Package ‘RBM’
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**biocViews** Microarray, DifferentialExpression

**Version** 1.6.0

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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)

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Yuan Liang <liang.tony@gmail.com>

References

Li D, Le Pape MA, Parikh NI, Chen WX, Dye TD (2013) Assessing Differential Expression in Two-
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 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


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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