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:

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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

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.
betr

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

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)
timeEset

Value

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

Author(s)

Martin Aryee

References


See Also

betr

data(timeEset)
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