Package ‘gDNAinRNAseqData’

April 2, 2024

Title RNA-seq data with different levels of gDNA contamination

Version 1.2.0

Description Provides access to BAM files generated from RNA-seq data produced with different levels of gDNA contamination. It currently allows one to download a subset of the data published by Li et al., BMC Genomics, 23:554, 2022. This subset of data is formed by BAM files with about 100,000 alignments with three different levels of gDNA contamination.

Depends R (>= 4.3)
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Suggests BiocStyle, knitr, rmarkdown
VignetteBuilder knitr
License Artistic-2.0
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biocViews ExperimentHub, ExperimentData, ExpressionData,
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URL https://github.com/functionalgenomics/gDNAinRNAseqData

BugReports https://github.com/functionalgenomics/gDNAinRNAseqData

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R topics documented:

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RNA-seq data with different levels of gDNA contamination

Description

This package provides access to RNA-seq BAM files containing different levels of genomic DNA (gDNA) contamination.

Usage

LiYu22subsetBAMfiles(path = tempdir(), offline = FALSE)

LiYu22phenoData(bamfiles)

Arguments

path (Default='tempdir()') Filesystem path where to store the BAM files.
offline (Default='FALSE') If there is no internet connection, but the data has been previously downloaded, setting `offline=TRUE` allows one to retrieve the data from the ExperimentHub cache.
bamfiles full filesystem paths to where the BAM files were downloaded with `LiYu22subsetBAMfiles()`.

Details

Currently, this package allows one to download a subset of the data published in:

The subset of the data accessible through this package corresponds to BAM files containing about 100,000 alignments sampled uniformly at random for the RNA-seq experiments produced from total RNA libraries mixed with different concentrations of gDNA, concretely 0% (no contamination), 1% and 10%; see Fig. 2 from Li et al. (2022).

Value

`LiYu22subsetBAMfiles()` returns a string character vector of filesystem paths to the downloaded BAM files.

`LiYu22phenoData()` returns a `data.frame` object with the gDNA contamination levels for the BAM files specified in the `bamfiles` parameter, according to the publication by Li et al. (2022).
Functions

- `LiYu22subsetBAMfiles()`: downloads the BAM files from the RNA-seq data through the ExperimentHub, and returns the path in the filesystem where the BAM files are stored.
- `LiYu22phenoData()`: retrieves phenotypic data from the BAM files downloaded with `LiYu22subsetBAMfiles()`.

References


Examples

```r
## for LiYu22subsetBAMfiles()
bamfiles <- LiYu22subsetBAMfiles()
bamfiles

## for LiYu22phenoData()
bamfiles <- LiYu22subsetBAMfiles()
LiYu22phenoData(bamfiles)
```
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