

Package: TumourMethData (via r-universe)

October 10, 2026

Title A Collection of DNA Methylation Datasets for Human Tumour Samples and Matching Normal Samples

Version 1.11.0

Date 2023-09-29

Description TumourMethData collects tumour methylation data from a variety of different tumour types (and also matching normal samples where available) and produced with different technologies (e.g. WGBS, RRBS and methylation arrays) and provides them as RangedSummarizedExperiments. This facilitates easy extraction of methylation data for regions of interest across different tumour types and studies.

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URL <https://github.com/richardheery/TumourMethData>

BugReports <https://support.bioconductor.org/tag/TumourMethData>

biocViews ExperimentData, ExperimentHub, MethylSeqData, CancerData, Homo_sapiens_Data,

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

Depends R (>= 4.2), SummarizedExperiment

Imports base, BSgenome.Hsapiens.UCSC.hg19, dplyr, ExperimentHub, ExperimentHubData, GenomicRanges, HDF5Array, knitr, methodical, methrix, openxlsx, R.utils, readr, rhdf5, rmarkdown, stringr, TCGAutils, tibble, usethis, xlsx

Suggests ggplot2

VignetteBuilder knitr

LazyData false

Config/pak/sysreqs cmake libfontconfig1-dev libfreetype6-dev libfribidi-dev git make libharfbuzz-dev default-jdk libbz2-dev libgit2-dev libicu-dev libjpeg-dev liblzma-dev libpng-dev libtiff-dev libuv1-dev libwebp-dev libxml2-dev libssl-dev libx11-dev xz-utils zlib1g-dev

Repository <https://bioc.r-universe.dev>
Date/Publication 2026-04-28 12:37:04 UTC
RemoteUrl <https://github.com/bioc/TumourMethData>
RemoteRef HEAD
RemoteSha 46455f70ceff767d8f1b8bda17d5c89e3f7e815b

Contents

TumourMethData-package	2
download_meth_dataset	3
download_rnaseq_dataset	4
TumourMethDatasets	4
Index	5

TumourMethData-package

TumourMethData: A collection of DNA methylation datasets for human tumour samples and matching normal samples

Description

TumourMethData collects tumour methylation data from a variety of different tumour types (and also matching normal samples where available) and produced with different technologies (e.g. WGBS, RRBS and methylation arrays) and provides them as RangedSummarizedExperiments, facilitating easy extraction of methylation data for regions of interest. At present, includes the following datasets:

Details

- cpgea_wgbs_hg38: WGBS Data from 187 pairs of matching human prostate tumours and normal prostate samples.
- tcga_wgbs_hg38: WGBS Data from 39 bladder, breast, colon, glioblastoma, lung, rectal stomach and uterine tumour samples and 8 matching normal samples.
- mcrpc_wgbs_hg38: WGBS data from 100 prostate cancer metastases.
- mcrpc_wgbs_hg38_chr11: Subset of mcrpc_wgbs_hg38 with methylation values for just chromosome 11.
- cao_esophageal_wgbs_hg19: WGBS data for 10 squamous esophageal tumours and 9 matching normal samples.
- target_rhabdoid_wgbs_hg19: WGBS data for 69 childhood rhabdoid tumours.

Author(s)

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See Also

Useful links:

- <https://github.com/richardheery/TumourMethData>
- Report bugs at <https://support.bioconductor.org/tag/TumourMethData>

download_meth_dataset *Download a WGBS methylation dataset from TumourMethData*

Description

The HDF5 file and RDS file to construct a `RangedSummarizedExperiment` for the specified dataset are downloaded into the ExperimentHub cache located at `ExperimentHub::getExperimentHubOption("cache")`. A copy of the RDS file pointing to the HDF5 file in the cache is saved in the specified directory.

Usage

```
download_meth_dataset(dataset, dir = getwd())
```

Arguments

dataset	Name of the dataset to download WGBS data from. Must be one of the datasets listed in <code>data(TumourMethDatasets)</code> .
dir	Directory in which to save a the copy of the RDS file pointing to the location of the HDF5 file in the ExperimentHub cache. Default is the current directory.

Value

A `RangedSummarizedExperiment` with methylation values from the specified dataset.

Examples

```
mcrpc_wgbs_hg38_chr11 = TumourMethData::download_meth_dataset(dataset = "mcrpc_wgbs_hg38_chr11")
print(mcrpc_wgbs_hg38_chr11)
```

```
download_rnaseq_dataset
```

Download a RNA-Seq counts dataset from TumourMethData

Description

Download a RNA-Seq counts dataset from TumourMethData

Usage

```
download_rnaseq_dataset(dataset)
```

Arguments

dataset	Name of the dataset to download. Must be one of the datasets listed in <code>data(TumourMethDatasets)</code> where <code>transcript_counts_available</code> is TRUE.
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Value

A data.frame with RNA-Seq counts calculated using Kallisto.

Examples

```
mcrpc_rnaseq = TumourMethData::download_rnaseq_dataset(dataset = "mcrpc_wgbs_hg38_chr11")
print(mcrpc_rnaseq)
```

TumourMethDatasets	<i>TumourMethDatasets</i>
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Description

A table describing the datasets available from TumourMethData.

Usage

```
TumourMethDatasets
```

Format

A data.frame with one row for each dataset

Index

* **datasets**

TumourMethDatasets, [4](#)

download_meth_dataset, [3](#)

download_rnaseq_dataset, [4](#)

TumourMethData

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

TumourMethData-package, [2](#)

TumourMethDatasets, [4](#)