

# Package ‘phantasusLite’

November 22, 2024

**Type** Package

**Title** Loading and annotation RNA-seq counts matrices

**Version** 1.5.0

**Description** PhantasusLite – a lightweight package with helper functions of general interest extracted from phantasus 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

**License** MIT + file LICENSE

**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>

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createH5	<i>Creates metafiles for HDF5-files</i>
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### Description

Creates metafiles for HDF5-files

### Usage

```
createH5(data, file, dataset_name)
```

### Arguments

data	contains metadata
file	contains file name
dataset_name	contains dataset name

**Value**

Returns NULL

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createIndexH5	<i>Writes indexes to the file</i>
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**Description**

Writes indexes to the file

**Usage**

```
createIndexH5(data, file)
```

**Arguments**

data	contains metadata
file	contains the file name

**Value**

Returns NULL

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createIndexH5Remote	<i>Creates HDF5-file with indexes</i>
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**Description**

Creates HDF5-file with indexes

**Usage**

```
createIndexH5Remote(  
  url,  
  collections = c("archs4", "dee2"),  
  destfile = "index.h5"  
)
```

**Arguments**

url	contains URL to the root of counts files
collections	vector of collection names to process
destfile	where to put resulting index file

**Value**

Returns NULL

---

createMetaH5	<i>Converts collection meta.txt files to meta.h5, putting them to the respective collection folders</i>
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---

**Description**

Converts collection meta.txt files to meta.h5, putting them to the respective collection folders

**Usage**

```
createMetaH5(counts_dir)
```

**Arguments**

counts_dir	contains directory name
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**Value**

Returns NULL

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createPriorityH5	<i>Creates HDF5-File with priority</i>
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**Description**

Creates HDF5-File with priority

**Usage**

```
createPriorityH5(counts_dir, force = FALSE, verbose = FALSE)
```

**Arguments**

counts_dir	contains counts directory
force	logical value which lets function replace existing priority file
verbose	logical value which determines a content of the output.

**Value**

Returns NULL

---

getCountsMetaPart	<i>Gets list with metadata</i>
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**Description**

Gets list with metadata

**Usage**

```
getCountsMetaPart(counts_dir, collection_name, verbose)
```

**Arguments**

counts_dir	contains counts directory
collection_name	contains name of the collection
verbose	logical value which determines a content of the output.

**Value**

list with metadata

---

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)
```

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getIndexRemote	<i>Creates a data table with indexes and chunks of samples in remote HDF5-files</i>
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---

**Description**

Creates a data table with indexes and chunks of samples in remote HDF5-files

**Usage**

```
getIndexRemote(url, collections)
```

**Arguments**

url	contains url to the root of counts files
collections	contains names of the collections

**Value**

table with samples, indexes and chunks in all HDF5-files

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gsmToChunk	<i>Gets chunk from GSE identifiers.</i>
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**Description**

Gets chunk from GSE identifiers.

**Usage**

```
gsmToChunk(samples)
```

**Arguments**

samples	containing a list of samples
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**Value**

list of chunks

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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
```

---

inferConditionImpl	<i>Creates condition from the samples titles</i>
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**Description**

Creates condition from the samples titles

**Usage**

```
inferConditionImpl(gse_titles)
```

**Arguments**

gse\_titles            contains titles

**Value**

List of conditions and replicates

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`loadCountsFromH5FileHSDS`*Load count matrix from remote HDF5-file*

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**Description**

Load count matrix from remote HDF5-file

**Usage**

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

**Arguments**

<code>es</code>	containing ExpressionSet loaded from GEO. Contains empty expression matrix.
<code>url</code>	containing url of the server and root domain.
<code>file</code>	containing name of the file (relative to the root domain)
<code>sampleIndexes</code>	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)
```

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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

**Value**

ExpressionSet object

**Examples**

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

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removeRepeatWords	<i>Removes repeated words from conditions</i>
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**Description**

Removes repeated words from conditions

**Usage**

```
removeRepeatWords(titles)
```

**Arguments**

titles	contains titles
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**Value**

titles without repeated words

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updateARCHS4meta	<i>Creates meta.txt file, which describes typical archs4 and archs4Zoo files.</i>
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---

**Description**

Creates meta.txt file, which describes typical archs4 and archs4Zoo files.

**Usage**

```
updateARCHS4meta(  
  archDir = file.path(getOption("phantasusCacheDir"), "counts/archs4")  
)
```

**Arguments**

archDir	path to directory with arch4 .h5 files.
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**Value**

Returns NULL

---

updateDEE2meta	<i>Creates meta.txt file, which describes typical dee2 files.</i>
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---

**Description**

Creates meta.txt file, which describes typical dee2 files.

**Usage**

```
updateDEE2meta(  
  destDir = file.path(getOption("phantasusCacheDir"), "counts/dee2")  
)
```

**Arguments**

destDir            path to directory with DEE2 .h5 files.

**Value**

Returns NULL

---

updateIndexH5	<i>Updates indexes from HDF5-files</i>
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---

**Description**

Updates indexes from HDF5-files

**Usage**

```
updateIndexH5(counts_dir, force = FALSE, verbose = FALSE)
```

**Arguments**

counts\_dir        contains counts directory  
force             logical value which lets function replace existing index file  
verbose          logical value which determines a content of the output.

**Value**

Returns NULL

---

validateCountsCollection  
*Validates counts collection*

---

**Description**

Validates counts collection

**Usage**

```
validateCountsCollection(collectionDir, verbose = FALSE)
```

**Arguments**

collectionDir contains directory name  
verbose logical value which determines a content of the output.

**Value**

false if collection is not valid

---

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 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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