Package ‘RBM’

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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)**

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**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

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

RBM_F

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

```r
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

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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