Package 'biotmleData'

October 16, 2025
Title Example experimental microarray data set for the ``biotmle" R package
Version 1.32.0
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_21
git_last_commit cf91e5f
git_last_commit_date 2025-04-15
Repository Bioconductor 3.21
Date/Publication 2025-10-16
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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 20 study	007
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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 3

rnaseqTMLEout	Results obtained from running biomarkertmle on simulated RNA-Seq data
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Description

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

Usage

 ${\tt rnaseqTMLEout}$

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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