Package 'NanoporeRNASeq'

October 27, 2026

Type Package

Title Nanopore RNA-Seq Example data

Version 1.22.0

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

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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)

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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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