

Package: phantasmLite (via r-universe)

May 29, 2026

Type Package

Title Loading and annotation RNA-seq counts matrices

Version 1.10.0

Description PhantasmLite – a lightweight package with helper functions of general interest extracted from phantasm package. In particular 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/phantasmLite/>

BugReports <https://github.com/ctlab/phantasmLite/issues>

Config/pak/sysreqs libicu-dev libssl-dev zlib1g-dev

Repository <https://bioc-release.r-universe.dev>

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RemoteUrl <https://github.com/bioc/phantasmLite>

RemoteRef RELEASE_3_23

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getHSDSFileList	<i>Returns list of all HDF5-files on HSDS-server</i>
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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	<i>Adds condition to the annotation.</i>
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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)

```

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	<i>Reads ExpressionSet from a GCT file.</i>
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Description

Only versions 1.2 and 1.3 are supported.

Usage

```
readGct(gct)
```

Arguments

gct	Path to gct file
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Value

ExpressionSet object

Examples

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

writeGct	<i>Saves ExpressionSet to a GCT file (version 1.3).</i>
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Description

Saves ExpressionSet to a GCT file (version 1.3).

Usage

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

Arguments

es	ExpressionSet object 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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