

# Package ‘glmSparseNet’

January 27, 2025

**Type** Package

**Title** Network Centrality Metrics for Elastic-Net Regularized Models

**Version** 1.24.0

**Description** glmSparseNet is an R-package that generalizes sparse regression models when the features (e.g. genes) have a graph structure (e.g. protein-protein interactions), by including network-based regularizers. glmSparseNet uses the glmnet R-package, by including centrality measures of the network as penalty weights in the regularization. The current version implements regularization based on node degree, i.e. the strength and/or number of its associated edges, either by promoting hubs in the solution or orphan genes in the solution. All the glmnet distribution families are supported, namely ```gaussian```, ```poisson```, ```binomial```, ```multinomial```, ```cox```, and ```mgaussian```.

**License** GPL-3

**URL** <https://www.github.com/sysbiomed/glmSparseNet>

**BugReports** <https://www.github.com/sysbiomed/glmSparseNet/issues>

**Depends** R (>= 4.3.0)

**Imports** biomaRt, checkmate, dplyr, forcats, futile.logger, ggplot2, glue, httr, lifecycle, methods, parallel, readr, rlang, glmnet, Matrix, MultiAssayExperiment, SummarizedExperiment, survminer, TCGAutils, utils

**Suggests** BiocStyle, curatedTCGAData, knitr, magrittr, reshape2, pROC, rmarkdown, survival, testthat, VennDiagram, withr

**VignetteBuilder** knitr

**RdMacros** lifecycle

**biocViews** Software, StatisticalMethod, DimensionReduction, Regression, Classification, Survival, Network, GraphAndNetwork

**Encoding** UTF-8

**Language** en-US

**LazyData** false

**NeedsCompilation** no

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.1

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

**git\_branch** RELEASE\_3\_20

**git\_last\_commit** b034036

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.20

**Date/Publication** 2025-01-27

**Author** André Veríssimo [aut, cre] (<<https://orcid.org/0000-0002-2212-339X>>),  
Susana Vinga [aut],  
Eunice Carrasquinha [ctb],  
Marta Lopes [ctb]

**Maintainer** André Veríssimo <[andre.verissimo@tecnico.ulisboa.pt](mailto:andre.verissimo@tecnico.ulisboa.pt)>

## Contents

glmSparseNet-package . . . . .	3
.baseDir . . . . .	4
.biomartLoad . . . . .	4
.buildFunctionDigest . . . . .	5
.cacheCompression . . . . .	6
.calcPenalty . . . . .	6
.calculateResult . . . . .	7
.combinedScore . . . . .	8
.createDirectoryForCache . . . . .	8
.curlWorkaround . . . . .	9
.degreeGeneric . . . . .	9
.digestCache . . . . .	10
.glmSparseNetPrivate . . . . .	11
.networkGenericParallel . . . . .	12
.networkWorker . . . . .	13
.runCache . . . . .	13
.saveRunCache . . . . .	15
.showMessage . . . . .	15
.tempdirCache . . . . .	16
.writeReadme . . . . .	16
balancedCvFolds . . . . .	17
buildLambda . . . . .	17
buildStringNetwork . . . . .	18
cv.glmDegree . . . . .	19
degreeCor . . . . .	22
degreeCov . . . . .	23
downloadFileLocal . . . . .	25
ensemblGeneNames . . . . .	25
geneNames . . . . .	26
glmSparseNet . . . . .	27
hallmarks . . . . .	29
heuristicScale . . . . .	30
hubHeuristic . . . . .	31
myColors . . . . .	32
mySymbols . . . . .	32

<i>glmSparseNet</i> -package	3
networkCorParallel	33
networkCovParallel	34
networkOptions	35
orphanHeuristic	36
protein2EnsemblGeneNames	36
separate2GroupsCox	37
string.network.700.cache	39
stringDBhomoSapiens	39
<b>Index</b>	<b>41</b>

---

*glmSparseNet*-package    *glmSparseNet: Network Centrality Metrics for Elastic-Net Regularized Models*

---

## Description

*glmSparseNet* is an R-package that generalizes sparse regression models when the features (e.g. genes) have a graph structure (e.g. protein-protein interactions), by including network-based regularizers. *glmSparseNet* uses the *glmnet* R-package, by including centrality measures of the network as penalty weights in the regularization. The current version implements regularization based on node degree, i.e. the strength and/or number of its associated edges, either by promoting hubs in the solution or orphan genes in the solution. All the *glmnet* distribution families are supported, namely "gaussian", "poisson", "binomial", "multinomial", "cox", and "mgaussian".

## Author(s)

**Maintainer:** André Veríssimo <andre.verissimo@tecnico.ulisboa.pt> ([ORCID](#))

Authors:

- Susana Vinga <susanavinga@tecnico.ulisboa.pt>

Other contributors:

- Eunice Carrasquinha <eunice.trigueirao@tecnico.ulisboa.pt> [contributor]
- Marta Lopes <marta.lopes@tecnico.ulisboa.pt> [contributor]

## See Also

Useful links:

- <https://www.github.com/sysbiomed/glmSparseNet>
- Report bugs at <https://www.github.com/sysbiomed/glmSparseNet/issues>

---

`.baseDir` *Change base dir for '.runCache*

---

### Description

Change base dir for '.runCache

### Usage

```
.baseDir(path = NULL)
```

### Arguments

`path` to base directory where cache is saved

### Value

the new path

### Examples

```
glmSparseNet:::.baseDir("/tmp/cache")
```

---

`.biomartLoad` *Common call to biomaRt to avoid repetitive code*

---

### Description

Common call to biomaRt to avoid repetitive code

### Usage

```
.biomartLoad(attributes, filters, values, useCache, verbose)
```

### Arguments

<code>attributes</code>	Attributes you want to retrieve. A possible list of attributes can be retrieved using the function <code>biomaRt::listAttributes</code> .
<code>filters</code>	Filters (one or more) that should be used in the query. A possible list of filters can be retrieved using the function <code>biomaRt::listFilters</code> .
<code>values</code>	Values of the filter, e.g. vector of affy IDs. If multiple filters are specified then the argument should be a list of vectors of which the position of each vector corresponds to the position of the filters in the filters argument
<code>useCache</code>	Boolean indicating if biomaRt cache should be used
<code>verbose</code>	When using biomaRt in webservice mode and setting <code>verbose</code> to <code>TRUE</code> , the XML query to the webservice will be printed.

### Value

data.frame with attributes as columns and values translated to them

**See Also**

geneNames  
ensemblGeneNames  
protein2EnsemblGeneNames  
biomaRt::getBM()  
biomaRt::useEnsembl()

**Examples**

```
glmSparseNet:::.biomartLoad(  
  attributes = c("external_gene_name", "ensembl_gene_id"),  
  filters = "external_gene_name",  
  values = c("MOB1A", "RFLNB", "SPIC", "TP53"),  
  useCache = TRUE,  
  verbose = FALSE  
)
```

---

*.buildFunctionDigest*    *Build digest of function from the actual code*

---

**Description**

Build digest of function from the actual code

**Usage**

```
.buildFunctionDigest(fun)
```

**Arguments**

fun                    function call name

**Value**

a digest

**Examples**

```
glmSparseNet:::.buildFunctionDigest(sum)  
glmSparseNet:::.buildFunctionDigest(c)
```

---

.cacheCompression	<i>Change cache.compression for run_cache</i>
-------------------	---

---

**Description**

Change cache.compression for run\_cache

**Usage**

```
.cacheCompression(compression = NULL)
```

**Arguments**

compression      see compression parameter in save function

**Value**

the new compression

**Examples**

```
glmSparseNet:::.cacheCompression("bzip2")
```

---

.calcPenalty	<i>Calculate penalty based on data</i>
--------------	--

---

**Description**

Internal method to calculate the network using data-dependant methods

**Usage**

```
.calcPenalty(xdata, penaltyType, options = networkOptions())
```

**Arguments**

xdata              input data  
penaltyType        which method to use  
options            options to be used

**Value**

vector with penalty weights

### Examples

```
xdata <- matrix(rnorm(1000), ncol = 200)
glmSparseNet:::.calcPenalty(xdata, "none")
glmSparseNet:::.calcPenalty(
  xdata, "correlation",
  networkOptions(cutoff = .6)
)
glmSparseNet:::.calcPenalty(xdata, "correlation")
glmSparseNet:::.calcPenalty(
  xdata, "covariance",
  networkOptions(cutoff = .6)
)
glmSparseNet:::.calcPenalty(xdata, "covariance")
```

---

.calculateResult	<i>Calculate/load result and save if necessary</i>
------------------	--

---

### Description

This is where the actual work is done

### Usage

```
.calculateResult(path, compression, forceRecalc, showMessage, fun, ...)
```

### Arguments

path	path to save cache
compression	compression used in save
forceRecalc	force to recalculate cache
showMessage	boolean to show messages
fun	function to be called
...	arguments to said function ,

### Value

result of fun(...)

### Examples

```
glmSparseNet:::.calculateResult(
  file.path(tempdir(), "calculate_result.Rdata"),
  "gzip",
  FALSE,
  TRUE,
  sum,
  1, 2, 3
)
```

---

<code>.combinedScore</code>	<i>Calculate combined score for STRINGdb interactions</i>
-----------------------------	---

---

**Description**

Please note that all the interactions have duplicates as it's a two way interaction (`score(ProteinA-Protein) == score(ProteinB, ProteinA)`)

**Usage**

```
.combinedScore(allInteractions, scoreThreshold, removeText)
```

**Arguments**

<code>allInteractions</code>	table with score of all interactions
<code>scoreThreshold</code>	threshold to keep interactions
<code>removeText</code>	remove text-based interactions

**Details**

To better understand how the score is calculated, please see: <https://string-db.org/help/faq/#how-are-the-scores-computed>

**Value**

table with combined score

---

<code>.createDirectoryForCache</code>	<i>Create directories for cache</i>
---------------------------------------	-------------------------------------

---

**Description**

Create directories for cache

**Usage**

```
.createDirectoryForCache(baseDir, parentPath)
```

**Arguments**

<code>baseDir</code>	tentative base dir to create.
<code>parentPath</code>	first 4 characters of digest that will become parent directory for the actual cache file (this reduces number of files per folder)

**Value**

a list of updated baseDir and parentDir



### Examples

```
glmSparseNet:::.createDirectoryForCache(tempdir(), "abcd")

glmSparseNet:::.createDirectoryForCache(
  file.path(getwd(), "run-cache"), "abcd"
)
```

---

.curlWorkaround      *Workaround for bug with curl when fetching specific ensembl mirror*

---

### Description

Should be solved in issue #39, will test to remove it.

### Usage

```
.curlWorkaround(expr)
```

### Arguments

expr                  expression

### Value

result of expression

### Examples

```
glmSparseNet:::.curlWorkaround({
  biomaRt::useEnsembl(
    biomart = "genes",
    dataset = "hsapiens_gene_ensembl"
  )
})
```

---

.degreeGeneric      *Generic function to calculate degree based on data*

---

### Description

The assumption to use this function is that the network represented by a matrix is symmetric and without any connection the node and itself.

**Usage**

```
.degreeGeneric(
  fun = stats::cor,
  funPrefix = "operator",
  xdata,
  cutoff = 0,
  considerUnweighted = FALSE,
  chunks = 1000,
  forceRecalcDegree = FALSE,
  forceRecalcNetwork = FALSE,
  nCores = 1,
  ...
)
```

**Arguments**

fun	function that will calculate the edge weight between 2 nodes
funPrefix	used to store low-level information on network as it can become too large to be stored in memory
xdata	calculate correlation matrix on each column
cutoff	positive value that determines a cutoff value
considerUnweighted	consider all edges as 1 if they are greater than 0
chunks	calculate function at batches of this value (default is 1000)
forceRecalcDegree	force recalculation of penalty weights (but not the network), instead of going to cache
forceRecalcNetwork	force recalculation of network and penalty weights, instead of going to cache
nCores	number of cores to be used
...	extra parameters for fun

**Value**

a vector of the degrees

---

.digestCache	<i>Default digest method</i>
--------------	------------------------------

---

**Description**

Sets a default caching algorithm to use with .runCache

**Usage**

```
.digestCache(val)
```

**Arguments**

val	object to calculate hash over
-----	-------------------------------

**Value**

a hash of the sha256

**Examples**

```
glmSparseNet:::.digestCache(c(1, 2, 3, 4, 5))  
glmSparseNet:::.digestCache("some example")
```

---

`.glmSparseNetPrivate` *Calculate GLM model with network-based regularization*

---

**Description**

Calculate GLM model with network-based regularization

**Usage**

```
.glmSparseNetPrivate(  
  fun,  
  xdata,  
  ydata,  
  network,  
  experiment = NULL,  
  options = networkOptions(),  
  ...  
)
```

**Arguments**

<code>fun</code>	function to be called (glmnet or cv.glmnet)
<code>xdata</code>	input data, can be a matrix or MultiAssayExperiment
<code>ydata</code>	response data compatible with glmnet
<code>network</code>	type of network, see below
<code>experiment</code>	when <code>xdata</code> is a MultiAssayExperiment object this parameter is required
<code>options</code>	options to calculate network
<code>...</code>	parameters that glmnet accepts

**Value**

an object just as glmnet network parameter accepts:

- string to calculate network based on data (correlation, covariance)
- matrix representing the network
- vector with already calculated penalty weights (can also be used directly with glmnet)

```
.networkGenericParallel
```

*Calculate the upper triu of the matrix*

---

### Description

Calculate the upper triu of the matrix

### Usage

```
.networkGenericParallel(  
  fun,  
  funPrefix,  
  xdata,  
  buildOutput = "matrix",  
  nCores = 1,  
  forceRecalcNetwork = FALSE,  
  showMessage = FALSE,  
  ...  
)
```

### Arguments

fun	function that will calculate the edge weight between 2 nodes
funPrefix	used to store low-level information on network as it can become to large to be stored in memory
xdata	base data to calculate network
buildOutput	if output returns a 'matrix', 'vector' of the upper triu without the diagonal or NULL with any other argument
nCores	number of cores to be used
forceRecalcNetwork	force recalculation, instead of going to cache
showMessage	shows cache operation messages
...	extra parameters for fun

### Value

depends on buildOutput parameter

---

.networkWorker	<i>Worker to calculate edge weight for each pair of ixI node and following</i>
----------------	--

---

**Description**

Note that it assumes it does not calculate for index below and equal to ixI

**Usage**

```
.networkWorker(fun, xdata, ixI, ...)
```

**Arguments**

fun	function to be used, can be cor, cov or any other defined function
xdata	original data to calculate the function over
ixI	starting index, this can be used to save ony upper triu
...	extra parameters for fun

**Value**

a vector with size ncol(xdata) - ixI

---

.runCache	<i>Run function and save cache</i>
-----------	------------------------------------

---

**Description**

This method saves the function that's being called

**Usage**

```
.runCache(  
  fun,  
  ...,  
  seed = NULL,  
  baseDir = NULL,  
  cachePrefix = "generic_cache",  
  cacheDigest = list(),  
  showMessage = NULL,  
  forceRecalc = FALSE,  
  addToHash = NULL  
)  
  
## S4 method for signature 'function'  
.runCache(  
  fun,  
  ...,  
  seed = NULL,
```

```

    baseDir = NULL,
    cachePrefix = "generic_cache",
    cacheDigest = list(),
    showMessage = NULL,
    forceRecalc = FALSE,
    addToHash = NULL
)

```

### Arguments

fun	function call name
...	parameters for function call
seed	when function call is random, this allows to set seed beforehand
baseDir	directory where data is stored
cachePrefix	prefix for file name to be generated from parameters (...)
cacheDigest	cache of the digest for one or more of the parameters
showMessage	show message that data is being retrieved from cache
forceRecalc	force the recalculation of the values
addToHash	something to add to the filename generation

### Value

the result of fun(...)

### Functions

- `.runCache(`function`)`: accepts function as first argument and save cache

### Examples

```

# [optional] save cache in a temporary directory
#
glmSparseNet:::.baseDir(tempdir())
glmSparseNet:::.runCache(c, 1, 2, 3, 4)
#
# next three should use the same cache
# note, the middle call should be a little faster as digest is not
# calculated
# for the first argument
glmSparseNet:::.runCache(c, 1, 2, 3, 4)
glmSparseNet:::.runCache(c, a = 1, 2, c = 3, 4)

# Using a local folder
# glmSparseNet:::.runCache(c, 1, 2, 3, 4, baseDir = "runcache")

```

---

.saveRunCache                    *Saving the cache*

---

**Description**

Saving the cache

**Usage**

```
.saveRunCache(result, path, compression, showMessage)
```

**Arguments**

result	main result to save
path	path to the file to save
compression	compression method to be used
showMessage	TRUE to show messages, FALSE otherwise

**Value**

result of save operation

**Examples**

```
glmSparseNet:::.saveRunCache(  
  35, file.path(tempdir(), "save_run_cache.Rdata"), FALSE, TRUE  
)
```

---

.showMessage                    *Show messages option in .runCache*

---

**Description**

Show messages option in .runCache

**Usage**

```
.showMessage(showMessage = NULL)
```

**Arguments**

showMessage	boolean indicating to show messages or not
-------------	--

**Value**

the show.message option

**Examples**

```
glmSparseNet:::.showMessage(FALSE)
```

`.tempdirCache`      *Temporary directory for runCache*

---

**Description**

Temporary directory for runCache

**Usage**

```
.tempdirCache()
```

**Value**

a path to a temporary directory used by runCache

---

`.writeReadme`      *Write a file in run-cache directory to explain the origin*

---

**Description**

Write a file in run-cache directory to explain the origin

**Usage**

```
.writeReadme(baseDir)
```

**Arguments**

`baseDir`      directory where to build this file

**Value**

the path to the file it has written

**Examples**

```
glmSparseNet:::.writeReadme(tempdir())
```



---

balancedCvFolds	<i>Create balanced folds for cross validation using stratified sampling</i>
-----------------	---

---

**Description**

Create balanced folds for cross validation using stratified sampling

**Usage**

```
balancedCvFolds(..., nfolds = 10)

# deprecated, please use balancedCvFolds()
balanced.cv.folds(..., nfolds = 10)
```

**Arguments**

...	vectors representing data
nfolds	number of folds to be created

**Value**

list with given input, nfolds and result. The result is a list matching the input with foldid attributed to each position.

**Examples**

```
balancedCvFolds(seq(10), seq(11, 15), nfolds = 2)

# will give a warning
balancedCvFolds(seq(10), seq(11, 13), nfolds = 10)

balancedCvFolds(seq(100), seq(101, 133), nfolds = 10)
```

---

buildLambda	<i>Auxiliary function to generate suitable lambda parameters</i>
-------------	--

---

**Description**

Auxiliary function to generate suitable lambda parameters

**Usage**

```
buildLambda(
  lambdaLargest = NULL,
  xdata = NULL,
  ydata = NULL,
  family = NULL,
  ordersOfMagnitudeSmaller = 3,
  lambdaPerOrderMagnitude = 150,
  lambda.largest = deprecated(),
```

```

orders.of.magnitude.smaller = deprecated(),
lambda.per.order.magnitude = deprecated()
)

```

### Arguments

lambdaLargest    numeric value for largest number of lambda to consider (usually with a target of 1 selected variable)

xdata            X parameter for glmnet function

ydata            Y parameter for glmnet function

family           family parameter to glmnet function

ordersOfMagnitudeSmaller  
                  minimum value for lambda ( $\text{lambda.largest} / 10^{\text{orders.of.magnitude.smaller}}$ )

lambdaPerOrderMagnitude  
                  how many lambdas to create for each order of magnitude

lambda.largest   **[Deprecated]**

orders.of.magnitude.smaller  
                  **[Deprecated]**

lambda.per.order.magnitude  
                  **[Deprecated]**

### Value

a numeric vector with suitable lambdas

### Examples

```
buildLambda(5.4)
```

---

buildStringNetwork	<i>Build gene network from peptide ids</i>
--------------------	--

---

### Description

This can reduce the dimension of the original network, as there may not be a mapping between peptide and gene id

### Usage

```

buildStringNetwork(
  stringTbl,
  useNames = c("protein", "ensembl", "external"),
  string.tbl = deprecated(),
  use.names = deprecated()
)

```

**Arguments**

stringTbl	data.frame or tibble with colnames and rownames as ensembl peptide id ( <i>same order</i> ).
useNames	character(1) that defaults to use protein names _('protein'), other options are 'ensembl' for ensembl gene id or 'external' for external gene names.
string.tbl	<b>[Deprecated]</b>
use.names	<b>[Deprecated]</b>

**Value**

a new matrix with gene ids instead of peptide ids. The size of matrix can be different as there may not be a mapping or a peptide mapping can have multiple genes.

**See Also**

[stringDBhomoSapiens\(\)](#)

**Examples**

```
interactions <- stringDBhomoSapiens(scoreThreshold = 100)
string_network <- buildStringNetwork(interactions)

# number of edges
sum(string_network != 0)
```

---

cv.glmDegree	<i>Calculate cross validating GLM model with network-based regularization</i>
--------------	---

---

**Description**

network parameter accepts:

**Usage**

```
cv.glmDegree(
  xdata,
  ydata,
  network,
  options = networkOptions(),
  experiment = NULL,
  network.options = deprecated(),
  experiment.name = deprecated(),
  ...
)

cv.glmHub(
  xdata,
  ydata,
  network,
```

```

    options = networkOptions(),
    experiment = NULL,
    network.options = deprecated(),
    experiment.name = deprecated(),
    ...
)

cv.glmOrphan(
  xdata,
  ydata,
  network,
  options = networkOptions(),
  experiment = NULL,
  network.options = deprecated(),
  experiment.name = deprecated(),
  ...
)

cv.glmSparseNet(
  xdata,
  ydata,
  network,
  options = networkOptions(),
  experiment = NULL,
  network.options = deprecated(),
  experiment.name = deprecated(),
  ...
)

```

### Arguments

xdata	input data, can be a matrix or MultiAssayExperiment.
ydata	response data compatible with glmnet.
network	type of network, see below.
options	options to calculate network.
experiment	name of experiment to use as input in MultiAssayExperiment object (only if xdata is an object of this class).
network.options	<b>[Deprecated]</b>
experiment.name	<b>[Deprecated]</b>
...	parameters that <code>glmnet::cv.glmnet()</code> accepts.

### Details

- string to calculate network based on data (correlation, covariance)
- matrix representing the network
- vector with already calculated penalty weights (can also be used directly glmnet)

### Value

an object just as `cv.glmnet`

## Functions

- `cv.glmDegree()`: penalizes nodes with small degree (*inversion penalization*  $h(x) = 1 / x$ ).
- `cv.glmHub()`: penalizes nodes with small degree (*normalized heuristic that promotes nodes with many edges*).
- `cv.glmOrphan()`: penalizes nodes with high degree (*normalized heuristic that promotes nodes with few edges*).

## See Also

Model with the same penalizations [glmSparseNet\(\)](#).

## Examples

```
# Degree penalization

xdata <- matrix(rnorm(100), ncol = 5)
cv.glmDegree(
  xdata,
  rnorm(nrow(xdata)),
  "correlation",
  family = "gaussian",
  nfolds = 5,
  options = networkOptions(minDegree = .2)
)

# Hub penalization

xdata <- matrix(rnorm(100), ncol = 5)
cv.glmHub(
  xdata,
  rnorm(nrow(xdata)),
  "correlation",
  family = "gaussian",
  nfolds = 5,
  options = networkOptions(minDegree = .2)
)

# Orphan penalization

xdata <- matrix(rnorm(100), ncol = 5)
cv.glmOrphan(
  xdata,
  rnorm(nrow(xdata)),
  "correlation",
  family = "gaussian",
  nfolds = 5,
  options = networkOptions(minDegree = .2)
)

# Gaussian model
xdata <- matrix(rnorm(500), ncol = 5)
cv.glmSparseNet(
  xdata, rnorm(nrow(xdata)), "correlation",
  family = "gaussian"
)
cv.glmSparseNet(
  xdata, rnorm(nrow(xdata)), "covariance",
```

```

    family = "gaussian"
  )

#
#
# Using MultiAssayExperiment with survival model
library(MultiAssayExperiment)
data("miniACC", package = "MultiAssayExperiment")

xdata <- miniACC

#
# build valid data with days of last follow up or to event
event.ix <- which(!is.na(xdata$days_to_death))
cens.ix <- which(!is.na(xdata$days_to_last_followup))
xdata$surv_event_time <- array(NA, nrow(colData(xdata)))
xdata$surv_event_time[event.ix] <- xdata$days_to_death[event.ix]
xdata$surv_event_time[cens.ix] <- xdata$days_to_last_followup[cens.ix]

#
# Keep only valid individuals
valid.ix <- as.vector(!is.na(xdata$surv_event_time) &
  !is.na(xdata$vital_status) &
  xdata$surv_event_time > 0)
xdata.valid <- xdata[, rownames(colData(xdata))[valid.ix]]
ydata.valid <- colData(xdata.valid)[, c("surv_event_time", "vital_status")]
colnames(ydata.valid) <- c("time", "status")

#
cv.glmSparseNet(
  xdata.valid,
  ydata.valid,
  nfolds = 5,
  family = "cox",
  network = "correlation",
  experiment = "RNASeq2GeneNorm"
)

```

---

degreeCor

*Calculate the degree of the correlation network based on xdata*


---

## Description

Calculate the degree of the correlation network based on xdata

## Usage

```

degreeCor(
  xdata,
  cutoff = 0,
  considerUnweighted = FALSE,
  forceRecalcDegree = FALSE,

```

```

    forceRecalcNetwork = FALSE,
    nCores = 1,
    ...,
    consider.unweighted = deprecated(),
    force.recalc.degree = deprecated(),
    force.recalc.network = deprecated(),
    n.cores = deprecated()
)

```

### Arguments

`xdata` calculate correlation matrix on each column.

`cutoff` positive value that determines a cutoff value.

`considerUnweighted` consider all edges as 1 if they are greater than 0.

`forceRecalcDegree` force recalculation of penalty weights (but not the network), instead of going to cache.

`forceRecalcNetwork` force recalculation of network and penalty weights, instead of going to cache.

`nCores` number of cores to be used.

`...` extra parameters for `cor` function.

`consider.unweighted` **[Deprecated]**

`force.recalc.degree` **[Deprecated]**

`force.recalc.network` **[Deprecated]**

`n.cores` **[Deprecated]**

### Value

a vector of the degrees.

### Examples

```

n.col <- 6
xdata <- matrix(rnorm(n.col * 4), ncol = n.col)
degreeCor(xdata)
degreeCor(xdata, cutoff = .5)
degreeCor(xdata, cutoff = .5, considerUnweighted = TRUE)

```

---

degreeCov

*Calculate the degree of the covariance network based on xdata*

---

### Description

Calculate the degree of the covariance network based on `xdata`

**Usage**

```

degreeCov(
  xdata,
  cutoff = 0,
  considerUnweighted = FALSE,
  forceRecalcDegree = FALSE,
  forceRecalcNetwork = FALSE,
  nCores = 1,
  ...,
  consider.unweighted = deprecated(),
  force.recalc.degree = deprecated(),
  force.recalc.network = deprecated(),
  n.cores = deprecated()
)

```

**Arguments**

xdata	calculate correlation matrix on each column.
cutoff	positive value that determines a cutoff value.
considerUnweighted	consider all edges as 1 if they are greater than 0.
forceRecalcDegree	force recalculation of penalty weights (but not the network), instead of going to cache.
forceRecalcNetwork	force recalculation of network and penalty weights, instead of going to cache.
nCores	number of cores to be used.
...	extra parameters for cov function.
consider.unweighted	<b>[Deprecated]</b>
force.recalc.degree	<b>[Deprecated]</b>
force.recalc.network	<b>[Deprecated]</b>
n.cores	<b>[Deprecated]</b>

**Value**

a vector of the degrees

**Examples**

```

n.col <- 6
xdata <- matrix(rnorm(n.col * 4), ncol = n.col)
degreeCov(xdata)
degreeCov(xdata, cutoff = .5)
degreeCov(xdata, cutoff = .5, considerUnweighted = TRUE)

```



---

downloadFileLocal      *Download files to local temporary path*

---

**Description**

In case of new call it uses the temporary cache instead of downloading again.

**Usage**

```
downloadFileLocal(urlStr, oD = tempdir())
```

**Arguments**

urlStr	url of file to download
oD	temporary directory to store file

**Details**

Inspired by STRINGdb Bioconductor package, but using curl as file may be too big to handle.

**Value**

path to file

**Examples**

```
glmSparseNet::downloadFileLocal(  
  "https://string-db.org/api/tsv-no-header/version"  
)
```

---

ensemblGeneNames      *Retrieve ensembl gene names from biomaRt*

---

**Description**

Retrieve ensembl gene names from biomaRt

**Usage**

```
ensemblGeneNames(  
  geneId,  
  useCache = TRUE,  
  verbose = FALSE,  
  gene.id = deprecated(),  
  use.cache = deprecated()  
)
```

**Arguments**

geneId	character vector with gene names
useCache	Boolean indicating if biomaRt cache should be used
verbose	When using biomaRt in webservice mode and setting verbose to TRUE, the XML query to the webservice will be printed.
gene.id	<b>[Deprecated]</b>
use.cache	<b>[Deprecated]</b>

**Value**

a dataframe with external gene names, `ensembl_id`

**Examples**

```
ensemblGeneNames(c("MOB1A", "RFLNB", "SPIC", "TP53"))
```

---

geneNames	<i>Retrieve gene names from biomaRt</i>
-----------	---

---

**Description**

Retrieve gene names from biomaRt

**Usage**

```
geneNames(
  ensemblGenes,
  useCache = TRUE,
  verbose = FALSE,
  ensembl.genes = deprecated(),
  use.cache = deprecated()
)
```

**Arguments**

ensemblGenes	character vector with gene names in <code>ensembl_id</code> format
useCache	Boolean indicating if biomaRt cache should be used
verbose	When using biomaRt in webservice mode and setting verbose to TRUE, the XML query to the webservice will be printed.
ensembl.genes	<b>[Deprecated]</b>
use.cache	<b>[Deprecated]</b>

**Value**

a dataframe with external gene names, `ensembl_id`

**Examples**

```
geneNames(c("ENSG00000114978", "ENSG00000166211", "ENSG00000183688"))
```

**Description**

network parameter accepts:

- string to calculate network based on data (correlation, covariance)
- matrix representing the network
- vector with already calculated penalty weights (can also be used directly with glmnet)

**Usage**

```
glmSparseNet(  
  xdata,  
  ydata,  
  network,  
  options = networkOptions(),  
  experiment = NULL,  
  network.options = deprecated(),  
  experiment.name = deprecated(),  
  ...  
)
```

```
glmDegree(  
  xdata,  
  ydata,  
  network,  
  options = networkOptions(),  
  experiment = NULL,  
  network.options = deprecated(),  
  experiment.name = deprecated(),  
  ...  
)
```

```
glmHub(  
  xdata,  
  ydata,  
  network,  
  options = networkOptions(),  
  experiment = NULL,  
  network.options = deprecated(),  
  experiment.name = deprecated(),  
  ...  
)
```

```
glmOrphan(  
  xdata,  
  ydata,  
  network,
```

```

options = networkOptions(),
experiment = NULL,
network.options = deprecated(),
experiment.name = deprecated(),
...
)

```

### Arguments

xdata	input data, can be a matrix or MultiAssayExperiment.
ydata	response data compatible with glmnet.
network	type of network, see below.
options	options to calculate network.
experiment	name of experiment to use as input in MultiAssayExperiment object (only if xdata is an object of this class).
network.options	<b>[Deprecated]</b>
experiment.name	<b>[Deprecated]</b>
...	parameters that <code>glmnet::glmnet()</code> accepts.

### Value

an object just as glmnet

### Functions

- `glmDegree()`: penalizes nodes with small degree (*inversion penalization*  $h(x) = 1 / x$ ).
- `glmHub()`: Penalizes nodes with small degree (*normalized heuristic that promotes nodes with many edges*).
- `glmOrphan()`: Penalizes nodes with high degree (*normalized heuristic that promotes nodes with few edges*).

### See Also

Cross-validation functions `cv.glmSparseNet()`.

### Examples

```

xdata <- matrix(rnorm(100), ncol = 20)
glmSparseNet(xdata, rnorm(nrow(xdata)), "correlation", family = "gaussian")
glmSparseNet(xdata, rnorm(nrow(xdata)), "covariance", family = "gaussian")

#
#
# Using MultiAssayExperiment
# load data
library(MultiAssayExperiment)
data("miniACC", package = "MultiAssayExperiment")

xdata <- miniACC

```

```

# TODO aking out x individuals missing values
# build valid data with days of last follow up or to event
event.ix <- which(!is.na(xdata$days_to_death))
cens.ix <- which(!is.na(xdata$days_to_last_followup))

xdata$surv_event_time <- array(NA, nrow(colData(xdata)))
xdata$surv_event_time[event.ix] <- xdata$days_to_death[event.ix]
xdata$surv_event_time[cens.ix] <- xdata$days_to_last_followup[cens.ix]

# Keep only valid individuals
valid.ix <- as.vector(!is.na(xdata$surv_event_time) &
  !is.na(xdata$vital_status) &
  xdata$surv_event_time > 0)
xdata.valid <- xdata[, rownames(colData(xdata))[valid.ix]]
ydata.valid <- colData(xdata.valid)[, c("surv_event_time", "vital_status")]
colnames(ydata.valid) <- c("time", "status")

glmSparseNet(
  xdata.valid,
  ydata.valid,
  family = "cox",
  network = "correlation",
  experiment = "RNASeq2GeneNorm"
)

# Degree penalization

xdata <- matrix(rnorm(100), ncol = 5)
glmDegree(
  xdata,
  rnorm(nrow(xdata)),
  "correlation",
  family = "gaussian",
  options = networkOptions(minDegree = .2)
)
xdata <- matrix(rnorm(100), ncol = 5)
glmHub(
  xdata,
  rnorm(nrow(xdata)),
  "correlation",
  family = "gaussian",
  options = networkOptions(minDegree = .2)
)

# Orphan penalization

xdata <- matrix(rnorm(100), ncol = 5)
glmOrphan(
  xdata,
  rnorm(nrow(xdata)),
  "correlation",
  family = "gaussian",
  options = networkOptions(minDegree = .2)
)

```

**Description**

**[Defunct]** The API has been removed and this function is no longer available.

**Usage**

```
hallmarks(
  genes,
  metric = "count",
  hierarchy = "full",
  generate.plot = TRUE,
  show.message = FALSE
)
```

**Arguments**

genes	gene names
metric	see below
hierarchy	see below
generate.plot	flag to indicate if return object has a ggplot2 object
show.message	flag to indicate if run_cache method shows messages

**Value**

data.frame with choosen metric and hierarchy It also returns a vector with genes that do not have any hallmarks.

See <http://chat.lionproject.net/api> for more details on the metric and hallmarks parameters

To standardize the colors in the gradient you can use `scale_fill_gradientn(limits=c(0,1), colours=topo.colors(3))` to limit between 0 and 1 for cprob and -1 and 1 for npmi

---

heuristicScale	<i>Heuristic function to use in high dimensions</i>
----------------	---

---

**Description**

Heuristic function to use in high dimensions

**Usage**

```
heuristicScale(
  x,
  subExp10 = -1,
  expMult = -1,
  subExp = -1,
  sub.exp10 = deprecated(),
  exp.mult = deprecated(),
  sub.exp = deprecated()
)
```

**Arguments**

x	vector of values to scale
subExp10	value to subtract to base 10 exponential, for example: $10^0 - \text{subExp10} = 1 - \text{subExp10}$
expMult	parameter to multiply exponential, i.e. to have a negative exponential or positive
subExp	value to subtract for exponential, for example if $x = 0$ , $\exp(0) - \text{sub.exp} = 1 - \text{sub.exp}$
sub.exp10	<b>[Deprecated]</b>
exp.mult	<b>[Deprecated]</b>
sub.exp	<b>[Deprecated]</b>

**Value**

a vector of scaled values

**Examples**

```
heuristicScale(rnorm(1:10))
```

---

hubHeuristic	<i>Heuristic function to penalize nodes with low degree</i>
--------------	---

---

**Description**

Heuristic function to penalize nodes with low degree

**Usage**

```
hubHeuristic(x)
```

**Arguments**

x	single value of vector
---	------------------------

**Value**

transformed

**Examples**

```
hubHeuristic(rnorm(1:10))
```

myColors *Custom pallete of colors*

---

**Description**

Custom pallete of colors

**Usage**

```
myColors(ix = NULL)

# deprecated, please use myColors()
my.colors(ix = NULL)
```

**Arguments**

ix                    index for a color

**Value**

a color

**Examples**

```
myColors()
myColors(5)
```

---

mySymbols *Custom pallete of symbols in plots*

---

**Description**

Custom pallete of symbols in plots

**Usage**

```
mySymbols(ix = NULL)

# deprecated, please use mySymbols()
my.symbols(ix = NULL)
```

**Arguments**

ix                    index for symbol

**Value**

a symbol

**Examples**

```
mySymbols()
mySymbols(2)
```



---

networkCorParallel     *Calculates the correlation network*

---

### Description

Calculates the correlation network

### Usage

```
networkCorParallel(
  xdata,
  buildOutput = "matrix",
  nCores = 1,
  forceRecalcNetwork = FALSE,
  showMessage = FALSE,
  ...,
  build.output = deprecated(),
  n.cores = deprecated(),
  force.recalc.network = deprecated(),
  show.message = deprecated()
)
```

### Arguments

xdata	base data to calculate network
buildOutput	if output returns a 'matrix', 'vector' of the upper triu without the diagonal or NULL with any other argument
nCores	number of cores to be used
forceRecalcNetwork	force recalculation, instead of going to cache
showMessage	shows cache operation messages
...	extra parameters for fun
build.output	lifecycle::badge("deprecated") without the diagonal or NULL with any other argument
n.cores	lifecycle::badge("deprecated")
force.recalc.network	lifecycle::badge("deprecated")
show.message	lifecycle::badge("deprecated")

### Value

depends on build.output parameter

### Examples

```
n_col <- 6
xdata <- matrix(rnorm(n_col * 4), ncol = n_col)
networkCorParallel(xdata)
```

---

networkCovParallel     *Calculates the covariance network*

---

### Description

Calculates the covariance network

### Usage

```
networkCovParallel(
  xdata,
  buildOutput = "matrix",
  nCores = 1,
  forceRecalcNetwork = FALSE,
  showMessage = FALSE,
  ...,
  build.output = deprecated(),
  n.cores = deprecated(),
  force.recalc.network = deprecated(),
  show.message = deprecated()
)
```

### Arguments

xdata	base data to calculate network
buildOutput	if output returns a 'matrix', 'vector' of the upper triu without the diagonal or NULL with any other argument
nCores	number of cores to be used
forceRecalcNetwork	force recalculation, instead of going to cache
showMessage	shows cache operation messages
...	extra parameters for fun
build.output	lifecycle::badge("deprecated") without the diagonal or NULL with any other argument
n.cores	lifecycle::badge("deprecated")
force.recalc.network	lifecycle::badge("deprecated")
show.message	lifecycle::badge("deprecated")

### Value

depends on build.output parameter

### Examples

```
n.col <- 6
xdata <- matrix(rnorm(n.col * 4), ncol = n.col)
networkCovParallel(xdata)
```

---

networkOptions	<i>Setup network options</i>
----------------	------------------------------

---

### Description

Setup network options, such as using weighted or unweighted degree, which centrality measure to use

### Usage

```
networkOptions(
  method = "pearson",
  unweighted = TRUE,
  cutoff = 0,
  centrality = "degree",
  minDegree = 0,
  nCores = 1,
  transFun = function(x) x,
  min.degree = deprecated(),
  n.cores = deprecated(),
  trans.fun = deprecated()
)
```

### Arguments

method	in case of correlation and covariance, which method to use.
unweighted	calculate degree using unweighted network.
cutoff	cutoff value in network edges to trim the network.
centrality	centrality measure to use, currently only supports degree.
minDegree	minimum value that individual penalty weight can take.
nCores	number of cores to use, default to 1.
transFun	See details below.
min.degree	<b>[Deprecated]</b>
n.cores	<b>[Deprecated]</b>
trans.fun	<b>[Deprecated]</b>

The transFun argument takes a function definition that will apply a transformation to the penalty vector calculated from the degree. This transformation allows to change how the penalty is applied.

### Value

a list of options

### See Also

[glmOrphan\(\)](#) and [glmDegree\(\)](#)

### Examples

```
networkOptions(unweighted = FALSE)
```

---

orphanHeuristic      *Heuristic function to penalize nodes with high degree*

---

**Description**

Heuristic function to penalize nodes with high degree

**Usage**

```
orphanHeuristic(x)
```

**Arguments**

x                      single value of vector

**Value**

transformed

**Examples**

```
orphanHeuristic(rnorm(1:10))
```

---

protein2EnsemblGeneNames

*Retrieve ensembl gene ids from proteins*

---

**Description**

Retrieve ensembl gene ids from proteins

**Usage**

```
protein2EnsemblGeneNames(
  ensemblProteins,
  useCache = TRUE,
  verbose = FALSE,
  ensembl.proteins = deprecated(),
  use.cache = deprecated()
)
```

**Arguments**

ensemblProteins      character vector with gene names in ensembl\_peptide\_id format

useCache              Boolean indicating if biomaRt cache should be used

verbose                When using biomaRt in webservice mode and setting verbose to TRUE, the XML query to the webservice will be printed.

ensembl.proteins      **[Deprecated]**

use.cache              **[Deprecated]**

**Value**

a dataframe with external gene names, ensembl\_peptide\_id

**Examples**

```
protein2EnsemblGeneNames(c(
  "ENSP00000235382",
  "ENSP00000233944",
  "ENSP00000216911"
))
```

---

separate2GroupsCox      *Separate data in High and Low risk groups (based on Cox model)*

---

**Description**

Draws multiple kaplan meyer survival curves (or just 1) and calculates logrank test

**Usage**

```
separate2GroupsCox(
  chosenBetas,
  xdata,
  ydata,
  probs = c(0.5, 0.5),
  noPlot = FALSE,
  plotTitle = "SurvivalCurves",
  xlim = NULL,
  ylim = NULL,
  expandYZero = FALSE,
  legendOutside = FALSE,
  stopWhenOverlap = TRUE,
  ...,
  chosen.betas = deprecated(),
  no.plot = deprecated(),
  plot.title = deprecated(),
  expand.yzero = deprecated(),
  legend.outside = deprecated(),
  stop.when.overlap = deprecated()
)
```

**Arguments**

chosenBetas	list of testing coefficients to calculate prognostic indexes, for example list(Age = some_vector).
xdata	n x m matrix with n observations and m variables.
ydata	Survival object.
probs	How to separate high and low risk patients 50%-50% is the default, but for top and bottom 40% -> c(.4, .6).
noPlot	Only calculate p-value and do not generate survival curve plot.

plotTitle	Name of file if.
xlim	Optional argument to limit the x-axis view.
ylim	Optional argument to limit the y-axis view.
expandYZero	expand to y = 0.
legendOutside	If TRUE legend will be outside plot, otherwise inside.
stopWhenOverlap	when probs vector allows for overlapping of samples in both groups, then stop.
...	additional parameters to <code>survminer::ggsurvplot</code>
chosen.btas	<b>[Deprecated]</b>
no.plot	<b>[Deprecated]</b>
plot.title	<b>[Deprecated]</b>
expand.yzero	<b>[Deprecated]</b>
legend.outside	<b>[Deprecated]</b>
stop.when.overlap	<b>[Deprecated]</b>
	Otherwise it will calculate with duplicate samples, i.e. simply adding them to xdata and ydata (in a different group).

### Value

object with logrank test and kaplan-meier survival plot

A list with plot, p-value and kaplan-meier object. The plot was drawn from `survminer::ggsurvplot` with only the palette, data and fit arguments being defined and keeping all other defaults that can be customized as additional parameters to this function.

### See Also

[survminer::ggsurvplot\(\)](#)

### Examples

```
xdata <- survival::ovarian[, c("age", "resid.ds")]
ydata <- data.frame(
  time = survival::ovarian$futime,
  status = survival::ovarian$fustat
)
separate2GroupsCox(c(age = 1, 0), xdata, ydata)
separate2GroupsCox(c(age = 1, 0.5), xdata, ydata)
separate2GroupsCox(
  c(age = 1), c(1, 0, 1, 0, 1, 0),
  data.frame(time = runif(6), status = rbinom(6, 1, .5))
)
separate2GroupsCox(list(
  aa = c(age = 1, 0.5),
  bb = c(age = 0, 1.5)
), xdata, ydata)
```

---

string.network.700.cache

*Cache of protein-protein network, as it takes some time to retrieve and process this will facilitate the vignette building*

---

### Description

It was filtered with combined\_scores and individual scores below 700 without text-based scores

### Usage

```
data('string.network.700.cache', package = 'glmSparseNet')
```

### Format

An object of class dgCMatrix with 11033 rows and 11033 columns.

### References

<https://string-db.org/>

---

stringDBhomoSapiens *Download protein-protein interactions from STRING DB*

---

### Description

Download protein-protein interactions from STRING DB

### Usage

```
stringDBhomoSapiens(
  version = "11.0",
  scoreThreshold = 0,
  removeText = TRUE,
  score_threshold = deprecated(),
  remove.text = deprecated()
)
```

### Arguments

version	version of the database to use
scoreThreshold	remove scores below threshold
removeText	remove text mining-based scores
score_threshold	<b>[Deprecated]</b>
remove.text	<b>[Deprecated]</b>

**Value**

a data.frame with rows representing an interaction between two proteins, and columns the count of scores above the given `score_threshold`

**Examples**

```
stringDBhomoSapiens(scoreThreshold = 800)
```



# Index

- \* **data**
  - string.network.700.cache, 39
- \* **internal**
  - .glmSparseNetPrivate, 11
  - glmSparseNet-package, 3
- .baseDir, 4
- .biomartLoad, 4
- .buildFunctionDigest, 5
- .cacheCompression, 6
- .calcPenalty, 6
- .calculateResult, 7
- .combinedScore, 8
- .createDirectoryForCache, 8
- .curlWorkaround, 9
- .degreeGeneric, 9
- .digestCache, 10
- .glmSparseNetPrivate, 11
- .networkGenericParallel, 12
- .networkWorker, 13
- .runCache, 13
- .runCache, function-method (.runCache), 13
- .saveRunCache, 15
- .showMessage, 15
- .tempdirCache, 16
- .writeReadme, 16

balanced.cv.folds (balancedCvFolds), 17

balancedCvFolds, 17

buildLambda, 17

buildStringNetwork, 18

cv.glmDegree, 19

cv.glmHub (cv.glmDegree), 19

cv.glmOrphan (cv.glmDegree), 19

cv.glmSparseNet (cv.glmDegree), 19

cv.glmSparseNet(), 28

degreeCor, 22

degreeCov, 23

downloadFileLocal, 25

ensemblGeneNames, 25

geneNames, 26

glmDegree (glmSparseNet), 27

glmDegree(), 35

glmHub (glmSparseNet), 27

glmnet::cv.glmnet(), 20

glmnet::glmnet(), 28

glmOrphan (glmSparseNet), 27

glmOrphan(), 35

glmSparseNet, 27

glmSparseNet(), 21

glmSparseNet-package, 3

hallmarks, 29

heuristicScale, 30

hubHeuristic, 31

my.colors (myColors), 32

my.symbols (mySymbols), 32

myColors, 32

mySymbols, 32

networkCorParallel, 33

networkCovParallel, 34

networkOptions, 35

orphanHeuristic, 36

protein2EnsemblGeneNames, 36

separate2GroupsCox, 37

string.network.700.cache, 39

stringDBhomoSapiens, 39

stringDBhomoSapiens(), 19

survminer::ggsurvplot(), 38