Package ‘leeBamViews’

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

Version 1.40.0

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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

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BamViews instance construction related to yeast RNA-seq

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-
  de vel/library/leeBamViews/bam/rlp5_13e.bam" "/Users/stvjc/ExternalSoft/R-devel/library/leeBamViews/bam/rlp6_13e.bam"
  ...
  ..@ bamIndices : 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-
  de vel/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
  ... ..@ elementType : chr "ANY"
  "... ...@ metadata : list()
  ... ...@ rowData : 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 2199 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"
Details

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

Source


References


Examples

library(leeBamViews) # bam files stored in package
bpaths = dir(system.file("bam", package="leeBamViews"), full=TRUE, patt="bam$")
#
# extract genotype and lane information from filenames
#
gt = gsub(".*", "", bpaths)
lane = gsub(".*", "", gt)
gen = gsub(".*", "", gt)
# format the sample-level information appropriately
#
pd = DataFrame(geno=geno, lane=lane, row.names=paste(geno, lane, sep="."))
prd = new("DFrame") # protocol data could go here
#
# create the views object, adding some arbitrary experiment-level information
#
bs1 = BamViews(bamPaths=bpaths, bamSamples=pd,
    bamExperiment=list(annotation="org.Sc.sgd.db"))
bs1
# add ranges and tabulate reads
START=c(861250, 863000)
END=c(862750, 864000)
exc = GRanges(IRanges(start=START, end=END), seqnames="Scchr13", strand="+")
values(exc)$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**

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

---

**Description**

supplemental data extracts on existing evidence of transcription in yeast

**Usage**

```r
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 unnannotated transcripts for which some evidence of transcription was obtained in this experiment
tabulateReads  

tabulate counts of alignments occurring in specified genomic regions

Description

tabulate counts of alignments occurring in specified genomic regions

Usage

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

Arguments

- **bv**: BamViews-class 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)

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Examples

```r
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, "+")
#```
totalReadCounts

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

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

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