

Package ‘RNAmoD.R.Data’

April 14, 2020

Type Package

Title Example data for the RNAmoD.R package

Version 1.0.0

Date 2020-01-14

Description RNAmoD.R.Data contains example data, which is used for vignettes and example workflows in the RNAmoD.R and dependent packages.

biocViews ExperimentData, SequencingData, RNASeqData

License Artistic-2.0

Encoding UTF-8

LazyData false

Depends R (>= 3.6), ExperimentHub, ExperimentHubData (>= 1.9.2)

Imports utils

Suggests knitr, rmarkdown, BiocStyle, GenomicRanges, sessioninfo

Collate 'RNAmoD.R.Data.R' 'zzz.R'

RoxygenNote 7.0.2

VignetteBuilder knitr

BugReports <https://github.com/FelixErnst/RNAmoD.R.Data/issues>

URL <https://github.com/FelixErnst/RNAmoD.R.Data>

git_url <https://git.bioconductor.org/packages/RNAmoD.R.Data>

git_branch RELEASE_3_10

git_last_commit 4bde57b

git_last_commit_date 2020-01-14

Date/Publication 2020-04-14

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R topics documented:

example.man.fasta	2
RNAmoDR.Data	2
RNAmoDR.Data.AAS	3
RNAmoDR.Data.example	4
RNAmoDR.Data.RMS	4
RNAmoDR.Data.snoRNadb	5
Index	6

example.man.fasta	<i>RNAmoDR example data for tests and man pages</i>
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Description

This dataset contains a small data set for tests and man page examples. The individual identifiers are `RNAmoDR.Data.` plus the header from the Datasets section.

Datasets

example.man.fasta: sequence of artificial genome for *S. cerevisiae* containing partial sequences of the 18S rRNA

example.man.gff3: annotation of artificial genome for *S. cerevisiae* containing partial sequences of the 18S rRNA

Examples

```
RNAmoDR.Data.example.man.fasta()
RNAmoDR.Data.example.man.gff3()
```

RNAmoDR.Data	<i>RNAmoDR.Data</i>
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Description

`RNAmoDR.Data` contains example data, which is used for vignettes and example workflows in the `RNAmoDR` and dependent packages.

Author(s)

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`RNAmodR.Data.AAS`*RNAmodR AlkAnilineSeq example data*

Description

This dataset contains example data for AlkAnilineSeq. The individual identifiers are `RNAmodR.Data.` plus the header from the Datasets section.

Datasets

example.AAS.fasta: sequence of artificial genome for *S. cerevisiae* containing only the 18S rRNA sequence and 10 tRNA sequences

example.AAS.gff3: annotation of artificial genome for *S. cerevisiae* containing only the 18S rRNA sequence and 10 tRNA sequences

example.bud23.1: sequencing reads mapped to artificial genome from bud23del strain - replicate 1

example.bud23.2: sequencing reads mapped to artificial genome from bud23del strain - replicate 2

example.trm8.1: sequencing reads mapped to artificial genome from trm8del strain - replicate 1

example.trm8.2: sequencing reads mapped to artificial genome from trm8del strain - replicate 2

example.wt.1: sequencing reads mapped to artificial genome from wild type strain - replicate 1

example.wt.2: sequencing reads mapped to artificial genome from wild type strain - replicate 2

example.wt.3: sequencing reads mapped to artificial genome from wild type strain - replicate 3

Examples

```
RNAmodR.Data.example.AAS.fasta()  
RNAmodR.Data.example.AAS.gff3()  
RNAmodR.Data.example.bud23.1()  
RNAmodR.Data.example.bud23.2()  
RNAmodR.Data.example.trm8.1()  
RNAmodR.Data.example.trm8.2()  
RNAmodR.Data.example.wt.1()  
RNAmodR.Data.example.wt.2()  
RNAmodR.Data.example.wt.3()
```

RNAmodR.Data.example *RNAmodR general example data*

Description

This dataset contains general example data used for different purposes. The individual identifiers are RNAmodR.Data. plus the header from the Datasets section.

Datasets

example.fasta: sequences of artificial genome for *S. cerevisiae* containing only rRNA and tRNA sequences

example.gff3: annotation of artificial genome for *S. cerevisiae* containing only rRNA and tRNA sequences

example.bam.1: sequencing reads mapped to artificial genome - replicate 1

example.bam.2: sequencing reads mapped to artificial genome - replicate 2

example.bam.3: sequencing reads mapped to artificial genome - replicate 3

Examples

```
RNAmodR.Data.example.fasta()  
RNAmodR.Data.example.gff3()  
RNAmodR.Data.example.bam.1()  
RNAmodR.Data.example.bam.2()  
RNAmodR.Data.example.bam.3()
```

RNAmodR.Data.RMS *RNAmodR RiboMethSeq example data*

Description

This dataset contains example data for RiboMethSeq. The individual identifiers are RNAmodR.Data. plus the header from the Datasets section.

Datasets

example.RMS.fasta: sequence of artificial genome for *H. sapiens* containing only the 5.8S rRNA sequence

example.RMS.gff3: annotation of artificial genome for *H. sapiens* containing only the 5.8S rRNA sequence

example.RMS.1: sequencing reads mapped to artificial genome - replicate 1

example.RMS.2: sequencing reads mapped to artificial genome - replicate 2

Examples

```
RNAmodR.Data.example.RMS.fasta()  
RNAmodR.Data.example.RMS.gff3()  
RNAmodR.Data.example.RMS.1()  
RNAmodR.Data.example.RMS.2()
```

```
RNAmodR.Data.snoRNAdb snoRNAdb data
```

Description

The csv files contains a copy of data from the snoRNAdb (<https://www-snorna.biotoul.fr/>) downloaded on the 2019-02-11. The coordinates were updated to current rRNA sequences of hg38.

Examples

```
RNAmodR.Data.snoRNAdb()
```

Index

example.man.fasta, 2

RNAmodR.Data, 2

RNAmodR.Data.AAS, 3

RNAmodR.Data.example, 4

RNAmodR.Data.example.AAS.fasta
(RNAmodR.Data.AAS), 3

RNAmodR.Data.example.AAS.gff3
(RNAmodR.Data.AAS), 3

RNAmodR.Data.example.bud23.1
(RNAmodR.Data.AAS), 3

RNAmodR.Data.example.bud23.2
(RNAmodR.Data.AAS), 3

RNAmodR.Data.example.man.fasta
(example.man.fasta), 2

RNAmodR.Data.example.man.gff3
(example.man.fasta), 2

RNAmodR.Data.example.RMS.1
(RNAmodR.Data.RMS), 4

RNAmodR.Data.example.RMS.2
(RNAmodR.Data.RMS), 4

RNAmodR.Data.example.RMS.fasta
(RNAmodR.Data.RMS), 4

RNAmodR.Data.example.RMS.gff3
(RNAmodR.Data.RMS), 4

RNAmodR.Data.example.trm8.1
(RNAmodR.Data.AAS), 3

RNAmodR.Data.example.trm8.2
(RNAmodR.Data.AAS), 3

RNAmodR.Data.example.wt.1
(RNAmodR.Data.AAS), 3

RNAmodR.Data.example.wt.2
(RNAmodR.Data.AAS), 3

RNAmodR.Data.example.wt.3
(RNAmodR.Data.AAS), 3

RNAmodR.Data.RMS, 4

RNAmodR.Data.snoRNadb, 5