

# Package ‘betr’

April 14, 2017

**Type** Package

**Title** Identify differentially expressed genes in microarray time-course data

**Version** 1.32.0

**Date** 2011-03-15

**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

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betr-package	<i>Identify differentially expressed genes in microarray time-course experiments</i>
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## 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)
```

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betr	<i>Bayesian Estimation of Temporal Regulation (BETR): Calculate the probability of differential expression in time-course data</i>
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## 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)
```

## 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)
```

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isRepetitive	<i>betr package: internal function</i>
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**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	<i>Smooth sample covariance matrices</i>
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**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](#)

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timeEset

*Example data set for the betr package*

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**Description**

A dummy dataset for the examples in the betr package

**Usage**

```
data(timeEset)
```

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