

# Package: msgbsR (via r-universe)

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**Type** Package

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

**Version** 1.36.0

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**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.rm6

**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-release.r-universe.dev>

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## Contents

checkCuts . . . . .	2
cuts . . . . .	3
diffMeth . . . . .	4
msgbsR . . . . .	4
plotCircos . . . . .	5
plotCounts . . . . .	6
ratdata . . . . .	6
ratdata2 . . . . .	7
rawCounts . . . . .	8
<b>Index</b>	<b>9</b>

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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>
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**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>
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**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>
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**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*

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**Description**

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

**Usage**

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

**Arguments**

`bamFilepath`     The path to the location of the bam file(s).  
`threads`         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)
```

# Index

## \* datasets

cuts, [3](#)

ratdata, [6](#)

ratdata2, [7](#)

checkCuts, [2](#)

cuts, [3](#)

diffMeth, [4](#)

msgbsR, [4](#)

msgbsR-package (msgbsR), [4](#)

plotCircos, [5](#)

plotCounts, [6](#)

ratdata, [6](#)

ratdata2, [7](#)

rawCounts, [8](#)