Package ‘rnaSeqMap’

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Imports GenomicRanges, IRanges, edgeR, DESeq, DBI

Description The rnaSeqMap library provides classes and functions to analyze the RNA-sequencing data using the coverage profiles in multiple samples at a time

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biocViews Annotation, ReportWriting, Transcription, GeneExpression, DifferentialExpression, Sequencing, RNASeq, SAGE, Visualization

NeedsCompilation yes

R topics documented:

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addBamData

Description

Add data from experimental samples stored in BAM file.

Usage

addBamData(rs, file, exp, phenoDesc=NULL)

Arguments

rs SeqReads object to modify
file BAM file to read
exp Numbers of sample slot in the object
phenoDesc A vector to add to phenoData

Value

SeqReads object with samples added from the BAM files. List of BAM files comes from the covdesc. The covdesc content becomes phenoData of the object.
addDataToReadset

Author(s)

Michal Okoniewski, Anna Lesniewska

Examples

```r
# if (xmapConnected())
# {
#   rs <- newSeqReads(1,1,20000,1)
#   rs <- addBamData(rs,1:3)
# }
```

Description

Add another reads matrix to the readset. No control of region consistency, the matrix needs just 2 columns: starts and ends.

Usage

```r
addDataToReadset(rs, datain, spl)
```

Arguments

- `rs`
- `datain`
- `spl` Number or name of the experimental sample

Value

SeqReads object with one more sample added.

Author(s)

Michal Okoniewski, Anna Lesniewska

Examples

```r
# rs <- newSeqReads(1,1,20000,1)
# my.data1 <- rbind(c(1,50), c(3,53), c(11,60))
# rs <- addDataToReadset(rs, my.data1, 1)
```
addExperimentsToReadset

`addExperimentsToReadset` - getting sample data from the database.

### Description
Add data from experimental samples in the xXMAP database to the readset. Connection to the database required.

### Usage
```r
addExperimentsToReadset(rs, exps)
```

### Arguments
- `rs` SeqReads object to modify
- `exps` Vector of numbers of experimental samples in xXMAP

### Value
SeqReads object with samples added from the database.

### Author(s)
Michal Okoniewski, Anna Lesniewska

### Examples
```r
# if (xmapConnected())
# {
#   rs <- newSeqReads(1,1,20000,1)
#   rs <- addExperimentsToReadset(rs, 1:3)
# }
```

averageND

`averageND, sumND, combineNS, log2ND` - operations on distributions

Set of functions to operate on NucleotideDistr objects.

averageND calculates the mean for samples, sumND adds up selected samples' distributions, combineND adds two objects with the same size of distribution matrix, log2ND transforms all numeric data in the object into log space.

### Usage
```r
averageND(nd, exps);
sumND(nd, exps);
combineND(nd1, nd2);
log2ND(nd);
```
bam2sig

Arguments

nd, nd1, nd2  NucleotideDistr objects
exps  a pair of numbers of samples in the experiment

Value

NucleotideDistr object of the same type as input objects

Author(s)

Michal Okoniewski, Anna Lesniewska

Examples

# if (xmapConnected())
# {
#   rs <- newSeqReads(1,1,20000,1)
#   nd.cov <- getCoverageFromRS(rs,1:3)
#   nd.avg <- averageND(nd.cov,c(1,3))
#   nd.sum <- averageND(nd.cov,c(1,3))
#   nd.sum <- combineND(nd.cov,nd.cov)
#   nd.log <- log2ND(nd.cov)
# }

---

bam2sig  "bam2sig - encapsulated pipeline of finding significant expression"

Description

Reads BAM files according to annotation and produces output table processed with DESeq negative binomial test.

Usage

bam2sig(annotlib, covdesc="covdesc", species=NULL, level="gene")

Arguments

annotlib  Character table or data frame with columns: chr, start, end, strand, name
covdesc  Name of the file that includes BAM files (experiment description file)
species  Species name - needed for .chr.convert function - to match BAM and annotation chromosome names
level  The level of annotation for calculating the counts: gene, transcript of exon

Value

Output table with significant expression results, as from DESeq

Author(s)

Michal Okoniewski, Anna Lesniewska
Examples

```r
if (1==0)
{
  all.g <- all.genes(as.vector=F)
  ss <- sample(1:20000, 10)
  genes <- as.data.frame(all.g[ss,])

deseqRes <- bam2sig("cassava.db")
deseqRes[1:10,]
}
```

```
buildDESeq
buildDESeq - create CountDataSet

Description

Creates CountDataSet from the data in the database using the list of genes supplied - for further analysis with DESeq

Usage

```r
buildDESeq(genes, exps, conds=NULL)
```

Arguments

genes vector of Ensembl gene IDs
exps vector of experiments
conds Vector of experimental condition descriptions for the samples

Value

CountDataSet object filled with the data of gene-level counts of reads

Author(s)

Michal Okoniewski, Anna Lesniewska

See Also

buildDGEList

Examples

```r
# if (xmapConnected())
# {
#   data(sample_data_rnaSeqMap)
#   gg <- names(rs.list)
#   cds <- buildDESeq(gg,1:6, c("a","b","b","a","a","b"))
# }
```
**buildDGEList**

*buildDGEList - create DGEList (edgeR)*

**Description**

Creates DGEList from the data in the database using the list of genes supplied - for further analysis with edgeR

**Usage**

```r
buildDGEList(genes, exps, conds=NULL)
```

**Arguments**

- `genes` vector of Ensembl gene IDs
- `exps` vector of experiments
- `conds` Vector of experimental condition descriptions for the samples

**Value**

DGEList object filled with the data of gene-level counts of reads

**Author(s)**

Michal Okoniewski, Anna Lesniewska

**See Also**

`buildDESeq`

**Examples**

```r
# if (xmapConnected())
# {
#   data(sample_data_rnaSeqMap)
#   gg <- names(rs.list)
#   cds <- buildDGEList(gg, 1:6, c("a","b","b","a","a","b"))
# }
```

**findRegionsAsIR**

*findRegionsAsIR - finding regions of high coverage using Lindell-Aumann algorithm.*

**Description**

The function is running Lindell-Aumann algorithm to find regions of irreducible expression on the coverage data in the NucleotideDistr object. The function may be used to find the location and boundaries of significant expression of exons and small RNA.
Usage

```
findRegionsAsIR(nd, mi, minsup=5, exp)
```

Arguments

- `nd`: An object of `NucleotideDistr` class that has coverage values for a given region
- `mi`: The threshold of coverage that makes the region significant
- `minsup`: Minimal support of the numeric association rule - namely, in this case, the minimal length of the discovered region
- `exp`: Sample (experiment) number

Value

IRanges object with irreducible regions with high coverage.

Author(s)

Michal Okoniewski, Anna Lesniewska

Examples

```
# if (xmapConnected())
# {
#   rs <- newSeqReads(1,1,20000,1)
#   rs <- addExperimentsToReadset(rs,1:3)
#   nd.cov <- getCoverageFromRS(rs,1:3)
#   nd.regs <- findRegionsAsND(nd.cov, 10)
# }
```

Description

The function is running Lindell-Aumann algorithm to find regions of irreducible expression on the coverage data in the `NucleotideDistr` object. The function may be used to find the location and boundaries of significant expression of exons and small RNA.

Usage

```
findRegionsAsND(nd, mi, minsup=5)
```

Arguments

- `nd`: An object of `NucleotideDistr` class that has coverage values for a given region
- `mi`: The threshold of coverage that makes the region significant
- `minsup`: Minimal support of the numeric association rule - namely, in this case, the minimal length of the discovered region
**Value**

NucleotideDistr object that includes a matrix with zeros where no region was found and the value of mi for all the nucleotides included in the region. The type of the object is "REG".

**Author(s)**

Michal Okoniewski, Anna Lesniewska

**Examples**

```r
# if (xmapConnected())
# {
#   rs <- newSeqReads(1,1,20000,1)
#   rs <- addExperimentsToReadset(rs,1:3)
#   nd.cov <- getCoverageFromRS(rs,1:3)
#   nd.regs <- findRegionsAsND(nd.cov, 10)
# }
```

---

**Description**

Set of functions to operate on NucleotideDistr objects.

averageND calculates the mean for samples, sumND adds up selected samples' distributions, combineND adds two objects with the same size of distribution matrix, log2ND transforms all numeric data in the object into log space.

**Usage**

```r
fiveCol2GRanges(t)
```

**Arguments**

- `t` A matrix or data frame including genomic regions in 5 columns: ID, chr/contig name, start, end, strand

**Value**

GenomicRanges object with the same values

**Author(s)**

Michal Okoniewski
geneInChromosome

Description
Finds all the genes in the given chromosome regions

Usage
geneInChromosome(chr, start, end, strand)

Arguments
- chr: Chromosome
- start: Start of the region on a chromosome
- end: End of the region on a chromosome
- strand: Genome strand: 1 or -1

Value
table of the genes in a given regions, produced with stored procedure

Author(s)
Michał Okoniewski, Anna Lesniewska

Examples
# if (xmapConnected())
# {
#     geneInChromosome(1, 1, 80000, 1)
# }

generators

Generators for synt data and

Description
Various generators for experiments.

Usage
generatorAddSquare(nd, deg, length.prop=0.5)
generatorAdd(nd, deg, length.prop=0.5)
generatorMultiply(nd, deg, length.prop=0.5)
generatorTrunc(nd, deg)
generatorSynth(nd, deg, length.prop=0.5)
generatorPeak(nd, deg, sr=10, mult=10)
getBamData - getting sample data from BAM file.

Description

Add data from experimental samples stored in BAM file.

Usage

getBamData(rs, exps = NULL, cvd = NULL, covdesc.file = "covdesc")

Arguments

rs  SeqReads object to modify
exps  Vector of numbers of experimental samples
cvd  Covdesc-like data frame - BAM files are read from row names
covdesc.file  Alternatively, the experiment description file

Value

SeqReads object with samples added from the BAM files. List of BAM files comes from the covdesc. The covdesc content becomes phenoData of the object.
getCoverageFromRS

Author(s)

Michal Okoniewski, Anna Lesniewska

Examples

```r
# if (xmapConnected())
# {
#   rs <- newSeqReads(1,1,20000,1)
#   rs <- getBamData(rs,1:3)
# }
```

getCoverageFromRS - conversion to coverage object

Description

Calculates the coverage function for the reads encapsulated in the SeqReads object.

Usage

```r
getCoverageFromRS(rs, exps)
```

Arguments

- `rs`: SeqReads object to modify
- `exps`: Vector of numbers of experimental samples in xXMAP

Value

NucleotideDistr object with coverage matrix in assayData slot and type "COV".

Author(s)

Michal Okoniewski, Anna Lesniewska

Examples

```r
# if (xmapConnected())
# {
#   rs <- newSeqReads(1,1,20000,1)
#   rs <- addExperimentsToReadset(rs,1:6)
#   nd.cov <- getCoverageFromRS(rs,1:3)
# }
```
**getData**

*Data accessor function for rnaSeqMap objects containing 'data' field*

**Description**

This function gets the 'data' field from rnaSeqMap objects.

**Usage**

`getData(iND)`

**Arguments**

- `iND`  
  rnaSeqMap object containing 'data' field

**Value**

A list containing 'data' field

**Author(s)**

Michal Okoniewski, Anna Lesniewska, Marek Wiewiorka

---

**getExpDescription**  

*getExpDescription*

**Description**

Gets the bio_sample table from the database. May be used as phenoData.

**Usage**

`getExpDescription()`

**Value**

Table of experimental factors assigned to numbers of samples.

**Author(s)**

Michal Okoniewski, Anna Lesniewska
getFCFromND

getFCFromND - calculating fold change of coverages

Description
This function calculates the fold change of two sample coverages from a NucleotideDistr object. The coverages are assumed to be after logarithmic transformation, so the function basically subtracts the value and generates new NucleotideDistr object with a single vector of fold changes.

Usage
getFCFromND(nd, exps)

Arguments
nd NucleotideDistr object with coverages
exps a pair of numbers of samples in the experiment

Value
NucleotideDistr object of type "FC" with a single vector of fold changes

Author(s)
Michal Okoniewski, Anna Lesniewska

Examples
# if (xmapConnected())
# {
# rs <- newSeqReads(1,1,20000,1)
# rs <- addExperimentsToReadset(rs,1:3)
# nd.cov <- getCoverageFromRS(rs,1:3)
# nd.fc <- getFCFromND(nd.cov,c(1,3))
# }

getSIFromND

getSIFromND - calculating splicing index of two coverages

Description
This function calculates the splicing index value of two sample coverages from a NucleotideDistr object. It is assumed that the region in the NucleotideDistr is a single gene. Splicing index is calculated in similar way to the implementation for exon Affy microarrays (see Gardina et al, Genome Biology, 2007 for details), but it is run for each nucleotide in the region and instead of gene-level average expression values, it uses sums of reads for both samples.

Usage
getSIFromND(nd, exps)
**getSumsExp**

**Arguments**

- **nd**
  - NucleotideDistr object with coverages
- **exps**
  - a pair of numbers of samples in the experiment

**Value**

NucleotideDistr object of type "FC" with a single vector of splicing index values

**Author(s)**

Michal Okoniewski, Anna Lesniewska

**Examples**

```
# if (xmapConnected())
# {
#   rs <- newSeqReads(1,1,20000,1)
#   nd.cov <- getCoverageFromRS(rs,1:3)
#   nd.fc <- getSIFromND(nd.cov,c(1,3))
# }
```

---

**Description**

Gets the sum of reads in all the samples present in the database in the seq_read table

**Usage**

```
getSumsExp()
```

**Value**

Vector of sums

**Author(s)**

Michal Okoniewski, Anna Lesniewska

**Examples**

```
# if (xmapConnected())
# {
#   sums <- getSumsExp()
#   nsums
# }
```
**measures**

---

**gRanges2CamelMeasures** *Genomic plots based upon NucleotideDistr objects*

**Description**

Various plots of genomic coverage for data from NucleotideDistr objects

**Usage**

```r
gRanges2CamelMeasures(gR, cvd, sample.idx1, sample.idx2, sums=NULL, progress=NULL)
allCamelMeasuresForRegion(ch, st, en, str, cvd, sample.idx1, sample.idx2, sums=NULL)
```

**Arguments**

- `ch`: chromosome name
- `st`: genomic start
- `en`: genomic end
- `str`: strand
- `cvd`: name of the file with BAM description - covdesc
- `gR`: GenomicRanges object to use as a set of genomic regions to query
- `sample.idx1`, `sample.idx2`: sample indices
- `sums`: the vector of sums for normalization
- `progress`: every how many regions print a dot for progress indicator

**Author(s)**

Michal Okoniewski

**Examples**

```r
#
```

---

**measures** *Measures*

**Description**

Various measures to find differential expression.
**Usage**

```r
ks_test(dd)
diff_area(dd, cconst)
diff_derivative_area(dd, cconst)
qq_plot(dd)
qq_derivative_plot(dd)
pp_plot(dd)
pp_derivative_plot(dd)
hump_diff1(dd)
hump_diff2 (dd)
```

**Arguments**

- `dd`: a matrix with 2 columns for samples and rows for nucleotides, containing coverage data (like from BED files)
- `cconst`: NULL default

The measures give various assessment of the difference between two sequencing samples shapes. Full description will follow in the paper.

**Author(s)**

Anna Lesniewska, Michal Okoniewski

**Examples**

```r
# if (xmapConnected())
# {
#   # ks_test(dd)
#   # }
```

---

**NDplots**

*Genomic plots based upon NucleotideDistr objects*

**Description**

Various plots of genomic coverage for data from NucleotideDistr objects

**Usage**

```r
distrCOVPlot(nd, exps)
distrSIPlot(nd, ex1, ex2, mi, minsup=5)
```

**Arguments**

- `nd`: NucleotideDistr object
- `exps`: vectors of experiment numbers to plot
- `ex1, ex2`: experiment numbers to plot
- `mi`: threshold in the region mining algorithm
- `minsup`: minimal support - minimal length of the irreducible region found
### Normalizations

**Normalization Methods**

**Description**

Various normalization methods.

**Usage**

- `standarizationNormalize(nd)`
- `min_maxNormalize(nd)`
- `densityNormalize(nd)`
- `globalCountsNormalize(nd, sums)`

**Arguments**

- `nd` nucleotide distribution object
- `sums` sum of reads in a sequencing sample

Normalizations of a single coverage profile for multiple samples contained in the NucleotideDistr object. Full description will follow in a paper.

**Author(s)**

Anna Lesniewska, Michal Okoniewski

**Examples**

```r
# if (xmapConnected())
# {
#   s <- newSeqReads('chr2', 220238268, 220254744, -1)
#   f <- c("test1.bam", "test2.bam", "test3.bam", "test4.bam", "test5.bam")
#   ff <- sapply(f, function(x) system.file("extdata", x, package = "rnaSeqMap"))
#   rs <- getBamData(rs, 1:5, files = ff)
#   nd <- getCoverageFromRS(rs, 1:5)
#   min_maxNormalize(nd)
# }
```
normalizeBySum

Normalization of NucleotideDistr by global number of reads

Description

normalizeBySum function normalizes the coverage values in NucleotideDistr by dividing all the numbers for all samples by the sum of reads for each sample. The number of reads from each sample may be taken from the database by the function getSumsExp, which is a wrapper for an appropriate SQL procedure. Alternatively, it is passed directly as a vector of numeric values of the same length as the number of samples analyzed. Such simple normalization allows comparisons of the coverage values for samples with different number of reads

Usage

normalizeBySum(nd, r=NULL)

Arguments

nd NucleotideDistr object with raw read counts
r Vector of numbers. If there is no such parameter, a database procedure summarizing reads is run

Value

NucleotideDistr object

Author(s)

Michal Okoniewski, Anna Lesniewska

See Also

getSumsExp

Examples

# if (xmapConnected())
# {
#   rs <- newSeqReads(1,10000,20000,1)
#   nd.cov <- getCoverageFromRS(rs,1:3)
#   nd.norm <- normalizeBySum(nd.cov)
#   nd.norm <- normalizeBySum(nd.cov, r=c(100, 200, 1000))
# }
NucleotideDistr-class  Numeric distributions by nucleotide - class

Description
An S4 class that inherits from eSet and holds all the numeric distributions of functions defined over the genome. The values may include coverage, splicing, fold change, etc. for a region defined by genomic coordinates.

Slots/List Components
Objects of this class contain (at least) the following list components:
chr: numeric matrix containing the read counts.
start: data.frame containing the library size and group labels.
end: data.frame containing the library size and group labels.
strand: data.frame containing the library size and group labels.
start: data.frame containing the library size and group labels.

Methods
distribs gives the matrix of distributions from assayData
getDistr gives a single distributions from assayData as a vector
newNucleotideDistr (distribs, chr, start, end, strand, type="UNKNOWN", phenoData=NULL, featureData=NULL)
constructor from a matrix of data and chromosome coordinates.

Author(s)
Anna Lesniewska, Michal Okoniewski

See Also
SeqReads, NDtransforms

parseGff3  parseGff3 - parsing gff3 file format

Description
Parses gff3 file into genes, transcripts and exons.

Usage
parseGff3(filegff, fileg="genes.txt", filet="transcripts.txt", filee="exons.txt", nofiles=FALSE)
**plotGeneCoverage**

**Arguments**

- **filegff**: Input file in GFF3 format
- **fileg**: Filename for output: genes
- **filet**: Filename for output: transcripts
- **filee**: Filename for output: exons
- **nofiles**: Flag: just output list, no files

**Value**

List with elements "genes", "transcripts", "exons" with appropriate tables.

**Author(s)**

Michal Okoniewski, Anna Lesniewska

**Examples**

```r
# if (xmapConnected())
# {
#   parseGff3("Athaliana.gff3")
# }
```

**Description**

Various plots of genomic coverage for experiments.

**Usage**

```r
plotGeneCoverage(gene_id, ex)
plotRegionCoverage(chr, start, end, strand, ex)
plotExonCoverage (exon_id, ex)
plotCoverageHistogram (chr, start, end, strand, ex, skip)
plotGeneExonCoverage(gene_id, ex)
plotSI(chr, start, end, strand, exp1, exp2)
```

**Arguments**

- **ex**: vectors of experiment numbers to plot
- **exp1, exp2**: experiment numbers for splicing index
- **gene_id**: Ensembl gene ID
- **exon_id**: Ensembl exon ID
- **chr**: Chromosome
- **start**: Start position of region on the chromosome
- **end**: Start position of region on the chromosome
- **strand**: Strand
- **skip**: size of the bucket in histogram
readsInRange

Author(s)
Michal Okoniewski, Anna Lesniewska

Examples

# if (xmapConnected())
# {
#   plotGeneCoverage("ENSG00000144567", 1:3) # plotting FAM134A for experiments 1,2,3
#   plotRegionCoverage(2, 220040947, 220050201, 1, 1:3) # the same, using coordinates
# }

Description
Finds all the reads for a genomic range

Usage
readsInRange(chr, start, end, strand, ex)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>chr</td>
<td>Chromosome</td>
</tr>
<tr>
<td>start</td>
<td>Start of the region on a chromosome</td>
</tr>
<tr>
<td>end</td>
<td>End of the region on a chromosome</td>
</tr>
<tr>
<td>strand</td>
<td>Genome strand: 1 or -1</td>
</tr>
<tr>
<td>ex</td>
<td>experiment</td>
</tr>
</tbody>
</table>

Value
table of reads, as in the database

Author(s)
Michal Okoniewski, Anna Lesniewska

Examples

# if (xmapConnected())
# {
#   tmp <- readsInRange(1, 10000, 20000, 1,3)
# }
regionBasedCoverage

regionBasedCoverage - transformation of the region coverage by the Lindell-Aumann regions

Description

The function builds a NucleotideDistr object from another object of coverage, using sequential call of Lindell-Aumann algorithm on the same data with a sequence of mi-levels. Each nucleotide is assigned the maximum mi-value of a region that covers it.

The output NucleotideDistr object has the distribution without peaks and small drops of coverage, but the thade-off is that the level of coverage are discrete: seq\*maxexp.

Usage

regionBasedCoverage(nd, seqq=1:10, maxexp=20, minsup=5)

Arguments

nd An object of NucleotideDistr class that has coverage values for a given region
seqq Vector of numbers used to divide the range of coverage for subsequent mi-levels
maxexp The maximal mi-level for coverage
minsup Minimal support of the numeric association rule - namely, in this case, the minimal length of the discovered region

Value

NucleotideDistr object that includes a matrix with zeros where no region was found and a maximum of mi-levels used for the sequential region searched. The distributions are similar to coverage, but have removed outliers of coverage peaks and short drops of coverage.

Author(s)

Michal Okoniewski, Anna Lesniewska

Examples

# if (xmapConnected())
# {
# rs <- newSeqReads(1,1,20000,1)
# rs <- addExperimentsToReadset(rs,1:3)
# nd.cov <- getCoverageFromRS(rs,1:3)
# nd.regs <- regionBasedCoverage(nd.cov, 1:10, 100)
# runs the Lindell-Aumann algorithm at 100, 90, ... and picks maximal mi-level, where the nucleotide has a region
# }
regionCoverage

Description

Finds all the reads for a genomic range

Usage

regionCoverage(chr, start, end, strand, ex, db = "FALSE")

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>chr</td>
<td>Chromosome</td>
</tr>
<tr>
<td>start</td>
<td>Start of the region on a chromosome</td>
</tr>
<tr>
<td>end</td>
<td>End of the region on a chromosome</td>
</tr>
<tr>
<td>strand</td>
<td>Genome strand: 1 or -1</td>
</tr>
<tr>
<td>ex</td>
<td>experiment</td>
</tr>
<tr>
<td>db</td>
<td>Use database (SQL) implementation of the algorithm</td>
</tr>
</tbody>
</table>

Value

coverage vector, independent from NucleotideDistr

Author(s)

Michal Okoniewski, Anna Lesniewska

Examples

```r
# if (xmapConnected())
# {
#  tmp <- regionCoverage( 1, 10000, 20000, 1,3)
# }
```

RleList2matrix

Description

Function transforms list of Rle objects to matrix.

Usage

RleList2matrix(ll);

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ll</td>
<td>list of Rle objects.</td>
</tr>
</tbody>
</table>
Value

Produces the full, unpacked coverage matrix from a list of Rle objects. Used to re-format the coverage data.

Author(s)

Michal Okoniewski, Anna Lesniewska

Description

A fragment of sequencing data from 6 samples - human.

Usage

data(sample_data_rnaSeqMap)

Format

A list with 17 SeqReads objects, each with sequencing reads from 6 samples sequenced with ABI SOLID machine.

Examples

# data(sample_data_rnaSeqMap)
# length(rs.list)
# gene1rs <- rs.list[[1]]

SeqReads

SeqReads - a container for RNAseq reads

Description

SeqReads objects keep the reads information in the form of a list, containing one matrix of reads per experiment. Matrices of dimension n x 2 should come from a mapping to the regions defined by genome coordinates (chromosome, start, end, strand) in the SeqReads object.

The object may be filled in from the database or from list with read data. It is recommended to create one SeqReads object per gene or intergenic region. The object are used then to create object of class NucleotideDistr

Usage

newSeqReads(chr, start, end, strand, datain=NULL, phenoData=NULL, featureData=NULL, covdesc=NULL)
newSeqReadsFromGene(g)
setData

Data accessor function for rnaSeqMap objects containing 'data' field

Description

This function sets the 'data' field from one rnaSeqMap object with 'data' field from the other one.

Usage

setData(iND1,iND2)

Arguments

iND1: target rnaSeqMap object containing 'data' field
iND2: source rnaSeqMap object containing 'data' field

Value

NULL

Author(s)

Michal Okoniewski, Anna Lesniewska, Marek Wiewiorka
setSAXPYData

Data accessor function for rnaSeqMap objects containing 'data' field

Description

This function sets the 'data' field at i position. The new value is the old one multiplied by iParam.

Usage

setSAXPYData(iND1,iParam,i)

Arguments

iND1 rnaSeqMap object containing 'data' field
iParam Scalining parameter
i Index of the 'data' field to be modified

Value

NULL

Author(s)

Michal Okoniewski, Anna Lesniewska, Marek Wiewiorka

setSpecies

setSpecies

Description

Sets the species name for chromosomes X, Y and MT translation into consecutive numbers. If you use xmap.connect, no need to call setSpecies. Both set the internal variable of xmapcore.

Usage

setSpecies(name=NULL)

Arguments

name Species name

Author(s)

Michal Okoniewski, Anna Lesniewska

Examples

setSpecies("mus_musculus")
simplePlot  

**Description**  
Plots 2 or 3 coverages with fixed colors.

**Usage**  
```
simplePlot (nd, exps, xlab="genome coordinates", ylab="coverage")
```

**Arguments**  
- `nd` : NucleotideDistr object to plot  
- `exps` : Samples to plot - numeric vector  
- `xlab` :  
- `ylab` :  

**Author(s)**  
Michal Okoniewski

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spaceInChromosome  

**Description**  
Finds all the intergenic spaces in the given chromosome region

**Usage**  
```
spaceInChromosome(chr, start, end, strand)
```

**Arguments**  
- `chr` : Chromosome  
- `start` : Start of the region on a chromosome  
- `end` : End of the region on a chromosome  
- `strand` : Genome strand: 1 or -1

**Value**  
Table of the intergenic spaces in a given regions, produced with stored procedure

**Author(s)**  
Michal Okoniewski, Anna Lesniewska
Examples

//# if (xmapConnected())
//# {
//#     spaceInChromosome(1, 1, 80000, 1)
//# }
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