Package ‘DMRcatedata’

April 4, 2024

Type Package
Title Data Package for DMRcate
Version 2.20.3
Date 2024-08-03
Author Tim Peters
Maintainer Tim Peters <t.peters@garvan.org.au>
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
git_url https://git.bioconductor.org/packages/DMRcatedata
git_branch RELEASE_3_18
git_last_commit 8575f6c
git_last_commit_date 2024-03-08
Repository Bioconductor 3.18
Date/Publication 2024-04-04

R topics documented:

  DMRcatedata-package ........................................... 2
  ALLbetas ......................................................... 2
## DMRcatedata-package

**Dataset to use with the DMRcate pipeline**

### Description

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

### Author(s)

Tim Peters, Immunogenomics Laboratory, Garvan Institute of Medical Research

Maintainer: Tim Peters<tpeters@garvan.org.au>

### Examples

```r
data(crosshyb)
data(snpsall)
data(hg19.grt)
data(hg19.generanges)
data(mm10.grt)
data(mm10.generanges)
data(snpsall)
data(XY.probes)
```

## 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

```r
data(ALLbetas)
```
crosshyb

Format
data.frame

Source

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

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)
**hg19.grt**

**Format**

data.frame

**Source**


---

**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**


---

**hg19.grt**

**GeneRegionTrack for hg19**

**Description**

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

**Usage**

data(hg19.grt)

**Format**

GeneRegionTrack
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


Description

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

Usage

data(hg38.grt)

Format

GeneRegionTrack
mm10.generanges  

**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  

**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**

```r
data(snpsall)
```

**Format**

`data.frame`

**Source**


**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**

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

**Format**

`character`
Index

* datasets
  ALLbetas, 2
  crosshyb, 3
  DMRcatedata-package, 2
  epicv2snps, 3
  hg19.generanges, 4
  hg19.grt, 4
  hg38.generanges, 5
  hg38.grt, 5
  mm10.generanges, 6
  mm10.grt, 6
  snpsall, 7
  XY.probes, 7

ALLbetas, 2

crosshyb, 3

DMRcatedata (DMRcatedata-package), 2
DMRcatedata-package, 2

epicv2snps, 3

hg19.generanges, 4
hg19.grt, 4
hg38.generanges, 5
hg38.grt, 5

mm10.generanges, 6
mm10.grt, 6

snpsall, 7

XY.probes, 7