Package ‘RNAmodR.Data’

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Type Package

Title Example data for the RNAmodR package

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Description RNAmodR.Data contains example data, which is used for vignettes and example workflows in the RNAmodR 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, testthat

Collate 'RNAmodR.Data.R' 'zzz.R'

RoxygenNote 7.3.3

VignetteBuilder knitr

BugReports `https://github.com/FelixErnst/RNAmodR.Data/issues`

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Author Felix G.M. Ernst [aut, cre],
Denis L.J. Lafontaine [ctb, fnd]

Maintainer Felix G.M. Ernst <`felix.gm.ernst@outlook.com`>

Contents

`example.man.fasta` *RNAmodR example data for tests and man pages*

Description

This dataset contains a small data set for tests and man page examples. The indivicual 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` *RNAmodR.Data*

Description

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

Author(s)

Felix G.M. Ernst [aut], Denis L.J. Lafontaine [ctb]

See Also

Useful links:

- `https://github.com/FelixErnst/RNAmodR.Data`
- Report bugs at `https://github.com/FelixErnst/RNAmodR.Data/issues`

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

Description

This dataset contains exmaple data for AlkAnilineSeq. The indivicual 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 indivicual 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 indivicual 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()
```

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