

Package ‘TumourMethData’

July 23, 2024

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

Version 1.2.0

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.

License Artistic-2.0

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 RELEASE_3_19

git_last_commit 6422f23

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-07-23

Author Richard Heery [aut, cre] (<<https://orcid.org/0000-0001-8067-3114>>)

Maintainer Richard Heery <richardheery@gmail.com>

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)

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

<code>dataset</code>	Name of the dataset to download WGBS data from. Must be one of the datasets listed in <code>data(TumourMethDatasets)</code> .
<code>dir</code>	Parent directory to create links to the HDF5 SummarizedExperiment dataset. A subdirectory with the dataset name will be created within this directory. Default is <code>tempdir()</code> . If a directory named <code>paste(dir, dataset, sep = "/")</code> 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, [4](#)

TumourMethData

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

TumourMethData-package, [2](#)

TumourMethDatasets, [4](#)