Package: phantasusLite (via r-universe)

July 23, 2024

Type Package

Title Loading and annotation RNA-seq counts matrices

Version 1.3.2

Description PhantasusLite – a lightweight package with helper functions of general interest extracted from phantasus package. In parituclar it simplifies working with public RNA-seq datasets from GEO by providing access to the remote HSDS repository with the precomputed gene counts from ARCHS4 and DEE2 projects.

Depends R (>= 4.2)

Imports data.table, rhdf5client(>= 1.25.1), httr, stringr, stats, utils, Biobase, methods

biocViews GeneExpression, Transcriptomics, RNASeq

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Encoding UTF-8

LazyData true

RoxygenNote 7.3.1

Suggests testthat (>= 3.0.0), knitr, rmarkdown, BiocStyle, rhdf5, GEOquery

VignetteBuilder knitr

Config/testthat/edition 3

URL https://github.com/ctlab/phantasusLite/

BugReports https://github.com/ctlab/phantasusLite/issues

Repository https://bioc.r-universe.dev

RemoteUrl https://github.com/bioc/phantasusLite

RemoteRef HEAD

RemoteSha 3e4299f3be7dbbf90115a3bb0f50e205ebdf5fd6

Contents

`getHSDSFileList` *Returns list of all HDF5-files on HSDS-server*

Description

Returns list of all HDF5-files on HSDS-server

Usage

```
getHSDSFileList(
  url = "https://alserglab.wustl.edu/hsds/?domain=/counts",
  directory = NULL
)
```

Arguments

`url`	containing url of the server and root domain.
`directory`	containing name of the directory

Value

List of all HDF5-files on the server or all files of the collection

Examples

```
url <- 'https://alserglab.wustl.edu/hsds/?domain=/counts'
getHSDSFileList(url)
```

inferCondition *Adds condition to the annotation.*

Description

Adds condition to the annotation.

Usage

```
inferCondition(es)
```

Arguments

es	contains ExpressionSet object

Value

Annotated ExpressionSet with conditions and replicates

Examples

```
ess <- GEOquery::getGEO("GSE143903")
es <- ess[[1]]
es <- inferCondition(es)
es$condition # contains inferred groups
es$replicate # contains inferred replicate numbers
```

loadCountsFromH5FileHSDS *Load count matrix from remote HDF5-file*

Description

Load count matrix from remote HDF5-file

Usage

```
loadCountsFromH5FileHSDS(
  es,
  url = "https://alserglab.wustl.edu/hsds/?domain=/counts",
  file,
  sampleIndexes = NULL
)
```

Arguments

es	containing ExpressionSet loaded from GEO. Contains empty expression matrix.
url	containing url of the server and root domain.
file	containing name of the file (relative to the root domain)
sampleIndexes	containing sample indexes list

Value

ExpressionSet object with loaded count matrix

Examples

```
ess <- GEOquery::getGEO("GSE53053")
es <- ess[[1]]
url <- 'https://alserglab.wustl.edu/hsds/?domain=/counts'
file <- "/dee2/mmusculus_star_matrix_20240409.h5"
es <- loadCountsFromH5FileHSDS(es, url, file)
```

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loadCountsFromHSDS *Load count matrix from HDF5-files.*

Description

Load count matrix from HDF5-files.

Usage

```
loadCountsFromHSDS(
  es,
  url = "https://alserglab.wustl.edu/hsds/?domain=/counts"
)
```

Arguments

es	containing ExpressionSet loaded from GEO. Contains empty expression matrix.
url	containing url of the server and root domain.

Value

ExpressionSet with loaded count matrix

Examples

```
ess <- GEOquery::getGEO("GSE85653")
es <- ess[[1]]
url <- 'https://alserglab.wustl.edu/hsds/?domain=/counts'
es <- loadCountsFromHSDS(es, url)
```

readGct — *Reads ExpressionSet from a GCT file.*

Description

Only versions 1.2 and 1.3 are supported.

Usage

```
readGct(gct)
```

Arguments

gct	Path to gct file

Value

ExpressionSet object

Examples

```
es <- readGct(system.file("extdata/testdata/gct/test.gct", package="phantasusLite"))
```

writeGct — *Saves ExpressionSet to a GCT file (version 1.3).*

Description

Saves ExpressionSet to a GCT file (version 1.3).

Usage

```
writeGct(es, file, gzip = FALSE)
```

Arguments

es	ExpresionSet obeject to save
file	Path to output gct file
gzip	Whether to gzip apply gzip-compression for the output file#'

Value

Result of the closing file (as in ‘close()‘ function‘)

Examples

```
es <- readGct(system.file("extdata/testdata/gct/test.gct", package="phantasusLite"))
out <- tempfile(fileext = ".gct.gz")
writeGct(es, out, gzip=TRUE)
```

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