

# 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(dmratedata)
```

Three 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()`.

```
str(crosshyb)
## chr [1:63707] "cg00001510" "cg00003969" "cg00004121" "cg00004192" ...
```

`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.

```
class(snpsall)
## [1] "data.frame"

dim(snpsall)
## [1] 208568      3

head(snpsall)
##                SNP Distance MinorAlleleFrequency
## cg00000108      rs9857774          16          0.056801
## cg00000109      rs9864492          17          0.010135
## cg00000165      rs76771611         25          0.027778
## cg00000769      rs74996347          51           0.5
## cg00000807 rs113612339;rs114523815    1, 38    0.500000, 0.025424
## cg00000884      rs115955687          39          0.033898
```

`myBetas` is a matrix of 450K probe beta values, matching to Homo Sapiens chromosome 20, sourced from the colon and rectal adenocarcinoma section of The Cancer Genome Atlas (TCGA) Repository. It contains 38 matched tumour/normal pairs.

```
class(myBetas)
## [1] "matrix"
dim(myBetas)
## [1] 10042 76
```

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

```
class(XY.probes)
## [1] "character"
length(XY.probes)
## [1] 20710
```

`CpGs` is a GRanges object containing simulated WGBS data, generated by WGBSSuite[3] v0.3 with the command `Rscript simulate_WGBS.R 100000 0.87605280264016 0.125787302952703 0.2 0.2 18.5989386821267 18.5989386821267 3 2 0.2 0.5 0.112588288740425,0.00330228672976263 . truncated.`

```
CpGs
## GRanges object with 100000 ranges and 12 metadata columns:
##           seqnames      ranges strand | Treatment1.C Treatment1.cov
##           <Rle> <IRanges> <Rle> |   <integer>      <integer>
##      [1]   chr1         1      * |         11           13
##      [2]   chr1        54      * |          9           15
##      [3]   chr1        58      * |         14           20
##      [4]   chr1       320      * |         12           15
##      [5]   chr1       325      * |         10           19
##      ...     ...         ...     ... .         ...           ...
## [99996]   chr1 19705499      * |         13           15
## [99997]   chr1 19705511      * |         11           13
## [99998]   chr1 19705521      * |         15           15
## [99999]   chr1 19705567      * |         19           20
## [100000]   chr1 19705760      * |         11           21
##           Treatment2.C Treatment2.cov Treatment3.C Treatment3.cov
##           <integer>      <integer>      <integer>      <integer>
```

```

##      [1]          9          14          16          19
##      [2]         16         26         18         20
##      [3]         19         20         19         27
##      [4]         14         14         17         20
##      [5]         13         18         14         22
##      ...         ...         ...         ...         ...
## [99996]         13         13         12         20
## [99997]         16         19         16         19
## [99998]         13         13         15         17
## [99999]         11         17         18         20
## [100000]        14         14         21         28
##          Control1.C Control1.cov Control2.C Control2.cov Control3.C
##          <integer> <integer> <integer> <integer> <integer>
##      [1]          11          15          16          23          11
##      [2]          17          18          10          17          19
##      [3]          16          16          12          14          15
##      [4]          13          25          15          21          18
##      [5]           5          14          16          23          20
##      ...         ...         ...         ...         ...
## [99996]          13          32          12          20          15
## [99997]          12          27          14          22          11
## [99998]          16          17           8          16          22
## [99999]          18          24          18          20          16
## [100000]         17          21          12          17          12
##          Control3.cov
##          <integer>
##      [1]          14
##      [2]          21
##      [3]          19
##      [4]          22
##      [5]          26
##      ...         ...
## [99996]          15
## [99997]          19
## [99998]          22
## [99999]          17
## [100000]         25
## -----
## seqinfo: 1 sequence from an unspecified genome; no seqlengths

```

tx.hg19, tx.hg38 and tx.mm10 are GRanges objects containing complete transcript annotation generated from [ftp://ftp.ensembl.org/pub/release-75/gtf/homo\\_sapiens/Homo\\_sapiens.GRCh37.75.gtf.gz](ftp://ftp.ensembl.org/pub/release-75/gtf/homo_sapiens/Homo_sapiens.GRCh37.75.gtf.gz), [ftp://ftp.ensembl.org/pub/release-81/gtf/homo\\_sapiens/Homo\\_sapiens.GRCh38.81.gtf.gz](ftp://ftp.ensembl.org/pub/release-81/gtf/homo_sapiens/Homo_sapiens.GRCh38.81.gtf.gz) and [ftp://ftp.ensembl.org/pub/release-81/gtf/mus\\_musculus/Mus\\_musculus.GRCm38](ftp://ftp.ensembl.org/pub/release-81/gtf/mus_musculus/Mus_musculus.GRCm38).

81.gtf.gz respectively.

```
tx.hg19
## GRanges object with 215170 ranges and 4 metadata columns:
##                               seqnames      ranges strand |
##                               <Rle>         <IRanges> <Rle> |
## ENST00000000233                chr7 127228399-127231759   + |
## ENST00000000412                chr12  9092961-9102551    - |
## ENST00000000442                chr11  64073050-64084210   + |
## ENST00000001008                chr12  2904119-2913124    + |
## ENST00000001146                chr2   72356367-72375167   - |
##                               ...           ...         ... .
## ENST00000610276                chr21  33108045-33108720   + |
## ENST00000610277 chrHSCHR19LRC_LRC_I_CTG1 54677109-54693666   - |
## ENST00000610278                chr22  21335650-21336044   - |
## ENST00000610279                chr10  69609283-69610504   + |
## ENST00000610280                chr11  58059298-58060237   - |
##                               gene_name      gene_type      gene_id
##                               <character>    <character>    <character>
## ENST00000000233                ARF5 protein_coding ENSG00000004059
## ENST00000000412                M6PR protein_coding ENSG00000003056
## ENST00000000442                ESRRA protein_coding ENSG00000173153
## ENST00000001008                FKBP4 protein_coding ENSG00000004478
## ENST00000001146                CYP26B1 protein_coding ENSG00000003137
##                               ...           ...         ...
## ENST00000610276                AP000255.6      lincRNA ENSG00000273091
## ENST00000610277                MBOAT7 protein_coding ENSG00000273130
## ENST00000610278 XXbac-B135H6.18      lincRNA ENSG00000272829
## ENST00000610279                RP11-57G10.8    lincRNA ENSG00000272892
## ENST00000610280                OR10Q2P      pseudogene ENSG00000272900
##                               tx_name
##                               <character>
## ENST00000000233                ARF5-001
## ENST00000000412                M6PR-001
## ENST00000000442                ESRRA-002
## ENST00000001008                FKBP4-001
## ENST00000001146                CYP26B1-001
##                               ...           ...
## ENST00000610276                AP000255.6-001
## ENST00000610277                MBOAT7-001
## ENST00000610278 XXbac-B135H6.18-001
## ENST00000610279                RP11-57G10.8-001
## ENST00000610280                OR10Q2P-001
## -----
## seqinfo: 265 sequences from an unspecified genome; no seqlengths
```

## Sources

- myBetas sourced from The Cancer Genome Atlas (TCGA) data repository, colon and rectal adenocarcinoma
- 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_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_MOESM5_ESM.csv), [https://static-content.springer.com/esm/art\%3A10.1186\%2Fs13059-016-1066-1/MediaObjects/13059\\_2016\\_1066\\_MOESM6\\_ESM.csv](https://static-content.springer.com/esm/art\%3A10.1186\%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM6_ESM.csv) (accessed October 2016) and [http://supportres.illumina.com/documents/myillumina/88bab663-307c-444a-848e-0ed6c338ee4d/humanmethylation450\\_15017482\\_v.1.2.snupdate.table.v3.txt](http://supportres.illumina.com/documents/myillumina/88bab663-307c-444a-848e-0ed6c338ee4d/humanmethylation450_15017482_v.1.2.snupdate.table.v3.txt), (accessed February 2014)
- 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_MOESM2_ESM.csv), [https://static-content.springer.com/esm/art\%3A10.1186\%2Fs13059-016-1066-1/MediaObjects/13059\\_2016\\_1066\\_MOESM3\\_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).
- tx.hg19, tx.hg38 and tx.mm10 sourced from <ftp://ftp.ensembl.org>, accessed July 2015.

## 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).
- [3] Rackham, OJL, Dellaportas P, Petretto E, Bottolo, L. (2015). WGBSSuite: Simulating Whole Genome Bisulphite Sequencing data and benchmarking differential DNA methylation analysis tools. *Bioinformatics* (Oxford, England), (March), btv114. <http://doi.org/10.1093/bioinformatics/btv114>