Package ‘TENET.ExperimentHub’

May 5, 2026

Title Experiment data for the TENET package

Description ExperimentHub package containing datasets for use in the TENET package's vignette and function examples. These include a variety of different objects to illustrate different datasets used in TENET functions. Where applicable, all datasets are aligned to the hg38 human genome.

Version 1.5.0

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BugReports https://github.com/rhielab/TENET.ExperimentHub/issues

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Contents

`exampleTENETClinicalDataFrame`

Example TENET clinical data frame

Description

A data frame containing example and simulated clinical information corresponding to the samples in the `exampleTENETMultiAssayExperiment` object, used to demonstrate how TENET functions can import clinical data from a specified data frame. Clinical data are utilized by the `step2GetDifferentiallyMethylatedS` `step7TopGenesSurvival`, and `step7ExpressionVsDNAMethylationScatterplots` functions. The data frame consists of vital status and time variables for use by the `step7TopGenesSurvival` function, simulated purity data for each sample, and simulated copy number variation (CNV) and somatic mutation (SM) data for the top 10 genes by number of linked hypermethylated and hypomethylated probes derived from analyses done using the `exampleTENETMultiAssayExperiment` object. These data are a subset of the clinical data contained in the colData of the `exampleTENETMultiAssayExperiment` object.

Usage

```
exampleTENETClinicalDataFrame(metadata = FALSE)
```

Arguments

`metadata`	If TRUE, retrieve the ExperimentHub metadata instead of the object itself. Defaults to FALSE.

Value

A data frame with 231 rows and 43 variables.

`vital_status` (character) Contains vital status data for each sample, listed as either "Alive", "Dead", or NA. Values are derived directly from the TCGA patient data.

`time` (double) Contains survival time values, in days, for each sample. Values are derived directly from the TCGA patient data.

`purity` (double) Contains simulated purity data for each sample, ranging from 0 to 1.

`ENSG00000165821_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000165821 (SALL2) gene, ranging from -2 to 2.

`ENSG00000165821_SM` (integer) Contains simulated SM data for each sample for the ENSG00000165821 (SALL2) gene, either 0 or 1.

`ENSG00000169989_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000169989 (TIGD4) gene, ranging from -2 to 2.

`ENSG00000169989_SM` (integer) Contains simulated SM data for each sample for the ENSG00000169989 (TIGD4) gene, either 0 or 1.

`ENSG00000197343_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000197343 (ZNF655) gene, ranging from -2 to 2.

`ENSG00000197343_SM` (integer) Contains simulated SM data for each sample for the ENSG00000197343 (ZNF655) gene, either 0 or 1.

`ENSG00000169083_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000169083 (AR) gene, ranging from -2 to 2.

`ENSG00000169083_SM` (integer) Contains simulated SM data for each sample for the ENSG00000169083 (AR) gene, either 0 or 1.

`ENSG00000177842_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000177842 (ZNF620) gene, ranging from -2 to 2.

`ENSG00000177842_SM` (integer) Contains simulated SM data for each sample for the ENSG00000177842 (ZNF620) gene, either 0 or 1.

`ENSG00000234284_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000234284 (ZNF879) gene, ranging from -2 to 2.

`ENSG00000234284_SM` (integer) Contains simulated SM data for each sample for the ENSG00000234284 (ZNF879) gene, either 0 or 1.

`ENSG00000177853_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000177853 (ZNF518A) gene, ranging from -2 to 2.

`ENSG00000177853_SM` (integer) Contains simulated SM data for each sample for the ENSG00000177853 (ZNF518A) gene, either 0 or 1.

`ENSG00000196345_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000196345 (ZKSCAN7) gene, ranging from -2 to 2.

`ENSG00000196345_SM` (integer) Contains simulated SM data for each sample for the ENSG00000196345 (ZKSCAN7) gene, either 0 or 1.

`ENSG00000196653_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000196653 (ZNF502) gene, ranging from -2 to 2.

`ENSG00000196653_SM` (integer) Contains simulated SM data for each sample for the ENSG00000196653 (ZNF502) gene, either 0 or 1.

`ENSG00000162599_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000162599 (NFIA) gene, ranging from -2 to 2.

`ENSG00000162599_SM` (integer) Contains simulated SM data for each sample for the ENSG00000162599 (NFIA) gene, either 0 or 1.

`ENSG00000129514_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000129514 (FOXA1) gene, ranging from -2 to 2.

`ENSG00000129514_SM` (integer) Contains simulated SM data for each sample for the ENSG00000129514 (FOXA1) gene, either 0 or 1.

`ENSG00000124664_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000124664 (SPDEF) gene, ranging from -2 to 2.

`ENSG00000124664_SM` (integer) Contains simulated SM data for each sample for the ENSG00000124664 (SPDEF) gene, either 0 or 1.

`ENSG00000107485_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000107485 (GATA3) gene, ranging from -2 to 2.

`ENSG00000107485_SM` (integer) Contains simulated SM data for each sample for the ENSG00000107485 (GATA3) gene, either 0 or 1.

`ENSG00000091831_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000091831 (ESR1) gene, ranging from -2 to 2.

`ENSG00000091831_SM` (integer) Contains simulated SM data for each sample for the ENSG00000091831 (ESR1) gene, either 0 or 1.

`ENSG00000118513_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000118513 (MYB) gene, ranging from -2 to 2.

`ENSG00000118513_SM` (integer) Contains simulated SM data for each sample for the ENSG00000118513 (MYB) gene, either 0 or 1.

`ENSG00000100219_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000100219 (XBP1) gene, ranging from -2 to 2.

`ENSG00000100219_SM` (integer) Contains simulated SM data for each sample for the ENSG00000100219 (XBP1) gene, either 0 or 1.

`ENSG00000152192_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000152192 (POU4F1) gene, ranging from -2 to 2.

`ENSG00000152192_SM` (integer) Contains simulated SM data for each sample for the ENSG00000152192 (POU4F1) gene, either 0 or 1.

`ENSG00000105261_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000105261 (OVOL3) gene, ranging from -2 to 2.

`ENSG00000105261_SM` (integer) Contains simulated SM data for each sample for the ENSG00000105261 (OVOL3) gene, either 0 or 1.

`ENSG00000178935_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000178935 (ZNF552) gene, ranging from -2 to 2.

`ENSG00000178935_SM` (integer) Contains simulated SM data for each sample for the ENSG00000178935 (ZNF552) gene, either 0 or 1.

`ENSG00000115163_CNV` (integer) Contains simulated CNV data for each sample for the ENSG00000115163 (CENPA) gene, ranging from -2 to 2.

`ENSG00000115163_SM` (integer) Contains simulated SM data for each sample for the ENSG00000115163 (CENPA) gene, either 0 or 1.

Examples

```
exampleTENETClinicalDataFrame()
```

`exampleTENETMultiAssayExperiment` *Example TENET MultiAssayExperiment object*

Description

A MultiAssayExperiment dataset created using a modified version of the `TCGADownloader` function from the TENET package utilizing TCGAbiolinks package functionality. This object contains two SummarizedExperiment objects, `expression` and `methylation`, with expression data for 11,637 genes annotated to the GENCODE v36 dataset, including all 1,637 identified human TF genes, and DNA methylation data for 20,000 probes from the Illumina HM450 methylation array. The data are aligned to the human hg38 genome. Expression and methylation values were matched from 200 tumor and 42 adjacent normal tissue samples subset from the TCGA BRCA dataset. Additionally, results from running the TENET step 1-6 functions on these samples are included in the metadata of this MultiAssayExperiment object. Clinical data for these samples are included in the colData of the MultiAssayExperiment object. (A separate data frame object containing a subset of the clinical data for these samples is available as `exampleTENETClinicalDataFrame`.) This dataset is included to demonstrate TENET functions. Note: Because this dataset is a small subset of the overall BRCA dataset, results generated by TENET from this dataset differ from those presented for the BRCA dataset at large in TENET publications.

Usage

```
exampleTENETMultiAssayExperiment(metadata = FALSE)
```

Arguments

`metadata`	If TRUE, retrieve the ExperimentHub metadata instead of the object itself. Defaults to FALSE.

Value

A MultiAssayExperiment object composed of "expression" and "methylation" SummarizedExperiment objects, clinical information about the patients in the colData, and information about sample pairing and type ('Case' vs. 'Control') in the sampleMap.

Examples

```
exampleTENETMultiAssayExperiment()
```

`exampleTENETPeakRegions` *Example TENET peak regions*

Description

A GenomicRanges dataset with example genomic regions (peaks) of interest, used to demonstrate TENET's `step7TopGenesUserPeakOverlap` function. The peaks are derived from a ChIP-seq experiment on FOXA1 in MCF-7 cells and aligned to the human hg38 genome. They were downloaded from the ENCODE portal (file ENCFF112JVK in experiment ENCSR126YEB). **Citation:** ENCODE Project Consortium; Moore JE, Purcaro MJ, Pratt HE, et al. Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature. 2020 Jul;583(7818):699-710. doi: 10.1038/s41586-020-2493-4. Epub 2020 Jul 29. Erratum in: Nature. 2022 May;605(7909):E3. PMID: 32728249; PMCID: PMC7410828.

Usage

```
exampleTENETPeakRegions(metadata = FALSE)
```

Arguments

`metadata`	If TRUE, retrieve the ExperimentHub metadata instead of the object itself. Defaults to FALSE.

Value

A GRanges object with 37,386 ranges and no metadata.

Source

https://www.encodeproject.org/files/ENCFF112JVK/

Examples

```
exampleTENETPeakRegions()
```

---

exampleTENETStep1MakeExternalDatasetsGRanges

Example TENET `step1MakeExternalDatasets` *GRanges object*

Description

A GenomicRanges dataset representing putative enhancer regions relevant to BRCA, created using the `step1MakeExternalDatasets` function in the TENET package with the `consensusEnhancer`, `consensusNDR`, `publicEnhancer`, `publicNDR`, and `ENCODEdELS` arguments all set to TRUE, and the `cancerType` argument set to "BRCA". The data are aligned to the human hg38 genome. This dataset is included to demonstrate TENET's `step2GetDifferentiallyMethylatedSites` function.

Usage

```
exampleTENETStep1MakeExternalDatasetsGRanges(metadata = FALSE)
```

Arguments

`metadata`	If TRUE, retrieve the ExperimentHub metadata instead of the object itself. Defaults to FALSE.

Value

A GRanges object with 1,971,031 ranges and no metadata.

Examples

```
exampleTENETStep1MakeExternalDatasetsGRanges()
```

`exampleTENETStep2GetDifferentiallyMethylatedSitesPuritySummarizedExperiment` *Example TENET* `step2GetDifferentiallyMethylatedSites` *purity SummarizedExperiment object*

Description

A SummarizedExperiment object with three DNA methylation datasets each composed of 10 adjacent normal colorectal adenocarcinoma (COAD) samples from The Cancer Genome Atlas (TCGA), retrieved using the TCGAbiolinks package. Each dataset has data for 20,000 probes from the Illumina HM450 methylation array, to match the number of probes in the `exampleTENETMultiAssayExperiment` object. The data are aligned to the human hg38 genome. This object is representative of a `purity` dataset, which would contain DNA methylation data from potentially confounding sources, used with TENET's `step2GetDifferentiallyMethylatedSites` function.

Usage

```
exampleTENETStep2GetDifferentiallyMethylatedSitesPuritySummarizedExperiment(
  metadata = FALSE
)
```

Arguments

`metadata`	If TRUE, retrieve the ExperimentHub metadata instead of the object itself. Defaults to FALSE.

Value

A SummarizedExperiment object with two methylation datasets, "purityMethylationExampleA" and "purityMethylationExampleB", each containing data for 20,000 HM450 probes in 10 samples.

Examples

```
exampleTENETStep2GetDifferentiallyMethylatedSitesPuritySummarizedExperiment()
```

`exampleTENETTADRegions` *Example TENET topologically associating domain (TAD) regions*

Description

A GenomicRanges dataset with example topologically associating domains (TADs), used to demonstrate TENET's `step7TopGenesTADTables` function. The TADs are derived from T47D cells (mistakenly labeled as 'T470'), and aligned to the human hg38 genome. They were downloaded from the 3D Genome Browser at `http://3dgenome.fsm.northwestern.edu`. **Citation:** Wang Y, Song F, Zhang B, et al. The 3D Genome Browser: a web-based browser for visualizing 3D genome organization and long-range chromatin interactions. Genome Biol. 2018 Oct 4;19(1):151. doi: 10.1186/s13059-018-1519-9. PMID: 30286773; PMCID: PMC6172833.

Usage

```
exampleTENETTADRegions(metadata = FALSE)
```

Arguments

`metadata`	If TRUE, retrieve the ExperimentHub metadata instead of the object itself. Defaults to FALSE.

Value

A GRanges object with 1,889 ranges and no metadata.

Source

`http://3dgenome.fsm.northwestern.edu/publications.html`

Examples

```
exampleTENETTADRegions()
```

`TENET.ExperimentHub` *TENET.ExperimentHub (Experiment data for the TENET package)*

Description

The TENET.ExperimentHub package contains datasets for use in the TENET package's vignette and function examples. These include a variety of different objects to illustrate different datasets used in TENET functions. Where applicable, all datasets are aligned to the hg38 human genome.

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See Also

Useful links:

- `https://github.com/rhielab/TENET.ExperimentHub`
- Report bugs at `https://github.com/rhielab/TENET.ExperimentHub/issues`

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