

# Package ‘NBAMSeq’

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**Type** Package

**Title** Negative Binomial Additive Model for RNA-Seq Data

**Version** 1.24.1

**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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**Author** Xu Ren [aut, cre],  
Pei Fen Kuan [aut]

**Maintainer** Xu Ren <xuren2120@gmail.com>

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|             |                                       |
|-------------|---------------------------------------|
| makeExample | <i>Make an example NBAMSeqDataSet</i> |
|-------------|---------------------------------------|

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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 <a href="#">plot.gam</a> |

**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**

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

**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 | <i>NBAMSeqDataSet constructor</i> |
|----------------|-----------------------------------|

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### 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. $\sim s(\text{pheno})$ or $\sim s(\text{pheno}) + \text{var1} + \text{var2}$ |
| ...       | 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))
```

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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.

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|         |                           |
|---------|---------------------------|
| results | <i>Pulling out result</i> |
|---------|---------------------------|

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## 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 <a href="#">NBAMSeq</a>                                                                                                                                                                                         |
| 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 threshold for declaring genes as differentially expressed. Default is 0.1.                                                                                                                                                              |
| pAdjustMethod | pvalue adjustment method. Default is "BH". See <a href="#">p.adjust</a> for details.                                                                                                                                                                |
| parallel      | either TRUE or FALSE indicating whether parallel should be used. Default is FALSE.                                                                                                                                                                  |
| BPPARAM       | an argument provided to <a href="#">bplapply</a> . See <a href="#">register</a> for details.                                                                                                                                                        |
| ...           | additional arguments provided to pvalueAdjustment function in DESeq2. See <a href="#">results</a> 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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