Package 'MMAPPR2data'

October 17, 2024

Type Package

Title Sample Data for MMAPPR2

Version 1.18.0

Description Contains data for illustration purposes in the MMAPPR2 package, namely simulated BAM files containing RNA-Seq data for a mutation in the slc24a5 gene, taken from the GRCz11 genome. Also contains reference sequence and annotation files for the region.

Depends R (>= 3.6.0)

VignetteBuilder knitr

Enhances MMAPPR2

Suggests knitr, rmarkdown, BiocStyle, roxygen2, seqinr, readr

Imports Rsamtools

License GPL-3

Encoding UTF-8

biocViews RNASeqData, Danio_rerio_Data, SequencingData, Genome

URL https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3613585/, https://github.com/kjohnsen/MMAPPR2

RoxygenNote 6.1.1

PackageStatus Deprecated

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MMAPPR2data   *MMAPPR2data: Example Data for MMAPPR2*

Description

Contains BAM files and indices for example use in MMAPPR2. The data is artificial, meant to
simulate sequencing of the zebrafish slc24a5 gene in mutant and wild-type pools resulting from the
cross of a novel mutant from a forward genetics screen with a wild-type line, as described in Hill et
al. 2013.

Usage

```
exampleMutBam()

exampleWTbam()

goldenFasta()

goldenGFF()
```

Details

Besides BAM files and indices, the package also contains fasta and gtf files for just the region of
the slc24a5 gene, which are also used in demonstrating MMAPPR2's functionality. They are based
on the GRCz11 assembly and were obtained from Ensembl version 95.

Value

A `BamFile` object referencing a BAM file and its index.

A `BamFile` object referencing a BAM file and its index.

A path to the bgzipped slc24a5 fasta file

The path to the bgzipped GFF file

Functions

- `exampleMutBam`: Easy access to example mutant pool BAM file.

- `exampleWTbam`: Easy access to example wild-type pool BAM file.

- `goldenFasta`: Easy access to example fasta file for slc24a5 gene.

- `goldenGFF`: Easy access to example GFF file for slc24a5 gene.

Examples

```
mutFile <- exampleMutBam()
wtFile <- exampleWTbam()
goldenFasta <- goldenFasta()
goldenGFF()
```

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