

Package ‘yeastRNASeq’

April 7, 2026

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

Version 0.49.0

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 c4feb7b

git_last_commit_date 2025-10-29

Repository Bioconductor 3.23

Date/Publication 2026-04-07

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](#)