

# An overview of yeastRNASeq

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```
> require(yeastRNASeq)
```

This package contains data from

```
> x <- citation(package = "yeastRNASeq")[[1]]
```

```
> print(x, bibtex = FALSE)
```

Albert Lee, Kasper D. Hansen, James Bullard, Sandrine Dudoit, Gavin Sherlock (2008). Novel low abundance and transient RNAs in yeast revealed by tiling microarrays and ultra high-throughput sequencing are not conserved across closely related yeast species.  
PLoS Genet 4(12): e1000299.  
doi:10.1371/journal.pgen.1000299

A BibTeX entry for LaTeX users is

```
@Article{  
  title = {Novel low abundance and transient RNAs in yeast revealed by tiling mi  
  author = {Albert Lee and Kasper D. Hansen and James Bullard and Sandrine Dudoit  
  year = {2008},  
  journal = {PLoS Genet},  
  volume = {4},  
  number = {12},  
  pages = {e1000299},  
  url = {http://dx.doi.org/10.1371/journal.pgen.1000299},  
  doi = {10.1371/journal.pgen.1000299},  
  note = {R package version 0.0.6},  
}
```

which describes some experiments in *S. cerevisiae* comparing various mutant strains to a wild-type strain. A full BibTex entry can be obtained by

```
> citation("yeastRNASeq")
```

The subset of the data which this package contains is more specifically data from a wild-type and a single mutant yeast. For each condition (mutant, wild-type) there is two lanes worth of data, each lane containing a sample of 500,000 raw (unaligned) reads from each of 2 lanes each. Each of the four lanes have been aligned against the yeast genome using Bowtie.

The raw reads are contained in 4 FASTQ files and the Bowtie alignment are contained in 4 Bowtie output files. There are 500,000 reads in each of the FASTQ files and fewer reads in each of the Bowtie files. The filenames are

```
> list.files(file.path(system.file(package = "yeastRNASeq"), "reads"))

[1] "mut_1_f.bowtie.gz" "mut_1_f.fastq.gz" "mut_2_f.bowtie.gz"
[4] "mut_2_f.fastq.gz" "wt_1_f.bowtie.gz" "wt_1_f.fastq.gz"
[7] "wt_2_f.bowtie.gz" "wt_2_f.fastq.gz"
```

The reads were aligned to the yeast genome obtained from <ftp://ftpmips.gsf.de/yeast/sequences> (which was the basis for the Bowtie index available at the Bowtie website at the time of alignment).

These files are ready to be parsed by the tools in the `ShortRead` package. As an example we read the alignment files by

```
> require(ShortRead)
> files <- list.files(file.path(system.file(package = "yeastRNASeq"), "reads"),
+                    pattern = "bowtie", full.names = TRUE)
> names(files) <- gsub("\\.bowtie.*", "", basename(files))
> names(files)

[1] "mut_1_f" "mut_2_f" "wt_1_f" "wt_2_f"

> aligned <- lapply(files, readAligned, type = "Bowtie")
```

The constructed object `aligned` is a list with 4 elements. Each element correspond to a lane and is an object of class `AlignedRead`.

The output from this operation has already been stored as an R object and is accessible by

```

> data(yeastAligned)
> yeastAligned[["mut_1_f"]]

class: AlignedRead
length: 423318 reads; width: 26 cycles
chromosome: Scchr05 Scchr15 ... Scchr08 Scchr13
position: 541317 885627 ... 488228 667296
strand: - + ... - +
alignQuality: NumericQuality
alignData varLabels: similar mismatch

```

The percent of aligned reads is

```

> round(sapply(aligned, length) / 500000, 2)

```

```

mut_1_f mut_2_f wt_1_f wt_2_f
  0.85   0.84   0.82   0.86

```

There are two additional objects available in the package, purely for illustrative purposes (do not use them for analysis). The object `yeastAnno` is annotation obtained from Ensembl using `biomaRt` and is a `data.frame` of annotation:

```

> data(yeastAnno)
> dim(yeastAnno)

```

```

[1] 7124    6

```

```

> head(yeastAnno, n = 2)

```

```

  ensembl_gene_id chromosome_name start_position end_position strand
1          YHR055C           VIII      214535      214720      -1
2          YPR161C           XVI       864445      866418      -1
  gene_biotype
1 protein_coding
2 protein_coding

```

```

> table(yeastAnno$gene_biotype)

```

ncRNA	protein_coding	pseudogene	rRNA
9	6698	21	14
snRNA	snoRNA	tRNA	
6	77	299	

The other object is called `geneLevelData` and is a **matrix** of counts per gene.

```
> data(geneLevelData)
> head(geneLevelData, n = 2)
```

	mut_1	mut_2	wt_1	wt_2
YHR055C	0	0	0	0
YPR161C	38	39	35	34

Such a matrix may be constructed from `yeastAligned` and `yeastAnno` using either the functionality in the `IRanges` and `ShortRead` packages or by using the functionality of the `Genominator` package (which also contains a vignette describing a simplified differential analysis of this dataset).

Note that the data does not contain any biological replicates. In the original publication this was addressed by also analyzing a set of tiling microarrays.