Package 'RUVnormalizeData'

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Title Gender data for the RUVnormalize package

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Description Microarray gene expression data from the study of Vawter et al., 2004.

License GPL-3

LazyLoad yes

Depends R (>= 2.10.0), Biobase

NeedsCompilation no

biocViews MicroarrayData

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gender *Gene expression matrix and sample annotation of the Vawter et al., 2004 study.*

Description

The ExpressionSet object describes the data from the Vawter et al., "Gender-specific gene expression in post-mortem human brain: localization to sex chromosomes", Neuropsychopharmacology, 2004 study. The expression of 12600 genes was systematically measured for 5 male and 5 female patients, with the goal to study gender related differential expression. The samples come from different brain regions and are hybridized from different labs, both of which affect gene expression.

The assayData field contains the 12600 x 84 gene expression matrix.

The phenoData field contains an AnnotatedDataFrame object describing the samples. The first column indicates the gender ('F' for female, 'M' for male). The next three columns indicate the lab: a one in the second, third or fourth column indicates that the sample was hybridized and scanned at UC Davis, UC Irvine or University of Michigan, Ann Arbor respectively. The last three columns contain brain regions. A one in the fifth, sixth or seventh column indicates that the sample was extracted from the anterior cingulate cortex, cerebellum or dorsolateral prefrontal cortex respectively.

The featureData field contains an AnnotatedDataFrame object with a single logical vectors indicating which probesets where used as negative controls in the Gagnon-Bartsch and Speed, "Using control genes to correct for unwanted variation in microarray data" 2012 paper.

The annotation field indicates the chip type, among HGU-95A and HGU-95Av2 Affymetrix arrays.

Usage

```
gender
```

Format

An ExpressionSet object.

Author(s)

Laurent Jacob

Examples

```
data('gender')
str(gender)
```

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