Package 'BMAseq'

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Title A Bayesian Model Averaging Approach for High-throughput RNA-seq Count Data (BMAseq)

Version 1.0.0

Description A Bayesian Model Averaging Approach for High-throughput RNA-seq Count Data (BMAseq) and Its Applications.

Depends limma, BHH2, stats, R(>= 2.10.1)

License GPL-2

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Suggests knitr, rmarkdown

VignetteBuilder knitr

R topics documented:

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`BMAseq.multi` *BMAseq.multi*

Description

Multivariate analysis using BMAseq approach

Usage

```
BMAseq.multi(
  dat.expr.counts,
  dat.pheno,
  var.pool,
  max.nvar,
  interaction = NULL,
  ind.incl.add = NULL,
  cut.BF = 1,
  cut.FDR = 0.05,
  laplace = FALSE
)
```

Arguments

dat.expr.counts	RNA-seq count data matrix (rows for genes and columns for subjects).
dat.pheno	Phenotypic data matrix (rows for subjects and columns for variables).
var.pool	Variables of interest, a vector.
max.nvar	The maximum number of variables in a model.
interaction	Specific interaction terms with input format 'A&B', default is Null.
ind.incl.add	Indices of additional included model.
cut.BF	Bayes factor criterion, default value is 1.
cut.FDR	False discovery rate criterion for identifying DE genes, default value is 0.05.

Details

Multivariate analysis on RNA-seq count data using BMAseq approach

Value

A list consisting of

dat.expr.logcpm	Normalized RNA-seq data matrix (rows for genes and columns for subjects).
weights	Estimated voom weights.
dat.pheno.new	Phenotypic data matrix including new interaction variables, will be same as input dat.pheno if interaction is NULL.
model.space	Model space including all possible models.
post.modelprob	Posterior model probability for each gene.
post.incl.modelprob	Posterior inclusive model probability for each gene associated with main effect of each variables if interaction is NULL; with main, interaction, main or interaction effects if interaction not NULL.
post.incl.modelprob.JointMain	Posterior inclusive model probability for each gene associated with joint main effects of variables, will be output if interaction is NULL.
post.incl.modelprob.Add	Posterior inclusive model probability for each gene associated with additional inclusive models, will be output if ind.incl.add is not Null.

`index.incl` Indices of the inclusive models.

`eFDR` Estimated FDR for each gene associated with main effect of each variables if interaction is NULL; with main, interaction, main or interaction effects if interaction is not NULL.

`eFDR.JointMain` Estimated FDR for each gene associated with all possible joint effect of variables, will be output if interaction is NULL.

`eFDR.Add` Estimated FDR for each gene associated with additional inclusive models, will be output if ind.incl.add is not Null.

`summary.nDEG` A summary table of the number of identified DE gene associated with main effect of each variable if interaction is NULL; with main, interaction, main or interaction effects if interaction is not NULL.

`summary.nDEG.JointMain`
A summary table of the number of identified DE gene associated with joint main effcts of variables, will be output if interaction is NULL.

`summary.nDEG.Add`
A summary table of the number of identified DE gene associated with additional inclusive models, will be output if ind.incl.add is not Null.

`DEG.bestmodel` DE genes associated with main effect of each variable if interaction is NULL; with main, interaction, main or interaction effects of each variable if interaction is not NULL; and the best model used to identify each DE gene.

Author(s)

Lingsong Meng

`BMAseq.multi.DEG` *BMAseq.multi.DEG*

Description

DE genes identification with obtained posterior model probability for each gene in multivariate analysis using BMAseq approach

Usage

```
BMAseq.multi.DEG(postprob.output, ind.incl.add = NULL, cut.FDR = 0.05)
```

Arguments

`postprob.output`
The output from BMAseq.multi.postprob function, a list.

`ind.incl.add` Indices of additional included model.

`cut.FDR` False discovery rate criterion for identifying DE genes, default value is 0.05.

Details

DE genes identification with obtained posterior model probability for each gene in multivariate analysis on RNA-seq count data using BMAseq approach

Value

A list consisting of

`post.incl.modelprob`
: Posterior inclusive model probability for each gene associated with main effect of each variables if interaction is NULL; with main, interaction, main or interaction effects if interaction not NULL..

`post.incl.modelprob.JointMain`
: Posterior inclusive model probability for each gene associated with all possible joint effect of variables, will be output if interaction is NULL.

`post.incl.modelprob.Add`
: Posterior inclusive model probability for each gene associated with additional inclusive models, will be output if ind.incl.add is not Null.

`index.incl`
: Indices of the inclusive models.

`eFDR`
: Estimated FDR for each gene associated with main effect of each variables if interaction is NULL; with main, interaction, main or interaction effects if interaction is not NULL.

`eFDR.JointMain`
: Estimated FDR for each gene associated with all possible joint effect of variables, will be output if interaction is NULL.

`eFDR.Add`
: Estimated FDR for each gene associated with additional inclusive models, will be output if ind.incl.add is not Null.

`summary.nDEG`
: A summary table of the number of identified DE gene associated with main effect of each variable if interaction is NULL; with main, interaction, main or interaction effects if interaction is not NULL.

`summary.nDEG.JointMain`
: A summary table of the number of identified DE gene associated with all possible joint effcts of variables, will be output if interaction is NULL.

`summary.nDEG.Add`
: A summary table of the number of identified DE gene associated with additional inclusive models, will be output if ind.incl.add is not Null.

`DEG.bestmodel`
: DE genes associated with main effect of each variable if interaction is NULL; with main, interaction, main or interaction effects of each variable if interaction is not NULL; and the best model used to identify each DE gene.

Author(s)

Lingsong Meng

`BMAseq.multi.Laplace` *BMAseq.multi*

Description

Multivariate analysis using BMAseq approach

Usage

```
BMAseq.multi.Laplace(
  dat.expr.counts,
  dat.pheno,
  var.pool,
  max.nvar,
  interaction = NULL,
  ind.incl.add = NULL,
  cut.BF = 1,
  cut.FDR = 0.05
)
```

Arguments

dat.expr.counts	RNA-seq count data matrix (rows for genes and columns for subjects).
dat.pheno	Phenotypic data matrix (rows for subjects and columns for variables).
var.pool	Variables of interest, a vector.
max.nvar	The maximum number of variables in a model.
interaction	Specific interaction terms with input format 'A&B', default is Null.
ind.incl.add	Indices of additional included model.
cut.BF	Bayes factor criterion, default value is 1.
cut.FDR	False discovery rate criterion for identifying DE genes, default value is 0.05.

Details

Multivariate analysis on RNA-seq count data using BMAseq approach

Value

A list consisting of

dat.expr.logcpm	Normalized RNA-seq data matrix (rows for genes and columns for subjects).
weights	Estimated voom weights.
dat.pheno.new	Phenotypic data matrix including new interaction variables, will be same as input dat.pheno if interaction is NULL.
model.space	Model space including all possible models.
post.modelprob	Posterior model probability for each gene.
post.incl.modelprob	Posterior inclusive model probability for each gene associated with main effect of each variables if interaction is NULL; with main, interaction, main or interaction effects if interaction not NULL.
post.incl.modelprob.JointMain	Posterior inclusive model probability for each gene associated with joint main effects of variables, will be output if interaction is NULL.
post.incl.modelprob.Add	Posterior inclusive model probability for each gene associated with additional inclusive models, will be output if ind.incl.add is not Null.

`index.incl` Indices of the inclusive models.

`eFDR` Estimated FDR for each gene associated with main effect of each variables if interaction is NULL; with main, interaction, main or interaction effects if interaction is not NULL.

`eFDR.JointMain` Estimated FDR for each gene associated with all possible joint effect of variables, will be output if interaction is NULL.

`eFDR.Add` Estimated FDR for each gene associated with additional inclusive models, will be output if ind.incl.add is not Null.

`summary.nDEG` A summary table of the number of identified DE gene associated with main effect of each variable if interaction is NULL; with main, interaction, main or interaction effects if interaction is not NULL.

`summary.nDEG.JointMain`
A summary table of the number of identified DE gene associated with joint main effcts of variables, will be output if interaction is NULL.

`summary.nDEG.Add`
A summary table of the number of identified DE gene associated with additional inclusive models, will be output if ind.incl.add is not Null.

`DEG.bestmodel` DE genes associated with main effect of each variable if interaction is NULL; with main, interaction, main or interaction effects of each variable if interaction is not NULL; and the best model used to identify each DE gene.

Author(s)

Lingsong Meng

`BMAseq.multi.postprob` *BMAseq.multi.postprob*

Description

Calculation of posterior model probability for each gene in multivariate analysis using BMAseq approach

Usage

```
BMAseq.multi.postprob(
  dat.expr.counts,
  dat.pheno,
  var.pool,
  max.nvar,
  interaction = NULL,
  cut.BF = 1,
  laplace = FALSE
)
```

Arguments

dat.expr.counts	RNA-seq count data matrix (rows for genes and columns for subjects).
dat.pheno	Phenotypic data matrix (rows for subjects and columns for variables).
var.pool	Variables of interest, a vector.
max.nvar	The maximum number of variables in a model.
interaction	Specific interaction terms with input format 'A&B', default is Null.
cut.BF	Bayes factor criterion, default value is 1.

Details

Calculation of posterior model probability for each gene in multivariate analysis on RNA-seq count data using BMAseq approach

Value

A list consisting of

dat.expr.logcpm	Normalized RNA-seq data matrix (rows for genes and columns for subjects).
weights	Estimated voom weights.
dat.pheno.new	Phenotypic data matrix including new interaction variables, will be same as input dat.pheno if interaction=NULL.
model.space	Model space including all possible models.
post.modelprob	Posterior model probability for each gene.
var.pool	Variables of interest, a vector.
interaction	Specific interaction terms with format 'A&B', default is Null.

Author(s)

Lingsong Meng

BMAseq.multi.postprob.MSout

BMAseq.multi.postprob

Description

Calculation of posterior model probability for each gene in multivariate analysis using BMAseq approach

Usage

```
BMAseq.multi.postprob.MSout(
  dat.expr.counts,
  dat.pheno,
  model.space,
  var.pool,
  interaction = NULL,
  cut.BF = 1,
  laplace = FALSE
)
```

Arguments

dat.expr.counts	RNA-seq count data matrix (rows for genes and columns for subjects).
dat.pheno	Phenotypic data matrix (rows for subjects and columns for variables).
model.space	Model space.
var.pool	Variables of interest, a vector.
interaction	Specific interaction terms with input format 'A&B', default is Null.
cut.BF	Bayes factor criterion, default value is 1.

Details

Calculation of posterior model probability for each gene in multivariate analysis on RNA-seq count data using BMAseq approach

Value

A list consisting of

dat.expr.logcpm	Normalized RNA-seq data matrix (rows for genes and columns for subjects).
weights	Estimated voom weights.
dat.pheno.new	Phenotypic data matrix including new interaction variables, will be same as input dat.pheno if interaction is NULL.
model.space	Model space including all possible models.
post.modelprob	Posterior model probability for each gene.
var.pool	Variables of interest, a vector.
interaction	Specific interaction terms with format 'A&B', default is Null.

Author(s)

Lingsong Meng

`BMAseq.uni` *BMAseq.uni*

Description

Univariate analysis using BMAseq approach

Usage

```
BMAseq.uni(
  dat.expr.counts,
  dat.pheno,
  var.pool,
  cut.BF = 1,
  cut.FDR = 0.25,
  laplace = FALSE
)
```

Arguments

`dat.expr.counts`	RNA-seq count data matrix (rows for genes and columns for subjects).
`dat.pheno`	Phenotypic data matrix (rows for subjects and columns for variables).
`var.pool`	Variables of interest, a vector.
`cut.BF`	Bayes factor criterion, default value is 1.
`cut.FDR`	False discovery rate criterion for identifying DE genes, default value is 0.25.

Details

Univariate analysis on RNA-seq count data using BMAseq approach

Value

A list consisting of

`dat.expr.logcpm`	Normalized RNA-seq data matrix (rows for genes and columns for subjects).
`weights`	Estimated voom weights.
`eFDR`	Estimated false discovery rate matrix (rows for genes and columns for variables of interest).
`nDEG`	The number of DE genes associated with each variable of interest.
`DEG`	DE genes associated with each variable of interest.

Author(s)

Lingsong Meng

get.jointMain *get.jointMain*

Description

Obtain specific joint main effects output

Usage

```
get.jointMain(postprob.output, joint = NULL, cut.FDR = 0.05)
```

Arguments

postprob.output	The output from BMAseq.multi.postprob function, a list.
joint	specific joint main effects with format 'A.B', a vector.
cut.FDR	False discovery rate criterion for identifying DE genes, default value is 0.05.

Details

Obtain specific joint main effects output

Value

A list consisting of

post.incl.modelprob.JointMain	Posterior inclusive model probability for specific joint effect of variables, only use if interaction is NULL.
eFDR.JointMain	Estimated FDR for specific joint effect, only use if interaction is NULL.
summary.nDEG.JointMain	A summary table of the number of identified DE gene for specific joint effcts of variables, only use if interaction is NULL.
ind.incl.JointMain	Indices of the inclusive models for specific joint effcts of variables, only use if interaction is NULL.

Author(s)

Lingsong Meng

`lmFit.single` *BMAseq.multi*

Description

Analysis using single model approach

Usage

```
lmFit.single(
  dat.expr.counts,
  dat.pheno,
  var.pool,
  max.nvar,
  interaction = NULL
)
```

Arguments

`dat.expr.counts`	RNA-seq count data matrix (rows for genes and columns for subjects).
`dat.pheno`	Phenotypic data matrix (rows for subjects and columns for variables).
`var.pool`	Variables of interest, a vector.
`max.nvar`	The maximum number of variables in a model.
`interaction`	Interactions.

Details

Analysis on RNA-seq count data using single model approach

Value

A list consisting of

`dat.expr.logcpm`	Normalized RNA-seq data matrix (rows for genes and columns for subjects).
`weights`	Estimated voom weights.
`summary.lmFit`	Output results of single linear models

Author(s)

Lingsong Meng

Modelspace *Modelspace*

Description

Create default model space

Usage

```
Modelspace(dat.pheno, var.pool, max.nvar, interaction = NULL)
```

Arguments

dat.pheno	Phenotypic data matrix (rows for subjects and columns for variables).
var.pool	Variables of interest, a vector.
max.nvar	The maximum number of variables in a model.
interaction	Specific interaction terms with input format 'A&B', default is Null.

Details

Create default model space consisting of all possible models

Value

A list consisting of

model.space	Model space including all possible models.
dat.pheno.new	Phenotypic data matrix including new interaction variables, will be same as input dat.pheno if interaction=NULL.
var.pool	Variables of interest, a vector.
interaction	Specific interaction terms with format 'A&B', default is Null.

Author(s)

Lingsong Meng

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