Package ‘NanoporeRNASeq’

March 21, 2024

Type Package
Title Nanopore RNA-Seq Example data
Version 1.12.0
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.
License GPL-3 + file LICENSE
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
SystemRequirements
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_18
git_last_commit 6b89b97
git_last_commit_date 2023-10-24
**Repository**  Bioconductor 3.18

**Date/Publication**  2024-03-21

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### R topics documented:

- **HsChr22BambuAnnotation**
- **NanoporeRNASeq**
- **SGNexSamples**

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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**

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

**Format**

SummarizedExperiment

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**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.
SGNexSamples

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

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**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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