# Package: EBSeq (via r-universe)

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**Type** Package

**Title** An R package for gene and isoform differential expression analysis of RNA-seq data

**Version** 2.12.0

**Date** 2015-12-8

**Depends** blockmodeling, gplots, testthat, R (>= 3.0.0)

**Description** Differential Expression analysis at both gene and isoform level using RNA-seq data

**License** Artistic-2.0

**LazyLoad** yes

**Collate** 'MedianNorm.R' 'GetNg.R' 'beta.mom.R' 'EBTest.R' 'GetPatterns.R' 'EBMultiTest.R' 'PostFC.R' 'GetPPMat.R' 'GetMultiPP.R' 'GetMultiFC.R' 'PlotPostVsRawFC.R' 'crit_fun.R' 'DenNHist.R' 'GetNormalizedMat.R' 'PlotPattern.R' 'PolyFitPlot.R' 'QQP.R' 'QuantileNorm.R' 'RankNorm.R' 'GetDEResults.R' 'EBSeqTest.R' 'Likefun.R' 'LikefunMulti.R' 'LogN.R' 'LogNMulti.R' 'f0.R' 'f1.R' 'GetSelectedPatterns.R'

**BuildVignettes** no

**Imports** Rcpp (>= 0.12.11), RcppEigen (>= 0.3.2.9.0), BH

**LinkingTo** Rcpp,RcppEigen,BH

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**RoxygenNote** 7.1.0

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# Contents

EBSeq_NingLeng-package . . . 3
beta.mom . . . 4
crit_fun . . . 5
DenNHist . . . 6
EBMultiTest . . . 7
EBSeqTest . . . 9
EBTest . . . 10
f0 . . . 12
f1 . . . 13
GeneMat . . . 14
GetDEResults . . . 15
GetMultiFC . . . 17
GetMultiPP . . . 18
GetNg . . . 19
GetNormalizedMat . . . 21
GetPatterns . . . 22
GetPPMat . . . 22
GetSelectedPatterns . . . 23
IsoList . . . 24
IsoMultiList . . . 25
Likefun . . . 25
LikefunMulti . . . 26
LogN . . . 27
LogNMulti . . . 28
MedianNorm . . . 29
MultiGeneMat . . . 30
PlotPattern . . . 31
PlotPostVsRawFC . . . 31
PolyFitPlot . . . 32
PostFC . . . 34
QQP . . . 35
QuantileNorm . . . 36
RankNorm . . . 37

**Index** **39**

EBSeq_NingLeng-package

*EBSeq: RNA-Seq Differential Expression Analysis on both gene and isoform level*

## Description

In 'EBSeq_NingLeng-package,' a Negative Binomial-beta model was built to analyze the RNASeq data. We used the empirical bayes method and EM algrithom.

## Details

| | |
|---|---|
| Package: | EBSeq_NingLeng |
| Type: | Package |
| Version: | 1.0 |
| Date: | 2011-06-13 |
| License: | What license is it under? |
| LazyLoad: | yes |

## Author(s)

Ning Leng,Xiuyu Ma, Christina Kendziorski, Michael A. Newton

Maintainer: Ning Leng <lengning1@gmail.com» Xiuyu Ma <watsonforfun@gmail.com>

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## See Also

EBTest, EBMultiTest

## Examples

```
data(GeneMat)
GeneMat.small = GeneMat[c(1:10,511:550),]
Sizes = MedianNorm(GeneMat.small)
EBOut = EBTest(Data=GeneMat.small,
 Conditions=as.factor(rep(c("C1","C2"), each=5)),
 sizeFactors=Sizes, maxround=5)
```

beta.mom *Fit the beta distribution by method of moments*

## Description

'beta.mom' fits the beta distribution by method of moments.

## Usage

```
beta.mom(qs.in)
```

## Arguments

| | |
|---|---|
| qs.in | A vector contains the numbers that are assumed to follow a beta distribution. |

## Value

| | |
|---|---|
| alpha.hat | Returns the estimation of alpha. |
| beta.hat | Returns the estimation of beta. |

## Author(s)

Ning Leng

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## See Also

DenNHist, DenNHistTable

## Examples

```
#tmp = rbeta(5, 5, 100)
#param = beta.mom(tmp)
```

crit_fun *Calculate the soft threshold for a target FDR*

## Description

'crit_fun' calculates the soft threshold for a target FDR.

## Usage

```
crit_fun(PPEE, thre)
```

## Arguments

| | |
|---|---|
| PPEE | The posterior probabilities of being EE. |
| thre | The target FDR. |

## Details

Regarding a target FDR alpha, both hard threshold and soft threshold could be used. If the hard threshold is preferred, user could simply take the transcripts with PP(DE) greater than (1-alpha). Using the hard threshold, any DE transcript in the list is with FDR <= alpha.

If the soft threshold is preferred, user could take the transcripts with PP(DE) greater than crit_fun(PPEE, alpha). Using the soft threshold, the list of DE transcripts is with average FDR alpha.

## Value

The adjusted FDR threshold of target FDR.

## Author(s)

Ning Leng

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## Examples

```
data(GeneMat)
GeneMat.small = GeneMat[c(1:10, 500:600),]
Sizes = MedianNorm(GeneMat.small)
EBOut = EBTest(Data = GeneMat.small,
 Conditions = as.factor(rep(c("C1","C2"), each=5)),
 sizeFactors = Sizes, maxround = 5)
PP = GetPPMat(EBOut)
DEfound = rownames(PP)[which(PP[,"PPDE"] >= 0.95)]
```

```
str(DEfound)

SoftThre = crit_fun(PP[,"PPEE"], 0.05)
DEfound_soft = rownames(PP)[which(PP[,"PPDE"] >= SoftThre)]
```

---

DenNHist *Density plot to compare the empirical q's and the simulated q's from the fitted beta distribution.*

---

## Description

'DenNHist' gives the density plot that compares the empirical q's and the simulated q's from the fitted beta distribution.

## Usage

```
DenNHist(EBOut, GeneLevel = F)
```

## Arguments

| | |
|---|---|
| EBOut | The output of EBTest or EBMultiTest. |
| GeneLevel | Indicate whether the results are from data at gene level. |

## Value

For data with n1 conditions and n2 uncertainty groups, n1*n2 plots will be generated. Each plot represents a subset of the data. The empirical estimation of q's will be represented as blue histograms and the density of the fitted beta distribution will be represented as the green line.

## Author(s)

Ning Leng

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## See Also

beta.mom, QQP, EBTest, EBMultiTest

## Examples

```
data(GeneMat)
GeneMat.small = GeneMat[c(500:1000),]
Sizes = MedianNorm(GeneMat.small)
EBOut = EBTest(Data = GeneMat.small,
 Conditions = as.factor(rep(c("C1","C2"), each=5)),
 sizeFactors = Sizes, maxround = 5)
par(mfrow = c(2,2))
DenNHist(EBOut)
```

---

`EBMultiTest` *Using EM algorithm to calculate the posterior probabilities of interested patterns in a multiple condition study*

---

## Description

'EBMultiTest' is built based on the assumption of NB-Beta Empirical Bayes model. It utilizes the EM algorithm to give the posterior probability of the interested patterns.

## Usage

```
EBMultiTest(Data, NgVector = NULL, Conditions, sizeFactors, uc = 0, AllParti = NULL, fast = T,
    Alpha = NULL, Beta = NULL, Qtrm = 1, QtrmCut = 0, maxround = 50,
    step1 = 1e-6, step2 = 1e-4, thre = 1.15, sthre = 0,
    filter = 1, stopthre = 1e-04, nequal = 0)
```

## Arguments

| | |
|---|---|
| `Data` | A data matrix contains expression values for each transcript (gene or isoform level). In which rows should be transcripts and columns should be samples. |
| `NgVector` | A vector indicates the uncertainty group assignment of each isoform. e.g. if we use number of isoforms in the host gene to define the uncertainty groups, suppose the isoform is in a gene with 2 isoforms, Ng of this isoform should be 2. The length of this vector should be the same as the number of rows in Data. If it's gene level data, Ngvector could be left as NULL. |
| `Conditions` | A vector indicates the condition in which each sample belongs to. |
| `sizeFactors` | The normalization factors. It should be a vector with lane specific numbers (the length of the vector should be the same as the number of samples, with the same order as the columns of Data). |
| `uc` | number of unceratin positions, unit levels |
| `AllParti` | user specified set of partitions, a matrix, with each row represent a partition |
| `fast` | boolean indicator whether to use fast EBSeq or full EBSeq |
| `Alpha` | start value of hyper parameter alpha |
| `Beta` | start value of hyper parameter beta |

| | |
|---|---|
| Qtrm, QtrmCut | Transcripts with Qtrm th quantile < = QtrmCut will be removed before testing. The default value is Qtrm = 1 and QtrmCut=0. By default setting, transcripts with all 0's won't be tested. |
| maxround | Number of iterations. The default value is 50. Users should always check the convergency by looking at the Alpha and Beta in output. If the hyper-parameter estimations are not converged in 50 iterations, larger number is suggested. |
| step1 | stepsize for gradient ascent of alpha |
| step2 | stepsize for gradietn ascent of beta |
| thre | threshold for determining the state of a position |
| sthre | shrinkage threshold for iterative pruning during the EM updates |
| filter | filterthreshold for low expression units |
| stopthre | stopping threshold for EM |
| nequal | when there is a chain of equal states with the number of equal states bigger than nequal, equalhandle algorithm will be used to further checking the homogeneity between the group means |

## Value

| | |
|---|---|
| Alpha | Fitted parameter alpha of the prior beta distribution. |
| Beta | Fitted parameter beta of the prior beta distribution. |
| P | Global proportion of DE patterns. |
| RList | The fitted values of r for each transcript. |
| MeanList | The mean of each transcript (across conditions). |
| VarList | The variance of each transcript (across conditions). |
| QList | The fitted q values of each transcript within the two conditions |
| Mean | The mean of each transcript within the two conditions (adjusted by normalization factors). |
| Var | The estimated variance of each transcript within the two conditions (adjusted by normalization factors). |
| PoolVar | The variance of each transcript (The pooled value of within condition EstVar). |
| DataNorm | Normalized expression matrix. |
| Iso | same as NgVector |
| AllZeroIndex | The transcript with expression 0 for all samples (which are not tested). |
| PPMat | The Posterior Probability of following each pattern (columns) for each transcript (rows). Transcripts with expression 0 for all samples are not shown in this matrix. |
| AllParti | selected patterns |
| PPMatWith0 | The Posterior Probability of following each pattern (columns) for each transcript (rows). Transcripts with expression 0 for all samples are shown in this matrix with PP(any_pattrn)=NA. The transcript order is exactly the same as the order of the input data. |
| Conditions | The input conditions. |
| NumUC | The number of uncertain positions at each unit |

## Author(s)

Ning Leng, Xiuyu Ma

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## See Also

EBTest, GetMultiPP, GetMultiFC

## Examples

```
data(MultiGeneMat)
Conditions = c("C1","C1","C2","C2","C3","C3")
MultiSize = MedianNorm(MultiGeneMat)
MultiOut = EBMultiTest(MultiGeneMat,Conditions=Conditions,uc = 2,
                    sizeFactors=MultiSize)
MultiPP = GetMultiPP(MultiOut)
```

---

# EBSeqTest *EBSeq core*

---

## Description

core function of EBSeq computation. Users are expected to use the wrappers, 2 conditions scenario, using EBTest, more than 2 condtiions, using EBMultiTest

## Usage

```
EBSeqTest(data, conditions, uc, AllParti = NULL, iLabel = 1, sizefactor = 1,
  iter = 50, alpha = 0.4, beta = 0, step1 = 1e-6, step2 = 1e-4,
  thre = 1.15, sthre = 0, filter = 1, stopthre = 1e-4, nequal = 0)
```

## Arguments

| | |
|---|---|
| data | A data matrix contains expression values for each transcript (gene or isoform level). In which rows should be transcripts and columns should be samples. For single cell data, normalized counts are required |
| conditions | condition label for samples |
| uc | number of unceratin positions, unit level |
| AllParti | user specified set of partitions |
| iLabel | label for isoform, indicating how beta are shared among units |

| | |
|---|---|
| sizefactor | The normalization factors. It should be a vector with lane specific numbers (the length of the vector should be the same as the number of samples, with the same order as the columns of Data). |
| iter | maximum iteration step of EM |
| alpha | start value of hyper parameter alpha |
| beta | start value of hyper parameter beta |
| step1 | stepsize for gradient ascent of alpha |
| step2 | stepsize for gradietn ascent of beta |
| thre | threshold for determining the state of a position |
| sthre | shrinkage threshold for iterative pruning during the EM updates |
| filter | filterthreshold for low expression units |
| stopthre | stopping threshold for EM |
| nequal | when there is a chain of equal states with the number of equal states bigger than nequal, equalhandle algorithm will be used to further checking the homogeneity between the group means |

## Value

a list containing selected DE patterns and their posterior probabilities, values for alpha and beta, some moments of the data

---

# EBTest *Using EM algorithm to calculate the posterior probabilities of being DE*

---

## Description

Base on the assumption of NB-Beta Empirical Bayes model, the EM algorithm is used to get the posterior probability of being DE.

## Usage

```
EBTest(Data, NgVector = NULL, Conditions, sizeFactors, fast = T,
    Alpha = NULL, Beta = NULL, Qtrm = 1, QtrmCut = 0, maxround = 50,
    step1 = 1e-6, step2 = 1e-4, thre = 1.15, sthre = 0,
    filter = 1, stopthre = 1e-4)
```

## Arguments

| | |
|---|---|
| Data | A data matrix contains expression values for each transcript (gene or isoform level). In which rows should be transcripts and columns should be samples. |
| NgVector | A vector indicates the uncertainty group assignment of each isoform. e.g. if we use number of isoforms in the host gene to define the uncertainty groups, suppose the isoform is in a gene with 2 isoforms, Ng of this isoform should be 2. The length of this vector should be the same as the number of rows in Data. If it's gene level data, Ngvector could be left as NULL. |

| | |
|---|---|
| Conditions | A factor indicates the condition which each sample belongs to. |
| sizeFactors | The normalization factors. It should be a vector with lane specific numbers (the length of the vector should be the same as the number of samples, with the same order as the columns of Data). |
| fast | boolean indicator whether to use fast EBSeq or full EBSeq |
| Alpha | start value of hyper parameter alpha |
| Beta | start value of hyper parameter beta |
| Qtrm, QtrmCut | Transcripts with Qtrm th quantile < = QtrmCut will be removed before testing. The default value is Qtrm = 1 and QtrmCut=0. By default setting, transcripts with all 0's won't be tested. |
| maxround | Number of iterations. The default value is 50. Users should always check the convergency by looking at the Alpha and Beta in output. If the hyper-parameter estimations are not converged in 50 iterations, larger number is suggested. |
| step1 | stepsize for gradient ascent of alpha |
| step2 | stepsize for gradietn ascent of beta |
| thre | threshold for determining the state of a position |
| sthre | shrinkage threshold for iterative pruning during the EM updates |
| filter | filterthreshold for low expression units |
| stopthre | stopping threshold for EM |

## Details

For each transcript gi within condition, the model assumes: X_gis|mu_gi ~ NB (r_gi0 * l_s, q_gi) q_gi|alpha, beta^N_g ~ Beta (alpha, beta^N_g) In which the l_s is the sizeFactors of samples.

The function will test "H0: q_gi^C1 = q_gi^C2" and "H1: q_gi^C1 != q_gi^C2."

## Value

| | |
|---|---|
| Alpha | Fitted parameter alpha of the prior beta distribution. |
| Beta | Fitted parameter beta of the prior beta distribution. |
| P | Global proportion of DE patterns. |
| RList | The fitted values of r for each transcript. |
| MeanList | The mean of each transcript (across conditions). |
| VarList | The variance of each transcript (across conditions). |
| QList | The fitted q values of each transcript within the two conditions |
| Mean | The mean of each transcript within the two conditions (adjusted by normalization factors). |
| Var | The estimated variance of each transcript within the two conditions (adjusted by normalization factors). |
| PoolVar | The variance of each transcript (The pooled value of within condition EstVar). |
| DataNorm | Normalized expression matrix. |

| | |
|---|---|
| AllZeroIndex | The transcript with expression 0 for all samples (which are not tested). |
| Iso | same as NgVector |
| PPMat | A matrix contains posterior probabilities of being EE (the first column) or DE (the second column). Rows are transcripts. Transcripts with expression 0 for all samples are not shown in this matrix. |
| AllParti | selected patterns |
| PPMatWith0 | A matrix contains posterior probabilities of being EE (the first column) or DE (the second column). Rows are transcripts. Transcripts with expression 0 for all samples are shown as PP(EE) = PP(DE) = NA in this matrix. The transcript order is exactly the same as the order of the input data. |
| Conditions | The input conditions. |

## Author(s)

Ning Leng, Xiuyu Ma

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## See Also

EBMultiTest, PostFC, GetPPMat

## Examples

```
data(GeneMat)
str(GeneMat)
Sizes = MedianNorm(GeneMat)
EBOut = EBTest(Data=GeneMat, Conditions=as.factor(rep(c("C1","C2"),each=5)),
       sizeFactors = Sizes)
PP = GetPPMat(EBOut)
```

---

# f0 *The Prior Predictive Distribution of being EE*

---

## Description

'f0' gives the Prior Predictive Distribution of being EE.

## Usage

```
f0(Input, AlphaIn, BetaIn, EmpiricalR, NumOfGroups, log)
```

### Arguments

| | |
|---|---|
| Input | Expression Values. |
| AlphaIn, BetaIn, EmpiricalR | The parameters estimated from last iteration of EM. |
| NumOfGroups | How many transcripts within each Ng group. |
| log | If true, will give the log of the output. |

### Value

The function will return the prior predictive distribution values of being EE.

### Author(s)

Ning Leng

### References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

### See Also

f1

### Examples

```
#
#f0(matrix(rnorm(100,100,1),ncol=10), .5, .6,
# matrix(rnorm(100,200,1),ncol=10), 100, TRUE)
```

---

## f1 *The Prior Predictive Distribution of being DE*

---

### Description

'f1' gives the Prior Predictive Distribution of DE.

### Usage

```
f1(Input1, Input2, AlphaIn, BetaIn, EmpiricalRSP1,
 EmpiricalRSP2, NumOfGroup, log)
```

## Arguments

| | |
|---|---|
| Input1 | Expressions from Condition1. |
| Input2 | Expressions from Condition2. |
| AlphaIn, BetaIn, EmpiricalRSP1, EmpiricalRSP2 | The parameters estimated from last iteration of EM. |
| NumOfGroup | How many transcripts within each Ng group. |
| log | If true, will give the log of the output. |

## Value

The function will return the prior predictive distribution values of being DE.

## Author(s)

Ning Leng

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## See Also

f0

## Examples

```
#f1(matrix(rnorm(100,100,1),ncol=10),
# matrix(rnorm(100,100,1),ncol=10), .5, .6,
# matrix(rnorm(100,200,1),ncol=10),
# matrix(rnorm(100,200,1),ncol=10), 100, TRUE)
```

---

# GeneMat *The simulated data for two condition gene DE analysis*

---

## Description

'GeneMat' gives the simulated data for two condition gene DE analysis.

## Usage

```
data(GeneMat)
```

## Source

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## See Also

IsoList

## Examples

```
data(GeneMat)
```

---

`GetDEResults` *Obtain Differential Expression Analysis Results in a Two-condition Test*

---

## Description

Obtain DE analysis results in a two-condition test using the output of EBTest()

## Usage

```
GetDEResults(EBPrelim, FDR=0.05, Method="robust",
         FDRMethod="hard", Threshold_FC=0.7,
        Threshold_FCRatio=0.3, SmallNum=0.01)
```

## Arguments

| | |
|---|---|
| `EBPrelim` | Output from the function EBTest(). |
| `FDR` | Target FDR, defaut is 0.05. |
| `FDRMethod` | "hard" or "soft". Giving a target FDR alpha, either hard threshold and soft threshold may be used. If the hard threshold is preferred, DE transcripts are defined as the the transcripts with PP(DE) greater than (1-alpha). Using the hard threshold, any DE transcript in the list has FDR <= alpha.<br>If the soft threshold is preferred, the DE transcripts are defined as the transcripts with PP(DE) greater than crit_fun(PPEE, alpha). Using the soft threshold, the list of DE transcripts has average FDR alpha.<br>Based on results from our simulation studies, hard thresholds provide a better-controlled empirical FDR when sample size is relatively small(Less than 10 samples in each condition). User may consider the soft threshold when sample size is large to improve power. |
| `Method` | "robust" or "classic". Using the "robust" option, EBSeq is more robust to genes with outliers and genes with extremely small variances. Using the "classic" option, the results will be more comparable to those obtained by using the GetPPMat() function from earlier version (<= 1.7.0) of EBSeq. Default is "robust". |

`Threshold_FC` Threshold for the fold change (FC) statistics. The default is 0.7. The FC statistics are calculated as follows. First the posterior FC estimates are calculated using PostFC() function. The FC statistics is defined as exp(-|log posterior FC|) and therefore is always less than or equal to 1. The default threshold was selected as the optimal threshold learned from our simulation studies. By setting the threshold as 0.7, the expected FC for a DE transcript is less than 0.7 (or greater than 1/0.7=1.4). User may specify their own threshold here. A higher (less conservative) threshold may be used here when sample size is large. Our simulation results indicated that when there are more than or equal to 5 samples in each condition, a less conservative threshold will improve the power when the FDR is still well-controlled. The parameter will be ignored if Method is set as "classic".

`Threshold_FCRatio` Threshold for the fold change ratio (FCRatio) statistics. The default is 0.3. The FCRatio statistics are calculated as follows. First we get another revised fold change statistic called Median-FC statistic for each transcript. For each transcript, we calculate the median of normalized expression values within each condition. The MedianFC is defined as exp(-|log((C1Median+SmallNum)/(C2Median+SmallNum))|). Note a small number is added to avoid Inf and NA. See SmallNum for more details. The FCRatio is calculated as exp(-|log(FCstatistics/MedianFC)|). Therefore it is always less than or equal to 1. The default threshold was selected as the optimal threshold learned from our simulation studies. By setting the threshold as 0.3, the FCRatio for a DE transcript is expected to be larger than 0.3.

`SmallNum` When calculating the FCRatio (or Median-FC), a small number is added for each transcript in each condition to avoid Inf and NA. Default is 0.01.

## Details

GetDEResults() function takes output from EBTest() function and output a list of DE transcripts under a target FDR. It also provides posterior probability estimates for each transcript.

## Value

`DEfound` A list of DE transcripts.

`PPMat` Posterior probability matrix. Transcripts are following the same order as in the input matrix. Transcripts that were filtered by magnitude (in EBTest function), FC, or FCR are assigned with NA for both PPDE and PPEE.

`Status` Each transcript will be assigned with one of the following values: "DE", "EE", "Filtered: Low Expression", "Filtered: Fold Change" and "Filtered: Fold Change Ratio". Transcripts are following the same order as in the input matrix.

## Author(s)

Ning Leng, Yuan Li

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical

Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## See Also

EBTest

## Examples

```
data(GeneMat)
str(GeneMat)
GeneMat.small = GeneMat[c(1:10,511:550),]
Sizes = MedianNorm(GeneMat.small)
EBOut = EBTest(Data = GeneMat.small,
 Conditions = as.factor(rep(c("C1","C2"), each = 5)),
 sizeFactors = Sizes, maxround = 5)
Out = GetDEResults(EBOut)
```

---

# GetMultiFC *Calculate the Fold Changes for Multiple Conditions*

---

## Description

'GetMultiFC' calculates the Fold Changes for each pair of conditions in a multiple condition study.

## Usage

```
GetMultiFC(EBMultiOut, SmallNum = 0.01)
```

## Arguments

| | |
|---|---|
| EBMultiOut | The output of EBMultiTest function. |
| SmallNum | A small number will be added for each transcript in each condition to avoid Inf and NA. Default is 0.01. |

## Details

Provide the FC (adjusted by the normalization factors) for each pair of comparisons. A small number will be added for each transcript in each condition to avoid Inf and NA. Default is set to be 0.01.

## Value

| | |
|---|---|
| FCMat | The FC of each pair of comparison (adjusted by the normalization factors). |
| Log2FCMat | The log 2 FC of each pair of comparison (adjusted by the normalization factors). |
| PostFCMat | The posterior FC of each pair of comparison. |
| Log2PostFCMat | The log 2 posterior FC of each pair of comparison. |
| CondMean | The mean of each transcript within each condition (adjusted by the normalization factors). |
| ConditionOrder | The condition assignment for C1Mean, C2Mean, etc. |

## Author(s)

Ning Leng

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## See Also

EBMultiTest, PostFC

## Examples

```
data(MultiGeneMat)
MultiGeneMat.small = MultiGeneMat[201:210,]

Conditions = c("C1","C1","C2","C2","C3","C3")

PosParti = GetPatterns(Conditions)
Parti = PosParti[-3,]

MultiSize = MedianNorm(MultiGeneMat.small)

MultiOut = EBMultiTest(MultiGeneMat.small,
 NgVector=NULL, Conditions=Conditions,
 AllParti=Parti, sizeFactors=MultiSize,
 maxround=5)

MultiFC = GetMultiFC(MultiOut)
```

---

# GetMultiPP *Posterior Probability of Each Transcript*

---

## Description

'GetMultiPP' generates the Posterior Probability of being each pattern of each transcript based on the EBMultiTest output.

## Usage

```
GetMultiPP(EBout)
```

## Arguments

| | |
|---|---|
| EBout | The output of EBMultiTest function. |

## Value

| | |
|---|---|
| PP | The poster probabilities of being each pattern. |
| MAP | Gives the most likely pattern. |
| Patterns | The Patterns. |

## Author(s)

Ning Leng

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## See Also

GetPPMat

## Examples

```
data(MultiGeneMat)
MultiGeneMat.small = MultiGeneMat[201:210,]

Conditions = c("C1","C1","C2","C2","C3","C3")
PosParti = GetPatterns(Conditions)
Parti = PosParti[-3,]
MultiSize = MedianNorm(MultiGeneMat.small)

MultiOut = EBMultiTest(MultiGeneMat.small,
 NgVector=NULL, Conditions=Conditions,
 AllParti=Parti, sizeFactors=MultiSize,
 maxround=5)
MultiPP = GetMultiPP(MultiOut)
```

---

# GetNg *Ng Vector*

---

## Description

'GetNg' generates the Ng vector for the isoform level data. (While using the number of isoform in the host gene to define the uncertainty groups.)

## Usage

```
GetNg(IsoformName, GeneName, TrunThre = 3)
```

## Arguments

| | |
|---|---|
| IsoformName | A vector contains the isoform names. |
| GeneName | The gene names of the isoforms in IsoformNames (Should be in the same order). |
| TrunThre | The number of uncertainty groups the user wish to define. The default is 3. |

## Value

| | |
|---|---|
| GeneNg | The number of isoforms that are contained in each gene. |
| GeneNgTrun | The truncated Ng of each gene. (The genes contain more than 3 isoforms are with Ng 3.) |
| IsoformNg | The Ng of each isoform. |
| IsoformNgTrun | The truncated Ng of each isoform (could be used to define the uncertainty group assignment). |

## Author(s)

Ning Leng

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## Examples

```
data(IsoList)

IsoMat = IsoList$IsoMat
IsoNames = IsoList$IsoNames
IsosGeneNames = IsoList$IsosGeneNames
IsoSizes = MedianNorm(IsoMat)
NgList = GetNg(IsoNames, IsosGeneNames)

#IsoNgTrun = NgList$IsoformNgTrun
#IsoEBOut = EBTest(Data = IsoMat, NgVector = IsoNgTrun,
# Conditions = as.factor(rep(c("C1","C2"), each=5)),
# sizeFactors = IsoSizes, maxround = 5)
```

GetNormalizedMat *Calculate normalized expression matrix*

## Description

'GetNormalizedMat' calculates the normalized expression matrix. (Note: this matrix is only used for visualization etc. EBTes and EBMultiTest request *un-adjusted* expressions and normalization factors.)

## Usage

```
GetNormalizedMat(Data, Sizes)
```

## Arguments

| | |
|---|---|
| Data | The data matrix with transcripts in rows and lanes in columns. |
| Sizes | A vector contains the normalization factor for each lane. |

## Value

The function will return a normalized matrix.

## Author(s)

Ning Leng

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## Examples

```
data(GeneMat)
str(GeneMat)
Sizes = MedianNorm(GeneMat)
NormData = GetNormalizedMat(GeneMat, Sizes)
```

## GetPatterns *Generate all possible patterns in a multiple condition study*

### Description

'GetPatterns' generates all possible patterns in a multiple condition study.

### Usage

```
GetPatterns(Conditions)
```

### Arguments

| | |
|---|---|
| Conditions | The names of the Conditions in the study. |

### Value

A matrix describe all possible patterns.

### Author(s)

Ning Leng

### References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

### Examples

```
Conditions = c("C1","C1","C2","C2","C3","C3")
PosParti = GetPatterns(Conditions)
```

## GetPPMat *Posterior Probability of Transcripts*

### Description

'GetPPMat' generates the Posterior Probability of being each pattern of each transcript based on the EBTest output.

### Usage

```
GetPPMat(EBout)
```

### Arguments

| | |
|---|---|
| EBout | The output of EBTest function. |

### Value

The poster probabilities of being EE (first column) and DE (second column).

### Author(s)

Ning Leng

### References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

### Examples

```
data(GeneMat)
GeneMat.small = GeneMat[c(500:550),]
Sizes = MedianNorm(GeneMat.small)
EBOut = EBTest(Data = GeneMat.small,
 Conditions = as.factor(rep(c("C1","C2"), each=5)),
 sizeFactors = Sizes, maxround = 5)
PP = GetPPMat(EBOut)
str(PP)
head(PP)
```

---

## GetSelectedPatterns *Get selected patterns in a multiple condition study*

---

### Description

'GetSelectedPatterns' get selected patterns in a multiple condition study.

### Usage

```
GetSelectedPatterns(EBout)
```

### Arguments

| | |
|---|---|
| EBout | Results from EBMultiTest |

### Value

A matrix describe selected patterns.

## Author(s)

Ning Leng, Xiuyu Ma

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## Examples

```
data(MultiGeneMat)
Conditions=c("C1","C1","C2","C2","C3","C3")
MultiSize=MedianNorm(MultiGeneMat)
MultiOut=EBMultiTest(MultiGeneMat,Conditions=Conditions,
 sizeFactors=MultiSize)
PosParti=GetSelectedPatterns(MultiOut)
```

---

# IsoList *The simulated data for two condition isoform DE analysis*

---

## Description

'IsoList' gives the simulated data for two condition isoform DE analysis.

## Usage

```
data(IsoList)
```

## Source

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## See Also

GeteMat

## Examples

```
data(IsoList)
```

## IsoMultiList *The simulated data for multiple condition isoform DE analysis*

### Description

'IsoMultiList' gives a set of simulated data for multiple condition isoform DE analysis.

### Usage

```
data(IsoMultiList)
```

### Source

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

### See Also

IsoList

### Examples

```
data(IsoMultiList)
```

## Likefun *Likelihood Function of the NB-Beta Model*

### Description

'Likefun' specifies the Likelihood Function of the NB-Beta Model.

### Usage

```
Likefun(ParamPool, InputPool)
```

### Arguments

| | |
|---|---|
| ParamPool | The parameters that will be estimated in EM. |
| InputPool | The control parameters that will not be estimated in EM. |

### Value

The function will return the log-likelihood.

## Author(s)

Ning Leng

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## Examples

```
#x1 = c(.6,.7,.3)
#Input = matrix(rnorm(100,100,1), ncol=10)
#RIn = matrix(rnorm(100,200,1), ncol=10)
#InputPool = list(Input[,1:5], Input[,6:10], Input,
# rep(.1,100), 1, RIn, RIn[,1:5], RIn[,6:10], 100)
#Likefun(x1, InputPool)
```

---

`LikefunMulti` *Likelihood Function of the NB-Beta Model In Multiple Condition Test*

---

## Description

'LikefunMulti' specifies the Likelihood Function of the NB-Beta Model In Multiple Condition Test.

## Usage

```
LikefunMulti(ParamPool, InputPool)
```

## Arguments

| | |
|---|---|
| `ParamPool` | The parameters that will be estimated in EM. |
| `InputPool` | The control parameters that will not be estimated in EM. |

## Value

The function will return the log-likelihood.

## Author(s)

Ning Leng

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## Examples

```
#x1 = c(.6,.7,.3)
#Input = matrix(rnorm(100,100,1),ncol=10)
#RIn = matrix(rnorm(100,200,1),ncol=10)
#InputPool = list(list(Input[,1:5],Input[,6:10]),
# Input, cbind(rep(.1, 10), rep(.9,10)), 1,
# RIn, list(RIn[,1:5],RIn[,6:10]),
# 10, rbind(c(1,1),c(1,2)))
#LikefunMulti(x1, InputPool)
```

---

LogN *The function to run EM (one round) algorithm for the NB-beta model.*

---

## Description

'LogN' specifies the function to run (one round of) the EM algorithm for the NB-beta model.

## Usage

```
LogN(Input, InputSP, EmpiricalR, EmpiricalRSP, NumOfEachGroup,
 AlphaIn, BetaIn, PIn, NoneZeroLength)
```

## Arguments

| | |
|---|---|
| `Input`, `InputSP` | The expressions among all the samples. |
| `NumOfEachGroup` | Number of genes in each Ng group. |
| `AlphaIn`, `PIn`, `BetaIn`, `EmpiricalR`, `EmpiricalRSP` | The parameters from the last EM step. |
| `NoneZeroLength` | Number of Ng groups. |

## Author(s)

Ning Leng

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## Examples

```
#Input = matrix(rnorm(100,100,1), ncol=10)
#rownames(Input) = paste("g",1:10)
#RIn = matrix(rnorm(100,200,1), ncol=10)
#res = LogN(Input, list(Input[,1:5], Input[,6:10]),
# RIn, list(RIn[,1:5], RIn[,6:10]),
# 10, .6, .7, .3, 1)
```

---

`LogNMulti` *EM algorithm for the NB-beta model in the multiple condition test*

---

## Description

'LogNMulti' specifies the function to run (one round of) the EM algorithm for the NB-beta model in the multiple condition test.

## Usage

```
LogNMulti(Input, InputSP, EmpiricalR, EmpiricalRSP,
 NumOfEachGroup, AlphaIn, BetaIn, PIn,
 NoneZeroLength, AllParti, Conditions)
```

## Arguments

| | |
|---|---|
| `Input`, `InputSP` | The expressions among all the samples. |
| `NumOfEachGroup` | Number of genes in each Ng group. |
| `AlphaIn`, `PIn`, `BetaIn`, `EmpiricalR`, `EmpiricalRSP` | The parameters from the last EM step. |
| `NoneZeroLength` | Number of Ng groups. |
| `AllParti` | The patterns of interests. |
| `Conditions` | The condition assignment for each sample. |

## Author(s)

Ning Leng

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## Examples

```
#

#Input = matrix(rnorm(100,100,1),ncol=10)
#rownames(Input) = paste("g",1:10)
#RIn = matrix(rnorm(100,200,1), ncol=10)
#res = LogNMulti(Input, list(Input[,1:5], Input[,6:10]),
# RIn, list(RIn[,1:5], RIn[,6:10]), 10, .6, .7,
# c(.3,.7), 1, rbind(c(1,1), c(1,2)),
# as.factor(rep(c("C1","C2"), each=5)))
```

---

`MedianNorm` *Median Normalization*

---

## Description

'MedianNorm' specifies the median-by-ratio normalization function from Anders et. al., 2010.

## Usage

```
MedianNorm(Data, alternative = FALSE)
```

## Arguments

| | |
|---|---|
| `Data` | The data matrix with transcripts in rows and lanes in columns. |
| `alternative` | if alternative = TRUE, the alternative version of median normalization will be applied. The alternative method is similar to median-by-ratio normalization, but can deal with the cases when all of the genes/isoforms have at least one zero counts (in which case the median-by-ratio normalization will fail).<br>In more details, in median-by-ratio normalization (denote l_1 as libsize for sample 1 as an example, assume total S samples):<br>hatl_1 = median_g [ X_g1 / (X_g1*X_g2*...*X_gS)^-S ] (1)<br>which estimates l_1 / (l_1 * l_2 * ... * l_S)^-S. Since we have the constrain that (l_1 * l_2 * ... * l_S) = 1, equation (1) estimates l_1. Note (1) could also be written as:<br>hatl_1 = median_g [ (X_g1/X_g1 * X_g1/X_g2 * .... * X_g1/X_gS)^-S]<br>In the alternative method, we estimate l_1/l_1, l_1/l_2, ... l_1/l_S individually by taking median_g(X_g1/X_g1), median_g(X_g1/X_g2) ... Then estimate l_1 = l_1 / (l_1 * l_2 * ... * l_S)^-S by taking the geomean of these estimates:<br>hatl_1 = [ median_g(X_g1/X_g1) * median_g(X_g1/X_g2) * median_g(X_g1/X_g3) * ... * median_g(X_g1/X_gS) ] ^-S |

## Value

The function will return a vector contains the normalization factor for each lane.

## Author(s)

Ning Leng

## References

Simon Anders and Wolfgang Huber. Differential expression analysis for sequence count data. Genome Biology (2010) 11:R106 (open access)

## See Also

QuantileNorm

## Examples

```
data(GeneMat)
Sizes = MedianNorm(GeneMat)
#EBOut = EBTest(Data = GeneMat,
# Conditions = as.factor(rep(c("C1","C2"), each=5)),
# sizeFactors = Sizes, maxround = 5)
```

---

`MultiGeneMat` *The simulated data for multiple condition gene DE analysis*

---

## Description

'MultiGeneMat' generates a set of the simulated data for multiple condition gene DE analysis.

## Usage

```
data(MultiGeneMat)
```

## Source

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## See Also

GeneMat

## Examples

```
data(MultiGeneMat)
```

PlotPattern *Visualize the patterns*

## Description

'PlotPattern' generates the visualized patterns before the multiple condition test.

## Usage

```
PlotPattern(Patterns)
```

## Arguments

| | |
|---|---|
| Patterns | The output of GetPatterns function. |

## Value

A heatmap to visualize the patterns of interest.

## Author(s)

Ning Leng

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## Examples

```
Conditions = c("C1","C1","C2","C2","C3","C3")
Patterns = GetPatterns(Conditions)
PlotPattern(Patterns)
```

PlotPostVsRawFC *Plot Posterior FC vs FC*

## Description

'PlotPostVsRawFC' helps the users visualize the posterior FC vs FC in a two condition study.

## Usage

```
PlotPostVsRawFC(EBOut, FCOut)
```

### Arguments

| | |
|---|---|
| EBOut | The output of EBMultiTest function. |
| FCOut | The output of PostFC function. |

### Value

A figure shows fold change vs posterior fold change.

### Author(s)

Ning Leng

### References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

### See Also

PostFC

### Examples

```
data(GeneMat)
GeneMat.small = GeneMat[c(500:600),]
Sizes = MedianNorm(GeneMat.small)
EBOut = EBTest(Data = GeneMat.small,
 Conditions = as.factor(rep(c("C1","C2"), each=5)),
 sizeFactors = Sizes, maxround = 5)
FC = PostFC(EBOut)
PlotPostVsRawFC(EBOut,FC)
```

---

## PolyFitPlot *Fit the mean-var relationship using polynomial regression*

---

### Description

'PolyFitPlot' fits the mean-var relationship using polynomial regression.

### Usage

```
PolyFitPlot(X, Y, nterms, xname = "Estimated Mean",
 yname = "Estimated Var", pdfname = "",
 xlim =  c(-1,5), ylim = c(-1,7), ChangeXY = F,
 col = "red")
```

## Arguments

| | |
|---|---|
| X | The first group of values want to be fitted by the polynomial regression (e.g Mean of the data). |
| Y | The second group of values want to be fitted by the polynomial regression (e.g. variance of the data). The length of Y should be the same as the length of X. |
| nterms | How many polynomial terms want to be used. |
| xname | Name of the x axis. |
| yname | Name of the y axis. |
| pdfname | Name of the plot. |
| xlim | The x limits of the plot. |
| ylim | The y limits of the plot. |
| ChangeXY | If ChangeXY is setted to be TRUE, X will be treated as the dependent variable and Y will be treated as the independent one. Default is FALSE. |
| col | Color of the fitted line. |

## Value

The PolyFitPlot function provides a smooth scatter plot of two variables and their best fitting line of polynomial regression.

## Author(s)

Ning Leng

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## Examples

```
data(IsoList)
str(IsoList)
IsoMat = IsoList$IsoMat
IsoNames = IsoList$IsoNames
IsosGeneNames = IsoList$IsosGeneNames
IsoSizes = MedianNorm(IsoMat)
NgList = GetNg(IsoNames, IsosGeneNames)

IsoNgTrun = NgList$IsoformNgTrun
#IsoEBOut = EBTest(Data = IsoMat.small,
# NgVector = IsoNgTrun,
# Conditions = as.factor(rep(c("C1","C2"), each=5)),
# sizeFactors = IsoSizes, maxround = 5)

#par(mfrow=c(2,2))
```

```
#PolyFitValue = vector("list",3)

#for(i in 1:3)
# PolyFitValue[[i]] = PolyFitPlot(IsoEBOut$C1Mean[[i]],
#  IsoEBOut$C1EstVar[[i]], 5)

#PolyAll = PolyFitPlot(unlist(IsoEBOut$C1Mean),
# unlist(IsoEBOut$C1EstVar), 5)

#lines(log10(IsoEBOut$C1Mean[[1]][PolyFitValue[[1]]$sort]),
# PolyFitValue[[1]]$fit[PolyFitValue[[1]]$sort],
# col="yellow", lwd=2)
#lines(log10(IsoEBOut$C1Mean[[2]][PolyFitValue[[2]]$sort]),
# PolyFitValue[[2]]$fit[PolyFitValue[[2]]$sort],
# col="pink", lwd=2)
#lines(log10(IsoEBOut$C1Mean[[3]][PolyFitValue[[3]]$sort]),
# PolyFitValue[[3]]$fit[PolyFitValue[[3]]$sort],
# col="green", lwd=2)

#legend("topleft",c("All Isoforms","Ng = 1","Ng = 2","Ng = 3"),
# col = c("red","yellow","pink","green"),
# lty=1, lwd=3, box.lwd=2)
```

---

`PostFC` *Calculate the posterior fold change for each transcript across conditions*

---

## Description

'PostFC' calculates the posterior fold change for each transcript across conditions.

## Usage

```
PostFC(EBoutput, SmallNum = 0.01)
```

## Arguments

| | |
|---|---|
| `EBoutput` | The ourput from function EBTest. |
| `SmallNum` | A small number will be added for each transcript in each condition to avoid Inf and NA. Default is 0.01. |

## Value

Provide both FC and posterior FC across two conditions. FC is calculated as (MeanC1+SmallNum)/(MeanC2+SmallNum). And Posterior FC is calculated as:

# Post alpha P_a_C1 = alpha + r_C1 * n_C1

# Post beta P_b_C1 = beta + Mean_C1 * n_C1

# P_q_C1 = P_a_C1 / (P_a_C1 + P_b_C1)

# Post FC = ((1-P_q_C1)/P_q_c1) / ( (1-P_q_c2)/P_q_c2)

| | |
|---|---|
| PostFC | The posterior FC across two conditions. |
| RealFC | The FC across two conditions (adjusted by the normalization factors). |
| Direction | The diretion of FC calculation. |

## Author(s)

Ning Leng

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## See Also

EBTest, GetMultiFC

## Examples

```
data(GeneMat)
GeneMat.small = GeneMat[c(500:550),]
Sizes = MedianNorm(GeneMat.small)
EBOut = EBTest(Data = GeneMat.small,
 Conditions = as.factor(rep(c("C1","C2"), each=5)),
 sizeFactors = Sizes, maxround = 5)
FC=PostFC(EBOut)
```

---

# QQP *The Quantile-Quantile Plot to compare the empirical q's and simulated q's from fitted beta distribution*

---

## Description

'QQP' gives the Quantile-Quantile Plot to compare the empirical q's and simulated q's from fitted beta distribution.

## Usage

```
QQP(EBOut, GeneLevel = F)
```

## Arguments

| | |
|---|---|
| EBOut | The output of EBTest or EBMultiTest. |
| GeneLevel | Indicate whether the results are from data at gene level. |

## Value

For data with n1 conditions and n2 uncertainty groups, n1*n2 plots will be generated. Each plot represents a subset of the data.

## Author(s)

Ning Leng

## References

Ning Leng, John A. Dawson, James A. Thomson, Victor Ruotti, Anna I. Rissman, Bart M.G. Smits, Jill D. Haag, Michael N. Gould, Ron M. Stewart, and Christina Kendziorski. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments. Bioinformatics (2013)

## See Also

EBTest, EBMultiTest, DenNHist

## Examples

```
data(GeneMat)
GeneMat.small = GeneMat[c(500:1000),]
Sizes = MedianNorm(GeneMat.small)
EBOut = EBTest(Data = GeneMat.small,
 Conditions = as.factor(rep(c("C1","C2"), each=5)),
 sizeFactors = Sizes, maxround = 5)
par(mfrow=c(2,2))
QQP(EBOut)
```

---

# QuantileNorm *Quantile Normalization*

---

## Description

'QuantileNorm' gives the quantile normalization.

## Usage

```
QuantileNorm(Data, Quantile)
```

## Arguments

| | |
|---|---|
| Data | The data matrix with transcripts in rows and lanes in columns. |
| Quantile | The quantile the user wishs to use. Should be a number between 0 and 1. |

## Details

Use a quantile point to normalize the data.

## Value

The function will return a vector contains the normalization factor for each lane.

## Author(s)

Ning Leng

## References

Bullard, James H., et al. Evaluation of statistical methods for normalization and differential expression in mRNA-Seq experiments. BMC bioinformatics 11.1 (2010): 94.

## See Also

MedianNorm

## Examples

```
data(GeneMat)
Sizes = QuantileNorm(GeneMat,.75)
#EBOut = EBTest(Data = GeneMat,
# Conditions = as.factor(rep(c("C1","C2"), each=5)),
# sizeFactors = Sizes, maxround = 5)
```

---

# RankNorm *Rank Normalization*

---

## Description

'RankNorm' gives the rank normalization.

## Usage

```
RankNorm(Data)
```

## Arguments

| | |
|---|---|
| Data | The data matrix with transcripts in rows and lanes in columns. |

## Value

The function will return a matrix contains the normalization factor for each lane and each transcript.

## Author(s)

Ning Leng

## See Also

MedianNorm, QuantileNorm

## Examples

```
data(GeneMat)
Sizes = RankNorm(GeneMat)
# Run EBSeq
# EBres = EBTest(Data = GeneData, NgVector = rep(1,10^4),
# Vect5End = rep(1,10^4), Vect3End = rep(1,10^4),
# Conditions = as.factor(rep(c(1,2), each=5)),
# sizeFactors = Sizes, maxround=5)
```

# Index


∗ **DE**
EBMultiTest, 7
EBTest, 10
GetDEResults, 15
∗ **FDR**
crit_fun, 5
∗ **Fold Change**
PostFC, 34
∗ **Multiple Condition**
EBMultiTest, 7
∗ **Ng**
GetNg, 19
∗ **Normalization**
GetNormalizedMat, 21
MedianNorm, 29
QuantileNorm, 36
RankNorm, 37
∗ **Posterior Probability**
GetMultiFC, 17
GetMultiPP, 18
GetPPMat, 22
PlotPostVsRawFC, 31
∗ **Q-Q plot**
QQP, 35
∗ **Two condition**
EBTest, 10
GetDEResults, 15
∗ **beta**
beta.mom, 4
DenNHist, 6
∗ **datasets**
GeneMat, 14
IsoList, 24
IsoMultiList, 25
MultiGeneMat, 30
∗ **package**
EBSeq_NingLeng-package, 3
∗ **patterns**
PlotPattern, 31

beta.mom, 4

crit_fun, 5

DenNHist, 6

EBMultiTest, 7
EBSeq_NingLeng
*(*EBSeq_NingLeng-package*)*, 3
EBSeq_NingLeng-package, 3
EBSeqTest, 9
EBTest, 10

f0, 12
f1, 13

GeneMat, 14
GetDEResults, 15
GetMultiFC, 17
GetMultiPP, 18
GetNg, 19
GetNormalizedMat, 21
GetPatterns, 22
GetPPMat, 22
GetSelectedPatterns, 23

IsoList, 24
IsoMultiList, 25

Likefun, 25
LikefunMulti, 26
LogN, 27
LogNMulti, 28

MedianNorm, 29
MultiGeneMat, 30

PlotPattern, 31
PlotPostVsRawFC, 31
PolyFitPlot, 32
PostFC, 34

QQP, 35
QuantileNorm, 36

RankNorm, 37