# Package ‘sampleClassifierData’

*July 4, 2024*

**Type** Package  
**Title** Pre-processed data for use with the sampleClassifier package  
**Version** 1.28.0  
**Date** 2021-11-21  
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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**

```r
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**

```r
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)

se_rnaseq_testmat  RNA-seq gene expression data set

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
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