Package 'RBM'

July 4, 2025

biocViews Microarray, DifferentialExpression

Version 1.41.0

Date 2014-10-02

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

Author Dongmei Li and Chin-Yuan Liang

Maintainer Dongmei Li <`Dongmei_Li@urmc.rochester.edu`>

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

git_branch devel

git_last_commit 2ade9ac

git_last_commit_date 2025-04-15

Repository Bioconductor 3.22

Date/Publication 2025-07-03

Contents

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

Description

Use A Resampling-Based Empirical Bayes Approach to Assesse Differential Expression or Identifying differntially 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)

Dongmei Li and Chin-Yuan Liang Maintainer: Dongmei Li <dongmeiliur@gmail.com> and Chin-Yuan Liang <liang.tony@gmail.com>

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)
```

`ovarian_cancer_methylation`

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

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 methyaltion 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

`RBM_F`	*RBM_F: a R function for microarray and RNA-Seq data analysis for designs with more than two groups*

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 signifiance 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`	orignal 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)
```

`RBM_T` *RBM_T: a R function for microarray and RNA-Seq data analysis for two-group comparisons*

Description

Use A Resampling-Based Empirical Bayes Approach to Assess Differential Expression or Identify differntially 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 signifiance 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`	orignal 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)
```

Index