

# Package ‘biotmleData’

February 3, 2026

**Title** Example experimental microarray data set for the ‘‘biotmle’’ R package

**Version** 1.34.0

**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

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

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

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biomarkerTMLEout	<i>Results obtained from running biomarkertmle on the "illuminaData" sample data</i>
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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`.

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illuminaData	<i>Sample baseline covariates and Illumina microarray data from a 2007 study</i>
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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.

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<code>rnaseqTMLEout</code>	<i>Results obtained from running biomarkertmle on simulated RNA-Seq data</i>
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**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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