

Package ‘NanoporeRNASeq’

October 17, 2024

Type Package

Title Nanopore RNA-Seq Example data

Version 1.14.0

Description The NanoporeRNASeq package contains long read RNA-Seq data generated using Oxford Nanopore Sequencing. The data consists of 6 samples from two human cell lines (K562 and MCF7) that were generated by the SG-NEx project. Each of these cell lines has three replicates, with 1 direct RNA sequencing data and 2 cDNA sequencing data. Reads are aligned to chromosome 22 (Grch38) and stored as bam files. The original data is from the SG-NEx project.

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Encoding UTF-8

LazyData true

Depends R(>= 4.0.0), ExperimentHub (>= 1.15.3)

Suggests knitr, bambu, ggbio, BSgenome.Hsapiens.NCBI.GRCh38, circlize, ComplexHeatmap, apeglm, rlang, rmarkdown, GenomicAlignments, Rsamtools

Enhances parallel

biocViews ExperimentHub, ExperimentData, RNASeqData, Genome, SequencingData

bugReports <https://github.com/GoekeLab/NanoporeRNASeq/issues>

URL <https://github.com/GoekeLab/NanoporeRNASeq>

RoxygenNote 7.1.1

VignetteBuilder knitr

git_url <https://git.bioconductor.org/packages/NanoporeRNASeq>

git_branch RELEASE_3_19

git_last_commit ca3b82a

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-10-17

Author Jonathan Goeke [aut],
 Ying Chen [cre],
 Yuk Kei Wan [aut]

Maintainer Ying Chen <chen_ying@gis.a-star.edu.sg>

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HsChr22BambuAnnotation

BambuAnnotation of the first half of Human Sapiens Chr22

Description

Annotation GRangesList prepared from bambu for Granges of human genome (Grch38) chromosome 22 (1:25409234)

Usage

```
data("HsChr22BambuAnnotation")
```

Format

SummarizedExperiment

NanoporeRNASeq

NanoporeRNASeq package with long-read RNA sequencing data

Description

The NanoporeRNASeq package contains long-read RNA-Seq data generated using Oxford Nanopore Sequencing. The data consists of 6 samples from two human cell lines (K562 and MCF7). Each of these cell lines has three replicates, with 1 direct RNA sequencing data and 2 cDNA sequencing data. Reads are aligned to chromosome 22 (Grch38) and stored as bam files. The original data is from the SG-NEx project. Please see the package vignette for examples and use cases.

Details

Data objects include:

- [SGNexSamples](#) - sample information of the bam files
- [HsChr22BambuAnnotation](#) - annotation GRangesList

For detailed information on usage, see the package vignette, by typing `vignette("NanoporeRNASeq")`, or the workflow linked to on the first page of the vignette.

Author(s)

Ying Chen, Yuk Kei Wan, Jonathan Göke

SGNexSamples

SG-Nex samples from Nanopore RNA-Seq

Description

Sample information description for K562 and MCF7 samples from SG-Nex

Usage

```
data("SGNexSamples")
```

Format

DataFrame

Details

SGNexSamples is a DataFrame containing the following information:

- `sample_id` - sample names of the bam files
- `Platform` - sequencing platform
- `cellLine` - cell line used
- `protocol` - sequencing protocols
- `cancer_type` - cancer type of the cell line

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