

beadarrayExampleData

March 23, 2012

`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)
```

Index

*Topic **datasets**

exampleBLData, [1](#)

exampleSummaryData, [1](#)

beadLevelData, [1](#)

exampleBLData, [1](#)

exampleSummaryData, [1](#)