Package ‘biotmleData’

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Title Example experimental microarray data set for the ``biotmle'' R package

Version 1.37.0

Description Microarray data (from the Illumina Ref-8 BeadChips platform) and phenotype-level data from an epidemiological investigation of benzene exposure, packaged using ``SummarizedExperiemnt'', for use as an example with the ``biotmle'' R package.

Depends R (>= 3.0)

Suggests Biobase, SummarizedExperiment

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LazyData true

RoxygenNote 6.0.1

biocViews GeneExpression, DifferentialExpression, Sequencing, Microarray, RNASeq

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Contents

`biomarkerTMLEout` *Results obtained from running biomarkertmle on the "illuminaData" sample data*

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` *Sample baseline covariates and Illumina microarray data from a 2007 study*

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` *Results obtained from running biomarkertmle on simulated RNA-Seq data*

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`.

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