Package 'NanoporeRNASeq'

July 11, 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

Repository Bioconductor 3.19

Date/Publication 2024-07-11

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

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

Contents

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

Index