Package ‘TumourMethData’

February 27, 2025

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

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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)

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Depends R (>= 4.2), SummarizedExperiment

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Suggests ggplot2

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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

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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")`. 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 datsets listed in data(TumourMethDatasets).
`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 data(TumourMethDatasets) where `transcript_counts_available` is TRUE.

Value

A data.frame with RNA-Seq counts calcualted 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