

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(dmrcatedata)
```

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
##           <Rle>             <IRanges> <Rle> | <integer>
##      [1]   chr1             [ 1,  1]   * |           11
##      [2]   chr1             [ 54, 54]  * |            9
##      [3]   chr1             [ 58, 58]  * |           14
##      [4]   chr1            [320, 320] * |           12
##      [5]   chr1            [325, 325] * |           10
##      ...     ...             ...     ... |           ...
## [99996]   chr1 [19705499, 19705499] * |           13
## [99997]   chr1 [19705511, 19705511] * |           11
## [99998]   chr1 [19705521, 19705521] * |           15
## [99999]   chr1 [19705567, 19705567] * |           19
## [100000]   chr1 [19705760, 19705760] * |           11
##           Treatment1.cov Treatment2.C Treatment2.cov Treatment3.C
##           <integer>     <integer>     <integer>     <integer>
```

```

##      [1]          13          9          14          16
##      [2]          15          16          26          18
##      [3]          20          19          20          19
##      [4]          15          14          14          17
##      [5]          19          13          18          14
##      ...          ...          ...          ...          ...
## [99996]          15          13          13          12
## [99997]          13          16          19          16
## [99998]          15          13          13          15
## [99999]          20          11          17          18
## [100000]         21          14          14          21
##      Treatment3.cov Control1.C Control1.cov Control2.C Control2.cov
##      <integer> <integer> <integer> <integer> <integer>
##      [1]          19          11          15          16          23
##      [2]          20          17          18          10          17
##      [3]          27          16          16          12          14
##      [4]          20          13          25          15          21
##      [5]          22           5          14          16          23
##      ...          ...          ...          ...          ...          ...
## [99996]          20          13          32          12          20
## [99997]          19          12          27          14          22
## [99998]          17          16          17           8          16
## [99999]          20          18          24          18          20
## [100000]         28          17          21          12          17
##      Control3.C Control3.cov
##      <integer> <integer>
##      [1]          11          14
##      [2]          19          21
##      [3]          15          19
##      [4]          18          22
##      [5]          20          26
##      ...          ...          ...
## [99996]          15          15
## [99997]          11          19
## [99998]          22          22
## [99999]          16          17
## [100000]          12          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-81/gtf/homo_sapiens/Homo_sapiens.GRCh38.81.gtf.gz and 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 chrH5CHR19LRC_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_MOESM5_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, (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_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>