Package ‘leeBamViews’

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

Version 1.38.0

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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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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-devel/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-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
... ...@ 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 933 636 234 108 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"
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)
gt = gsub("_.*", "", gt)
lane = gsub(".*\([^\s]+\)\s+\d+$", "\\\1", gt)
genom = gsub(".\s+\d+$", "", gt)
# # format the sample-level information appropriately
#
pd = DataFrame(genom=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, "+")

---

### 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,]

supplemental data extracts on existing evidence of transcription in yeast

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 unnannotated transcripts for which some evidence of transcription was obtained in this experiment
Examples
   data(leeUnn)
   leeUnn[1:5,]

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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

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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

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)
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Examples
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