Package 'HighlyReplicatedRNASeq'

January 22, 2026

Type Package

Title Collection of Bulk RNA-Seq Experiments With Many Replicates

Version 1.22.0

Description Gene-level count matrix data for bulk RNA-seq dataset with many replicates. The data are provided as easy to use SummarizedExperiment objects. The source data that is made accessible through this package comes from https://github.com/bartongroup/profDGE48.

URL https://github.com/const-ae/HighlyReplicatedRNASeq

BugReports https://github.com/const-ae/HighlyReplicatedRNASeq/issues

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Encoding UTF-8

Depends SummarizedExperiment, ExperimentHub

Imports S4Vectors

Suggests BiocStyle, BiocFileCache, knitr, rmarkdown

biocViews ExperimentHub, ExperimentData, ExpressionData, SequencingData, RNASeqData

RoxygenNote 7.1.0

Roxygen list(markdown = TRUE)

VignetteBuilder knitr

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Contents

HighlyReplicatedRNASeq

> *HighlyReplicatedRNASeq: Collection of Bulk RNA-Seq Experiments With Many Replicates*

Description

The HighlyReplicatedRNASeq package provides access to the count matrix results from studies with many replicates. These datasets can be valuable for benchmarking tools designed to handle RNA-seq data.

Details

Available datasets:

- Schurch et al. (2016): 86 samples of S. *cerevisiae* in two conditions
    - [Schurch16()](#) / [Schurch16_metadata()](#)

At the moment, this package contains only one dataset, but more datasets can be added in the future.

Schurch16

> *Get the RNA-seq counts from Schurch et al. (2016)*

Description

The data contains bulk RNA-seq count on 86 samples in two conditions. The first condition is wild type S. *cerevisiae* (taxonomic id: 1247190). The second condition is the same strain with a snf2 knockout.

Usage

```
Schurch16(hub = ExperimentHub())

Schurch16_metadata(hub = ExperimentHub())
```

Arguments

hub   an [ExperimentHub](#) object that is used to load the resource "EH3315" and "EH3316". Default: [ExperimentHub()](#)

Details

Schurch et al. originally generated this dataset to benchmark RNA-seq differential expression tools and find out how many replicates are necessary to detect most differentially expressed genes. The data that is returned by this packge comes from the GitHub [repository](#) that accompanied the study.

Value

Schurch16() returns a SummarizedExperiment with 7126 genes and 86 samples.

Schurch16_metadata() returns a ExperimentHub object with the metadata on the Schurch16 dataset.

Author(s)

Constantin Ahlmann-Eltze

References

Schurch, N. J., Schofield, P., Gierliński, M., Cole, C., Sherstnev, A., Singh, V., . . . Barton, G. J. (2016). How many biological replicates are needed in an RNA-seq experiment and which differential expression tool should you use? *RNA*, 22(6), 839–851. https://doi.org/10.1261/rna.053959.115

Examples

```
Schurch16_metadata()

se <- Schurch16()

dim(se)
colData(se)
summary(c(assay(se, "counts")))
```

Index