

Package ‘yeastRNASeq’

July 31, 2025

Title Yeast RNA-Seq Experimental Data from Lee et al. 2008
Version 0.47.0
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 65d0ea2
git_last_commit_date 2025-04-15
Repository Bioconductor 3.22
Date/Publication 2025-07-31

Contents

geneLevelData	1
yeastAligned	2
yeastAnno	2
Index	3

geneLevelData	<i>Yeast gene-level counts from: Lee et al. PloS Genetics 2008.</i>
---------------	---

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	<i>AlignedRead</i> 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	<i>Yeast Annotation</i>
-----------	-------------------------

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, [1](#)

yeastAligned, [2](#)

yeastAnno, [2](#)

geneLevelData, [1](#)

yeastAligned, [2](#)

yeastAnno, [2](#)