Package ‘RBM’

February 1, 2017

biocViews  Microarray, DifferentialExpression
Version     1.6.0
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)
NeedsCompilation no

R topics documented:

RBM-package .................................................. 1
ovarian_cancer_methylation ..................................... 3
RBM_F .................................................. 3
RBM_T .................................................. 5

Index

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)
```
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
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

daData  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: 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,mydesign,100,0.05)
```
Index

*Topic Microarray and RNA-Seq
  RBM_F, 3
  RBM_T, 5

*Topic Resampling, Empirical Bayes, Microarray, RNA-Seq
  RBM-package, 1

*Topic Resampling
  RBM_F, 3
  RBM_T, 5

*Topic datasets
  ovarian_cancer_methylation, 3

ovarian_cancer_methylation, 3

RBM (RBM-package), 1
RBM-package, 1
RBM_F, 2, 3, 5
RBM_T, 2, 4, 5