

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.

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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.gsfc.nasa.gov/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"),
+                               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 corresponds 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.