

Package ‘HighlyReplicatedRNASeq’

November 5, 2024

Type Package

Title Collection of Bulk RNA-Seq Experiments With Many Replicates

Version 1.19.0

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>

License MIT + file LICENSE

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

git_url <https://git.bioconductor.org/packages/HighlyReplicatedRNASeq>

git_branch devel

git_last_commit 202c6b5

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2024-11-05

Author Constantin Ahlmann-Eltze [aut, cre] (ORCID:
<<https://orcid.org/0000-0002-3762-068X>>)

Maintainer Constantin Ahlmann-Eltze <artjom31415@googlemail.com>

Contents

HighlyReplicatedRNASeq	2
Schurch16	2
Index	4

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 package 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

ExperimentHub, [2](#), [3](#)
ExperimentHub(), [2](#)

HighlyReplicatedRNASeq, [2](#)

Schurch16, [2](#)
Schurch16(), [2](#)
Schurch16_metadata (Schurch16), [2](#)
Schurch16_metadata(), [2](#)
SummarizedExperiment, [3](#)