

Package ‘biotmleData’

April 12, 2018

Title Example experimental microarray data set for the “biotmle” R package

Version 1.2.0

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

NeedsCompilation no

Author Nima Hejazi [aut, cre]

Maintainer Nima Hejazi <nhejazi@berkeley.edu>

R topics documented:

biomarkerTMLEout	1
illuminaData	2
rnaseqTMLEout	2

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`.

<code>illuminaData</code>	<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.

<code>rnaseqTMLEout</code>	<i>Results obtained from running <code>biomarkertmle</code> 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

*Topic **datasets**

biomarkerTMLEout, [1](#)

illuminaData, [2](#)

rnaseqTMLEout, [2](#)

biomarkerTMLEout, [1](#)

illuminaData, [2](#)

rnaseqTMLEout, [2](#)