

# Package ‘RBM’

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**Version** 1.28.0

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**Title** RBM: a R package for microarray and RNA-Seq data analysis

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**Depends** R (>= 3.2.0), limma, marray

**Description** Use A Resampling-Based Empirical Bayes Approach to Assess Differential Expression in Two-Color Microarrays and RNA-Seq data sets.

**License** GPL (>= 2)

**git\_url** <https://git.bioconductor.org/packages/RBM>

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## R topics documented:

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RBM-package

*RBM: a package for microarray and RNA-Seq data analysis*

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## Description

Use A Resampling-Based Empirical Bayes Approach to Assesse Differential Expression or Identifying differentially methylated loci in Two-Color Microarrays and RNA-Seq data sets. Significant features selected through RBM\_T or RBM\_F functions could be further used as input for pathway analysis or experimental vilidations.

## Details

Package: RBM  
Type: Package  
Version: 0.99.0  
Date: 2014-10-05  
Depends: R (>= 3.0.0), limma, marray  
License: GPL (>= 2)

## Author(s)

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## References

Li D, Le Pape MA, Parikh NI, Chen WX, Dye TD (2013) Assessing Differential Expression in Two-Color Microarrays: A Resampling-Based Empirical Bayes Approach. PLoS ONE 8(11): e80099. doi: 10.1371/journal.pone.0080099

## See Also

The [RBM\\_T](#) and [RBM\\_F](#) functions defined in this package. The [limma](#) and [marray](#) packages.

## Examples

```
normal_data <- matrix(rnorm(200*6), 200, 6)
mydesign <- c(0,0,0,1,1,1)
norm_result <- RBM_T(normal_data,mydesign,50,0.05)

unif_data <- matrix(runif(200*7, 0.10, 0.95), 200, 7)
mydesign2 <- c(0,0,0, 1,1,1,1)
unif_result <- RBM_T(unif_data,mydesign2,100,0.05)
```

```
normdata_F <- matrix(rnorm(200*9, 0, 2), 200, 9)
mydesign_F <- c(0, 0, 0, 1, 1, 1, 2, 2, 2)
aContrast <- c("X1-X0", "X2-X1", "X2-X0")
normresult_F <- RBM_F(normdata_F, mydesign_F, aContrast, 100, 0.05)

unifdata_F <- matrix(runif(200*18, 0.15, 0.98), 200, 18)
mydesign2_F <- c(rep(0, 6), rep(1, 6), rep(2, 6))
aContrast <- c("X1-X0", "X2-X1", "X2-X0")
unifresult_F <- RBM_F(unifdata_F, mydesign2_F, aContrast, 100, 0.05)
```

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ovarian\_cancer\_methylation

*ovarian cancer methylation example from United Kingdom Ovarian Cancer Population Study (UKOPS)*

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## Description

This data set contains DNA methylation level from 1000 DNA methylation loci in 8 randomly selected women with 4 ovarian cancer cases (pre-treatment) and 4 age-matched healthy controls.

## Usage

```
ovarian_cancer_methylation
```

## Format

A matrix containing 1000 rows and 8 columns with each row denoting a methylation locus and each column denoting a subject.

## Value

The ovarian cancer methylation example data set contains the following information:

|         |                              |
|---------|------------------------------|
| IlmnID  | Name of DNA methylation loci |
| case    | Ovarian cancer patients      |
| control | Healthy controls             |

## Source

NCBI GEO website with access number GSE19711

## References

Teschendorff AE, Menon U, Gentry-Maharaj A, Ramus SJ et al. Age-dependent DNA methylation of genes that are suppressed in stem cells is a hallmark of cancer. *Genome Res* 2010 Apr;20(4):440-6. PMID: 20219944

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RBM\_F *RBM\_F: a R function for microarray and RNA-Seq data analysis for designs with more than two groups*

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### Description

Use A Resampling-Based Empirical Bayes Approach to Assess Differential Expression in Two-Color Microarrays and RNA-Seq data sets for designs with more than two groups.

### Usage

```
RBM_F(aData, vec_trt, aContrast, repetition, alpha)
```

### Arguments

|            |   |
|------------|---|
| aData      | The input data set with rows and columns denoting features and samples, respectively  |
| vec_trt    | A vector for group notation such as 1s denote treatment group and 0s denote control group   |
| aContrast  | A vector for contrast. For example: if we want to compare group 1 with group 0, group 2 with group 1, and group 2 with group 0, then the contrast vector will be ("X1-X0", "X2"- "X1", "X2-X0") |
| repetition | The number of resamplings used in the analysis. You could use 1000 or higher number   |
| alpha      | The significance level  |

### Details

Combine resampling with empirical Bayes approach for Microarrays and RNA-Seq data analysis.

### Value

RBM\_F produces a named list with the following components:

|               |  |
|---------------|--|
| ordfit_t      | original t statistics  |
| ordfit_pvalue | original p-values from lmFit and eBayes  |
| ordfit_beta0  | estimated mean for the control group   |
| ordfit_beta1  | estimated mean difference between treatment and control group                  |
| permutation_p | calculated p-values from permutation method based on resampled test statistics |
| bootstrap_p   | calculated p-values from bootstrap method based on resampled test statistics   |

### Author(s)

Dongmei Li and Chin-Yuan Liang

## References

Li D, Le Pape MA, Parikh NI, Chen WX, Dye TD (2013) Assessing Differential Expression in Two-Color Microarrays: A Resampling-Based Empirical Bayes Approach. PLoS ONE 8(11): e80099. doi: 10.1371/journal.pone.0080099

## See Also

The [RBM\\_T](#) function defined in this package. The [limma](#) and [marray](#) packages.

## Examples

```
normdata_F <- matrix(rnorm(200*9, 0, 2), 200, 9)
mydesign_new <- c(0, 0, 0, 1, 1, 1, 2, 2, 2)
aContrast <- c("X1-X0", "X2-X1", "X2-X0")
normresult_F <- RBM_F(normdata_F, mydesign_new, aContrast, 100, 0.05)

unifdata_F <- matrix(runif(200*18, 0.15, 0.98), 200, 18)
mydesign2_new <- c(rep(0, 6), rep(1, 6), rep(2, 6))
aContrast <- c("X1-X0", "X2-X1", "X2-X0")
unifresult_F <- RBM_F(unifdata_F, mydesign2_new, aContrast, 100, 0.05)
```

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RBM\_T

*RBM\_T: a R function for microarray and RNA-Seq data analysis for two-group comparisons*

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## Description

Use A Resampling-Based Empirical Bayes Approach to Assess Differential Expression or Identify differentially methylated loci in Two-Color Microarrays and RNA-Seq data sets.

## Usage

```
RBM_T(aData, vec_trt, repetition, alpha)
```

## Arguments

|            |   |
|------------|---|
| aData      | The input data set with rows and columns denoting features and samples, respectively      |
| vec_trt    | A vector for group notation such as 1s denote treatment group and 0s denote control group |
| repetition | The number of resamplings used in the analysis. You could use 1000 or higher number       |
| alpha      | The significance level  |

## Details

Combine resampling with empirical Bayes approach for Microarrays and RNA-Seq data analysis.

**Value**

RBM\_T produces a named list with the following components:

|               |  |
|---------------|--|
| ordfit_t      | original t statistics  |
| ordfit_pvalue | original p-values from lmFit and eBayes  |
| ordfit_beta0  | estimated mean for the control group   |
| ordfit_beta1  | estimated mean difference between treatment and control group                  |
| permutation_p | calculated p-values from permutation method based on resampled test statistics |
| bootstrap_p   | calculated p-values from bootstrap method based on resampled test statistics   |

**Author(s)**

Dongmei Li and Chin-Yuan Liang

**References**

Li D, Le Pape MA, Parikh NI, Chen WX, Dye TD (2013) Assessing Differential Expression in Two-Color Microarrays: A Resampling-Based Empirical Bayes Approach. PLoS ONE 8(11): e80099. doi: 10.1371/journal.pone.0080099

**See Also**

The [RBM\\_F](#) function defined in this package. The `limma` and `marray` packages.

**Examples**

```
normal_data <- matrix(rnorm(200*6), 200, 6)
mydesign <- c(0,0,0,1,1,1)
norm_result <- RBM_T(normal_data,mydesign,50,0.05)

unif_data <- matrix(runif(200*7, 0.10, 0.95), 200, 7)
mydesign2 <- c(0,0,0, 1,1,1,1)
unif_result <- RBM_T(unif_data,mydesign2,100,0.05)
```

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