

# Package ‘NBAMSeq’

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**Type** Package

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

**Version** 1.12.0

**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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**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()
```

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`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")
```

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`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)
```

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 NBAMSeq-methods

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*Accessor functions and replace methods for NBAMSeqDataSet object*


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**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
```

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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. $\sim s(\text{pheno})$ 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))
```

---

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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