Package 'NBAMSeq'

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Type Package

Title Negative Binomial Additive Model for RNA-Seq Data

Version 1.19.0

Description High-throughput sequencing experiments followed by differential expression analysis is a widely used approach to detect genomic biomarkers. A fundamental step in differential expression analysis is to model the association between gene counts and covariates of interest. NBAMSeq a flexible statistical model based on the generalized additive model and allows for information sharing across genes in variance estimation.

License GPL-2

URL https://github.com/reese3928/NBAMSeq

BugReports https://github.com/reese3928/NBAMSeq/issues

Encoding UTF-8

Imports DESeq2, mgcv(>= 1.8-24), BiocParallel, genefilter, methods, stats,

Depends R (>= 3.6), SummarizedExperiment, S4Vectors

Suggests knitr, rmarkdown, testthat, ggplot2

RoxygenNote 6.1.0

VignetteBuilder knitr

biocViews RNASeq, DifferentialExpression, GeneExpression, Sequencing, Coverage

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Contents

`makeExample` *Make an example NBAMSeqDataSet*

Description

This function makes an example NBAMSeqDataSet

Usage

```
makeExample(n = 200, m = 30)
```

Arguments

`n`	number of genes
`m`	number of samples

Value

a NBAMSeqDataSet object

References

Love, M.I., Huber, W., Anders, S. (2014) Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biology, 15:550. https://doi.org/10.1186/s13059-014-0550-8

Examples

```
gsd = makeExample()
```

makeplot *Making plots to visualize nonlinear associations*

Description

This function makes plots to visualize nonlinear associations.

Usage

```
makeplot(object, phenoname, genename, ...)
```

Arguments

object	a NBAMSeqDataSet object
phenoname	the name of nonlinear variable to be visualized
genename	the name of gene to be visualized
...	additional arguments provided to plot.gam

Value

the plot made by plot.gam() function

Examples

```
gsd = makeExample(n = 3, m = 10)
gsd = NBAMSeq(gsd)
makeplot(gsd, "pheno", "gene3", main = "gene10")
```

NBAMSeq *Differential expression analysis based on negative binomial additive model*

Description

This function performs differential expression analysis based on negative binomial additive model.

Usage

```
NBAMSeq(object, gamma = 2.5, parallel = FALSE, fitlin = FALSE,
  BPPARAM = bpparam(), ...)
```

Arguments

object	a NBAMSeqDataSet object
gamma	a number greater or equal to 1. Increase gamma to create smoother models. Default gamma is 2.5. See gam for details.
parallel	either TRUE or FALSE indicating whether parallel should be used. Default is FALSE
fitlin	either TRUE or FALSE indicating whether linear model should be fitted. Default is FALSE
BPPARAM	an argument provided to bplapply. See register for details.
...	additional arguments provided to gam

Value

a NBAMSeqDataSet object

References

Love, M.I., Huber, W., Anders, S. (2014) Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biology, 15:550. https://doi.org/10.1186/s13059-014-0550-8

Examples

```
gsd = makeExample(n = 3, m = 10)
gsd = NBAMSeq(gsd)
```

NBAMSeq-methods *Accessor functions and replace methods for NBAMSeqDataSet object*

Description

Accessor functions and replace methods for NBAMSeqDataSet object

For `getDesign()`: accessor to the design formula

For `getsf()`: accessor to the size factors

Replace methods for NBAMSeqDataSet object

For `setsf()`: replace size factors

Usage

```
getDesign(theObject)

## S4 method for signature 'NBAMSeqDataSet'
getDesign(theObject)

getsf(theObject)
```

```
## S4 method for signature 'NBAMSeqDataSet'
getsf(theObject)

setsf(theObject) <- value

## S4 replacement method for signature 'NBAMSeqDataSet,numeric'
setsf(theObject) <- value
```

Arguments

theObject	a NBAMSeqDataSet object
value	the values to be included in the object

Value

For `getDesign()`: design formula

For `getsf()`: size factor

For `setsf()`: NBAMSeq object

References

Love, M.I., Huber, W., Anders, S. (2014) Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biology, 15:550. https://doi.org/10.1186/s13059-014-0550-8

Examples

```
## For getDesign() ##
gsd = makeExample()
design_gsd = getDesign(gsd)
## For getsf() ##
gsd = makeExample()
sf = getsf(gsd)
## For setsf() ##
n = 100
m = 50
gsd = makeExample(n = n, m = m)
sf = sample(1:5, m, replace = TRUE)
setsf(gsd) = sf
```

`NBAMSeqDataSet` *NBAMSeqDataSet constructor*

Description

NBAMSeqDataSet constructor

Usage

```
NBAMSeqDataSet(countData, colData, design, ...)
```

Arguments

countData	a matrix or data frame contains gene count
colData	a DataFrame or data.frame
design	a mgcv type design. e.g. ~ s(pheno) or ~ s(pheno) + var1 + var2
...	optional arguments passed to SummarizedExperiment

Value

a NBAMSeqDataSet object

Examples

```
n = 100  ## n stands for number of genes
m = 20   ## m stands for sample size
countData = matrix(rnbinom(n*m, mu=100, size=1/3), ncol = m)
mode(countData) = "integer"
colnames(countData) = paste0("sample", 1:m)
rownames(countData) = paste0("gene", 1:n)
pheno = runif(m, 20, 80)
colData = data.frame(pheno = pheno)
rownames(colData) = paste0("sample", 1:m)
gsd = NBAMSeqDataSet(countData = countData,
colData = colData, design = ~s(pheno))
```

NBAMSeqDataSet-class *NBAMSeqDataSet class*

Description

NBAMSeqDataSet is a class inherited from SummarizedExperiment. It is used to store the count matrix, colData, and design formula in differential expression analysis.

Slots

design a mgcv-type design formula

References

Martin Morgan, Valerie Obenchain, Jim Hester and Hervé Pagès (2018). SummarizedExperiment: SummarizedExperiment container. R package version 1.12.0.

`results` *Pulling out result*

Description

This function pulls out result from NBAMSeqDataSet object returned by NBAMSeq

Usage

```
results(object, name, contrast, indepfilter = TRUE, alpha = 0.1,
  pAdjustMethod = "BH", parallel = FALSE, BPPARAM = bpparam(), ...)
```

Arguments

`object`	a NBAMSeqDataSet object returned by NBAMSeq
`name`	the name of nonlinear variable or continuous linear variable
`contrast`	a character of length 3. 1st element: name of factor variable; 2nd element: name of numerator level; 3rd element: name of denominator level. contrast = c("group", "treatment", "control") means comparing treatment vs control for group variable.
`indepfilter`	either TRUE or FALSE indicating whether independent filtering should be performed. Default is TRUE.
`alpha`	significant threhold for declaring genes as differentially expressed. Default is 0.1.
`pAdjustMethod`	pvalue adjustment method. Default is "BH". See `p.adjust` for details.
`parallel`	either TRUE or FALSE indicating whether parallel should be used. Default is FALSE.
`BPPARAM`	an argument provided to `bplapply`. See `register` for details.
`...`	additional arguments provided to `pvalueAdjustment` function in DESeq2. See `results` for details.

Value

a DataFrame which contains the result

References

Love, M.I., Huber, W., Anders, S. (2014) Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biology, 15:550. https://doi.org/10.1186/s13059-014-0550-8

Examples

```
gsd = makeExample(n = 3, m = 10)
gsd = NBAMSeq(gsd)
res = results(gsd, name = "pheno")
```

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