

# Package ‘betr’

October 8, 2015

**Type** Package

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

**Version** 1.24.0

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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

**NeedsCompilation** no

## R topics documented:

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

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

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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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