

# Package ‘biotmleData’

November 18, 2025

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

**Version** 1.35.0

**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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## Contents

|                            |   |
|----------------------------|---|
| biomarkerTMLEout . . . . . | 2 |
| illuminaData . . . . .     | 2 |
| rnaseqTMLEout . . . . .    | 3 |

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

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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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| rnaseqTMLEout | <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.

# Index

## \* **datasets**

biomarkerTMLEout, [2](#)

illuminaData, [2](#)

rnaseqTMLEout, [3](#)

biomarkerTMLEout, [2](#)

illuminaData, [2](#)

rnaseqTMLEout, [3](#)