

# Package: msgbsR (via r-universe)

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**Type** Package

**Title** msgbsR: methylation sensitive genotyping by sequencing (MS-GBS)  
R functions

**Version** 1.37.0

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**Author** Benjamin Mayne

**Maintainer** Benjamin Mayne <benjamin.mayne@adelaide.edu.au>

**Depends** R (>= 3.4), GenomicRanges, methods

**Imports** BSgenome, easyRNASeq, edgeR, GenomicAlignments,  
GenomicFeatures, Seqinfo, ggbio, ggplot2, IRanges, parallel,  
plyr, Rsamtools, R.utils, stats, SummarizedExperiment,  
S4Vectors, utils

**Suggests** roxygen2, BSgenome.Rnorvegicus.UCSC.rn6

**biocViews** ImmunoOncology, DifferentialMethylation, DataImport,  
Epigenetics, MethylSeq

**Description** Pipeline for the analysis of a MS-GBS experiment.

**License** GPL-2

**LazyLoad** yes

**Collate** 'msgbsR.R' 'rawCounts.R' 'checkCuts.R' 'plotCounts.R'  
'diffMeth.R' 'plotCircos.R'

**RoxygenNote** 5.0.1

**Config/pak/sysreqs** cmake make libbz2-dev libicu-dev libjpeg-dev liblzma-dev libpng-dev libuv1-  
dev libxml2-dev libssl-dev xz-utils zlib1g-dev

**Repository** <https://bioc.r-universe.dev>

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**RemoteRef** HEAD

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|           |                  |
|-----------|------------------|
| checkCuts | <i>checkCuts</i> |
|-----------|------------------|

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Description

Determines the sequence around a cut site using a fasta file or BSgenome

Usage

```
checkCuts(cutSites, genome, fasta = FALSE, seq)
```

Arguments

|          |                                                                                                                                                                       |
|----------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| cutSites | A GRanges object containing the locations of the cut sites to be checked for sequence match. The names of the correct cut sites will be returned as a GRanges object. |
| genome   | The path to a fasta file or a BSgenome object to check for genomic sequences.                                                                                         |
| fasta    | TRUE if a fasta file has been supplied. Default = FALSE                                                                                                               |
| seq      | The desired recognition sequence that the enzyme should have cut.                                                                                                     |

Value

A GRanges object containing the names of the sites that had the correct sequence.

Author(s)

Benjamin Mayne

## Examples

```
library(GenomicRanges)
library(SummarizedExperiment)
library(BSgenome.Rnorvegicus.UCSC.rn6)
# Load the positions of possible MspI cut sites
data(ratdata)
# Extract the cut sites
cutSites <- rowRanges(ratdata)
# Adjust the cut sites to overlap recognition site on each strand
start(cutSites) <- ifelse(test = strand(cutSites) == '+',
                          yes = start(cutSites) - 1, no = start(cutSites) - 2)
end(cutSites) <- ifelse(test = strand(cutSites) == '+',
                        yes = end(cutSites) + 2, no = end(cutSites) + 1)
correctCuts <- checkCuts(cutSites = cutSites, genome = "rn6", seq = "CCGG")
```

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|      |                                                                                                                       |
|------|-----------------------------------------------------------------------------------------------------------------------|
| cuts | <i>A GRanges object of differentially methylated MspI cut sites on chromosome 20 in Rat from a MS-GBS experiment.</i> |
|------|-----------------------------------------------------------------------------------------------------------------------|

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## Description

The GRanges object was created from a list of differentially methylated cut sites from a MS-GBS experiment between two groups of rats that were fed either a control diet or a high fat diet.

## Usage

```
data(cuts)
```

## Format

A GRanges object of length 10.

## Details

- Positions of MspI cut sites differentially methylated in the prostate on chromosome 20 in Rats.

The data set contains 10 differentially methylated sites in the prostate between rats fed a control or high fat diet.

## Value

A GRanges object of length 10.

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|          |                 |
|----------|-----------------|
| diffMeth | <i>diffMeth</i> |
|----------|-----------------|

---

### Description

Determines differential methylated sites from a RangedSummarizedExperiment

### Usage

```
diffMeth(se, category, condition1, condition2,
         block = NULL, cpmThreshold, thresholdSamples)
```

### Arguments

|                  |                                                                                                                          |
|------------------|--------------------------------------------------------------------------------------------------------------------------|
| se               | A RangedSummarizedExperiment containing meta data of the samples.                                                        |
| category         | The heading name in the sample data to be tested for differential methylation.                                           |
| condition1       | The reference group within the category.                                                                                 |
| condition2       | The experimental group within the category.                                                                              |
| block            | The heading name in the sample data if differential methylation is to be tested with a blocking factor. Default is NULL. |
| cpmThreshold     | Counts per million threshold of read counts to be filtered out of the analysis.                                          |
| thresholdSamples | Minimum number of samples to contain the counts per million threshold.                                                   |

### Value

A data frame containing which cut sites that are differentially methylated.

### Author(s)

Benjamin Mayne

### Examples

```
# Load data
data(ratdata2)
top <- diffMeth(se = ratdata2, category = "Group",
               condition1 = "Control", condition2 = "Experimental",
               cpmThreshold = 1, thresholdSamples = 1)
```

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|        |               |
|--------|---------------|
| msgbsR | <i>msgbsR</i> |
|--------|---------------|

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### Description

msgbsR

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|            |                   |
|------------|-------------------|
| plotCircos | <i>plotCircos</i> |
|------------|-------------------|

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## Description

Plot a circos representing the cut site locations

## Usage

```
plotCircos(cutSites, seqlengths, cutSite.colour, seqlengths.colour)
```

## Arguments

|                   |                                                                           |
|-------------------|---------------------------------------------------------------------------|
| cutSites          | A GRanges object containing the locations of the cut sites to be plotted. |
| seqlengths        | An integer with the lengths of the chromosomes.                           |
| cutSite.colour    | The colour of the cut sites.                                              |
| seqlengths.colour | The colour of the chromosomes                                             |

## Value

A circos plot showing the locations of the cut sites.

## Author(s)

Benjamin Mayne

## Examples

```
# load example cut site positions
data(cuts)
# Obtain the length of chromosome 20 in rn6
library(BSgenome.Rnorvegicus.UCSC.rn6)
chr20 <- seqlengths(BSgenome.Rnorvegicus.UCSC.rn6)["chr20"]
plotCircos(cutSites = cuts, seqlengths = chr20,
           cutSite.colour = "red", seqlengths.colour = "blue")
```

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|            |                   |
|------------|-------------------|
| plotCounts | <i>plotCounts</i> |
|------------|-------------------|

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**Description**

Plots the total number of reads vs total number of cut sites per sample

**Usage**

```
plotCounts(se, category)
```

**Arguments**

|          |                                                                   |
|----------|-------------------------------------------------------------------|
| se       | A RangedSummarizedExperiment containing meta data of the samples. |
| category | The heading name in the sample data to distinguish groups.        |

**Value**

Produces a plot showing the total number reads vs total number of cut sites per sample.

**Author(s)**

Benjamin Mayne

**Examples**

```
data(ratdata2)
plotCounts(se = ratdata2, category = "Group")
```

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|         |                                                                                                |
|---------|------------------------------------------------------------------------------------------------|
| ratdata | <i>Read counts of potential MspI cut sites from a MS-GBS experiment of prostates from rats</i> |
|---------|------------------------------------------------------------------------------------------------|

---

**Description**

A RangedSummarizedExperiment containing read counts generated from a MS-GBS experiment using the restriction enzyme MspI, focusing on chromosome 20 of Rat.

**Usage**

```
data(ratdata)
```

**Format**

RangedSummarizedExperiment

**Details**

- ratdata A RangedSummarizedExperiment with 16047 potential MspI cut sites on chromosome 20 in Rat and six samples (3 Control and 3 Experimental).

This dataset contains six prostate samples from rats: 3 control and 3 experimental high fat diet.

**Value**

RangedSummarizedExperiment

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|          |                                                                                              |
|----------|----------------------------------------------------------------------------------------------|
| ratdata2 | <i>Read counts of correct MspI cut sites from a MS-GBS experiment of prostates from rats</i> |
|----------|----------------------------------------------------------------------------------------------|

---

**Description**

A RangedSummarizedExperiment containing read counts generated from a MS-GBS experiment using the restriction enzyme MspI, focusing on chromosome 20 of Rat. The sites have been checked for the correct recognition site.

**Usage**

```
data(ratdata2)
```

**Format**

RangedSummarizedExperiment

**Details**

- ratdata2 A RangedSummarizedExperiment containing data for 13983 MspI cut sites on chromosome 20 in Rat and six samples (3 Control and 3 Experimental).

This dataset contains six prostate samples from rats: 3 control and 3 experimental high fat diet. The data can be used for differential methylation analyses.

**Value**

RangedSummarizedExperiment

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`rawCounts`*rawCounts*

---

**Description**

Imports the raw read counts from sorted and indexed bam file(s)

**Usage**

```
rawCounts(bamFilepath, threads = 1)
```

**Arguments**

|                          |                                                              |
|--------------------------|--------------------------------------------------------------|
| <code>bamFilepath</code> | The path to the location of the bam file(s).                 |
| <code>threads</code>     | The total number of usable threads to be used. Default is 1. |

**Value**

Produces a `RangedSummarizedExperiment`. Columns are samples and the rows are cut sites. The cut site IDs are in the format `chr:position-position:strand`.

**Author(s)**

Benjamin Mayne, Sam Buckberry

**Examples**

```
my_path <- system.file("extdata", package = "msgbsR")
my_data <- rawCounts(bamFilepath = my_path)
```

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