

# Package ‘gDNAinRNAseqData’

April 16, 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)

**Imports** RCurl, XML, ExperimentHub, BiocGenerics, Rsamtools

**Suggests** BiocStyle, knitr, rmarkdown

**VignetteBuilder** knitr

**License** Artistic-2.0

**NeedsCompilation** no

**Encoding** UTF-8

**biocViews** ExperimentHub, ExperimentData, ExpressionData, SequencingData, RNASeqData, Homo\_sapiens\_Data

**URL** <https://github.com/functionalgenomics/gDNAinRNAseqData>

**BugReports** <https://github.com/functionalgenomics/gDNAinRNAseqData>

**RoxygenNote** 7.2.3

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gDNAinRNAseqData-package

*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:

Li, X., Zhang, P., and Yu. Y. Gene expressed at low levels raise false discovery rates in RNA samples contaminated with genomic DNA. *BMC Genomics*, 23:554, 2022.

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

Li, X., Zhang, P., and Yu. Y. Gene expressed at low levels raise false discovery rates in RNA samples contaminated with genomic DNA. *BMC Genomics*, 23:554, 2022.

## Examples

```
## for LiYu2subsetBAMfiles()
bamfiles <- LiYu22subsetBAMfiles()
bamfiles
```

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

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