

# Package ‘phantasusLite’

June 30, 2025

**Type** Package

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

**Version** 1.6.0

**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>

**git\_url** <https://git.bioconductor.org/packages/phantasusLite>

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|          |                                         |
|----------|-----------------------------------------|
| createH5 | <i>Creates metafiles for HDF5-files</i> |
|----------|-----------------------------------------|

---

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

---

|               |                                   |
|---------------|-----------------------------------|
| createIndexH5 | <i>Writes indexes to the file</i> |
|---------------|-----------------------------------|

---

**Description**

Writes indexes to the file

**Usage**

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

**Arguments**

|      |                        |
|------|------------------------|
| data | contains metadata      |
| file | contains the file name |

**Value**

Returns NULL

---

|                     |                                       |
|---------------------|---------------------------------------|
| createIndexH5Remote | <i>Creates HDF5-file with indexes</i> |
|---------------------|---------------------------------------|

---

**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> |
|--------------|---------------------------------------------------------------------------------------------------------|

---

**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 |
|------------|-------------------------|

**Value**

Returns NULL

---

|                  |                                        |
|------------------|----------------------------------------|
| createPriorityH5 | <i>Creates HDF5-File with priority</i> |
|------------------|----------------------------------------|

---

**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> |
|-------------------|--------------------------------|

---

**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> |
|-----------------|------------------------------------------------------|

---

**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)
```

---

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

---

**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

---

|            |                                         |
|------------|-----------------------------------------|
| gsmToChunk | <i>Gets chunk from GSE identifiers.</i> |
|------------|-----------------------------------------|

---

**Description**

Gets chunk from GSE identifiers.

**Usage**

```
gsmToChunk(samples)
```

**Arguments**

|         |                              |
|---------|------------------------------|
| samples | containing a list of samples |
|---------|------------------------------|

**Value**

list of chunks

---

|                |                                          |
|----------------|------------------------------------------|
| inferCondition | <i>Adds condition to the annotation.</i> |
|----------------|------------------------------------------|

---

**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> |
|--------------------|--------------------------------------------------|

---

**Description**

Creates condition from the samples titles

**Usage**

```
inferConditionImpl(gse_titles)
```

**Arguments**

|            |                 |
|------------|-----------------|
| gse_titles | contains titles |
|------------|-----------------|

**Value**

List of conditions and replicates

---

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> |
|---------|---------------------------------------------|

---

**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"))
```

---

|                   |                                               |
|-------------------|-----------------------------------------------|
| removeRepeatWords | <i>Removes repeated words from conditions</i> |
|-------------------|-----------------------------------------------|

---

**Description**

Removes repeated words from conditions

**Usage**

```
removeRepeatWords(titles)
```

**Arguments**

titles            contains titles

**Value**

titles without repeated words

---

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

---

**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.

**Value**

Returns NULL

---

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

---

**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> |
|---------------|----------------------------------------|

---

**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 | <i>Validates counts collection</i> |
|--------------------------|------------------------------------|

---

**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 | <i>Saves ExpressionSet to a GCT file (version 1.3).</i> |
|----------|---------------------------------------------------------|

---

**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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