

Package ‘biotmleData’

October 31, 2024

Title Example experimental microarray data set for the ``biotmle" R package
Version 1.31.0
Description Microarray data (from the Illumina Ref-8 BeadChips platform) and phenotype-level data from an epidemiological investigation of benzene exposure, packaged using ``SummarizedExperiment", for use as an example with the ``biotmle" R package.
Depends R (>= 3.0)
Suggests Biobase, SummarizedExperiment
License file LICENSE
Encoding UTF-8
LazyData true
RoxygenNote 6.0.1
biocViews GeneExpression, DifferentialExpression, Sequencing, Microarray, RNASeq
git_url <https://git.bioconductor.org/packages/biotmleData>
git_branch devel
git_last_commit 6da33db
git_last_commit_date 2024-10-29
Repository Bioconductor 3.21
Date/Publication 2024-10-31
Author Nima Hejazi [aut, cre]
Maintainer Nima Hejazi <nhejazi@berkeley.edu>

Contents

biomarkerTMLEout	2
illuminaData	2
rnaseqTMLEout	3
Index	4

biomarkerTMLEout	<i>Results obtained from running biomarkertmle on the "illuminaData" sample data</i>
------------------	--------------------------------------------------------------------------------------

Description

Example results obtained from running the TMLE-based estimation procedure on the example data included with this package (illuminaData).

Usage

```
biomarkerTMLEout
```

Format

A biotmle object containing the results of running biomarkertmle.

These results are included here for the sake of making the vignettes build more quickly. The user will likely not benefit from using this data set.

Value

A biotmle object containing results from biomarkertmle.

illuminaData	<i>Sample baseline covariates and Illumina microarray data from a 2007 study</i>
--------------	----------------------------------------------------------------------------------

Description

A dataset containing various baseline covariates and microarray expression measures from Illumina arrays used in a 2007 study.

Usage

```
illuminaData
```

Format

A SummarizedExperiment containing Illumina microarray data from the Ref-8 BeadChips platform in the "assay" slot and phenotype data on subjects in the "colData" slot:

This is example data to be used in testing the biomarkertmle procedure. Consult the vignettes for how to use this data.

Value

A SummarizedExperiment containing biomarkers and baseline covariates.

rnaseqTMLEout	<i>Results obtained from running biomarkertmle on simulated RNA-Seq data</i>
---------------	------------------------------------------------------------------------------

Description

Example results obtained from running the TMLE-based estimation procedure on next-generation sequencing (count) data.

Usage

rnaseqTMLEout

Format

A biotmle object containing the results of running biomarkertmle.

These results are included here for the sake of making the vignettes build more quickly. The user will likely not benefit from using this data set.

Value

A biotmle object containing results from biomarkertmle.

Index

* **datasets**

biomarkerTMLEout, [2](#)

illuminaData, [2](#)

rnaseqTMLEout, [3](#)

biomarkerTMLEout, [2](#)

illuminaData, [2](#)

rnaseqTMLEout, [3](#)