Package 'biotmleData'

November 10, 2026

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

Version 1.36.0

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

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 RELEASE_3_23

git_last_commit 7007019

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-10

Author Nima Hejazi [aut, cre]

Maintainer Nima Hejazi <nhejazi@berkeley.edu>

Contents

biomarkerTMLEout 2
illuminaData 2
rnaseqTMLEout 3

Index **4**

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`.

Index

∗ **datasets**
biomarkerTMLEout, 2
illuminaData, 2
rnaseqTMLEout, 3

biomarkerTMLEout, 2

illuminaData, 2

rnaseqTMLEout, 3