

# Package ‘biotmleData’

November 28, 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** 2024-11-28

**Author** Nima Hejazi [aut, cre]

**Maintainer** Nima Hejazi <nhejazi@berkeley.edu>

## Contents

biomarkerTMLEout . . . . .	2
illuminaData . . . . .	2
rnaseqTMLEout . . . . .	3

<b>Index</b>	<b>4</b>
--------------	----------

---

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