: color of plotting symbols (same length as rankingStatistic)
- **bg**: background color of plotting symbols (same length as rankingStatistic)
- **cex**: size of plotting symbols (same length as rankingStatistic)

Author(s)

R. Scharpf

Examples

data(expressionSetList)
data(xmcmc)
pathToLogFiles <- system.file("logFiles", package="XDE")
load(file.path(pathToLogFiles, "BES.rda"))
load(file.path(pathToLogFiles, "postAvg.rda"))
op.conc <- symbolsInteresting(rankingStatistic=postAvg[, "concordant"])
graphics:::pairs(BES[op.conc$order, ], pch=op.conc$pch, col=op.conc$col,
thin

Description

How often to write MCMC iterations to file

A value greater than one means that not every MCMC iteration is written to file.

Usage

thin(x, ...)

Arguments

x

An object of class XdeParameter

... not implemented

Details

thin is an accessor for the first element in the vector returned by the method output.
The replacement method replaces the first element in the output vector.

Value

An integer.

Author(s)

R. Scharpf

See Also

output

tuning

Tuning parameters for Metropolis-Hastings proposals

Description

Accessor and replacement methods for tuning the Metropolis-Hastings proposal parameters.

Usage

tuning(object)

Arguments

object Object of class XdeParameter
**Details**

See the XdeParameterClass vignette

**Value**

A numerical vector

**Author(s)**

R. Scharpf

---

**updates**  
*Frequency of updating a parameter per MCMC iteration*

**Description**

Accessor and replacement methods for the class XdeParameter are available. Specifying an update of integer N for a Metropolis-Hastings parameter means that N values are proposed for that parameter for each MCMC iteration.

**Usage**

updates(object)

**Arguments**

object  
An object of class XdeParameter

**Details**

See the XdeParameterClass vignette

**Value**

A numerical vector

**Author(s)**

R. Scharpf
**Description**

Fits the Bayesian hierarchical model for cross-study differential gene expression.

**Usage**

```r
xde(paramsMcmc, esetList, outputMcmc, batchSize=NULL, NCONC=2,
    center=TRUE, ...)
```

**Arguments**

- `paramsMcmc`: Object of class `XdeParameter`
- `esetList`: Object of class `ExpressionSetList`
- `outputMcmc`: Object of class `XdeMcmc` (optional)
- `batchSize`: Integer or NULL. The number of iterations written to log files before summarizing the chain and then removing. Experimental.
- `NCONC`: The number of studies for which a gene must be differentially expressed in the same direction to be considered as concordantly differentially expressed.
- `center`: Logical. If TRUE, each study is centered to have mean zero.
- `...`: Additional arguments passed to `xdeFit`.

**Details**

Details for fitting the Bayesian model are discussed elsewhere (see citation below and `XdeParameterClass` vignette)

If an integer is specified for the `batchSize`, summary statistics for the log-files are calculated for every `batchSize` iterations. The log files are then removed and the next iteration will start a new log file. This allows one to do many iterations without creating enormous log files. This is only reasonable to do if one has already assessed convergence.

**Value**

Object of class `XdeMcmc`

**Note**

See the vignettes for `XdeParameterClass` and `XDE`.

**Author(s)**

R. Scharpf
References


See Also
XdeMcmc-class, XdeParameter-class, ExpressionSetList-class

Examples

## Not run:
data(expressionSetList)
xparam <- new("XdeParameter", phenotypeLabel="adenovsquamous", esetList=expressionSetList)
iterations(xparam) <- 10
fit <- xde(xparam, esetList=expressionSetList)
## End(Not run)

XdeMcmc-class

Class for storing output from the Bayesian model

Description

Stores output, including the last iteration of the MCMC.

Objects from the Class

Objects can be created by calls of the form new("XdeMcmc", studyNames, featureNames, iterations, seed, output).

Slots

  studyNames: Object of class "character"
  featureNames: Object of class "character"
  iterations: Object of class "numeric"
  directory: Object of class "character"
  seed: Object of class "integer"
  output: Object of class "numeric"
  lastMcmc: Object of class "environment"
  posteriorAvg: Object of class "NULLorMatrix"
  bayesianEffectSize: Object of class "NULLorMatrix"

Methods

  $ signature(x = "XdeMcmc")
  standardizedDelta signature(object = "XdeMcmc")
  bayesianEffectSize signature(object = "XdeMcmc")
  bayesianEffectSize<-. signature(object = "XdeMcmc", value = "matrix")
  calculatePosteriorAvg signature(object = "XdeMcmc"): See calculatePosteriorAvg
XdeParameter-class

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Author(s)
R. Scharpf

See Also
The class for storing the data: ExpressionSetList-class and the class that contains default options for fitting the Bayesian model: XdeParameter-class

Examples
```r
## See XDE vignette:
## Not run:
openVignette(package="XDE")
## End(Not run)
```

XdeParameter-class  Container class for storing options of the Bayesian hierarchical model

Description
This class contains initial values for the first iteration of the MCMC, options for saving MCMC chains, options for changing the tuning parameters of the Metropolis-Hastings algorithm, options for changing hyperparameters from their defaults, etc.

Objects from the Class
Objects can be created by calls of the form `new("XdeParameter", esetList, updates, tuning, hyperparameters...).`
Slots

updates: Object of class numeric. The frequency of updates for each iteration of the chain.
tuning: Object of class numeric. Tuning parameters for the Metropolis-Hastings proposals
hyperparameters: Object of class numeric. Hyperparameters for the Bayesian hierarchical model
output: Object of class numeric. Indicator for whether to save the MCMC chain to file. If the
        value is zero, the chain is not saved.
iterations: Object of class numeric. The total number of MCMC iterations.
burnin: Object of class logical. If set to FALSE, by default none of the chains will be saved
        (called for its side-effect of setting the output to zero for each parameter).
notes: Object of class character.
firstMcmc: Object of class environment. Values for the first iteration of the MCMC
seed: Object of class integer. Seed used for simulating random numbers.
showIterations: Object of class logical. Whether to show the MCMC iteration when fitting the
model
specifiedInitialValues: Object of class logical. If TRUE (the default), the values stored in
firstMcmc will be used for the first iteration of the MCMC.
directory: Object of class character. Specifies where to write the log files
phenotypeLabel: Object of class character. The name of the binary covariate used for differential
expression
verbose: Object of class logical
studyNames: Object of class character. Names of the datasets
one.delta: Logical. If TRUE, a gene is assumed to be differentially in all studies or none of the
studies.

Methods

burnin  signature(object = "XdeParameter") logical. See burnin
burnin<- signature(object = "XdeParameter", value = "logical") logical. See burnin
directory  signature(object = "XdeParameter") character string giving the path or relative
path to store log files from the MCMC chain
directory<- signature(object = "XdeParameter") Path to store log files.
firstMcmc  signature(object = "XdeParameter") See firstMcmc
firstMcmc<- signature(object = "XdeParameter", value = "environment")
firstMcmc<- signature(object = "XdeParameter", value = "list")
hyperparameters  signature(object = "XdeParameter") See the XdeParameterClass vignette
hyperparameters<- signature(object = "XdeParameter") See the XdeParameterClass vignette
initialize  signature(.Object = "XdeParameter") Method for initializing an instance of the
class. The default values provided work well in most cases.
iterations  signature(object = "XdeParameter") Accessor for the total number of MCMC
iterations to run
iterations<- signature(object = "XdeParameter", value = numeric) The replacement
method is useful for setting a different number of iterations.
iterations<- signature(object = "XdeParameter", value = "integer")
output signature(object = "XdeParameter") See also output. This method is also defined for class XdeMcmc

output<- signature(object = "XdeParameter") See also output

phenotypeLabel signature(object = "XdeParameter") The name of a binary covariate present in each study

phenotypeLabel<- signature(object = "XdeParameter", value = "character")

savedIterations signature(object = "XdeParameter") The number of MCMC iterations written to file. It is the value of the total number of iterations divided by the thinning parameter. See also output

seed signature(object = "XdeParameter") See seed

seed<- signature(object = "XdeParameter", value = "integer") Replacement method. See also seed.

show signature(object = "XdeParameter") Produces a short summary of objects that are instances of the XdeParameter class

showIterations signature(object = "XdeParameter") logical

showIterations<- signature(object = "XdeParameter")

studyNames signature(object = "XdeParameter") Names of the high-throughput gene expression studies

studyNames<- signature(object = "XdeParameter")

thin signature(x = "XdeParameter") See output and thin

thin<- signature(x = "XdeParameter", value = numeric) See thin

tuning signature(object = "XdeParameter") See also tuning

tuning<- signature(object = "XdeParameter")

updates signature(object = "XdeParameter") See also updates

updates<- signature(object = "XdeParameter")

Author(s)

R. Scharpf

References

R. Scharpf

See Also

ExpressionSetList-class

Examples

tshowClass("XdeParameter")

##See the XdeParameterClass vignette
**xmcnc**  
*Object of class XdeMcmc*

**Description**

An object of class XdeMcmc is created by fitting the Bayesian hierarchical model to the expressionSetList example data.

**Usage**

```r
data(xmcnc)
```

**Details**

The xmcnc data example was obtained as described in the XDE vignette.

**Examples**

```r
data(xmcnc)
xmcnc
```

```r
# ordinarily, one should not need to change the directory in an object
# of class XdeMcmc -- therefore, a replacement method is not defined
pathToLogFiles <- system.file("logFiles", package="XDE")
xmcnc@directory <- pathToLogFiles

# The $ operator can be used to extract chains. For instance, here we
# extract the c2 chain
c2 <- xmcnc$c2
plot.ts(c2)
```

---

**xsScores**  
*Alternative cross-study scores of differential expression*

**Description**

Alternative cross-study scores of differential expression

**Usage**

```r
xsScores(statistic, N)
```

**Arguments**

- **statistic**: a matrix of study-specific estimates of effect size. Rows are genes and columns are studies.
- **N**: numerical vector: the number of samples in each study (the length should be the number of columns in statistic)
**Value**

A matrix of cross-study scores for differential expression ("diffExpressed"), concordant differential expression, and discordant differential expression.

**Author(s)**

R. Scharpf

**References**


R. Scharpf et al., A Bayesian Model for Cross-Study Differential Gene Expression, Technical Report 158, Johns Hopkins University, Department of Biostatistics, 2007

**See Also**

the GeneMeta package, ssStatistic

**Examples**

```r
data(expressionSetList)
t <- ssStatistic(statistic="t", phenotypeLabel="adenovsquamous", esetList=expressionSetList)
tScores <- xsScores(t, N=nSamples(expressionSetList))
```

---

**zeroNu**  
*Option for not modeling Nu*

**Description**

Nu is the average expression value in each study.

**Usage**

`zeroNu(object, ...)`

**Arguments**

- `object`: object of class `ExpressionSetList`
- `...`: Not implemented
Details

This function should be regarded as experimental.

The nu parameter models the average expression value in each study. Modeling nu allows one to estimate differential expression across studies that may differ in location and scale (as often occurs when multiple platforms are used). The price to pay for modeling nu are additional assumptions (the nu's are assumed Gaussian) and a more heavily parameterized model.

The method zeroNu allows one to fit the Bayesian model without estimating nu:
- each gene is centered at zero
- initial values for the first MCMC are chosen on the basis of empirical starting values
- the initial values for a and rho are set to zero.
- the nu, a, gamma2, and rho parameters are not updated during MCMC

Value

object of class XdeParameter

Author(s)

R. Scharpf

References

R. Scharpf et al. (2007), A Bayesian Model for Cross-Study Differential Gene Expression, Technical Report 158, Johns Hopkins University, Department of Biostatistics
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