Package 'HarmanData'

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Type Package

Title Data for the Harman package

Version 1.10.0

Date 2016-02-01

Description Datasets of accompany Harman, a PCA and constrained optimisation based technique. Contains three datasets: IMR90, Human lung fibroblast cells exposed to nitric oxide; NPM, an experiment to test skin penetration of metal oxide nanoparticles following topical application of sunscreens in non-pregnant mice; OLF; an experiment to gauge the response of human olfactory neurosphere-derived (hONS) cells to ZnO nanoparticles.

NeedsCompilation no

Suggests BiocGenerics, BiocStyle, knitr, rmarkdown

Depends R (>= 3.2.3)

License GPL-3

LazyData true

VignetteBuilder knitr

biocViews ExpressionData, MicroarrayData, ExperimentData, Homo_sapiens_Data, Mus_musculus_Data

URL http://www.bioinformatics.csiro.au/harman/

BugReports https://github.com/JasonR055/Harman/issues

RoxygenNote 5.0.1

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R topics documented:

IMR90 *IMR90 data, a Human lung fibroblast cell line.*

Description

Data used in the batch effect correction paper of Johnson, Li and Rabinovich. The data are from a cell-line experimental designed to reveal whether exposing mammalian cells to nitric oxide (NO) stabilizes mRNAs. The data comprises one treatment, one control and 2 time points (0 h and 7.5 h), resulting in 4 distinct (2 treatment x 2 time points) experimental conditions. There were 3 batches and a total of 12 samples, with each batch consisting of 1 replicate from each of the experimental conditions. Affymetrix HG-U133A Arrays were normalised and background adjusted as a whole using the RMA procedure in MATLAB.

Usage

```
data(IMR90)
```

Format

Two data frames. `imr90.data` has 22,223 probesets (rows) and 12 samples (columns). While `imr90.info` is a description of the samples, with two columns:

`Treatment` the treatment applied to the cells

`Batch` batch processing number

Value

promise

References

Johnson et al. Biostatistics (2007). doi: 10.1093/biostatistics/kxj037

Examples

```
data(IMR90)
```

NPM   *Non-pregant mice study data*

Description

An experiment to test skin penetration of metal oxide nanoparticles following topical application of sunscreens. The data comprises three treatment groups plus a control group, with six replicates in each group, making a total of 24 Affymetrix MoGene 1.0 ST arrays. There were a total of three processing batches of eight arrays, each consisting of 2 replicates per group. Arrays were normalised and background adjusted as a whole using the RMA procedure in MATLAB.

Usage

```
data(NPM)
```

Format

Two data frames. `npm.data` has 35,512 probesets (rows) and 24 biological samples (columns). While `npm.info` is a description of the samples, with two columns:

`Treatment` the treatment applied to the mice

`Batch` batch processing number

Value

promise

References

Osmond-McLeod et al. Nanotoxicology (2014). doi: 10.3109/17435390.2013.855832

Examples

```
data(NPM)
```

OLF   *Olfactory stem cell study data*

Description

An experiment to gauge the response of human olfactory neurosphere-derived (hONS) cells established from adult donors to ZnO nanoparticles. The data comprises six treatment groups plus a control group, each consisting of four replicates, giving a total number of 28 Affymetrix HuGene 1.0 ST arrays. The arrays were broken up into four processing batches of seven arrays each, consisting of one replicate from each of the groups. Arrays were normalised and background adjusted as a whole using the RMA procedure in MATLAB.

Usage

```
data(OLF)
```

Format

Two data frames. `olf.data` has 33,297 probesets (rows) and 28 biological samples (columns). While `olf.info` is a description of the samples, with two columns:

`Treatment` the treatment applied

`Batch` batch processing number

Value

promise

Source

<http://www.example.com/>

References

Osmond-McLeod et al. Part Fibre Toxicol. (2013). doi: 10.1186/1743-8977-10-54

Examples

```
data(OLF)
```

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