The `DMRcatedata` package user's guide

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Package Contents

`DMRcatedata` accompanies the `DMRcate` package, providing data for examples, probe filtering and transcript annotation.

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

Nine objects are contained in `DMRcatedata`. `crosshyb` is a factor listing probe IDs potentially confounded by cross-hybridisation to other parts of the genome[1][2]. It is used internally by `rmSNPandCH()`.

`snpsall` is a data.frame containing probes that are potentially confounded by a SNP or indel variant[1]. It lists the ID, distance (in nucleotides) to the CpG in question, and minor allele frequency for each associated variant.

`XY.probes` is a vector of Illumina probes whose targets are on human sex chromosomes.

Objects named `.*{grt|generanges)` are annotation objects that are needed by `extractRanges()` and `DMR.plot()` respectively. hg38 and mm10 objects have been parsed from Release 96 of Ensembl, and hg19 from Release 75. These are accessed within the environment of the aforementioned functions.

Sources

- `snpsall` sourced from `https://static-content.springer.com/esm/art\%3A10.1186\%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM4_ESM.csv`, `https://static-content.springer.com/esm/art\%3A10.1186\%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM5_ESM.csv`, `https://static-content.springer.com/esm/art\%3A10.1186\%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM6_ESM.csv`, `http://www.sickkids.ca/MS-Office-Files/Research/WeksbergLab/48640-polymorphic-CpGs-Illumina450k.xlsx` (accessed October 2016)

- `crosshyb` sourced from `https://static-content.springer.com/esm/art\%3A10.1186\%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM2_ESM.csv`, `https://static-content.springer.com/esm/art\%3A10.1186\%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM3_ESM.csv` (accessed October 2016) and `http://www.sickkids.ca/MS-Office-Files/Research/WeksbergLab/48639-non-specific-probes-Illumina450k.xlsx`, (accessed February 2014).

References

[1] Pidsley R, Zotenko E, Peters TJ, Lawrence MG, Risbridger GP, Molloy P, Van Dijk S, Muhlhausler B, Stirzaker C, Clark SJ. Critical evaluation of the Illumina MethylationEPIC BeadChip microarray for whole-genome DNA methylation profiling. *Genome Biology*. 2016 17(1), 208.

[2] Chen YA, Lemire M, Choufani S, Butcher DT, Grafodatskaya D, Zanke BW, Gallinger S, Hudson TJ, Weksberg R. Discovery of cross-reactive probes and polymorphic CpGs in the Illumina Infinium HumanMethylation450 microarray. *Epigenetics*. 2013 Jan 11;8(2).