Package 'TumourMethData'

April 29, 2025

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

Version 1.7.0

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 7.2.3

Depends R (>= 4.2), SummarizedExperiment

Imports ExperimentHub, GenomicRanges, HDF5Array, R.utils, rhdf5

Suggests ggplot2, knitr, rmarkdown

VignetteBuilder knitr

LazyData false

git_url https://git.bioconductor.org/packages/TumourMethData

git_branch devel

git_last_commit 476278c

git_last_commit_date 2025-04-15

Repository Bioconductor 3.22

Date/Publication 2025-04-29

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Contents

TumourMethData-package 2
download_meth_dataset 3
download_rnaseq_dataset 3
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 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)

Richard Heery

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")` and symbolic links to these are created in the specified directory by `dir`.

Usage

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

Arguments

`dataset`	Name of the dataset to download WGBS data from. Must be one of the datsets listed in data(TumourMethDatasets).
`dir`	Parent directory to create links to the HDF5 SummarizedExperiment dataset. A subdirectory with the dataset name will be created within this directory. Default is tempdir(). If a directory named `paste(dir, dataset, sep = "/")` already exists, will attempt to load a HDF5 summarized experiment from there and return an error if this fails.

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 an RNA-Seq counts dataset from TumourMethData*

Description

A TSV file with the RNA-Seq counts is downloaded into the ExperimentHub cache located at `ExperimentHub::getExperimentHubOption("cache")` and is read into R as a data.frame.

Usage

```
download_rnaseq_dataset(dataset)
```

Arguments

`dataset`	Name of the dataset to download. Must be one of the datasets listed in data(TumourMethDatasets) where `transcript_counts_available` is TRUE.

Value

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

`TumourMethDatasets` *TumourMethDatasets*

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, 3

TumourMethData
*(*TumourMethData-package*)*, 2
TumourMethData-package, 2
TumourMethDatasets, 4