

# Package ‘NBAMSeq’

June 30, 2022

**Type** Package

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

**Version** 1.13.0

**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

**git\_url** <https://git.bioconductor.org/packages/NBAMSeq>

**git\_branch** master

**git\_last\_commit** c4ce64c

**git\_last\_commit\_date** 2022-04-26

**Date/Publication** 2022-06-30

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

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

## R topics documented:

|                                |          |
|--------------------------------|----------|
| makeExample . . . . .          | 2        |
| makeplot . . . . .             | 3        |
| NBAMSeq . . . . .              | 3        |
| NBAMSeq-methods . . . . .      | 4        |
| NBAMSeqDataSet . . . . .       | 5        |
| NBAMSeqDataSet-class . . . . . | 6        |
| results . . . . .              | 7        |
| <b>Index</b>                   | <b>8</b> |

---

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

---

### 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**

|                        |   |
|------------------------|---|
| <code>object</code>    | a NBAMSeqDataSet object                                   |
| <code>phenoname</code> | the name of nonlinear variable to be visualized           |
| <code>genename</code>  | the name of gene to be visualized                         |
| <code>...</code>       | 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**

|          |  |
|----------|--|
| object   | a NBAMSeqDataSet object  |
| gamma    | 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. |
| 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 <a href="#">bplapply</a> . See <a href="#">register</a> for details.   |
| ...      | 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

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

---

**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")
```

# Index

`bplapply`, [4](#), [7](#)

`gam`, [4](#)

`getDesign` (NBAMSeq-methods), [4](#)

`getDesign`, NBAMSeqDataSet-method  
(NBAMSeq-methods), [4](#)

`getsf` (NBAMSeq-methods), [4](#)

`getsf`, NBAMSeqDataSet-method  
(NBAMSeq-methods), [4](#)

`makeExample`, [2](#)

`makeplot`, [3](#)

NBAMSeq, [3](#), [7](#)

NBAMSeq-methods, [4](#)

NBAMSeqDataSet, [5](#)

NBAMSeqDataSet-class, [6](#)

`p.adjust`, [7](#)

`plot.gam`, [3](#)

`register`, [4](#), [7](#)

`results`, [7](#), [7](#)

`setsf<-` (NBAMSeq-methods), [4](#)

`setsf<-`, NBAMSeqDataSet, numeric-method  
(NBAMSeq-methods), [4](#)

SummarizedExperiment, [6](#)