

Package: DMRcatedata (via r-universe)

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Type Package

Title Data Package for DMRcate

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Description This package contains 9 data objects supporting functionality and examples of the Bioconductor package DMRcate.

License GPL-3

Depends R (>= 4.0), ExperimentHub

Imports GenomicFeatures, Gviz, readxl, plyr, rtracklayer,
IlluminaHumanMethylation450kanno.ilmn12.hg19,
IlluminaHumanMethylationEPICanno.ilm10b4.hg19

LazyData true

Suggests knitr

biocViews ExperimentHub, ExperimentData, SNPData, Homo_sapiens_Data,
Mus_musculus_Data, SequencingData, MicroarrayData, Genome

VignetteBuilder knitr

Config/pak/sysreqs cmake make libbz2-dev libicu-dev libjpeg-dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev libx11-dev xz-utils zlib1g-dev

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Contents

DMRcatedata-package	2
ALLbetas	3
crosshyb	3
epicv2snps	4
hg19.generanges	4
hg19.grt	5
hg38.generanges	5
hg38.grt	6
mm10.generanges	6
mm10.grt	7
snpsall	7
XY.probes	8
Index	9

DMRcatedata-package	<i>Dataset to use with the DMRcate pipeline</i>
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Description

SNP annotation, cross-hybridising probes, XY probes, and gene annotation for hg19, hg38 and mm10

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Examples

```
data(crosshyb)
data(snpsall)
data(hg19.grt)
data(hg19.generanges)
```

ALLbetas

EPICv2 beta values for DMR calling

Description

Matrix of EPICv2 beta values from Noguera-Castells et al. (2023) consisting of five B cell acute lymphoblastic leukaemia (BALL) and five T cell acute lymphoblastic leukaemia (TALL) samples for DMR calling.

Usage

`data(ALLbetas)`

Format

`data.frame`

Source

https://ftp.ncbi.nlm.nih.gov/geo/series/GSE222nnn/GSE222919/suppl/GSE222919_processed_data.txt.gz

crosshyb

Potentially cross-hybridising Illumina probes

Description

This is a character vector of Illumina probes whose probe sequence promiscuously aligns to non-target sections of the genome with a matching of 47bp or higher.

Usage

`data(crosshyb)`

Format

`character`

Source

https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM2_ESM.csv (accessed September 2019) https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM3_ESM.csv (accessed September 2019) <http://www.sickkids.ca/MS-Office-Files/Research/WeksbergLab/48639-non-specific-probes-Illumina450k.xlsx> (accessed September 2019)

`epicv2snps`*SNP information for EPICv2 Illumina probes*

Description

This is a data.frame of Illumina probes from EPICv2 whose target CpG lies on or near a known SNP. SNP ID, distance and minor allele frequency are all reported here.

Usage

```
data(snpsall)
```

Format

data.frame

Source

https://static-content.springer.com/esm/art%3A10.1186%2Fs12864-024-10027-5/MediaObjects/12864_2024_10027_MOESM4_ESM.csv

`hg19.generanges`*Start and stop positions of all genes in hg19*

Description

This data set gives the genomic intervals of all gene regions in the Ensembl Release 75 of hg19.

Usage

```
data(hg19.generanges)
```

Format

A GRanges object with 57773 intervals.

Source

ftp://ftp.ensembl.org/pub/release-75/gtf/homo_sapiens/Homo_sapiens.GRCh37.75.gtf.gz

hg19.grt*GeneRegionTrack for hg19*

Description

This is a GeneRegionTrack formulated from TxDb.Hsapiens.UCSC.hg19.knownGene.

Usage

```
data(hg19.grt)
```

Format

GeneRegionTrack

hg38.generanges*Start and stop positions of all genes in hg38*

Description

This data set gives the genomic intervals of all gene regions in the Ensembl Release 102 of hg38.

Usage

```
data(hg38.generanges)
```

Format

A GRanges object with 60616 intervals.

Source

ftp://ftp.ensembl.org/pub/release-102/gtf/homo_sapiens/Homo_sapiens.GRCh38.102.chr.gtf.gz

`hg38.grt`*GeneRegionTrack for hg38*

Description

This is a GeneRegionTrack formulated from TxDb.Hsapiens.UCSC.hg38.knownGene.

Usage

```
data(hg38.grt)
```

Format

GeneRegionTrack

`mm10.generanges`*Start and stop positions of all genes in mm10*

Description

This data set gives the genomic intervals of all gene regions in the Ensembl Release 102 of mm10.

Usage

```
data(mm10.generanges)
```

Format

A GRanges object with 55401 intervals.

Source

ftp://ftp.ensembl.org/pub/release-96/gtf/mus_musculus/Mus_musculus.GRCm38.102.chr.gtf.gz

mm10.grt

*GeneRegionTrack for mm10***Description**

This is a GeneRegionTrack formulated from TxDb.Mmusculus.UCSC.mm10.knownGene.

Usage

```
data(mm10.grt)
```

Format

GeneRegionTrack

snpsall

*SNP information for EPICv1 and 450K Illumina probes***Description**

This is a data.frame of Illumina probes from EPICv1 and 450K whose target CpG lies on or near a known SNP. SNP ID, distance and minor allele frequency are all reported here.

Usage

```
data(snpsall)
```

Format

data.frame

Source

https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM4_ESM.csv (accessed September 2019) https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM5_ESM.csv (accessed September 2019) https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM6_ESM.csv (accessed September 2019) <http://www.sickkids.ca/MS-Office-Files/Research/WeksbergLab/48640-polymorphic-CpGs-Illumina.xlsx> (accessed September 2019)

`XY.probes`*Sex chromosome Illumina probes*

Description

This is a character vector of Illumina probes whose target CpG site is on a sex chromosome.

Usage

```
data(XY.probes)
```

Format

character

Index

* datasets

- ALLbetas, [3](#)
- crosshyb, [3](#)
- DMRcatedata-package, [2](#)
- epicv2snps, [4](#)
- hg19.geranges, [4](#)
- hg19.grt, [5](#)
- hg38.geranges, [5](#)
- hg38.grt, [6](#)
- mm10.geranges, [6](#)
- mm10.grt, [7](#)
- snpsall, [7](#)
- XY.probes, [8](#)

ALLbetas, [3](#)

crosshyb, [3](#)

DMRcatedata (DMRcatedata-package), [2](#)
DMRcatedata-package, [2](#)

epicv2snps, [4](#)

hg19.geranges, [4](#)
hg19.grt, [5](#)
hg38.geranges, [5](#)
hg38.grt, [6](#)

mm10.geranges, [6](#)
mm10.grt, [7](#)

snpsall, [7](#)

XY.probes, [8](#)