

# Package ‘phantasus’

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**Title** Visual and interactive gene expression analysis

**Version** 1.24.0

**Description** Phantasus is a web-application for visual and interactive gene expression analysis. Phantasus is based on Morpheus – a web-based software for heatmap visualisation and analysis, which was integrated with an R environment via OpenCPU API. Aside from basic visualization and filtering methods, R-based methods such as k-means clustering, principal component analysis or differential expression analysis with limma package are supported.

**URL** <https://alserglab.wustl.edu/phantasus>

**BugReports** <https://github.com/ctlab/phantasus/issues>

**Depends** R (>= 4.3)

**biocViews** GeneExpression, GUI, Visualization, DataRepresentation, Transcriptomics, RNASeq, Microarray, Normalization, Clustering, DifferentialExpression, PrincipalComponent, ImmunoOncology

**Imports** ggplot2, protolite, Biobase, GEOquery, Rook, htmltools, httpuv, jsonlite, limma, edgeR, opencpu, assertthat, methods, httr, rhdf5, utils, parallel, stringr, fgsea (>= 1.9.4), svglite, gtable, stats, Matrix, pheatmap, scales, ccaPP, grid, grDevices, AnnotationDbi, DESeq2, data.table, curl, config (>= 0.3.2), rhdf5client (>= 1.25.1), yaml, fs, phantasusLite, XML

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adjustDataset	<i>Adjust dataset</i>
---------------	-----------------------

---

### Description

Adjust dataset

### Usage

```
adjustDataset(
  es,
  scaleColumnSum = NULL,
  log2 = FALSE,
  onePlusLog2 = FALSE,
  inverseLog2 = FALSE,
  quantileNormalize = FALSE,
  zScore = FALSE,
  robustZScore = FALSE,
  sweep = NULL
)
```

### Arguments

es	Expression set to perform adjustment on
scaleColumnSum	perform sum scaling of columns (default FALSE)
log2	perform logarithm2 adjustment (default FALSE)
onePlusLog2	perform log2(1+x) adjustment (default FALSE)
inverseLog2	perform 2 <sup>x</sup> adjustment (default FALSE)
quantileNormalize	perform quantile normalization (default FALSE)
zScore	perform zScore adjustment: subtract mean, divide by std (default FALSE)
robustZScore	perform robustZScore adjustment: subtract median, divide by MAD (default FALSE)
sweep	perform sweep adjustment on rows/columns (default FALSE)

**Value**

Nothing. Adjusted dataset will be assigned as ES in global environment

**Examples**

```
## Not run:  
es <- gseGSE('GSE53986')[[1]]  
adjustDataset(es, log2 = T, quantileNormalize = T)  
  
## End(Not run)
```

---

annotationDBMeta	<i>Create meta file for AnnotationDB</i>
------------------	--

---

**Description**

annotationDBMeta function creates txt files containing meta information of provided sqlite files for AnnotationDB.

**Usage**

```
annotationDBMeta(annotDir)
```

**Arguments**

annotDir            path to folder with annotationDB sqlite files

**Value**

nothing

**Examples**

```
## Not run:  
annotationDBMeta('/var/phantasus/cache')  
  
## End(Not run)
```

---

calcPCA                      *Principal Component Analysis.*

---

**Description**

calcPCA calculates PCA-matrix for the given ExpressionSet and returns this matrix encoded to JSON.

**Usage**

```
calcPCA(es, replacena = "mean")
```

**Arguments**

es                      an ExpressionSet object, should be normalized  
replacena              method for replacing NA values (mean by default)

**Value**

json with full description of the plot for plotly.js

**Examples**

```
## Not run:  
data(es)  
calcPCA(es)  
  
## End(Not run)
```

---

calculatedAnnotation    *Create calculated annotation*

---

**Description**

calculatedAnnotation adds a column calculated by operation

**Usage**

```
calculatedAnnotation(  
  es,  
  operation,  
  rows = c(),  
  columns = c(),  
  isColumns = FALSE,  
  name = NULL  
)
```

**Arguments**

es	ExpressionSet object.
operation	Name of the operation to perform calculation
rows	List of specified rows' indices (optional), indices start from 0
columns	List of specified columns' indices (optional), indices start from 0#'
isColumns	Apply fn to columns
name	Name of the new annotation

**Value**

Nothing. Annotated dataset will be assigned to es in environment

---

checkGPLsFallback      *Check possible annotations for GEO Dataset.*

---

**Description**

checkGPLs returns GPL-names for the specified GEO identifier.

**Usage**

```
checkGPLsFallback(name)
```

**Arguments**

name	String, containing GEO identifier of the dataset.
------	---

**Value**

Vector of filenames serialized in JSON format. If there is only one GPL for that dataset, the function will return name.

**Examples**

```
## Not run:  
checkGPLs('GSE27112')  
checkGPLs('GSE14308')  
  
## End(Not run)
```

---

checkGSEType	<i>Checks GSE to be supported</i>
--------------	-----------------------------------

---

**Description**

Checks GSE to be supported

**Usage**

```
checkGSEType(name, destDir, combine = any)
```

**Arguments**

name	GSE id, with optional GPL specification
destDir	path to cache directory
combine	function on how to combine results, when multiple platforms are present

**Value**

logical vector if the dataset is supported or not

---

collapseDataset	<i>Collapse dataset</i>
-----------------	-------------------------

---

**Description**

collapseDataset performs a collapse action on expression set

**Usage**

```
collapseDataset(
  es,
  isRows = TRUE,
  selectOne = FALSE,
  fn,
  fields,
  removeEmpty = TRUE
)
```

**Arguments**

es	Expression set
isRows	Work with rows. False if columns (default True - row mode)
selectOne	select best match or merge duplicates
fn	select/merge function
fields	fields to unique on
removeEmpty	remove unannotated genes

**Value**

Nothing. Collapsed dataset will be assigned to es in environment

**Examples**

```
## Not run:
es <- getGSE('GSE53986')[[1]]
collapseDataset(es, isRows = TRUE, selectOne = TRUE,
fn = mean, fields = c('Gene ID', 'Gene symbol'))

## End(Not run)
```

---

colMeansByGroups	<i>Calculate column averages in row groups</i>
------------------	--

---

**Description**

Calculate column averages in row groups

**Usage**

```
colMeansByGroups(m, groups)
```

**Arguments**

m	matrix n x m
groups	vector of size n of numbers from 1 to k

**Value**

matrix k\*m of column averages by groups

---

convertByAnnotationDB	<i>Map indexes using Annotation DB</i>
-----------------------	--

---

**Description**

convertByAnnotationDB function returns keyType ids from dbName mapped to columnName in es.



**Usage**

```

convertByAnnotationDB(
  es,
  dbName,
  columnName,
  columnType,
  keyType,
  otherOptions
)

```

**Arguments**

es	source ExpressionSet
dbName	name of AnnotationDB file
columnName	name of column in featureData of source ExpressionSet
columnType	Type of indexes in columnName
keyType	Type of mapped indexes
otherOptions	additional parameters for conversion. Currently only named boolean delete-DotVersion is not ignored.

**Value**

JSON object with a vector of converted IDs

---

createDockerConf	<i>Creates default docker conf file Function creates default docker user configuration file based on provided setup_file or on default parameters if setup_file doesn't exist. If user_conf_file exists function does nothing.</i>
------------------	--

---

**Description**

Creates default docker conf file Function creates default docker user configuration file based on provided setup\_file or on default parameters if setup\_file doesn't exist. If user\_conf\_file exists function does nothing.

**Usage**

```

createDockerConf(
  setup_file = confFile("setup.yml"),
  user_conf_file = confFile("user.conf")
)

```

**Arguments**

setup\_file      name of config from file. If unset or not existed, "default".  
 user\_conf\_file Location of the setup.yml file with setup parameters. If not existed use file from package

---

createES	<i>Create ExpressionSet.</i>
----------	------------------------------

---

**Description**

createES function produces an ExpressionSet object from given data, and exports it to global scope.

**Usage**

```
createES(data, pData, varLabels, fData, fvarLabels, eData)
```

**Arguments**

data            Gene expression matrix.  
 pData         Matrix with phenotypical data.  
 varLabels     Names of phenoData columns.  
 fData         Matrix with feature data.  
 fvarLabels    Names of featureData columns.  
 eData         List with experimentData

**Value**

produced ExpressionSet object

**Examples**

```
## Not run:
data <- matrix(1:15, 5, 3)
pData <- c("A", "B", "C")
varLabels <- "cat"
fData <- c("p", "r", "s", "t", "u")
fvarLabels <- "id"
eData <- list(name="", lab="", contact="", title="", url="", other=list(), pubMedIds="")
createES(data, pData, varLabels, fData, fvarLabels, eData)

## End(Not run)
```

---

es	<i>Example dataset</i>
----	------------------------

---

**Description**

Small slice from GSE27112-GPL6103 for runnable examples.

**Usage**

```
data(es)
```

**Format**

An object of class ExpressionSet with 20 rows and 5 columns.

**Examples**

```
## Not run:  
data(es)  
performKmeans(es, k = 2)  
  
## End(Not run)
```

---

fgseaExample	<i>Example pathway data.frame for fgsea tool</i>
--------------	--

---

**Description**

Example pathway data.frame for fgsea tool

---

generatePreloadedSession	<i>Generate files for preloaded session from a session link.</i>
--------------------------	--

---

**Description**

Generate files for preloaded session from a session link.

**Usage**

```
generatePreloadedSession(sessionURL, preloadedName, preloadedDir)
```

**Arguments**

sessionURL      String with session link produced by phantasus.  
 preloadedName   String with name that should be assigned to the session.  
 preloadedDir    Path to the directory with preloaded datasets and sessions.

**Value**

Function produces two files (preloadedName.rda with ExpressionSet and preloadedName.json with session features) in preloadedDir folder.

**Examples**

```
## Not run:
sessionURL <- "https://ctlab.itmo.ru/phantasus/?session=x063c1b365b9211" # link from 'Get dataset link...' tool in
newName <- "my_session" # user defined name
preloadedDir <- "../preloaded" # directory where files will be stored. In order too get access through phantasus web-
dir.create(preloadedDir, showWarnings = FALSE)
generatePreloadedSession(sessionURL= sessionURL,
                          preloadedName = newName,
                          preloadedDir = preloadedDir)

servePhantasus(preloadedDir=preloadedDir, openInBrowser=FALSE)
# open browser manually at http://0.0.0.0:8000/phantasus/index.html?preloaded=my_session

## End(Not run)
```

---

<code>getArchs4Files</code>	<i>Returns list of ARCHS4 hdf5 files with expression data</i>
-----------------------------	---

---

**Description**

Returns list of ARCHS4 hdf5 files with expression data

**Usage**

```
getArchs4Files(cacheDir)
```

**Arguments**

cacheDir          base directory for cache

**Value**

list of .h5 files

---

getCountsMetaPart	<i>Create meta-data for single counts collection</i>
-------------------	--

---

**Description**

Creates a part of counts collections meta-data

**Usage**

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

**Arguments**

counts_dir	path to directory with count collections
collection_name	name of collection and collection's directory
verbose	logical value which determines a content of the output.

**Details**

Function assumes that collection\_name contains meta.txt which is valid (in sense of [validateCountsCollection](#)). For each row in meta.txt function reads specified sample\_id dataset and writes every sample id to the resulting data.table with source file name and collection name.

**Value**

data.table with meta-data or nothing if destdir does not exist or does not contain files.

**See Also**

[validateCountsCollection](#), [getCountsMetaPart](#)

**Examples**

```
## Not run:
collDir <- "/path/to/my/collection"
valid_collection = validateCountsCollection(collectionDir = collDir, verbose = TRUE)
if (valid_collection){
  metaPart = getCountsMetaPart(destdir = collDir, verbose = TRUE)
}

## End(Not run)
```

---

`getES`*Load ExpressionSet by GEO identifier*

---

### Description

`getES` return the ExpressionSet object(s) corresponding to GEO identifier.

### Usage

```
getES(  
  name,  
  type = NA,  
  destdir = getPhantasusConf("cache_folders")$geo_path,  
  mirrorPath = getPhantasusConf("geo_mirrors")  
)
```

### Arguments

<code>name</code>	String, containing GEO identifier of the dataset. It should start with 'GSE' or 'GDS' and can include exact GPL to annotate dataset, separated with dash ('-') from the identifier.
<code>type</code>	Type of the dataset: 'GSE' or 'GDS'. If not specified, the function will take first three letters of name variable as type.
<code>destdir</code>	Directory for caching loaded Series and GPL files from GEO database.
<code>mirrorPath</code>	URL string which specifies the source of matrices.

### Value

List of ExpressionSet objects, that were available by given in name variable GEO identifier.

### Examples

```
## Not run:  
  getES('GSE14308', type = 'GSE', destdir = 'cache')  
  getES('GSE27112')  
  getES('GDS4922')  
  
## End(Not run)
```

---

`getGDS`*Load ExpressionSet from GEO Datasets*

---

**Description**

`getGDS` return the ExpressionSet object corresponding to GEO Dataset identifier.

**Usage**

```
getGDS(  
  name,  
  destdir = getPhantasusConf("cache_folders")$geo_path,  
  mirrorPath = getPhantasusConf("geo_mirrors")  
)
```

**Arguments**

<code>name</code>	String, containing GEO identifier of the dataset. It should start with 'GSE' or 'GDS' and can include exact GPL to annotate dataset, separated with dash ('-') from the identifier.
<code>destdir</code>	Directory for caching loaded Series and GPL files from GEO database.
<code>mirrorPath</code>	URL string which specifies the source of matrices.

**Value**

ExpressionSet object wrapped in list, that was available by given in name variable GEO identifier.

**Examples**

```
## Not run:  
  getGDS('GDS4922', destdir = tempdir(), mirrorPath = "https://ftp.ncbi.nlm.nih.gov")  
## End(Not run)
```

---

`getGSE`*Load ExpressionSet from GEO Series*

---

**Description**

`getGSE` return the ExpressionSet object(s) corresponding to GEO Series Identifier.

**Usage**

```
getGSE(
  name,
  destdir = getPhantasusConf("cache_folders")$geo_path,
  mirrorPath = getPhantasusConf("geo_mirrors")
)
```

**Arguments**

name	String, containing GEO identifier of the dataset. It should start with 'GSE' or 'GDS' and can include exact GPL to annotate dataset, separated with dash ('-') from the identifier.
destdir	Directory for caching loaded Series and GPL files from GEO database.
mirrorPath	URL string which specifies the source of matrices.

**Value**

List of ExpressionSet objects, that were available by given in name variable GEO identifier.

**Examples**

```
## Not run:
  getGSE('GSE14308', destdir = 'cache')
  getGSE('GSE27112')
  getGSE('GSE53986')

## End(Not run)
```

---

getPhantasusConf	<i>Read Phantasus Config</i>
------------------	------------------------------

---

**Description**

Read Phantasus Config

**Usage**

```
getPhantasusConf(
  value = NULL,
  configName = Sys.getenv("R_CONFIG_ACTIVE"),
  file = file.path(tools::R_user_dir(package = "phantasus", which = "config"),
    "user.conf")
)
```



**Arguments**

value	Value to retrieve from the config file.
configName	R_CONFIG_ACTIVE value. If unset, "default".
file	Location of the config file

---

gseaPlot	<i>Returns path to an svg file with enrichment plot</i>
----------	---

---

**Description**

Returns path to an svg file with enrichment plot

**Usage**

```
gseaPlot(
  es,
  rankBy,
  selectedGenes,
  width,
  height,
  vertical = FALSE,
  addHeatmap = FALSE,
  showAnnotation = NULL,
  annotationColors = NULL,
  pallete = c("blue", "white", "red")
)
```

**Arguments**

es	ExpressionSet object.
rankBy	name of the numeric column used for gene ranking
selectedGenes	indexes of selected genes (starting from one, in the order of fData)
width	width of the image (in inches)
height	height of the image (in inches)
vertical	whether to use vertical orientation (default: FALSE)
addHeatmap	whether to add an expression heatmap, sorted by rankBy (default: FALSE)
showAnnotation	a name of column annotation to add to the heatmap, default: NULL (no annotation)
annotationColors	a list of colors to use in annotation
pallete	a vector of colors to draw heatmap

**Value**

path to an svg file

---

isHSDS	<i>check if url responding as HSDS server TRUE - hsdS FALSE - web link but not working NULL - not web link</i>
--------	--

---

**Description**

check if url responding as HSDS server TRUE - hsdS FALSE - web link but not working NULL - not web link

**Usage**

```
isHSDS(url)
```

**Arguments**

url	URL to check
-----	--------------

---

limmaAnalysis	<i>Differential Expression analysis.</i>
---------------	--

---

**Description**

limmaAnalysis performs differential expression analysis from limma package and returns a ProtoBuf-serialized resulting de-matrix.

**Usage**

```
limmaAnalysis(
  es,
  fieldValues,
  version = "One-factor design",
  contrast = list("Comparison", "Target", "Reference"),
  designData = NULL
)
```

**Arguments**

es	ExpressionSet object. It should be normalized for more accurate analysis.
fieldValues	Vector of comparison values, mapping categories' names to columns/samples
version	name of the limma analysis implementation. Should be "One-factor design" or "Advanced design"
contrast	a character vector with exactly three elements: the name of a factor in the design formula, the name of the numerator level for the fold change, and the name of the denominator level for the fold change
designData	data.frame with design matrix

**Value**

Name of the file containing serialized de-matrix.

**Examples**

```
## Not run:
data(es)
limmaAnalysis(es, fieldValues = c("A", "A", "A", "B", "B"))

## End(Not run)
```

---

loadCounts	<i>Loads expression data from .h5 count files. Only samples with counted expression are kept. If es already contains expression data it is returned as is.</i>
------------	--

---

**Description**

Loads expression data from .h5 count files. Only samples with counted expression are kept. If es already contains expression data it is returned as is.

**Usage**

```
loadCounts(es, counts_dir)
```

**Arguments**

es	ExpressionSet from GEO to check for expression in ARCHS4/dee2 or other h5 files
counts_dir	directory with .h5 files collections. There must be meta.rda file in counts_dir and each collection's sub directory must have meta.txt file with description. Also counts_dir must contain counts_priority.txt file.

**Value**

either original es or an ExpressionSet with loaded count data from ARCHS4

---

loadFromARCHS4	<i>Loads expression data from ARCHS4 count files. Only samples with counted expression are kept. If es already contains expression data it is returned as is.</i>
----------------	---

---

### Description

Loads expression data from ARCHS4 count files. Only samples with counted expression are kept. If es already contains expression data it is returned as is.

### Usage

```
loadFromARCHS4(es, archs4_files)
```

### Arguments

es	ExpressionSet from GEO to check for expression in ARCHS4
archs4_files	list of available .h5 files from ARCHS4 project

### Value

either original es or an ExpressionSet with loaded count data from ARCHS4

---

loadGEO	<i>Load GEO Dataset.</i>
---------	--------------------------

---

### Description

loadGEO returns the file with serialized ExpressionSet using ProtoBuf, parsed from data downloaded from GEO by identifier.

### Usage

```
loadGEO(name, type = NA)
```

### Arguments

name	String, containing GEO identifier of the dataset. It should start with 'GSE' or 'GDS' and can include exact GPL to annotate dataset, separated with dash ('-') from the identifier.
type	Type of the dataset: 'GSE' or 'GDS'. If not specified, the function will take first three letters of name variable as type.

**Value**

File with ProtoBuf-serialized ExpressionSet-s that were downloaded by this identifier. For GSE-datasets there can be multiple annotations, so in file will be a list mapping name with GPL to ExpressionSet.

**Examples**

```
## Not run:
  loadGEO("GSE27112")
  loadGEO("GDS4922")

## End(Not run)
```

---

loadPreloaded	<i>Load GEO Dataset.</i>
---------------	--------------------------

---

**Description**

loadPreloaded returns the file with serialized ExpressionSets using ProtoBuf, that were preloaded on server.

**Usage**

```
loadPreloaded(name)
```

**Arguments**

name                   String, containing filename. Assuming that in the directory with preloaded files preloadedDir exists file filename.rda with list of ExpressionSets ess.

**Value**

File with ProtoBuf-serialized ExpressionSet-s that were loaded from specified file.

---

performKmeans	<i>K-means clusterisation.</i>
---------------	--------------------------------

---

**Description**

performKmeans returns a vector of corresponding clusters for each gene from a given Expression-Set.

**Usage**

```
performKmeans(es, k, replacena = "mean")
```

**Arguments**

es	ExpressionSet object.
k	Expected number of clusters.
replacena	Method for replacing NA values in series matrix (mean by default)

**Value**

Vector of corresponding clusters, serialized to JSON.

**Examples**

```
## Not run:  
data(es)  
performKmeans(es, k = 2)  
  
## End(Not run)
```

---

queryAnnotationDBMeta *Get meta list for annotationDB files*

---

**Description**

queryAnnotationDBMeta Function reads txt meta files for provided sqlite annotation databases.

**Usage**

```
queryAnnotationDBMeta()
```

**Value**

meta info in JSON

**Examples**

```
## Not run:  
queryAnnotationDBMeta()  
  
## End(Not run)
```

---

read.gct	<i>Reads ExpressionSet from a GCT file.</i>
----------	---

---

**Description**

Only versions 1.2 and 1.3 are supported.

**Usage**

```
read.gct(gct, ...)
```

**Arguments**

gct	Path to gct file
...	additional options for read.csv

**Value**

ExpressionSet object

**Examples**

```
read.gct(system.file("extdata", "centers.gct", package = "phantasus"))
```

---

reparseCachedESs	<i>Reparse cached expression sets from GEO.</i>
------------------	---

---

**Description**

The function should be used on phantasus version updates that change behavior of loading datasets from GEO. It finds all the datasets that were cached and runs 'getES' for them again. The function uses cached Series and other files from GEO.

**Usage**

```
reparseCachedESs(destdir, mirrorPath = getPhantasusConf("geo_mirrors"))
```

**Arguments**

destdir	Directory used for caching loaded Series files from GEO database.
mirrorPath	URL string which specifies the source of matrices.

**Value**

vector of previously cached GSE IDs

**Examples**

```
reparseCachedESs(destdir=tempdir(), "https://ftp.ncbi.nlm.nih.gov")
```

---

reproduceInR	<i>Reproduce session in R code</i>
--------------	------------------------------------

---

**Description**

Reproduce session in R code

**Usage**

```
reproduceInR(sessionName, leaf = T, step = 0, savedEnv = new.env())
```

**Arguments**

sessionName	String, OCPU session name
leaf	Boolean, is it leaf (default = F)
step	Integer, step of recursion (default = 0)
savedEnv	Environment, where to store complex arguments (default = new.env())

**Value**

JSON with R code

**Examples**

```
## Not run:  
  setwd(tempdir())  
  reproduceInR('x039f1672026678');  
  
## End(Not run)
```



---

servePhantasia	<i>Serve phantasia.</i>
----------------	-------------------------

---

### Description

servePhantasia starts http server handling phantasia static files and opencpu server.

### Usage

```
servePhantasia(  
  host = getPhantasiaConf("host"),  
  port = getPhantasiaConf("port"),  
  staticRoot = getPhantasiaConf("static_root"),  
  preloadedDir = getPhantasiaConf("preloaded_dir"),  
  openInBrowser = TRUE,  
  quiet = TRUE  
)
```

### Arguments

host	Host to listen.
port	Port to listen.
staticRoot	Path to static files with phantasia.js (on local file system).
preloadedDir	Full path to directory with preloaded files.
openInBrowser	Boolean value which states if application will be automatically loaded in default browser.
quiet	Boolean value which states whether the connection log should be hidden (default: TRUE)

### Value

Running instance of phantasia application.

### Examples

```
## Not run:  
servePhantasia()  
  
## End(Not run)
```

---

setupPhantasmus	<i>Setup phantasmus. Read user config file ( or create default one) and fill cache_root using sources in file.</i>
-----------------	--

---

**Description**

Setup phantasmus. Read user config file ( or create default one) and fill cache\_root using sources in file.

**Usage**

```
setupPhantasmus(setup_name = "default", file = confFile("setup.yml"))
```

**Arguments**

setup_name	name of config from file. If unset or not existed, "default".
file	Location of the setup.yml file with setup parameters. If not existed use file from package

---

shinyGAMAnalysis	<i>Constructs data frame with gene annotations and submits it into Shiny GAM web-server</i>
------------------	---

---

**Description**

Constructs data frame with gene annotations and submits it into Shiny GAM web-server

**Usage**

```
shinyGAMAnalysis(es)
```

**Arguments**

es	Expression set object
----	-----------------------

**Value**

URL for Shiny GAM

---

subsetES	<i>Subsets es, if rows or columns are not specified, all are retained</i>
----------	---

---

**Description**

Subsets es, if rows or columns are not specified, all are retained

**Usage**

```
subsetES(es, columns = c(), rows = c())
```

**Arguments**

es	ExpressionSet object.#'
columns	List of specified columns' indices (optional), indices start from 0#'
rows	List of specified rows' indices (optional), indices start from 0

**Value**

new expression set 'es'

---

updateARCHS4	<i>Update archs4 files.</i>
--------------	-----------------------------

---

**Description**

Download archs4 or archs4zoo counts in cacheDir. If directory does not exists function makes nothing and produce corresponding warnings.

**Usage**

```
updateARCHS4(
  cacheDir = file.path(getPhantasusConf("cache_folders")$rnaseq_counts, "archs4"),
  organism = c("all"),
  force = FALSE
)
```

**Arguments**

cacheDir	file path to <b>archs4</b> cache directory
organism	vector which determines organisms to download: human, mouse, zoo or all as default. Also can be a genus. Possible genus: <ol style="list-style-type: none"> <li>1. drosophila</li> <li>2. gallus</li> </ol>

	3. bos
	4. caenorhabditis
	5. danio
	6. rattus
	7. saccharomyces
	8. arabidopsis
force	logical value which let function replace current files

---

updateARCHS4meta	<i>Update ARCHS4 meta files</i>
------------------	---------------------------------

---

## Description

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

## Usage

```
updateARCHS4meta(
  archDir = file.path(getPhantasusConf("cache_folders")$rnaseq_counts, "archs4")
)
```

## Arguments

archDir            path to directory with arch4 .h5 files.

## Details

This function produces very specific "hardcoded" meta.txt file for arch4 and archs4ZOO counts collections. See [validateCountsCollection](#) for more common information and meta.txt file structure

## See Also

[validateCountsCollection](#)

---

updateCountsMeta	<i>Update meta-data for counts collections</i>
------------------	--

---

### Description

Creates meta.rda file which contain information about all samples in all collections. Also function checks priority.txt file. This file is used to manage collections with the same samples.

### Usage

```
updateCountsMeta(  
  counts_dir = getPhantasiaConf("cache_folders")$rnaseq_counts,  
  force = FALSE,  
  verbose = FALSE  
)
```

### Arguments

counts_dir	path to counts cache directory
force	logical value wich lets function replace existing meta.rda file
verbose	logical value which determines a content of the output.

### Details

First of all function checks validity of priority.txt file. **Every** Collection should have **unique** priority. If priority.txt is not valid function creates new one, setting priorities for each subdirectory(=collection) equal to order in list.dir output.

Function updates meta.rda if this file is older than at least one .h5 file in counts files. meta.rda is data.table which is a result of union data.tables produced by [getCountsMetaPart](#) for each collection

### See Also

[validateCountsCollection](#), [updateCountsMeta](#) @import data.table

---

updateDEE2meta	<i>Update DEE2 meta files</i>
----------------	-------------------------------

---

### Description

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

**Usage**

```
updateDEE2meta(
  destDir = file.path(getPhantasusConf("cache_folders")$rnaseq_counts, "dee2")
)
```

**Arguments**

destDir            path to directory with DEE2 .h5 files.

**Details**

This function produces very specific "hardcoded" meta.txt file for dee2 counts collection. See [validateCountsCollection](#) for more common information and meta.txt file structure

**See Also**

[validateCountsCollection](#)

---

validateCountsCollection

*Check a counts collection*

---

**Description**

Function checks existing and structure of meta.txt file in specified counts folder. Also it checks accessibility of specified datasets in corresponding .h5 files.

**Usage**

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

**Arguments**

collectionDir    path to directory with collection  
 verbose            logical value which determines a content of the output.

**Details**

collectionDir should contain a bunch of .h5 files and a single meta.txt. meta.txt is .tsv-like file where for each .h5 exists a row with columns:

**file\_name** name of .h5 file in collectionDir.

**sample\_id** name of dataset in file\_name which contains sample IDs (sample\_geo\_accession for example).

**sample\_dim** which dimension of the expression matrix in file\_name corresponds to samples. Should be one of c("rows", "columns")

**gene\_id** name of dataset in `file_name` which contains ids for genes and the "meaning" for that ids( column name in result ES). For correct work this dataset should contain unique values.  
Example: ENSEMBLID:/meta/genes/ensembl\_gene\_id

**genes\_annot** Names of datasets and their meanings to extract gene-related metadata from `file_name`.  
Can be empty or `gene_id`-like values separated with semicolon(;).

---

write.gct                      *Saves ExpressionSet to a GCT file (version 1.3).*

---

### Description

Saves ExpressionSet to a GCT file (version 1.3).

### Usage

```
write.gct(es, file, gzip = FALSE)
```

### Arguments

<code>es</code>	ExpressionSet object to save
<code>file</code>	Path to output gct file
<code>gzip</code>	Whether to gzip apply gzip-compression for the output file#'

### Value

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

### Examples

```
es <- read.gct(system.file("extdata", "centers.gct", package = "phantasus"))
out <- tempfile(fileext = ".gct.gz")
write.gct(es, out, gzip=TRUE)
```

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