

Package ‘yeastRNASeq’

July 4, 2024

Title Yeast RNA-Seq Experimental Data from Lee et al. 2008

Version 0.43.0

Author James H. Bullard and Kasper D. Hansen

Description A selection of RNA-Seq data from a yeast transcriptome experiment.

biocViews ExperimentData, Saccharomyces_cerevisiae_Data,
SequencingData, RNASeqData

Maintainer J. Bullard <bullard@stat.berkeley.edu>

License GPL

Depends R (>= 2.4)

Suggests Biobase, ShortRead, IRanges

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

git_branch devel

git_last_commit f0d3b6a

git_last_commit_date 2024-04-30

Repository Bioconductor 3.20

Date/Publication 2024-07-04

Contents

geneLevelData	2
yeastAligned	2
yeastAnno	3

Index	4
--------------	----------

`geneLevelData`*Yeast gene-level counts from: Lee et al. PloS Genetics 2008.*

Description

Gene counts for an Illumina sequencing experiment. These counts represent summarizations over the data in the `yeastAligned` object using the annotation from the `yeastAnno` object, both from this package.

Usage

```
data(geneLevelData)
```

Source

A citation for the dataset may be generated using `citation("yeastRNASeq")`.

See Also

The package vignette.

`yeastAligned`*AlignedRead list*

Description

A four element list of `AlignedRead` objects from the `ShortRead` package from 4 yeast lanes of a Solexa experiment: Lee et al. PloS Genetics 2008.

The data represents a random subsample of reads from 4 lanes (2 wild-type, 2 mutant lanes)

Usage

```
data(yeastAligned)
```

Source

A citation for the dataset may be generated using `citation("yeastRNASeq")`.

See Also

The package vignette.

yeastAnno

Yeast Annotation

Description

Annotation for *S. cerevisiae* downloaded from Ensembl using the **biomaRt** package in the fall of 2009 and post-processed. This file should not be used for analyses purposes, but rather demonstrates some functionality of various packages.

Usage

```
data(geneLevelData)
```

Source

A citation for the dataset may be generated using `citation("yeastRNASeq")`.

See Also

The package vignette.

Index

* datasets

geneLevelData, [2](#)

yeastAligned, [2](#)

yeastAnno, [3](#)

geneLevelData, [2](#)

yeastAligned, [2](#)

yeastAnno, [3](#)