Package ‘RBM’

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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)
NeedsCompilation no

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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 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 validations.
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


See Also

The `RBM_T` and `RBM_F` functions defined in this package. The limma and marray packages.

Examples

```r
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 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**


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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*

**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


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 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


See Also

The RBM_F function defined in this package. The limma and marray packages.
Examples

```r
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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