Package ‘betr’

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Type Package

Title Identify differentially expressed genes in microarray time-course data

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Depends R(>= 2.6.0)

Imports Biobase (>= 2.5.5), limma, mvtnorm, methods, stats

Suggests Biobase

Description The betr package implements the BETR (Bayesian Estimation of Temporal Regulation) algorithm to identify differentially expressed genes in microarray time-course data.

License LGPL

LazyLoad yes

biocViews Microarray, DifferentialExpression, TimeCourse

PackageStatus Deprecated

NeedsCompilation no

R topics documented:

`betr-package` *Identify differentially expressed genes in microarray time-course experiments*

Description

The betr package implements the BETR (Bayesian Estimation of Temporal Regulation) algorithm.

Details

Package:	betr
Type:	Package
License:	LGPL (>= 2.0)
LazyLoad:	yes

Author(s)

Martin Aryee Maintainer: <aryee@jhu.edu>

References

Smyth, G. Linear models and empirical bayes methods for assessing differential expression in microarray experiments. Statistical applications in genetics and molecular biology (2004) vol. 3, article 3 Tai, Y and Speed, T. A multivariate empirical Bayes statistic for replicated microarray time course data. Annals of Statistics (2006) vol. 34 (5) pp. 2387-2412

See Also

`betr`

Examples

```
library(Biobase)
data(timeEset)
prob <- betr(timeEset, cond=pData(timeEset)$strain,
    timepoint=pData(timeEset)$time, replicate=pData(timeEset)$rep, alpha=0.05)
head(prob)
```

`betr` *Bayesian Estimation of Temporal Regulation (BETR): Calculate the probability of differential expression in time-course data*

Description

Calculate the probability of differential expression of each feature in a microarray gene expression time-course data set.

Usage

```
betr(eset, cond=NULL, timepoint, replicate, twoColor = FALSE, twoCondition = NULL, alpha = 0.05, ve
```

Arguments

`eset`	object of class matrix, ExpressionSet or exprSet containing log-ratios or log-values of expression for a series of microarrays
`cond`	character or factor vector giving the experimental group for each sample of eset. Not required for a single-condition time-course.
`timepoint`	numeric vector giving the time point for each sample of eset
`replicate`	character or factor vector giving the replicate ID of each sample of eset
`twoColor`	boolean indicating whether the data is from a two-color microarray platform
`twoCondition`	boolean indicating whether the data is from a two condition experiment (as opposed to a single condition experiment where the comparison is between baseline and subsequent time points)
`alpha`	the desired False Discovery Rate
`verbose`	whether to output more detailed information about the model fitting

Details

This function fits a model to estimate the probability of differential for each feature of time-course data set.

Value

a numeric vector of the probability of differential expression for each feature in the data set.

Author(s)

Martin Aryee

References

The algorithm is described in detail in: Aryee et al., An improved empirical bayes approach to estimating differential gene expression in microarray time-course data: BETR (Bayesian Estimation of Temporal Regulation), BMC Bioinformatics. 2009 Dec 10;10:409.

Examples

```
library(Biobase)
data(timeEset)
prob <- betr(timeEset, cond=pData(timeEset)$strain,
    timepoint=pData(timeEset)$time, replicate=pData(timeEset)$rep, alpha=0.05)
head(prob)
```

`isRepetitive` *betr package: internal function*

Description

An internal function used to determine when the iterative model fitting process has converged.

Arguments

`x`	a list of numeric vectors

Details

This function takes a list of numeric vectors and returns TRUE if two of the vectors are the same.

Value

a boolean

Author(s)

Martin Aryee

See Also

`betr`

`squeezeMVar` *Smooth sample covariance matrices*

Description

An internal function to smooth a set of sample covariance matrices by computing empirical Bayes posterior means.

Usage

```
squeezeMVar(S, df, Lambda = NULL, nu = NULL)
```

Arguments

`S`	a list of covariance matrices
`df`	numeric vector of degrees of freedom for covariance matrices
`Lambda`	use this target covariance matrix instead of calculating it from the data
`nu`	use this nu instead of calculating it from the data

Details

Calculate shrinkage estimates for covariance matrices using the procedure of Tai and Speed (2006) and Smyth (2004)

Value

`varPost`	list of posterior covariance matrices
`varPrior`	target covariance matrix
`dfPrior`	prior degrees of freedom

Author(s)

Martin Aryee

References

Smyth, G. Linear models and empirical bayes methods for assessing differential expression in microarray experiments. Statistical applications in genetics and molecular biology (2004) vol. 3

Tai, Y and Speed, T. A multivariate empirical Bayes statistic for replicated microarray time course data. Annals of Statistics (2006) vol. 34 (5) pp. 2387-2412

See Also

`betr`

`timeEset` *Example data set for the betr package*

Description

A dummy dataset for the examples in the betr package

Usage

```
data(timeEset)
```

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