# Package 'beadarrayExampleData'

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**Title** Example data for the beadarray package

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**Description**
An small dataset that can be used to run examples from the beadarray vignette and examples

**Depends** R (>= 2.13.0), Biobase (>= 2.5.5), methods, beadarray (>= 2.0.0)

**License** GPL-2

**biocViews** ExperimentData, Homo_sapiens_Data, MicroarrayData

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## exampleBLData *beadLevelData object from an example experiment*

### Description

The data in this package are a subset of the MAQC bead-level data available in the beadarrayUseCases package. Bead-level refers to the availability of intensity and location information for each bead on each BeadArray in an experiment. In this dataset, BeadArrays were hybridized with either Universal Human Reference RNA (UHRR, Stratagene) or Brain Reference RNA (Ambion) as used in the MAQC project. This object is a representation of the bead-level data for 2 arrays and was created by the beadarray package.

### Usage

```
data(exampleBLdata)
```

### See Also

beadLevelData

## exampleSummaryData *ExpressionSetIllumina object for the example experiment*

### Description

exampleSummaryData is an object of class ExpressionSetIllumina which is a summarized version of the bead-level data distributed with the BeadArrayUseCases package. There are 12 MAQC samples in the object which are either Brain or UHRR. Unlogged and log2 versions of the data are provided. See the vignette for beadarrayExampleData for details of how these data were created.

### Usage

```
data(exampleSummaryData)
```

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