Package ‘sampleClassifierData’

February 1, 2017

**Type**  Package

**Title**  Pre-processed data for use with the sampleClassifier package

**Version**  0.99.2

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**Description**  This package contains two microarray and two RNA-seq datasets that have been preprocessed for use with the sampleClassifier package. The RNA-seq data are derived from Fagerberg et al. (2014) and the Illumina Body Map 2.0 data. The microarray data are derived from Roth et al. (2006) and Ge et al. (2005).

**License**  Artistic-2.0

**Depends**  R (>= 3.4), SummarizedExperiment

**Suggests**  BiocStyle

**biocViews**  ExperimentData, ExpressionData, MicroarrayData, SequencingData, RNASEqData, ArrayExpress

**NeedsCompilation**  no

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**Description**

This package contains two microarray and two RNA-seq datasets that have been preprocessed for use with the sampleClassifier package. The RNA-seq data are derived from Fagerberg et al. (2014) and the Illumina Body Map 2.0 data. The microarray data are derived from Roth et al. (2006) and Ge et al. (2005).

**Details**

This package contains a collection of publicly available microarray and RNA-seq datasets that have been pre-processed for use with the R-package 'sampleClassifier'.

The dataset `se_rnaseq_refmat` contains 71 samples from 24 tissues, derived from Fagerberg et al. (2014). Each tissue is represented by 3 replicates (except ovary which is represented by 2 replicates).

The dataset `se_micro_refmat` contains 78 samples from 26 tissues, derived from Roth et al. (2006). Each tissue is represented by 3 replicates.

The dataset `se_rnaseq_testmat` contains 12 samples from the Illumina Body Map 2.0 data.

The dataset `se_micro_testmat` contains 16 samples from Ge et al. (2005).

See the package vignette for details on the pre-processing of the data.

**Author(s)**

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**References**


The Illumina Body Map 2.0 data (https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-513/).

Description
Microarray gene expression data set with 78 samples from 26 tissues, derived from Roth et al. (2006). Each tissue is represented by 3 replicates.

Usage
```
data(se_micro_refmat)
```

Format
A `matrix` with 54675 probesets and 78 samples.

Value
microarray data matrix as SummarizedExperiment

References

Examples
```
data(se_micro_refmat)
```

---

Description
Microarray gene expression data set with 16 samples from Ge et al. (2005).

Usage
```
data(se_micro_testmat)
```

Format
A `matrix` with 22283 probesets and 16 samples.

Value
microarray data matrix as SummarizedExperiment
References


Examples

data(se_micro_testmat)

se_rnaseq_refmat RNA-seq gene expression data set

Description

RNA-seq gene expression data set with 71 samples from 24 tissues, derived from Fagerberg et al. (2014). Each tissue is represented by 3 replicates (except ovary which is represented by 2 replicates).

Usage

data(se_rnaseq_refmat)

Format

A matrix with 43819 genes and 71 samples.

Value

RNA-seq data matrix as SummarizedExperiment

References


Examples

data(se_rnaseq_refmat)
Description
RNA-seq gene expression data set with 12 samples from the Illumina Body Map 2.0 data.

Usage
data(se_rnaseq_testmat)

Format
A matrix with 43819 genes and 12 samples.

Value
RNA-seq data matrix as SummarizedExperiment

References
The Illumina Body Map 2.0 data (https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-513/).

Examples
data(se_rnaseq_testmat)
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