

# Package ‘leeBamViews’

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**Title** leeBamViews -- multiple yeast RNAseq samples excerpted from Lee 2009

**Version** 1.43.0

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**Description** data from PMID 19096707; prototype for managing multiple NGS samples

**Depends** R (>= 2.15.0), Biobase, Rsamtools (>= 0.1.50), BSgenome

**Imports** GenomicRanges, GenomicAlignments, methods, S4Vectors, parallel, IRanges

**Suggests** biomaRt, org.Sc.sgd.db, edgeR

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**License** Artistic 2.0

**LazyLoad** yes

**biocViews** ExperimentData, Saccharomyces\_cerevisiae\_Data, SequencingData, RNASeqData, SNPData

**RoxygenNote** 7.1.2

**git\_url** <https://git.bioconductor.org/packages/leeBamViews>

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**Description**

BamViews instance construction related to yeast RNA-seq

**Format**

The format is: Formal class 'BamViews' [package "Rsamtools"] with 5 slots

```

..@ bamPaths : chr [1:8] "/Users/stvjc/ExternalSoft/R-devel/library/leeBamViews/bam/isowt5_13e.bam"
"/Users/stvjc/ExternalSoft/R-devel/library/leeBamViews/bam/isowt6_13e.bam" "/Users/stvjc/ExternalSoft/R-
devel/library/leeBamViews/bam/rlp5_13e.bam" "/Users/stvjc/ExternalSoft/R-devel/library/leeBamViews/bam/rlp6_13e.bam"
...
..@ bamIndicies : chr [1:8] "/Users/stvjc/ExternalSoft/R-devel/library/leeBamViews/bam/isowt5_13e.bam"
"/Users/stvjc/ExternalSoft/R-devel/library/leeBamViews/bam/isowt6_13e.bam" "/Users/stvjc/ExternalSoft/R-
devel/library/leeBamViews/bam/rlp5_13e.bam" "/Users/stvjc/ExternalSoft/R-devel/library/leeBamViews/bam/rlp6_13e.bam"
...
..@ bamSamples :Formal class 'DataFrame' [package "IRanges"] with 6 slots
.. ..@ rownames : chr [1:8] "isowt.5" "isowt.6" "rlp.5" "rlp.6" ...
.. ..@ nrows : int 8
.. ..@ elementMetadata: NULL
.. ..@ elementType : chr "ANY"
" .. ..@ metadata : list()
.. ..@ listData :List of 2
.. .. .$ geno: chr [1:8] "isowt" "isowt" "rlp" "rlp" ...
.. .. .$ lane: chr [1:8] "5" "6" "5" "6" ...
..@ bamRanges :Formal class 'GRanges' [package "GenomicRanges"] with 7 slots
.. ..@ seqnames :Formal class 'Rle' [package "IRanges"] with 5 slots
.. .. ..@ values : Factor w/ 1 level "Scchr13": 1
.. .. ..@ lengths : int 27
.. .. ..@ elementMetadata: NULL
.. .. ..@ elementType : chr "ANY"
.. .. ..@ metadata : list()
.. ..@ ranges :Formal class 'IRanges' [package "IRanges"] with 6 slots
.. .. ..@ start : int [1:27] 798517 801771 804455 808999 810465 811088 818826 820255
822762 832338 ...
.. .. ..@ width : int [1:27] 2862 933 636 234 114 108 1122 2199 1869 915 ...
.. .. ..@ NAMES : NULL
.. .. ..@ elementMetadata: NULL
.. .. ..@ elementType : chr "integer"
.. .. ..@ metadata : list()
.. ..@ strand :Formal class 'Rle' [package "IRanges"] with 5 slots
.. .. ..@ values : Factor w/ 3 levels "+","-","*": 1
.. .. ..@ lengths : int 27
.. .. ..@ elementMetadata: NULL
.. .. ..@ elementType : chr "ANY"

```

```

.. .. ..@ metadata : list()
.. ..@ seqlengths : Named int NA
.. .. ..- attr(*, "names")= chr "Scchr13"
.. ..@ elementMetadata:Formal class 'DataFrame' [package "IRanges"] with 6 slots
.. .. ..@ rownames : NULL
.. .. ..@ nrows : int 27
.. .. ..@ elementMetadata: NULL
.. .. ..@ elementType : chr "ANY"
.. .. ..@ metadata : list()
.. .. ..@ listData :List of 1
.. .. .. ..$ name: chr [1:27] "YMR266W" "YMR267W" "YMR269W" "YMRWdelta20" ...
.. ..@ elementType : chr "ANY"
.. ..@ metadata : list()
..@ bamExperiment:List of 1
.. ..$ annotation: chr "org.Sc.sgd.db"

```

## Details

Illumina short reads from a very small segment of yeast chr XIII have been collected

## Source

FASTQ data available at <ftp://ftp.ncbi.nlm.nih.gov/sra/Studies/SRP000/SRP000632/>

## References

Albert Lee and Kasper Daniel Hansen and James Bullard and Sandrine Dudoit and Gavin Sherlock, 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, v4, e1000299, Dec 2008

## Examples

```

library(leeBamViews) # bam files stored in package
bpaths = dir(system.file("bam", package="leeBamViews"), full=TRUE, patt="bam$")
#
# extract genotype and lane information from filenames
#
gt = gsub(".*/", "", bpaths)
gt = gsub("_.*", "", gt)
lane = gsub(".*(.)$", "\\1", gt)
geno = gsub(".$", "", gt)
#
# format the sample-level information appropriately
#
pd = DataFrame(geno=geno, lane=lane, row.names=paste(geno,lane,sep="."))
prd = new("DFrame") # protocol data could go here
#
# create the views object, adding some arbitrary experiment-level information
#

```

```

bs1 = BamViews(bamPaths=bpaths, bamSamples=pd,
               bamExperiment=list(annotation="org.Sc.sgd.db"))
bs1
# add ranges and tabulate reads

START=c(861250, 863000)
END=c(862750, 864000)
exc = GRanges(IRanges(start=START, end=END), seqnames="Scchr13", strand="+")
values(exc)$name = c("intv1", "intv2") # necessary
bamRanges(bs1) = exc
bs1
tabulateReads(bs1, "+")

```

---

leeRPKM

*supplemental data extract on RNA seq results in yeast*


---

## Description

supplemental data extract on RNA seq results in yeast

## Usage

```
data(leeRPKM)
```

## Format

A data frame with 6291 observations on the following 16 variables.

chr a numeric vector

strand a numeric vector

start a numeric vector

end a numeric vector

name a factor with levels LSR1 NME1 YAL001C YAL002W YAL003W ...

feature a factor with levels CDS CDS\_unchar snRNA snoRNA

orf\_classification a factor with levels Uncharacterized Verified silenced\_gene3AVerified

gene a factor with levels AAC1 AAC3 AAD10 AAD14 AAD15 AAD16 AAD3 AAD4 ...

wt.reads a numeric vector

rrp.reads a numeric vector

ski.reads a numeric vector

xrn.reads a numeric vector

wt.rpkm a numeric vector

rrp.rpkm a numeric vector

ski.rpkm a numeric vector

xrn.rpkm a numeric vector

**Source**

imported from supplemental data

**References**

Lee et al PLOS genetics December 2008 ; Volume 4 ; Issue 12 ; e1000299

**Examples**

```
data(leeRPKM)
leeRPKM[1:5,]
```

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leeUnn	<i>supplemental data extracts on existing evidence of transcription in yeast</i>
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**Description**

supplemental data extracts on existing evidence of transcription in yeast

**Usage**

```
data(leeUnn)
```

**Format**

A data frame with 54822 observations on the following 11 variables.

chr a numeric vector

start a numeric vector

end a numeric vector

strand a numeric vector

lengthWithoutMask a numeric vector

length a numeric vector

lambda a numeric vector

background5 a logical vector

background20 a logical vector

reads a numeric vector

study a factor with levels David Davis Miura Nagalakshmi

**Source**

from Lee et al PLoS genetics December 2008 Volume 4 Issue 12 e1000299 supplemental data information on unannotated transcripts for which some evidence of transcription was obtained in this experiment

**Examples**

```
data(leeUnn)
leeUnn[1:5,]
```

---

tabulateReads	<i>tabulate counts of alignments occurring in specified genomic regions</i>
---------------	-----------------------------------------------------------------------------

---

**Description**

tabulate counts of alignments occurring in specified genomic regions

**Usage**

```
tabulateReads(bv, strandmarker=NULL, as.GRanges=FALSE, applier=lapply)
```

**Arguments**

bv	<a href="#">BamViews-class</a> instance
strandmarker	character atom: '+' or '-'; if missing, ignore strand
as.GRanges	logical directive to return a GRanges instance instead of a matrix
applier	lapply-like function; if unspecified and multicore is attached will use mclapply

**Details**

[readGAlignments](#) is the basic engine for this task

**Value**

annotated matrix with start, end, and samples as rows, regions as columns, and read counts as cell entries

**Author(s)**

VJ Carey <stvjc@channing.harvard.edu>

**Examples**

```
example(bs1)
#
# counts in a partition
#
myrn = GRanges(IRanges(start=seq(861250, 862750, 100), width=100),
  seqnames="Scchr13", strand="+")

values(myrn)$name = paste("til", 1:length(myrn), sep=".")
bamRanges(bs1) = myrn
tabulateReads(bs1, "+")
#
```

```
# a related computation based on countBam
lapply(bamPaths(bs1)[1:2], function(x)
  countBam(x, param=ScanBamParam(which=bamRanges(bs1))))
```

---

*totalReadCounts*      *scan BAM files for total read counts*

---

### **Description**

scan BAM files for total read counts

### **Usage**

```
totalReadCounts(x)
```

### **Arguments**

x                    [BamViews-class](#) instance

### **Details**

slow procedure – does lightweight scan of entire file

### **Value**

named integer vector of read counts per sample

### **Author(s)**

VJ Carey <stvjc@channing.harvard.edu>

### **Examples**

```
example(bs1)
totalReadCounts(bs1)
```

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