Package ‘betr’

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Type Package

Title Identify differentially expressed genes in microarray time-course data

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Author Martin Aryee

Maintainer Martin Aryee <aryee@jhu.edu>

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:

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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

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Author(s)
Martin Aryee Maintainer: <aryee@jhu.edu>

References

See Also
betr

Examples

```r
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, verbose=FALSE)

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


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*

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squeezeMVar  

*Smooth sample covariance matrices*

## Description

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

## Usage

```r
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

Value

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

Author(s)

Martin Aryee

References


See Also

- `betr`

**Description**

A dummy dataset for the examples in the betr package

**Usage**

```r
data(timeEset)
```
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