Package ‘RBM’

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Version  1.8.0  
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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)  
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 Assess 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:

<table>
<thead>
<tr>
<th>IlmnID</th>
<th>Name of DNA methylation loci</th>
</tr>
</thead>
<tbody>
<tr>
<td>case</td>
<td>Ovarian cancer patients</td>
</tr>
<tr>
<td>control</td>
<td>Healthy controls</td>
</tr>
</tbody>
</table>

**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**

```r
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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