

# Package: MLGL (via r-universe)

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**Type** Package

**Title** Multi-Layer Group-Lasso

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**Copyright** Inria

**Description** It implements a new procedure of variable selection in the context of redundancy between explanatory variables, which holds true with high dimensional data (Grimonprez et al. (2023) <[doi:10.18637/jss.v106.i03](https://doi.org/10.18637/jss.v106.i03)>).

**BugReports** <https://github.com/modal-inria/MLGL/issues>

**License** GPL (>=2)

**Imports** gglasso, MASS, Matrix, fastcluster, FactoMineR, parallelDist

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MLGL-package

*MLGL*


---

## Description

This package presents a method combining Hierarchical Clustering and Group-lasso. Usually, a single partition of the covariates is used in the group-lasso. Here, we provide several partitions from the hierarchical tree.

A post-treatment method based on statistical test (with FWER and FDR control) for selecting the regularization parameter and the optimal group for this value is provided. This method can be applied for the classical group-lasso and our method.

## Details

The [MLGL](#) function performs the hierarchical clustering and the group-lasso. The post-treatment method can be performed with [hierarchicalFWER](#) and [selfFWER](#) functions. The whole process can be run with the [fullProcess](#) function.

## Author(s)

Quentin Grimonprez

## References

Grimonprez Q, Blanck S, Celisse A, Marot G (2023). "MLGL: An R Package Implementing Correlated Variable Selection by Hierarchical Clustering and Group-Lasso." *Journal of Statistical Software*, 106(3), 1-33. doi:10.18637/jss.v106.i03.

## See Also

[MLGL](#), [cv.MLGL](#), [fullProcess](#), [hierarchicalFWER](#)

## Examples

```
# Simulate gaussian data with block-diagonal variance matrix containing 12 blocks of size 5
X <- simuBlockGaussian(50, 12, 5, 0.7)
# Generate a response variable
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)
# Apply MLGL method
res <- MLGL(X, y)
```

---

bootstrapHclust	<i>Hierarchical Clustering with distance matrix computed using bootstrap replicates</i>
-----------------	---

---

## Description

Hierarchical Clustering with distance matrix computed using bootstrap replicates

## Usage

```
bootstrapHclust(X, frac = 1, B = 50, method = "ward.D2", nCore = NULL)
```

## Arguments

X	data
frac	fraction of sample used at each replicate
B	number of replicates
method	desired method: "single", "complete", "average", "mcquitty", "ward.D", "ward.D2", "centroid", "median".
nCore	number of cores

## Value

An object of class hclust

## Examples

```
hc <- bootstrapHclust(USArrests, nCore = 1)
```

---

coef.cv.MLGL                    *Get coefficients from a cv.MLGL object*

---

**Description**

Get coefficients from a [cv.MLGL](#) object

**Usage**

```
## S3 method for class 'cv.MLGL'  
coef(object, s = c("lambda.1se", "lambda.min"), ...)
```

**Arguments**

object	<a href="#">cv.MLGL</a> object
s	Either "lambda.1se" or "lambda.min"
...	Not used. Other arguments to predict.

**Value**

A matrix with estimated coefficients for given values of s.

**Author(s)**

Quentin Grimonprez

**See Also**

[cv.MLGL](#), [predict.cv.MLGL](#)

---

coef.MLGL                    *Get coefficients from a MLGL object*

---

**Description**

Get coefficients from a [MLGL](#) object

**Usage**

```
## S3 method for class 'MLGL'  
coef(object, s = NULL, ...)
```

**Arguments**

object	<a href="#">MLGL</a> object
s	values of lambda. If NULL, use values from object
...	Not used. Other arguments to predict.

**Value**

A matrix with estimated coefficients for given values of s.

**Author(s)**

Quentin Grimonprez

**See Also**

[MLGL](#), [predict.MLGL](#)

---

computeGroupSizeWeight

*Compute the group size weight vector with an authorized maximal size*

---

**Description**

Compute the group size weight vector with an authorized maximal size

**Usage**

```
computeGroupSizeWeight(hc, sizeMax = NULL)
```

**Arguments**

hc	output of hclust
sizeMax	maximum size of cluster to consider

**Value**

the weight vector

**Examples**

```

set.seed(42)
# Simulate gaussian data with block-diagonal variance matrix containing 12 blocks of size 5
X <- simuBlockGaussian(50, 12, 5, 0.7)
# Generate a response variable
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)
# use 20 as the maximal number of group
hc <- hclust(dist(t(X)))
w <- computeGroupSizeWeight(hc, sizeMax = 20)
# Apply MLGL method
res <- MLGL(X, y, hc = hc, weightSizeGroup = w)

```

---

cv.MLGL

---

*Multi-Layer Group-Lasso with cross V-fold validation*


---

**Description**

V-fold cross validation for [MLGL](#) function

**Usage**

```

cv.MLGL(
  X,
  y,
  nfold = 5,
  lambda = NULL,
  hc = NULL,
  weightLevel = NULL,
  weightSizeGroup = NULL,
  loss = c("ls", "logit"),
  intercept = TRUE,
  sizeMaxGroup = NULL,
  verbose = FALSE,
  ...
)

```

**Arguments**

X	matrix of size n*p
y	vector of size n. If loss = "logit", elements of y must be in -1,1
nfolds	number of folds
lambda	lambda values for group lasso. If not provided, the function generates its own values of lambda
hc	output of <a href="#">hclust</a> function. If not provided, <a href="#">hclust</a> is run with ward.D2 method
weightLevel	a vector of size p for each level of the hierarchy. A zero indicates that the level will be ignored. If not provided, use 1/(height between 2 successive levels)

weightSizeGroup	a vector
loss	a character string specifying the loss function to use, valid options are: "ls" least squares loss (regression) and "logit" logistic loss (classification)
intercept	should an intercept be included in the model ?
sizeMaxGroup	maximum size of selected groups. If NULL, no restriction
verbose	print some informations
...	Others parameters for <a href="#">cv.glasso</a> function

### Details

Hierarchical clustering is performed with all the variables. Then, the partitions from the different levels of the hierarchy are used in the different run of MLGL for cross validation.

### Value

a cv.MLGL object containing:

**lambda** values of lambda.

**cvm** the mean cross-validated error.

**cvsd** estimate of standard error of cvm

**cvupper** upper curve = cvm+cvsd

**cvlower** lower curve = cvm-cvsd

**lambda.min** The optimal value of lambda that gives minimum cross validation error cvm.

**lambda.1se** The largest value of lambda such that error is within 1 standard error of the minimum.

**time** computation time

### Author(s)

Quentin Grimonprez

### See Also

[MLGL](#), [stability.MLGL](#), [predict.cv.glasso](#), [coef.cv.MLGL](#), [plot.cv.MLGL](#)

### Examples

```
set.seed(42)
# Simulate gaussian data with block-diagonal variance matrix containing 12 blocks of size 5
X <- simuBlockGaussian(50, 12, 5, 0.7)
# Generate a response variable
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)
# Apply cv.MLGL method
res <- cv.MLGL(X, y)
```

---

Ftest	<i>F-test</i>
-------	---------------

---

**Description**

Perform a F-test

**Usage**

Ftest(X, y, varToTest)

**Arguments**

X	design matrix of size n*p
y	response vector of length n
varToTest	vector containing the index of the column of X to test

**Details**

$y = X * \text{beta} + \text{epsilon}$

null hypothesis:  $\text{beta}[\text{varToTest}] = 0$  alternative hypothesis: it exists an index k in varToTest such that  $\text{beta}[k] \neq 0$

The test statistic is based on a full and a reduced model. full:  $y = X * \text{beta}[\text{varToTest}] + \text{epsilon}$   
 reduced: the null model

**Value**

a vector of the same length as varToTest containing the p-values of the test.

**See Also**

[partialFtest](#)

---

fullProcess	<i>Full process of MLGL</i>
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---

**Description**

Run hierarchical clustering following by a group-lasso on all the different partition and a hierarchical testing procedure. Only for linear regression problem.



**Usage**

```

fullProcess(X, ...)

## Default S3 method:
fullProcess(
  X,
  y,
  control = c("FWER", "FDR"),
  alpha = 0.05,
  test = partialFtest,
  hc = NULL,
  fractionSampleMLGL = 1/2,
  BHclust = 50,
  nCore = NULL,
  addRoot = FALSE,
  Shaffer = FALSE,
  ...
)

## S3 method for class 'formula'
fullProcess(
  formula,
  data,
  control = c("FWER", "FDR"),
  alpha = 0.05,
  test = partialFtest,
  hc = NULL,
  fractionSampleMLGL = 1/2,
  BHclust = 50,
  nCore = NULL,
  addRoot = FALSE,
  Shaffer = FALSE,
  ...
)

```

**Arguments**

X	matrix of size n*p
...	Others parameters for MLGL
y	vector of size n.
control	either "FDR" or "FWER"
alpha	control level for testing procedure
test	test used in the testing procedure. Default is <a href="#">partialFtest</a>
hc	output of <a href="#">hclust</a> function. If not provided, <a href="#">hclust</a> is run with ward.D2 method. User can also provide the desired method: "single", "complete", "average", "mc-quitty", "ward.D", "ward.D2", "centroid", "median".

<code>fractionSampleMLGL</code>	a real between 0 and 1: the fraction of individuals to use in the sample for MLGL (see Details).
<code>BHclust</code>	number of replicates for computing the distance matrix for the hierarchical clustering tree
<code>nCore</code>	number of cores used for distance computation. Use all cores by default.
<code>addRoot</code>	If TRUE, add a common root containing all the groups
<code>Shaffer</code>	If TRUE, a Shaffer correction is performed (only if control = "FWER")
<code>formula</code>	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted.
<code>data</code>	an optional data frame, list or environment (or object coercible by <code>as.data.frame</code> to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment (formula)

### Details

Divide the  $n$  individuals in two samples. Then the three following steps are done: 1) Bootstrap Hierarchical Clustering of the variables of  $X$  2) MLGL on the second sample of individuals 3) Hierarchical testing procedure on the first sample of individuals.

### Value

a list containing:

**res** output of [MLGL](#) function

**lambdaOpt** lambda values maximizing the number of rejects

**var** A vector containing the index of selected variables for the first `lambdaOpt` value

**group** A vector containing the values index of selected groups for the first `lambdaOpt` value

**selectedGroups** Selected groups for the first `lambdaOpt` value

**reject** Selected groups for all lambda values

**alpha** Control level

**test** Test used in the testing procedure

**control** "FDR" or "FWER"

**time** Elapsed time

### Author(s)

Quentin Grimonprez

### See Also

[MLGL](#), [hierarchicalFDR](#), [hierarchicalFWER](#), [selfFDR](#), [selfFWER](#)

**Examples**

```
# least square loss
set.seed(42)
X <- simuBlockGaussian(50, 12, 5, 0.7)
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)
res <- fullProcess(X, y)
```

---

hierarchicalFDR	<i>Hierarchical testing with FDR control</i>
-----------------	--

---

**Description**

Apply hierarchical test for each hierarchy, and test external variables for FDR control at level alpha

**Usage**

```
hierarchicalFDR(X, y, group, var, test = partialFtest, addRoot = FALSE)
```

**Arguments**

X	original data
y	associated response
group	vector with index of groups. group[i] contains the index of the group of the variable var[i].
var	vector with the variables contained in each group. group[i] contains the index of the group of the variable var[i].
test	function for testing the nullity of a group of coefficients in linear regression. The function has 3 arguments: X, the design matrix, y, response, and varToTest, a vector containing the indices of the variables to test. The function returns a p-value
addRoot	If TRUE, add a common root containing all the groups

**Details**

Version of the hierarchical testing procedure of Yekutieli for MLGL output. You can use the [selfFDR](#) function to select groups at a desired level alpha.

**Value**

a list containing:

**pvalues** pvalues of the different test (without correction)

**adjPvalues** adjusted pvalues

**groupId** Index of the group

**hierMatrix** Matrix describing the hierarchical tree.

**References**

Yekutieli, Daniel. "Hierarchical False Discovery Rate-Controlling Methodology." Journal of the American Statistical Association 103.481 (2008): 309-16.

**See Also**

[selFDR](#), [hierarchicalFWER](#)

**Examples**

```
set.seed(42)
X <- simuBlockGaussian(50, 12, 5, 0.7)
y <- X[, c(2, 7, 12)] %**% c(2, 2, -2) + rnorm(50, 0, 0.5)
res <- MLGL(X, y)
test <- hierarchicalFDR(X, y, res$group[[20]], res$var[[20]])
```

---

hierarchicalFWER

*Hierarchical testing with FWER control*

---

**Description**

Apply hierarchical test for each hierarchy, and test external variables for FWER control at level alpha

**Usage**

```
hierarchicalFWER(
  X,
  y,
  group,
  var,
  test = partialFtest,
  Shaffer = FALSE,
  addRoot = FALSE
)
```

**Arguments**

X	original data
y	associated response
group	vector with index of groups. group[i] contains the index of the group of the variable var[i].
var	vector with the variables contained in each group. group[i] contains the index of the group of the variable var[i].

<code>test</code>	function for testing the nullity of a group of coefficients in linear regression. The function has 3 arguments: X, the design matrix, y, response, and varToTest, a vector containing the indices of the variables to test. The function returns a p-value
<code>Shaffer</code>	boolean, if TRUE, a Shaffer correction is performed
<code>addRoot</code>	If TRUE, add a common root containing all the groups

### Details

Version of the hierarchical testing procedure of Meinshausen for MLGL output. You can use the [selFWER](#) function to select groups at a desired level alpha

### Value

a list containing:

**pvalues** pvalues of the different test (without correction)

**adjPvalues** adjusted pvalues

**groupId** Index of the group

**hierMatrix** Matrix describing the hierarchical tree.

### References

Meinshausen, Nicolai. "Hierarchical Testing of Variable Importance." *Biometrika* 95.2 (2008): 265-78.

### See Also

[selFWER](#), [hierarchicalFDR](#)

### Examples

```
set.seed(42)
X <- simuBlockGaussian(50, 12, 5, 0.7)
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)
res <- MLGL(X, y)
test <- hierarchicalFWER(X, y, res$group[[20]], res$var[[20]])
```

### Description

Apply Hierarchical Multiple Testing procedure on a [MLGL](#) object

**Usage**

```
HMT(
  res,
  X,
  y,
  control = c("FWER", "FDR"),
  alpha = 0.05,
  test = partialFtest,
  addRoot = FALSE,
  Shaffer = FALSE,
  ...
)
```

**Arguments**

<code>res</code>	MLGL object
<code>X</code>	matrix of size n*p
<code>y</code>	vector of size n.
<code>control</code>	either "FDR" or "FWER"
<code>alpha</code>	control level for testing procedure
<code>test</code>	test used in the testing procedure. Default is <a href="#">partialFtest</a>
<code>addRoot</code>	If TRUE, add a common root containing all the groups
<code>Shaffer</code>	If TRUE, a Shaffer correction is performed (only if control = "FWER")
<code>...</code>	extra parameters for <a href="#">selfDR</a>

**Value**

a list containing:

**lambdaOpt** lambda values maximizing the number of rejects  
**var** A vector containing the index of selected variables for the first lambdaOpt value  
**group** A vector containing the values index of selected groups for the first lambdaOpt value  
**selectedGroups** Selected groups for the first lambdaOpt value  
**indLambdaOpt** indices associated with optimal lambdas  
**reject** Selected groups for all lambda values  
**alpha** Control level  
**test** Test used in the testing procedure  
**control** "FDR" or "FWER"  
**time** Elapsed time  
**hierTest** list containing the output of the testing function for each lambda. Each element can be used with the [selfFWER](#) or [selfFDR](#) functions.  
**lambda** lambda path  
**nGroup** Number of groups before testing  
**nSelectedGroup** Numer of groups after testing

**See Also**

[hierarchicalFWER](#) [hierarchicalFDR](#) [selfFWER](#) [selfFDR](#)

**Examples**

```
set.seed(42)
X <- simuBlockGaussian(50, 12, 5, 0.7)
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)
res <- MLGL(X, y)

# perform hierarchical testing with FWER control
out <- HMT(res, X, y, alpha = 0.05)

# test a new value of alpha for a specific lambda
selfFWER(out$hierTest[[60]], alpha = 0.1)
```

---

listToMatrix

*Obtain a sparse matrix of the coefficients of the path*

---

**Description**

Obtain a sparse matrix of the coefficients of the path

**Usage**

```
listToMatrix(x, row = c("covariates", "lambda"))
```

**Arguments**

x	<a href="#">MLGL</a> object
row	"lambda" or "covariates". If row="covariates", each row of the output matrix represents a covariate else if row="lambda", it represents a value of lambda.

**Details**

This function can be used with a [MLGL](#) object to obtain a matrix with all estimated coefficients for the  $p$  original variables. In case of overlapping groups, coefficients from repeated variables are summed.

**Value**

a sparse matrix containing the estimated coefficients for different lambdas

**See Also**

[MLGL](#), [overlapglasso](#)

**Examples**

```

# Simulate gaussian data with block-diagonal variance matrix containing 12 blocks of size 5
X <- simuBlockGaussian(50, 12, 5, 0.7)
# Generate a response variable
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)
# Apply MLGL method
res <- MLGL(X, y)
# Convert output in sparse matrix format
beta <- listToMatrix(res)

```

---

MLGL

---

*Multi-Layer Group-Lasso*


---

**Description**

Run hierarchical clustering following by a group-lasso on all the different partitions.

**Usage**

```

MLGL(X, ...)

## Default S3 method:
MLGL(
  X,
  y,
  hc = NULL,
  lambda = NULL,
  weightLevel = NULL,
  weightSizeGroup = NULL,
  intercept = TRUE,
  loss = c("ls", "logit"),
  sizeMaxGroup = NULL,
  verbose = FALSE,
  ...
)

## S3 method for class 'formula'
MLGL(
  formula,
  data,
  hc = NULL,
  lambda = NULL,
  weightLevel = NULL,
  weightSizeGroup = NULL,
  intercept = TRUE,
  loss = c("ls", "logit"),
  verbose = FALSE,

```



```

    ...
  )

```

### Arguments

<code>X</code>	matrix of size $n \times p$
<code>...</code>	Others parameters for <code>gglasso</code> function
<code>y</code>	vector of size $n$ . If <code>loss = "logit"</code> , elements of <code>y</code> must be in $-1, 1$
<code>hc</code>	output of <code>hclust</code> function. If not provided, <code>hclust</code> is run with <code>ward.D2</code> method. User can also provide the desired method: "single", "complete", "average", "mc-quitty", "ward.D", "ward.D2", "centroid", "median".
<code>lambda</code>	lambda values for group lasso. If not provided, the function generates its own values of lambda
<code>weightLevel</code>	a vector of size $p$ for each level of the hierarchy. A zero indicates that the level will be ignored. If not provided, use $1/(\text{height between 2 successive levels})$ . Only if <code>hc</code> is provided
<code>weightSizeGroup</code>	a vector of size $2 \times p - 1$ containing the weight for each group. Default is the square root of the size of each group. Only if <code>hc</code> is provided
<code>intercept</code>	should an intercept be included in the model ?
<code>loss</code>	a character string specifying the loss function to use, valid options are: "ls" least squares loss (regression) and "logit" logistic loss (classification)
<code>sizeMaxGroup</code>	maximum size of selected groups. If NULL, no restriction
<code>verbose</code>	print some information
<code>formula</code>	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted.
<code>data</code>	an optional data.frame, list or environment (or object coercible by <code>as.data.frame</code> to a data.frame) containing the variables in the model. If not found in data, the variables are taken from environment (formula)

### Value

a MLGL object containing:

**lambda** lambda values

**b0** intercept values for lambda

**beta** A list containing the values of estimated coefficients for each values of lambda

**var** A list containing the index of selected variables for each values of lambda

**group** A list containing the values index of selected groups for each values of lambda

**nVar** A vector containing the number of non zero coefficients for each values of lambda

**nGroup** A vector containing the number of non zero groups for each values of lambda

**structure** A list containing 3 vectors. `var`: all variables used. `group`: associated groups. `weight`: weight associated with the different groups. `level`: for each group, the corresponding level of the hierarchy where it appears and disappears. 3 indicates the level with a partition of 3 groups.

**time** computation time  
**dim** dimension of X  
**hc** Output of hierarchical clustering  
**call** Code executed by user

### Author(s)

Quentin Grimonprez

### See Also

[cv.MLGL](#), [stability.MLGL](#), [listToMatrix](#), [predict.MLGL](#), [coef.MLGL](#), [plot.cv.MLGL](#)

### Examples

```
set.seed(42)
# Simulate gaussian data with block-diagonal variance matrix containing 12 blocks of size 5
X <- simuBlockGaussian(50, 12, 5, 0.7)
# Generate a response variable
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)
# Apply MLGL method
res <- MLGL(X, y)
```

---

overlappglasso

*Group-lasso with overlapping groups*

---

### Description

Group-lasso with overlapping groups

### Usage

```
overlappglasso(
  X,
  y,
  var,
  group,
  lambda = NULL,
  weight = NULL,
  loss = c("ls", "logit"),
  intercept = TRUE,
  ...
)
```

**Arguments**

<code>X</code>	matrix of size $n \times p$
<code>y</code>	vector of size $n$ . If <code>loss = "logit"</code> , elements of <code>y</code> must be in $-1,1$
<code>var</code>	vector containing the variable to use
<code>group</code>	vector containing the associated groups
<code>lambda</code>	lambda values for group lasso. If not provided, the function generates its own values of lambda
<code>weight</code>	a vector the weight for each group. Default is the square root of the size of each group
<code>loss</code>	a character string specifying the loss function to use, valid options are: "ls" least squares loss (regression) and "logit" logistic loss (classification)
<code>intercept</code>	should an intercept be included in the model ?
<code>...</code>	Others parameters for <code>gglasso</code> function

**Details**

Use a group-lasso algorithm (see `gglasso`) to solve a group-lasso with overlapping groups. Each variable  $j$  of the original matrix  $X$  is paste  $k(j)$  times in a new dataset with  $k(j)$  the number of different groups containing the variable  $j$ . The new dataset is used to solve the group-lasso with overlapping groups running a group-lasso algorithm.

**Value**

a MLGL object containing:

**lambda** lambda values

**b0** intercept values for lambda

**beta** A list containing the values of estimated coefficients for each values of lambda

**var** A list containing the index of selected variables for each values of lambda

**group** A list containing the values index of selected groups for each values of lambda

**nVar** A vector containing the number of non zero coefficients for each values of lambda

**nGroup** A vector containing the number of non zero groups for each values of lambda

**structure** A list containing 3 vectors. `var`: all variables used. `group`: associated groups. `weight`: weight associated with the different groups.

**time** computation time

**dim** dimension of  $X$

**Source**

Laurent Jacob, Guillaume Obozinski, and Jean-Philippe Vert. 2009. Group lasso with overlap and graph lasso. In Proceedings of the 26th Annual International Conference on Machine Learning (ICML '09).

**See Also**[listToMatrix](#)**Examples**

```
# Least square loss
set.seed(42)
X <- simuBlockGaussian(50, 12, 5, 0.7)
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)
var <- c(1:60, 1:8, 7:15)
group <- c(rep(1:12, each = 5), rep(13, 8), rep(14, 9))
res <- overlappglasso(X, y, var, group)

# Logistic loss
y <- 2 * (rowSums(X[, 1:4]) > 0) - 1
var <- c(1:60, 1:8, 7:15)
group <- c(rep(1:12, each = 5), rep(13, 8), rep(14, 9))
res <- overlappglasso(X, y, var, group, loss = "logit")
```

---

partialFtest

*Partial F-test*


---

**Description**

Perform a partial F-test

**Usage**

```
partialFtest(X, y, varToTest)
```

**Arguments**

X	design matrix of size n*p
y	response vector of length n
varToTest	vector containing the index of the column of X to test

**Details**

$$y = X * \beta + \epsilon$$

null hypothesis:  $\beta[\text{varToTest}] = 0$  alternative hypothesis: it exists an index k in varToTest such that  $\beta[k] \neq 0$

The test statistic is based on a full and a reduced model. full:  $y = X * \beta + \epsilon$  reduced:  $y = X * \beta[-\text{varToTest}] + \epsilon$

**Value**

a vector of the same length as varToTest containing the p-values of the test.

**See Also**[Ftest](#)

---

`plot.cv.MLGL`*Plot the cross-validation obtained from [cv.MLGL](#) function*

---

**Description**

Plot the cross-validation obtained from [cv.MLGL](#) function

**Usage**

```
## S3 method for class 'cv.MLGL'  
plot(x, log.lambda = FALSE, ...)
```

**Arguments**

<code>x</code>	<a href="#">cv.MLGL</a> object
<code>log.lambda</code>	If TRUE, use <code>log(lambda)</code> instead of <code>lambda</code> in abscissa
<code>...</code>	Other parameters for plot function

**See Also**[cv.MLGL](#)**Examples**

```
set.seed(42)  
# Simulate gaussian data with block-diagonal variance matrix containing 12 blocks of size 5  
X <- simuBlockGaussian(50, 12, 5, 0.7)  
# Generate a response variable  
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)  
# Apply cv.MLGL method  
res <- cv.MLGL(X, y)  
# Plot the cv error curve  
plot(res)
```

---

plot.fullProcess      *Plot the path obtained from fullProcess function*

---

### Description

Plot the path obtained from [fullProcess](#) function

### Usage

```
## S3 method for class 'fullProcess'
plot(
  x,
  log.lambda = FALSE,
  lambda.lines = FALSE,
  lambda.opt = c("min", "max", "both"),
  ...
)
```

### Arguments

x	<a href="#">fullProcess</a> object
log.lambda	If TRUE, use log(lambda) instead of lambda in abscissa
lambda.lines	If TRUE, add vertical lines at lambda values
lambda.opt	If there is several optimal lambdas, which one to print "min", "max" or "both"
...	Other parameters for plot function

### See Also

[fullProcess](#)

### Examples

```
set.seed(42)
# Simulate gaussian data with block-diagonal variance matrix containing 12 blocks of size 5
X <- simuBlockGaussian(50, 12, 5, 0.7)
# Generate a response variable
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)
# Apply MLGL method
res <- fullProcess(X, y)
# Plot the solution path
plot(res)
```

---

`plot.HMT`*Plot the path obtained from [HMT](#) function*

---

## Description

Plot the path obtained from [HMT](#) function

## Usage

```
## S3 method for class 'HMT'  
plot(  
  x,  
  log.lambda = FALSE,  
  lambda.lines = FALSE,  
  lambda.opt = c("min", "max", "both"),  
  ...  
)
```

## Arguments

<code>x</code>	<a href="#">fullProcess</a> object
<code>log.lambda</code>	If TRUE, use <code>log(lambda)</code> instead of <code>lambda</code> in abscissa
<code>lambda.lines</code>	If TRUE, add vertical lines at <code>lambda</code> values
<code>lambda.opt</code>	If there is several optimal lambdas, which one to print "min", "max" or "both"
<code>...</code>	Other parameters for plot function

## See Also

[HMT](#)

## Examples

```
set.seed(42)  
# Simulate gaussian data with block-diagonal variance matrix containing 12 blocks of size 5  
X <- simuBlockGaussian(50, 12, 5, 0.7)  
# Generate a response variable  
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)  
# Apply MLGL method  
res <- MLGL(X, y)  
  
out <- HMT(res, X, y)  
plot(out)
```

---

plot.MLGL                      *Plot the path obtained from MLGL function*

---

### Description

Plot the path obtained from [MLGL](#) function

### Usage

```
## S3 method for class 'MLGL'
plot(x, log.lambda = FALSE, lambda.lines = FALSE, ...)
```

### Arguments

x	<a href="#">MLGL</a> object
log.lambda	If TRUE, use log(lambda) instead of lambda in abscissa
lambda.lines	if TRUE, add vertical lines at lambda values
...	Other parameters for plot function

### See Also

[MLGL](#)

### Examples

```
# Simulate gaussian data with block-diagonal variance matrix containing 12 blocks of size 5
set.seed(42)
X <- simuBlockGaussian(50, 12, 5, 0.7)
# Generate a response variable
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)
# Apply MLGL method
res <- MLGL(X, y)
# Plot the solution path
plot(res)
```

---

plot.stability.MLGL            *Plot the stability path obtained from [stability.MLGL](#) function*

---

### Description

Plot the stability path obtained from [stability.MLGL](#) function

### Usage

```
## S3 method for class 'stability.MLGL'
plot(x, log.lambda = FALSE, threshold = 0.75, ...)
```



**Arguments**

x	<a href="#">stability.MLGL</a> object
log.lambda	If TRUE, use log(lambda) instead of lambda in abscissa
threshold	Threshold for selection frequency
...	Other parameters for plot function

**Value**

A list containing:

**var** Index of selected variables for the given threshold.

**group** Index of the associated group.

**threshold** Value of threshold

**See Also**

[stability.MLGL](#)

**Examples**

```
set.seed(42)
# Simulate gaussian data with block-diagonal variance matrix containing 12 blocks of size 5
X <- simuBlockGaussian(50, 12, 5, 0.7)

# Generate a response variable
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)

# Apply stability.MLGL method
res <- stability.MLGL(X, y)
selected <- plot(res)
print(selected)
```

---

predict.cv.MLGL

*Predict fitted values from a [cv.MLGL](#) object*

---

**Description**

Predict fitted values from a [cv.MLGL](#) object

**Usage**

```
## S3 method for class 'cv.MLGL'
predict(
  object,
  newx = NULL,
  s = c("lambda.1se", "lambda.min"),
  type = c("fit", "coefficients"),
  ...
)
```

**Arguments**

object	<a href="#">cv.MLGL</a> object
newx	matrix with new individuals for prediction. If type="coefficients", the parameter has to be NULL
s	Either "lambda.1se" or "lambda.min"
type	if "fit", return the fitted values for each values of s, if "coefficients", return the estimated coefficients for each s
...	Not used. Other arguments to predict.

**Value**

A matrix with fitted values or estimated coefficients for given values of s.

**Author(s)**

Quentin Grimonprez

**See Also**

[cv.MLGL](#)

---

predict.MLGL

*Predict fitted values from a [MLGL](#) object*

---

**Description**

Predict fitted values from a [MLGL](#) object

**Usage**

```
## S3 method for class 'MLGL'
predict(object, newx = NULL, s = NULL, type = c("fit", "coefficients"), ...)
```

**Arguments**

object	<a href="#">MLGL</a> object
newx	matrix with new individuals for prediction. If type="coefficients", the parameter has to be NULL
s	values of lambda. If NULL, use values from object
type	if "fit", return the fitted values for each values of s, if "coefficients", return the estimated coefficients for each s
...	Not used. Other arguments to predict.

**Value**

A matrix with fitted values or estimated coefficients for given values of s.

**Author(s)**

original code from **gglasso** package Author: Yi Yang <yiyang@umn.edu>, Hui Zou <hzou@stat.umn.edu>  
function inspired from predict function from gglasso package by Yi Yang and Hui Zou.

**See Also**

[MLGL](#)

**Examples**

```
X <- simuBlockGaussian(n = 50, nBlock = 12, sizeBlock = 5, rho = 0.7)
y <- drop(X[, c(2, 7, 12)] %*% c(2, 2, -1)) + rnorm(50, 0, 0.5)

m1 <- MLGL(X, y, loss = "ls")
predict(m1, newx = X)
predict(m1, s=3, newx = X)
predict(m1, s=1:3, newx = X)
```

---

print.fullProcess      *Print Values*

---

**Description**

Print a [fullProcess](#) object

**Usage**

```
## S3 method for class 'fullProcess'
print(x, ...)
```

**Arguments**

x                    [fullProcess](#) object  
...                   Not used.

**See Also**

[fullProcess](#) [summary.fullProcess](#)

**Examples**

```
set.seed(42)
# Simulate gaussian data with block-diagonal variance matrix containing 12 blocks of size 5
X <- simuBlockGaussian(50, 12, 5, 0.7)
# Generate a response variable
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)
# Apply MLGL method
res <- fullProcess(X, y)
print(res)
```

---

print.HMT

*Print Values*

---

**Description**

Print a [HMT](#) object

**Usage**

```
## S3 method for class 'HMT'
print(x, ...)
```

**Arguments**

x                    [HMT](#) object  
...                   Not used.

**See Also**

[HMT](#) [summary.HMT](#)

## Examples

```
set.seed(42)
# Simulate gaussian data with block-diagonal variance matrix containing 12 blocks of size 5
X <- simuBlockGaussian(50, 12, 5, 0.7)
# Generate a response variable
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)
# Apply MLGL method
res <- MLGL(X, y)
out <- HMT(res, X, y)
print(out)
```

---

print.MLGL

*Print Values*

---

## Description

Print a [MLGL](#) object

## Usage

```
## S3 method for class 'MLGL'
print(x, ...)
```

## Arguments

x	<a href="#">MLGL</a> object
...	Not used.

## See Also

[MLGL summary.MLGL](#)

## Examples

```
set.seed(42)
# Simulate gaussian data with block-diagonal variance matrix containing 12 blocks of size 5
X <- simuBlockGaussian(50, 12, 5, 0.7)
# Generate a response variable
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)
# Apply MLGL method
res <- MLGL(X, y)
print(res)
```

---

`selFDR`*Selection from hierarchical testing with FDR control*

---

**Description**

Select groups from hierarchical testing procedure with FDR control ([hierarchicalFDR](#))

**Usage**

```
selFDR(out, alpha = 0.05, global = TRUE, outer = TRUE)
```

**Arguments**

<code>out</code>	output of <a href="#">hierarchicalFDR</a> function
<code>alpha</code>	control level for test
<code>global</code>	if FALSE the provided alpha is the desired level control for each family.
<code>outer</code>	if TRUE, the FDR is controlled only on outer node (rejected groups without rejected children). If FALSE, it is controlled on the full tree.

**Details**

See the reference for more details about the method.

If each family is controlled at a level  $\alpha$ , we have the following control: FDR control of full tree:  $\alpha * \delta * 2$  ( $\delta = 1.44$ ) FDR control of outer node:  $\alpha * L * \delta * 2$  ( $\delta = 1.44$ )

**Value**

a list containing:

**toSel** vector of boolean. TRUE if the group is selected

**groupId** Names of groups

**local.alpha** control level for each family of hypothesis

**global.alpha** control level for the tree (full tree or outer node)

**References**

Yekutieli, Daniel. "Hierarchical False Discovery Rate-Controlling Methodology." Journal of the American Statistical Association 103.481 (2008): 309-16.

**See Also**

[hierarchicalFDR](#)

## Examples

```
set.seed(42)
X <- simuBlockGaussian(50, 12, 5, 0.7)
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)
res <- MLGL(X, y)
test <- hierarchicalFDR(X, y, res$group[[20]], res$var[[20]])
sel <- selFDR(test, alpha = 0.05)
```

---

selFWER

*Selection from hierarchical testing with FWER control*

---

## Description

Select groups from hierarchical testing procedure with FWER control ([hierarchicalFWER](#))

## Usage

```
selFWER(out, alpha = 0.05)
```

## Arguments

out	output of <a href="#">hierarchicalFWER</a> function
alpha	control level for test

## Details

Only outer nodes (rejected groups without rejected children) are returned as TRUE.

## Value

a list containing:

**toSel** vector of boolean. TRUE if the group is selected

**groupId** Names of groups

## References

Meinshausen, Nicolai. "Hierarchical Testing of Variable Importance." *Biometrika* 95.2 (2008): 265-78.

## See Also

[hierarchicalFWER](#)

### Examples

```
set.seed(42)
X <- simuBlockGaussian(50, 12, 5, 0.7)
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)
res <- MLGL(X, y)
test <- hierarchicalFWER(X, y, res$group[[20]], res$var[[20]])
sel <- selFWER(test, alpha = 0.05)
```

---

simuBlockGaussian	<i>Simulate multivariate Gaussian samples with block diagonal variance matrix</i>
-------------------	---

---

### Description

Simulate  $n$  samples from a gaussian multivariate law with 0 vector mean and block diagonal variance matrix with diagonal 1 and block of  $\rho$ .

### Usage

```
simuBlockGaussian(n, nBlock, sizeBlock, rho)
```

### Arguments

<code>n</code>	number of samples to simulate
<code>nBlock</code>	number of blocks
<code>sizeBlock</code>	size of blocks
<code>rho</code>	correlation within each block

### Value

a matrix of size  $n * (nBlock * sizeBlock)$  containing the samples

### Author(s)

Quentin Grimonprez

### Examples

```
X <- simuBlockGaussian(50, 12, 5, 0.7)
```



---

stability.MLGL

*Stability Selection for Multi-Layer Group-lasso*


---

**Description**

Stability selection for [MLGL](#)

**Usage**

```
stability.MLGL(
  X,
  y,
  B = 50,
  fraction = 0.5,
  hc = NULL,
  lambda = NULL,
  weightLevel = NULL,
  weightSizeGroup = NULL,
  loss = c("ls", "logit"),
  intercept = TRUE,
  verbose = FALSE,
  ...
)
```

**Arguments**

X	matrix of size n*p
y	vector of size n. If loss = "logit", elements of y must be in -1,1
B	number of bootstrap sample
fraction	Fraction of data used at each of the B sub-samples
hc	output of <a href="#">hclust</a> function. If not provided, <a href="#">hclust</a> is run with ward.D2 method
lambda	lambda values for group lasso. If not provided, the function generates its own values of lambda
weightLevel	a vector of size p for each level of the hierarchy. A zero indicates that the level will be ignored. If not provided, use 1/(height between 2 successive levels)
weightSizeGroup	a vector
loss	a character string specifying the loss function to use, valid options are: "ls" least squares loss (regression) and "logit" logistic loss (classification)
intercept	should an intercept be included in the model ?
verbose	print some informations
...	Others parameters for <a href="#">gglasso</a> function

## Details

Hierarchical clustering is performed with all the variables. Then, the partitions from the different levels of the hierarchy are used in the different runs of MLGL for estimating the probability of selection of each group.

## Value

a stability.MLGL object containing:

**lambda** sequence of lambda.

**B** Number of bootstrap samples.

**stability** A matrix of size length(lambda)\*number of groups containing the probability of selection of each group

**var** vector containing the index of covariates

**group** vector containing the index of associated groups of covariates

**time** computation time

## Author(s)

Quentin Grimonprez

## References

Meinshausen and Bühlmann (2010). Stability selection. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)* 72.4, p. 417-473.

## See Also

[cv.MLGL](#), [MLGL](#)

## Examples

```
set.seed(42)
# Simulate gaussian data with block-diagonal variance matrix containing 12 blocks of size 5
X <- simuBlockGaussian(50, 12, 5, 0.7)

# Generate a response variable
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)

# Apply stability.MLGL method
res <- stability.MLGL(X, y)
```

---

summary.fullProcess     *Object Summaries*

---

**Description**

Summary of a [fullProcess](#) object

**Usage**

```
## S3 method for class 'fullProcess'  
summary(object, ...)
```

**Arguments**

object	<a href="#">fullProcess</a> object
...	Not used.

**See Also**

[fullProcess](#) [print.fullProcess](#)

**Examples**

```
set.seed(42)  
# Simulate gaussian data with block-diagonal variance matrix containing 12 blocks of size 5  
X <- simuBlockGaussian(50, 12, 5, 0.7)  
# Generate a response variable  
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)  
# Apply MLGL method  
res <- fullProcess(X, y)  
summary(res)
```

---

summary.HMT     *Object Summaries*

---

**Description**

Summary of a [HMT](#) object

**Usage**

```
## S3 method for class 'HMT'  
summary(object, ...)
```

**Arguments**

object	<a href="#">HMT</a> object
...	Not used.

**See Also**

[HMT print.HMT](#)

**Examples**

```
set.seed(42)
# Simulate gaussian data with block-diagonal variance matrix containing 12 blocks of size 5
X <- simuBlockGaussian(50, 12, 5, 0.7)
# Generate a response variable
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)
# Apply MLGL method
res <- MLGL(X, y)
out <- HMT(res, X, y)
summary(out)
```

---

summary.MLGL

*Object Summaries*

---

**Description**

Summary of a [MLGL](#) object

**Usage**

```
## S3 method for class 'MLGL'
summary(object, ...)
```

**Arguments**

object	<a href="#">MLGL</a> object
...	Not used.

**See Also**

[MLGL print.MLGL](#)

**Examples**

```
set.seed(42)
# Simulate gaussian data with block-diagonal variance matrix containing 12 blocks of size 5
X <- simuBlockGaussian(50, 12, 5, 0.7)
# Generate a response variable
y <- X[, c(2, 7, 12)] %*% c(2, 2, -2) + rnorm(50, 0, 0.5)
# Apply MLGL method
res <- MLGL(X, y)
summary(res)
```

---

uniqueGroupHclust      *Find all unique groups in [hclust](#) results*

---

**Description**

Find all unique groups in [hclust](#) results

**Usage**

```
uniqueGroupHclust(hc)
```

**Arguments**

hc                      output of [hclust](#) function

**Value**

A list containing:

**indexGroup** Vector containing the index of variables.

**varGroup** Vector containing the index of the group of each variable.

**Author(s)**

Quentin Grimonprez

**Examples**

```
hc <- hclust(dist(USArrests), "average")
res <- uniqueGroupHclust(hc)
```

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