Package ‘NanoporeRNASeq’

July 4, 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.
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
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
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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.
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.

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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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