Package ‘HighlyReplicatedRNASeq’

July 15, 2025

Type Package

Title Collection of Bulk RNA-Seq Experiments With Many Replicates

Version 1.20.0

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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`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")))
```

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