

# Package ‘adelie’

September 3, 2024

**Title** Group Lasso and Elastic Net Solver for Generalized Linear Models

**Version** 1.0.2

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**Description** Extremely efficient procedures for fitting the entire group lasso and group elastic net regularization path for GLMs, multinomial, the Cox model and multi-task Gaussian models. Similar to the R package glmnet in scope of models, and in computational speed. This package provides R bindings to the C++ code underlying the corresponding Python package 'adelie'. These bindings offer a general purpose group elastic net solver, a wide range of matrix classes that can exploit special structure to allow large-scale inputs, and an assortment of generalized linear model classes for fitting various types of data. The package includes  
The package is an implementation of Yang, J. and Hastie, T. (2024) <doi:10.48550/arXiv.2405.08631>.

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**Author** James Yang [aut, cph],  
Trevor Hastie [aut, cph, cre],  
Balasubramanian Narasimhan [aut]

**Maintainer** Trevor Hastie <hastie@stanford.edu>

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## Contents

cv.grpnet . . . . .	2
gaussian_cov . . . . .	5
glm.binomial . . . . .	7
glm.cox . . . . .	8
glm.gaussian . . . . .	9
glm.multigaussian . . . . .	10
glm.multinomial . . . . .	11
glm.poisson . . . . .	12
grpnet . . . . .	13
io.snp_phased_ancestry . . . . .	16
io.snp_unphased . . . . .	17
matrix.block_diag . . . . .	18
matrix.concatenate . . . . .	19
matrix.dense . . . . .	20
matrix.eager_cov . . . . .	21
matrix.interaction . . . . .	21
matrix.kronecker_eye . . . . .	22
matrix.lazy_cov . . . . .	23
matrix.one_hot . . . . .	24
matrix.snp_phased_ancestry . . . . .	25
matrix.snp_unphased . . . . .	26
matrix.sparse . . . . .	27
matrix.standardize . . . . .	28
matrix.subset . . . . .	29
plot.cv.grpnet . . . . .	30
plot.grpnet . . . . .	31
predict.cv.grpnet . . . . .	32
predict.grpnet . . . . .	33
print.cv.grpnet . . . . .	35
print.grpnet . . . . .	36
set_configs . . . . .	37
<b>Index</b>	<b>38</b>

---

 cv.grpnet

*Cross-validation for grpnet*


---

### Description

Does k-fold cross-validation for grpnet

**Usage**

```

cv.grpnet(
  X,
  glm,
  n_folds = 10,
  foldid = NULL,
  min_ratio = 0.01,
  lmda_path_size = 100,
  offsets = NULL,
  progress_bar = FALSE,
  n_threads = 1,
  ...
)

```

**Arguments**

<code>X</code>	Feature matrix. Either a regular R matrix, or else an <code>adelle</code> custom matrix class, or a concatenation of such.
<code>glm</code>	GLM family/response object. This is an expression that represents the family, the response and other arguments such as weights, if present. The choices are <code>glm.gaussian()</code> , <code>glm.binomial()</code> , <code>glm.poisson()</code> , <code>glm.multinomial()</code> , <code>glm.cox()</code> , <code>glm.multinomial()</code> , and <code>glm.multigaussian()</code> . This is a required argument, and there is no default. In the simple example below, we use <code>glm.gaussian(y)</code> .
<code>n_folds</code>	(default 10). Although <code>n_folds</code> can be as large as the sample size (leave-one-out CV), it is not recommended for large datasets. Smallest value allowable is <code>n_folds=3</code> .
<code>foldid</code>	An optional vector of values between 1 and <code>n_folds</code> identifying what fold each observation is in. If supplied, <code>n_folds</code> can be missing.
<code>min_ratio</code>	Ratio between smallest and largest value of lambda. Default is 1e-2.
<code>lmda_path_size</code>	Number of values for lambda, if generated automatically. Default is 100.
<code>offsets</code>	Offsets, default is NULL. If present, this is a fixed vector or matrix corresponding to the shape of the natural parameter, and is added to the fit.
<code>progress_bar</code>	Progress bar. Default is FALSE.
<code>n_threads</code>	Number of threads, default 1.
<code>...</code>	Other arguments that can be passed to <code>grpnet</code>

**Details**

The function runs `grpnet` `n_folds+1` times; the first to get the lambda sequence, and then the remainder to compute the fit with each of the folds omitted. The out-of-fold deviance is accumulated, and the average deviance and standard deviation over the folds is computed. Note that `cv.grpnet` does NOT search for values for alpha. A specific value should be supplied, else `alpha=1` is assumed by default. If users would like to cross-validate alpha as well, they should call `cv.grpnet` with a pre-computed vector `foldid`, and then use this same `foldid` vector in separate calls to `cv.grpnet` with different values of alpha. Note also that the results of `cv.grpnet` are random, since the folds are selected at random. Users can reduce this randomness by running `cv.grpnet` many times, and averaging the error curves.

**Value**

an object of class "cv.grpnet" is returned, which is a list with the ingredients of the cross-validation fit.

lambda	the values of lambda used in the fits.
cvm	The mean cross-validated deviance - a vector of length length(lambda).
cvsd	estimate of standard error of cvm.
cvup	upper curve = cvm+cvsd.
cvlo	lower curve = cvm-cvsd.
nzero	number of non-zero coefficients at each lambda.
name	a text string indicating type of measure (for plotting purposes). Currently this is "deviance"
grpnet.fit	a fitted grpnet object for the full data.
lambda.min	value of lambda that gives minimum cvm.
lambda.1se	largest value of lambda such that mean deviance is within 1 standard error of the minimum.
index	a one column matrix with the indices of lambda.min and lambda.1se in the sequence of coefficients, fits etc.

**Author(s)**

James Yang, Trevor Hastie, and Balasubramanian Narasimhan  
 Maintainer: Trevor Hastie <hastie@stanford.edu>

**References**

- Yang, James and Hastie, Trevor. (2024) A Fast and Scalable Pathwise-Solver for Group Lasso and Elastic Net Penalized Regression via Block-Coordinate Descent. arXiv [doi:10.48550/arXiv.2405.08631](https://arxiv.org/abs/2405.08631).
- Friedman, J., Hastie, T. and Tibshirani, R. (2008) *Regularization Paths for Generalized Linear Models via Coordinate Descent (2010)*, *Journal of Statistical Software*, Vol. 33(1), 1-22, [doi:10.18637/jss.v033.i01](https://doi.org/10.18637/jss.v033.i01).
- Simon, N., Friedman, J., Hastie, T. and Tibshirani, R. (2011) *Regularization Paths for Cox's Proportional Hazards Model via Coordinate Descent*, *Journal of Statistical Software*, Vol. 39(5), 1-13, [doi:10.18637/jss.v039.i05](https://doi.org/10.18637/jss.v039.i05).
- Tibshirani, Robert, Bien, J., Friedman, J., Hastie, T., Simon, N., Taylor, J. and Tibshirani, Ryan. (2012) *Strong Rules for Discarding Predictors in Lasso-type Problems*, *JRSSB*, Vol. 74(2), 245-266, <https://arxiv.org/abs/1011.2234>.

**Examples**

```
set.seed(0)
n <- 100
p <- 200
X <- matrix(rnorm(n * p), n, p)
y <- X[,1] * rnorm(1) + rnorm(n)
```

```
fit <- grpnet(X, glm.gaussian(y))
print(fit)
```

---

`gaussian_cov`*Solves group elastic net via covariance method.*

---

## Description

Solves group elastic net via covariance method.

## Usage

```
gaussian_cov(  
  A,  
  v,  
  constraints = NULL,  
  groups = NULL,  
  alpha = 1,  
  penalty = NULL,  
  lmda_path = NULL,  
  max_iters = as.integer(1e+05),  
  tol = 1e-07,  
  rdev_tol = 0.001,  
  newton_tol = 1e-12,  
  newton_max_iters = 1000,  
  n_threads = 1,  
  early_exit = TRUE,  
  screen_rule = "pivot",  
  min_ratio = 0.01,  
  lmda_path_size = 100,  
  max_screen_size = NULL,  
  max_active_size = NULL,  
  pivot_subset_ratio = 0.1,  
  pivot_subset_min = 1,  
  pivot_slack_ratio = 1.25,  
  check_state = FALSE,  
  progress_bar = TRUE,  
  warm_start = NULL  
)
```

## Arguments

<code>A</code>	Positive semi-definite matrix.
<code>v</code>	Linear term.
<code>constraints</code>	Constraints.
<code>groups</code>	Groups.

alpha	Elastic net parameter.
penalty	Penalty factor.
lmda_path	The regularization path.
max_iters	Maximum number of coordinate descents.
tol	Coordinate descent convergence tolerance.
rdev_tol	Relative percent deviance explained tolerance.
newton_tol	Convergence tolerance for the BCD update.
newton_max_iters	Maximum number of iterations for the BCD update.
n_threads	Number of threads.
early_exit	TRUE if the function should exit early.
screen_rule	Screen rule (currently the only value is the default "pivot").
min_ratio	Ratio between largest and smallest regularization parameter, default is 0.01.
lmda_path_size	Number of regularization steps in the path, default is 100.
max_screen_size	Maximum number of screen groups, default is NULL for no maximum.
max_active_size	Maximum number of active groups, default is NULL for no maximum.
pivot_subset_ratio	Subset ratio of pivot rule, default is 0.1.
pivot_subset_min	Minimum subset of pivot rule, default is 1.
pivot_slack_ratio	Slack ratio of pivot rule, default is 1.25.
check_state	Check state, default is FALSE.
progress_bar	Progress bar, default is TRUE.
warm_start	Warm start, default is NULL (no warm start).

**Value**

State of the solver.

**Examples**

```

set.seed(0)
n <- 100
p <- 200
X <- matrix(rnorm(n * p), n, p)
y <- X[,1] * rnorm(1) + rnorm(n)
A <- t(X) %*% X / n
v <- t(X) %*% y / n
state <- gaussian_cov(A, v)

```

---

glm.binomial	<i>Creates a Binomial GLM family object.</i>
--------------	--

---

### Description

A GLM family object specifies the type of model fit, provides the appropriate response object and makes sure it is represented in the right form for the model family, and allows for optional parameters such as a weight vector.

### Usage

```
glm.binomial(y, weights = NULL, link = "logit")
```

### Arguments

y	Binary response vector, with values 0 or 1, or a logical vector. Alternatively, if data are represented by a two-column matrix of proportions (with row-sums = 1), then one can provide one of the columns as the response. This is useful for grouped binomial data, where each observation represents the result of $m[i]$ successes out of $n[i]$ trials. Then the response is provided as $y[i] = m[i]/n[i]$ and the corresponding element of the weight vector as $w[i]=n[i]$ . Alternatively can use <code>glm.multinomial()</code> instead.
weights	Observation weight vector, with default NULL.
link	The link function type, with choice "logit" (default) or "probit").

### Value

Binomial GLM object.

### Author(s)

Trevor Hastie and James Yang  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

### See Also

`glm.gaussian`, `glm.binomial`, `glm.poisson`, `glm.multinomial`, `glm.multigaussian`, `glm.cox`.

### Examples

```
n <- 100
y <- rbinom(n, 1, 0.5)
obj <- glm.binomial(y)
```

---

`glm.cox`*Creates a Cox GLM family object.*

---

### Description

A GLM family object specifies the type of model fit, provides the appropriate response object and makes sure it is represented in the right form for the model family, and allows for optional parameters such as a weight vector.

### Usage

```
glm.cox(  
  stop,  
  status,  
  start = -Inf,  
  weights = NULL,  
  tie_method = c("efron", "breslow")  
)
```

### Arguments

<code>stop</code>	Stop time vector.
<code>status</code>	Binary status vector of same length as <code>stop</code> , with 1 a "death", and 0 censored.
<code>start</code>	Start time vector. Default is a vector of <code>-Inf</code> of same length as <code>stop</code> .
<code>weights</code>	Observation weights, with default <code>NULL</code> .
<code>tie_method</code>	The tie-breaking method - one of "efron" (default) or "breslow".

### Value

Cox GLM object.

### Author(s)

James Yang, Trevor Hastie, and Balasubramanian Narasimhan  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

### See Also

`glm.gaussian`, `glm.binomial`, `glm.poisson`, `glm.multinomial`, `glm.multigaussian`, `glm.cox`.

### Examples

```
n <- 100  
start <- sample.int(20, size=n, replace=TRUE)  
stop <- start + 1 + sample.int(5, size=n, replace=TRUE)  
status <- rbinom(n, 1, 0.5)  
obj <- glm.cox(start, stop, status)
```



---

glm.gaussian	<i>Creates a Gaussian GLM family object.</i>
--------------	--

---

**Description**

A GLM family object specifies the type of model fit, provides the appropriate response object and makes sure it is represented in the right form for the model family, and allows for optional parameters such as a weight vector.

**Usage**

```
glm.gaussian(y, weights = NULL, opt = TRUE)
```

**Arguments**

y	Response vector.
weights	Observation weight vector, with default NULL.
opt	If TRUE (default), an optimized routine is run.

**Value**

Gaussian GLM

**Author(s)**

James Yang, Trevor Hastie, and Balasubramanian Narasimhan  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

**See Also**

`glm.gaussian`, `glm.binomial`, `glm.poisson`, `glm.multinomial`, `glm.multigaussian`, `glm.cox`.

**Examples**

```
n <- 100  
y <- rnorm(n)  
obj <- glm.gaussian(y)
```

---

glm.multigaussian      *Creates a MultiGaussian GLM family object.*

---

### Description

A GLM family object specifies the type of model fit, provides the appropriate response object and makes sure it is represented in the right form for the model family, and allows for optional parameters such as a weight vector.

### Usage

```
glm.multigaussian(y, weights = NULL, opt = TRUE)
```

### Arguments

y	Response matrix, with two or more columns.
weights	Observation weight vector, with default NULL.
opt	If TRUE (default), an optimized routine is run.

### Value

MultiGaussian GLM object.

### Author(s)

James Yang, Trevor Hastie, and Balasubramanian Narasimhan  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

### See Also

`glm.gaussian`, `glm.binomial`, `glm.poisson`, `glm.multinomial`, `glm.multigaussian`, `glm.cox`.

### Examples

```
n <- 100
K <- 5
y <- matrix(rnorm(n*K), n, K)
obj <- glm.multigaussian(y)
```

---

glm.multinomial      *Creates a Multinomial GLM family object.*

---

### Description

A GLM family object specifies the type of model fit, provides the appropriate response object and makes sure it is represented in the right form for the model family, and allows for optional parameters such as a weight vector.

### Usage

```
glm.multinomial(y, weights = NULL)
```

### Arguments

y	Response matrix with $K > 1$ columns, and row sums equal to 1. This can either be a "one-hot" encoded version of a $K$ -category factor variable, or else a matrix of proportions. This is useful for grouped multinomial data, where column $y[i, k]$ represents the proportion of outcomes in category $k$ in $n[i]$ trials. Then the corresponding element of the weight vector is $w[i] = n[i]$ .
weights	Observation weights.

### Value

Multinomial GLM object.

### Author(s)

James Yang, Trevor Hastie, and Balasubramanian Narasimhan  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

### See Also

`glm.gaussian`, `glm.binomial`, `glm.poisson`, `glm.multinomial`, `glm.multigaussian`, `glm.cox`.

### Examples

```
n <- 100
K <- 5
y <- t(rmultinom(n, 1, rep(1/K, K)))
obj <- glm.multinomial(y)
```

---

glm.poisson	<i>Creates a Poisson GLM family object.</i>
-------------	---

---

### Description

A GLM family object specifies the type of model fit, provides the appropriate response object and makes sure it is represented in the right form for the model family, and allows for optional parameters such as a weight vector.

### Usage

```
glm.poisson(y, weights = NULL)
```

### Arguments

y	Response vector of non-negative counts.
weights	Observation weight vector, with default NULL.

### Value

Poisson GLM object.

### Author(s)

James Yang, Trevor Hastie, and Balasubramanian Narasimhan  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

### See Also

`glm.gaussian`, `glm.binomial`, `glm.poisson`, `glm.multinomial`, `glm.multigaussian`, `glm.cox`.

### Examples

```
n <- 100  
y <- rpois(n, 1)  
obj <- glm.poisson(y)
```

---

`grpnet`*fit a GLM with group lasso or group elastic-net regularization*

---

## Description

Computes a group elastic-net regularization path for a variety of GLM and other families, including the Cox model. This function extends the abilities of the `glmnet` package to allow for grouped regularization. The code is very efficient (core routines are written in C++), and allows for specialized matrix classes.

## Usage

```
grpnet(  
  X,  
  glm,  
  constraints = NULL,  
  groups = NULL,  
  alpha = 1,  
  penalty = NULL,  
  offsets = NULL,  
  lambda = NULL,  
  standardize = TRUE,  
  irls_max_iters = as.integer(10000),  
  irls_tol = 1e-07,  
  max_iters = as.integer(1e+05),  
  tol = 1e-07,  
  adev_tol = 0.9,  
  ddev_tol = 0,  
  newton_tol = 1e-12,  
  newton_max_iters = 1000,  
  n_threads = 1,  
  early_exit = TRUE,  
  intercept = TRUE,  
  screen_rule = c("pivot", "strong"),  
  min_ratio = 0.01,  
  lmda_path_size = 100,  
  max_screen_size = NULL,  
  max_active_size = NULL,  
  pivot_subset_ratio = 0.1,  
  pivot_subset_min = 1,  
  pivot_slack_ratio = 1.25,  
  check_state = FALSE,  
  progress_bar = FALSE,  
  warm_start = NULL  
)
```

**Arguments**

<code>X</code>	Feature matrix. Either a regular R matrix, or else an <code>adelie</code> custom matrix class, or a concatenation of such.
<code>glm</code>	GLM family/response object. This is an expression that represents the family, the response and other arguments such as weights, if present. The choices are <code>glm.gaussian()</code> , <code>glm.binomial()</code> , <code>glm.poisson()</code> , <code>glm.multinomial()</code> , <code>glm.cox()</code> , <code>glm.multinomial()</code> , and <code>glm.multigaussian()</code> . This is a required argument, and there is no default. In the simple example below, we use <code>glm.gaussian(y)</code> .
<code>constraints</code>	Constraints on the parameters. Currently these are ignored.
<code>groups</code>	This is an ordered vector of integers that represents the groupings, with each entry indicating where a group begins. The entries refer to column numbers in the feature matrix. If there are $p$ features, the default is $1:p$ (no groups). (Note that in the output of <code>grpnet</code> this vector might be shifted to start from 0, since internally <code>adelie</code> uses zero-based indexing.)
<code>alpha</code>	The elasticnet mixing parameter, with $0 \leq \alpha \leq 1$ . The penalty is defined as $(1 - \alpha)/2 \sum_j \ \beta_j\ _2^2 + \alpha \sum_j \ \beta_j\ _2,$ <p>where the sum is over groups. <code>alpha=1</code> is pure group lasso penalty, and <code>alpha=0</code> the pure ridge penalty.</p>
<code>penalty</code>	Separate penalty factors can be applied to each group of coefficients. This is a number that multiplies <code>lambda</code> to allow differential shrinkage for groups. Can be 0 for some groups, which implies no shrinkage, and that group is always included in the model. Default is square-root of group sizes for each group.
<code>offsets</code>	Offsets, default is NULL. If present, this is a fixed vector or matrix corresponding to the shape of the natural parameter, and is added to the fit.
<code>lambda</code>	A user supplied <code>lambda</code> sequence. Typical usage is to have the program compute its own <code>lambda</code> sequence based on <code>lmda_path_size</code> and <code>min_ratio</code> .
<code>standardize</code>	If TRUE (the default), the columns of <code>X</code> are standardized before the fit is computed. This is good practice if the features are a mixed bag, because it has an impact on the penalty. The regularization path is computed using the standardized features, and the standardization information is saved on the object for making future predictions.
<code>irls_max_iters</code>	Maximum number of IRLS iterations, default is $1e4$ .
<code>irls_tol</code>	IRLS convergence tolerance, default is $1e-7$ .
<code>max_iters</code>	Maximum total number of coordinate descent iterations, default is $1e5$ .
<code>tol</code>	Coordinate descent convergence tolerance, default $1e-7$ .
<code>adev_tol</code>	Fraction deviance explained tolerance, default $0.9$ . This can be seen as a limit on overfitting the training data.
<code>ddev_tol</code>	Difference in fraction deviance explained tolerance, default $0$ . If a step in the path changes the deviance by this amount or less, the algorithm truncates the path.

newton_tol	Convergence tolerance for the BCD update, default 1e-12. This parameter controls the iterations in each block-coordinate step to establish the block solution.
newton_max_iters	Maximum number of iterations for the BCD update, default 1000.
n_threads	Number of threads, default 1.
early_exit	TRUE if the function should be allowed to exit early.
intercept	Default TRUE to include an unpenalized intercept.
screen_rule	Screen rule, with default "pivot". Other option is "strong". (an empirical improvement over "strong", the other option.)
min_ratio	Ratio between smallest and largest value of lambda. Default is 1e-2.
lmda_path_size	Number of values for lambda, if generated automatically. Default is 100.
max_screen_size	Maximum number of screen groups. Default is NULL.
max_active_size	Maximum number of active groups. Default is NULL.
pivot_subset_ratio	Subset ratio of pivot rule. Default is 0.1. Users not expected to fiddle with this.
pivot_subset_min	Minimum subset of pivot rule. Defaults is 1. Users not expected to fiddle with this.
pivot_slack_ratio	Slack ratio of pivot rule, default is 1.25. Users not expected to fiddle with this. See reference for details.
check_state	Check state. Internal parameter, with default FALSE.
progress_bar	Progress bar. Default is FALSE.
warm_start	Warm start (default is NULL). Internal parameter.

### Value

A list of class "grpnet". This has a main component called state which represents the fitted path, and a few extra useful components such as the call, the family name, and group\_sizes. Users typically use methods like predict(), print(), plot() etc to examine the object.

### Author(s)

James Yang, Trevor Hastie, and Balasubramanian Narasimhan  
 Maintainer: Trevor Hastie <hastie@stanford.edu>

### References

Yang, James and Hastie, Trevor. (2024) A Fast and Scalable Pathwise-Solver for Group Lasso and Elastic Net Penalized Regression via Block-Coordinate Descent. arXiv doi:10.48550/arXiv.2405.08631.  
 Friedman, J., Hastie, T. and Tibshirani, R. (2008) *Regularization Paths for Generalized Linear Models via Coordinate Descent* (2010), *Journal of Statistical Software*, Vol. 33(1), 1-22, doi:10.18637/jss.v033.i01.

Simon, N., Friedman, J., Hastie, T. and Tibshirani, R. (2011) *Regularization Paths for Cox's Proportional Hazards Model via Coordinate Descent*, *Journal of Statistical Software*, Vol. 39(5), 1-13, doi:10.18637/jss.v039.i05.

Tibshirani, Robert, Bien, J., Friedman, J., Hastie, T., Simon, N., Taylor, J. and Tibshirani, Ryan. (2012) *Strong Rules for Discarding Predictors in Lasso-type Problems*, *JRSSB*, Vol. 74(2), 245-266, <https://arxiv.org/abs/1011.2234>.

### See Also

cv.grpnet, predict.grpnet, plot.grpnet, print.grpnet.

### Examples

```
set.seed(0)
n <- 100
p <- 200
X <- matrix(rnorm(n * p), n, p)
y <- X[,1] * rnorm(1) + rnorm(n)
fit <- grpnet(X, glm.gaussian(y))
print(fit)
```

---

io.snp\_phased\_ancestry

*IO handler for SNP phased, ancestry matrix.*

---

### Description

IO handler for SNP phased, ancestry matrix.

### Usage

```
io.snp_phased_ancestry(filename, read_mode = "file")
```

### Arguments

filename	File name.
read_mode	Reading mode.

### Value

IO handler for SNP phased, ancestry data.



**Examples**

```
n <- 123
s <- 423
A <- 8
filename <- paste(tempdir(), "snp_phased_ancestry_dummy.snpdat", sep="/")
handle <- io.snp_phased_ancestry(filename)
calldata <- matrix(
  as.integer(sample.int(
    2, n * s * 2,
    replace=TRUE,
    prob=c(0.7, 0.3)
  ) - 1),
  n, s * 2
)
ancestries <- matrix(
  as.integer(sample.int(
    A, n * s * 2,
    replace=TRUE,
    prob=rep_len(1/A, A)
  ) - 1),
  n, s * 2
)
handle$write(calldata, ancestries, A, 1)
handle$read()
file.remove(filename)
```

---

io.snp\_unphased

*IO handler for SNP unphased matrix.*

---

**Description**

IO handler for SNP unphased matrix.

**Usage**

```
io.snp_unphased(filename, read_mode = "file")
```

**Arguments**

filename	File name.
read_mode	Reading mode.

**Value**

IO handler for SNP unphased data.

## Examples

```
n <- 123
s <- 423
filename <- paste(tempdir(), "snp_unphased_dummy.snpdat", sep="/")
handle <- io.snp_unphased(filename)
mat <- matrix(
  as.integer(sample.int(
    3, n * s,
    replace=TRUE,
    prob=c(0.7, 0.2, 0.1)
  ) - 1),
  n, s
)
impute <- double(s)
handle$write(mat, "mean", impute, 1)
handle$read()
file.remove(filename)
```

---

matrix.block\_diag      *Creates a block-diagonal matrix.*

---

## Description

Creates a block-diagonal matrix.

## Usage

```
matrix.block_diag(mats, n_threads = 1)
```

## Arguments

mats	List of matrices.
n_threads	Number of threads.

## Value

Block-diagonal matrix.

## Author(s)

Trevor Hastie and James Yang  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

## Examples

```
n <- 100
ps <- c(10, 20, 30)
mats <- lapply(ps, function(p) {
  X <- matrix(rnorm(n * p), n, p)
  matrix.dense(t(X) %*% X, method="cov")
})
out <- matrix.block_diag(mats)
```

---

`matrix.concatenate`      *Creates a concatenation of the matrices.*

---

## Description

Creates a concatenation of the matrices.

## Usage

```
matrix.concatenate(mats, axis = 2, n_threads = 1)
```

## Arguments

<code>mats</code>	List of matrices.
<code>axis</code>	The axis along which the matrices will be joined. With <code>axis = 2</code> (default) this function is equivalent to <code>cbind()</code> and <code>axis = 1</code> is equivalent to <code>rbind()</code> .
<code>n_threads</code>	Number of threads.

## Value

Concatenation of matrices. The object is an S4 class with methods for efficient computation in C++ by *adelie*. Note that for the object itself `axis` is represented with base 0 (so 1 less than the argument here).

## Author(s)

Trevor Hastie and James Yang  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

## Examples

```
n <- 100
ps <- c(10, 20, 30)
ps <- c(10, 20, 30)
n <- 100
mats <- lapply(ps, function(p) {
  matrix.dense(matrix(rnorm(n * p), n, p))
})
out <- matrix.concatenate(mats, axis=2)
```

---

matrix.dense	<i>Creates a dense matrix object.</i>
--------------	---------------------------------------

---

## Description

Creates a dense matrix object.

## Usage

```
matrix.dense(mat, method = c("naive", "cov"), n_threads = 1)
```

## Arguments

mat	The dense matrix.
method	Method type, with default method="naive". If method="cov", the matrix is used with the solver <code>gaussian_cov()</code> . Used for <code>glm.gaussian()</code> and <code>glm.multigaussian()</code> families. Generally "naive" is used for wide matrices, and "cov" for tall matrices.
n_threads	Number of threads.

## Value

Dense matrix. The object is an S4 class with methods for efficient computation by *adelie*.

## Author(s)

Trevor Hastie and James Yang  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

## Examples

```
n <- 100
p <- 20
X_dense <- matrix(rnorm(n * p), n, p)
out <- matrix.dense(X_dense, method="naive")
A_dense <- t(X_dense) %*% X_dense
out <- matrix.dense(A_dense, method="cov")
```

---

matrix.eager\_cov      *Creates an eager covariance matrix.*

---

**Description**

Creates an eager covariance matrix.

**Usage**

```
matrix.eager_cov(mat, n_threads = 1)
```

**Arguments**

mat                    A dense matrix to be used with the gaussian\_cov() solver.  
n\_threads              Number of threads.

**Value**

The dense covariance matrix. This matrix is exactly `t(mat)%*%mat`, computed with some efficiency.

**Examples**

```
n <- 100  
p <- 20  
mat <- matrix(rnorm(n * p), n, p)  
out <- matrix.eager_cov(mat)
```

---

matrix.interaction      *Creates a matrix with pairwise interactions.*

---

**Description**

Creates a matrix with pairwise interactions.

**Usage**

```
matrix.interaction(  
  mat,  
  intr_keys = NULL,  
  intr_values,  
  levels = NULL,  
  n_threads = 1  
)
```

**Arguments**

mat	The dense matrix, which can include factors with levels coded as non-negative integers.
intr_keys	List of feature indices. This is a list of all features with which interactions can be formed. Default is 1:p where p is the number of columns in mat.
intr_values	List of list of feature indices. For each of the $m \leq p$ indices listed in intr_keys, there is a list of indices indicating which columns are candidates for interaction with that feature. If a list is <code>list(NULL)</code> , that means all other features are candidates for interactions. The default is a list of length m where each element is <code>list(NULL)</code> ; that is <code>rep(list(NULL), m)</code> .
levels	Number of levels for each of the columns of mat, with 1 representing a quantitative feature. A factor with K levels should be represented by the numbers 0, 1, ..., K-1.
n_threads	Number of threads.

**Value**

Pairwise interaction matrix. Logic is used to avoid repetitions. For each factor variable, the column is one-hot-encoded to form a basis for that feature. The object is an S4 class with methods for efficient computation by *adelle*. Note that some of the arguments are transformed to C++ base 0 for internal use, and if the object is examined, it will reflect that.

**Author(s)**

Trevor Hastie and James Yang  
 Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

**Examples**

```
n <- 10
p <- 20
X_dense <- matrix(rnorm(n * p), n, p)
X_dense[,1] <- rbinom(n, 4, 0.5)
intr_keys <- c(1, 2)
intr_values <- list(NULL, c(1, 3))
levels <- c(c(5), rep(1, p-1))
out <- matrix.interaction(X_dense, intr_keys, intr_values, levels)
```

---

`matrix.kronecker_eye` *Creates a Kronecker product with an identity matrix.*

---

**Description**

Creates a Kronecker product with an identity matrix.

**Usage**

```
matrix.kronecker_eye(mat, K = 1, n_threads = 1)
```

**Arguments**

mat	The matrix to view as a Kronecker product.
K	Dimension of the identity matrix (default is 1, which does essentially nothing).
n_threads	Number of threads.

**Value**

Kronecker product with identity matrix. If mat is  $n \times p$ , the the resulting matrix will be  $nK \times np$ . The object is an S4 class with methods for efficient computation by *adelle*.

**Author(s)**

James Yang, Trevor Hastie, and Balasubramanian Narasimhan  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

**Examples**

```
n <- 100
p <- 20
K <- 2
mat <- matrix(rnorm(n * p), n, p)
out <- matrix.kronecker_eye(mat, K)
mat <- matrix.dense(mat)
out <- matrix.kronecker_eye(mat, K)
```

---

matrix.lazy_cov	<i>Creates a lazy covariance matrix.</i>
-----------------	--

---

**Description**

Creates a lazy covariance matrix.

**Usage**

```
matrix.lazy_cov(mat, n_threads = 1)
```

**Arguments**

mat	A dense data matrix to be used with the <code>gaussian_cov()</code> solver.
n_threads	Number of threads.

**Value**

Lazy covariance matrix. This is essentially the same matrix, but with a setup to create covariance terms as needed on the fly. The object is an S4 class with methods for efficient computation by *adelie*.

**Author(s)**

James Yang, Trevor Hastie, and Balasubramanian Narasimhan  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

**Examples**

```
n <- 100
p <- 20
mat <- matrix(rnorm(n * p), n, p)
out <- matrix.lazy_cov(mat)
```

---

<code>matrix.one_hot</code>	<i>Creates a one-hot encoded matrix.</i>
-----------------------------	--

---

**Description**

Creates a one-hot encoded matrix.

**Usage**

```
matrix.one_hot(mat, levels = NULL, n_threads = 1)
```

**Arguments**

<code>mat</code>	A dense matrix, which can include factors with levels coded as non-negative integers.
<code>levels</code>	Number of levels for each of the columns of <code>mat</code> , with 1 representing a quantitative feature. A factor with $K$ levels should be represented by the numbers $0, 1, \dots, K-1$ .
<code>n_threads</code>	Number of threads.

**Value**

One-hot encoded matrix. All the factor columns, with `levels > 1`, are replaced by a collection of one-hot encoded versions (dummy matrices). The resulting matrix has `sum(levels)` columns. The object is an S4 class with methods for efficient computation by *adelie*. Note that some of the arguments are transformed to C++ base 0 for internal use, and if the object is examined, it will reflect that.



**Author(s)**

James Yang, Trevor Hastie, and Balasubramanian Narasimhan  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

**Examples**

```
n <- 100
p <- 20
mat <- matrix(rnorm(n * p), n, p)
out <- matrix.one_hot(mat)
```

---

matrix.snp\_phased\_ancestry

*Creates a SNP phased, ancestry matrix.*

---

**Description**

Creates a SNP phased, ancestry matrix.

**Usage**

```
matrix.snp_phased_ancestry(io, n_threads = 1)
```

**Arguments**

io	IO handler.
n_threads	Number of threads.

**Value**

SNP phased, ancestry matrix.

**Author(s)**

James Yang, Trevor Hastie, and Balasubramanian Narasimhan  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

**Examples**

```
n <- 123
s <- 423
A <- 8
filename <- paste(tempdir(), "snp_phased_ancestry_dummy.snpdat", sep="/")
handle <- io.snp_phased_ancestry(filename)
calldata <- matrix(
  as.integer(sample.int(
    2, n * s * 2,
    replace=TRUE,
```

```

        prob=c(0.7, 0.3)
      ) - 1),
      n, s * 2
    )
ancestries <- matrix(
  as.integer(sample.int(
    A, n * s * 2,
    replace=TRUE,
    prob=rep_len(1/A, A)
  ) - 1),
  n, s * 2
)
handle$write(calldata, ancestries, A, 1)
out <- matrix.snp_phased_ancestry(handle)
file.remove(filename)

```

---

matrix.snp\_unphased     *Creates a SNP unphased matrix.*

---

### Description

Creates a SNP unphased matrix.

### Usage

```
matrix.snp_unphased(io, n_threads = 1)
```

### Arguments

io	IO handler.
n_threads	Number of threads.

### Value

SNP unphased matrix.

### Examples

```

n <- 123
s <- 423
filename <- paste(tempdir(), "snp_unphased_dummy.snpdat", sep="/")
handle <- io.snp_unphased(filename)
mat <- matrix(
  as.integer(sample.int(
    3, n * s,
    replace=TRUE,
    prob=c(0.7, 0.2, 0.1)
  ) - 1),
  n, s
)

```

```

)
impute <- double(s)
handle$write(mat, "mean", impute, 1)
out <- matrix.snp_unphased(handle)
file.remove(filename)

```

---

matrix.sparse	<i>Creates a sparse matrix object.</i>
---------------	--

---

### Description

Creates a sparse matrix object.

### Usage

```
matrix.sparse(mat, method = c("naive", "cov"), n_threads = 1)
```

### Arguments

mat	A sparse matrix.
method	Method type, with default method="naive". If method="cov", the matrix is used with the solver <code>gaussian_cov()</code> . Used for <code>glm.gaussian()</code> and <code>glm.multigaussian()</code> families. Generally "naive" is used for wide matrices, and "cov" for tall matrices.
n_threads	Number of threads.

### Value

Sparse matrix object. The object is an S4 class with methods for efficient computation by *adelie*.

### Examples

```

n <- 100
p <- 20
X_dense <- matrix(rnorm(n * p), n, p)
X_sp <- as(X_dense, "dgCMatrix")
out <- matrix.sparse(X_sp, method="naive")
A_dense <- t(X_dense) %**% X_dense
A_sp <- as(A_dense, "dgCMatrix")
out <- matrix.sparse(A_sp, method="cov")

```

---

matrix.standardize      *Creates a standardized matrix.*

---

## Description

Creates a standardized matrix.

## Usage

```
matrix.standardize(  
  mat,  
  centers = NULL,  
  scales = NULL,  
  weights = NULL,  
  ddof = 0,  
  n_threads = 1  
)
```

## Arguments

mat	An <code>adelle</code> matrix.
centers	The center values. Default is to use the column means.
scales	The scale values. Default is to use the sample standard deviations.
weights	Observation weight vector, which defaults to $1/n$ per observation.
ddof	Degrees of freedom for standard deviations, with default 0 ( $1/n$ ). The alternative is 1 leading to $1/(n-1)$ .
n_threads	Number of threads.

## Value

Standardized matrix. The object is an S4 class with methods for efficient computation by `adelle`.

## Author(s)

James Yang, Trevor Hastie, and Balasubramanian Narasimhan  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

## Examples

```
n <- 100  
p <- 20  
X <- matrix(rnorm(n * p), n, p)  
out <- matrix.standardize(matrix.dense(X))
```

---

matrix.subset	<i>Creates a subset of the matrix along an axis.</i>
---------------	--

---

## Description

Creates a subset of the matrix along an axis.

## Usage

```
matrix.subset(mat, indices, axis = 1, n_threads = 1)
```

## Arguments

mat	The adelic matrix to subset.
indices	Vector of indices to subset the matrix.
axis	The axis along which to subset (2 is columns, 1 is rows).
n_threads	Number of threads.

## Value

Matrix subsetted along the appropriate axis. The object is an S4 class with methods for efficient computation by adelic.

## Author(s)

James Yang, Trevor Hastie, and Balasubramanian Narasimhan  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

## Examples

```
n <- 100
p <- 20
X <- matrix.dense(matrix(rnorm(n * p), n, p))
indices <- c(1, 3, 10)
out <- matrix.subset(X, indices, axis=1)
out <- matrix.subset(X, indices, axis=2)
```

---

`plot.cv.grpnet`*plot the cross-validation curve produced by cv.grpnet*

---

## Description

Plots the cross-validation curve, and upper and lower standard deviation curves, as a function of the lambda values used.

## Usage

```
## S3 method for class 'cv.grpnet'  
plot(x, sign.lambda = -1, ...)
```

## Arguments

<code>x</code>	fitted "cv.grpnet" object
<code>sign.lambda</code>	Either plot against $\log(\lambda)$ or its negative (default) if <code>sign.lambda=-1</code>
<code>...</code>	Other graphical parameters

## Details

A plot is produced, and nothing is returned.

## Author(s)

James Yang, Trevor Hastie, and Balasubramanian Narasimhan  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

## References

Yang, James and Hastie, Trevor. (2024) A Fast and Scalable Pathwise-Solver for Group Lasso and Elastic Net Penalized Regression via Block-Coordinate Descent. arXiv [doi:10.48550/arXiv.2405.08631](https://arxiv.org/abs/10.48550/arXiv.2405.08631).  
Adelie Python user guide <https://jamesyang007.github.io/adelie/>

## See Also

`grpnet` and `cv.grpnet`.

## Examples

```
set.seed(1010)  
n = 1000  
p = 100  
nzc = trunc(p/10)  
x = matrix(rnorm(n * p), n, p)  
beta = rnorm(nzc)  
fx = (x[, seq(nzc)] %*% beta)  
eps = rnorm(n) * 5
```

```

y = drop(fx + eps)
px = exp(fx)
px = px/(1 + px)
ly = rbinom(n = length(px), prob = px, size = 1)
cvob1 = cv.grpnet(x, glm.gaussian(y))
plot(cvob1)
title("Gaussian Family", line = 2.5)
frame()
set.seed(1011)
cvob2 = cv.grpnet(x, glm.binomial(ly))
plot(cvob2)
title("Binomial Family", line = 2.5)

```

---

plot.grpnet

*plot coefficients from a "grpnet" object*


---

## Description

Produces a coefficient profile plot of the coefficient paths for a fitted "grpnet" object.

## Usage

```

## S3 method for class 'grpnet'
plot(x, sign.lambda = -1, glm.name = TRUE, ...)

```

## Arguments

x	fitted "grpnet" model
sign.lambda	This determines whether we plot against $\log(\lambda)$ or its negative. values are -1(default) or 1
glm.name	This is a logical (default TRUE), and causes the glm name of the model to be included in the plot.
...	Other graphical parameters to plot

## Details

A coefficient profile plot is produced. If x is a multinomial or multigaussian model, the 2norm of the vector of coefficients is plotted.

## Author(s)

James Yang, Trevor Hastie, and Balasubramanian Narasimhan  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

## References

Yang, James and Hastie, Trevor. (2024) A Fast and Scalable Pathwise-Solver for Group Lasso and Elastic Net Penalized Regression via Block-Coordinate Descent. arXiv [doi:10.48550/arXiv.2405.08631](https://doi.org/10.48550/arXiv.2405.08631).

**See Also**

grpnet, and print, and coef methods, and cv.grpnet.

**Examples**

```
x=matrix(rnorm(100*20),100,20)
y=rnorm(100)
fit1=grpnet(x,glm.gaussian(y))
plot(fit1)
g4=diag(4)[sample(1:4,100,replace=TRUE),]
fit2=grpnet(x,glm.multinomial(g4))
plot(fit2,lwd=3)
fit3=grpnet(x,glm.gaussian(y),groups=c(1,5,9,13,17))
plot(fit3)
```

---

predict.cv.grpnet      *make predictions from a "cv.grpnet" object.*

---

**Description**

This function makes predictions from a cross-validated grpnet model, using the stored "grpnet.fit" object, and the optimal value chosen for lambda.

**Usage**

```
## S3 method for class 'cv.grpnet'
predict(object, newx, lambda = c("lambda.1se", "lambda.min"), ...)
```

**Arguments**

object	Fitted "cv.grpnet".
newx	Matrix of new values for x at which predictions are to be made. Can be a matrix, a sparse matrix as in Matrix package, or else any of the matrix forms allowable in the adelié package. This argument is not used for type="coefficients".
lambda	Value(s) of the penalty parameter lambda at which predictions are required. Default is the value lambda="lambda.1se" stored on the CV object. Alternatively lambda="lambda.min" can be used. If lambda is numeric, it is taken as the value(s) of lambda to be used.
...	Not used. Other arguments to predict.

**Details**

This function makes it easier to use the results of cross-validation to make a prediction.

**Value**

The object returned depends on the arguments.



**Author(s)**

James Yang, Trevor Hastie, and Balasubramanian Narasimhan  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

**References**

Yang, James and Hastie, Trevor. (2024) A Fast and Scalable Pathwise-Solver for Group Lasso and Elastic Net Penalized Regression via Block-Coordinate Descent. arXiv [doi:10.48550/arXiv.2405.08631](https://doi.org/10.48550/arXiv.2405.08631).

**See Also**

grpnet, and print, and coef methods, and cv.grpnet.

**Examples**

```
x = matrix(rnorm(100 * 20), 100, 20)
y = rnorm(100)
cv.fit = cv.grpnet(x, glm.gaussian(y))
predict(cv.fit, newx = x[1:5, ])
coef(cv.fit)
coef(cv.fit, lambda = "lambda.min")
predict(cv.fit, newx = x[1:5, ], lambda = c(0.001, 0.002))
```

---

predict.grpnet	<i>make predictions from a "grpnet" object.</i>
----------------	---

---

**Description**

Similar to other predict methods, this functions predicts linear predictors, coefficients and more from a fitted "grpnet" object.

**Usage**

```
## S3 method for class 'grpnet'
predict(
  object,
  newx,
  lambda = NULL,
  type = c("link", "response", "coefficients"),
  newoffsets = NULL,
  ...
)

## S3 method for class 'grpnet'
coef(object, lambda = NULL, ...)
```

**Arguments**

object	Fitted "grpnet" model.
newx	Matrix of new values for x at which predictions are to be made. Can be a matrix, a sparse matrix as in Matrix package, or else any of the matrix forms allowable in the adelic package. The number of columns must match that of the input matrix used in fitting object. If the model object was fit with standardize=TRUE, the saved centers and scaling will be applied to this matrix. This argument is not used for type="coefficients"
lambda	Value(s) of the penalty parameter lambda at which predictions are required. Default is the entire sequence used to create the model. If values of lambda are supplied, the function uses linear interpolation to make predictions for values of lambda that do not coincide with those used in the fitting algorithm.
type	Type of prediction required. Type "link" is the default, and gives the linear predictors. Type "response" applies the inverse link to these predictions. Type "coefficients" extracts the coefficients, intercepts and the active-set sizes.
newoffsets	If an offset is used in the fit, then one must be supplied for making predictions (except for type="coefficients" or type="nonzero")
...	Currently ignored.

**Details**

The shape of the objects returned are different for "multinomial" and "multigaussian" objects `coef(...)` is equivalent to `predict(type="coefficients", ...)`

**Value**

The object returned depends on type.

**Author(s)**

James Yang, Trevor Hastie, and Balasubramanian Narasimhan  
 Maintainer: Trevor Hastie <hastie@stanford.edu>

**References**

Yang, James and Hastie, Trevor. (2024) A Fast and Scalable Pathwise-Solver for Group Lasso and Elastic Net Penalized Regression via Block-Coordinate Descent. arXiv doi:10.48550/arXiv.2405.08631. Adelic Python user guide <https://jamesyang007.github.io/adelic/>

**See Also**

grpnet, and print, and coef methods, and cv.grpnet.

## Examples

```
set.seed(0)
n <- 100
p <- 200
X <- matrix(rnorm(n * p), n, p)
y <- X[,1] * rnorm(1) + rnorm(n)
fit <- grpnet(X, glm.gaussian(y))
coef(fit)
predict(fit, newx = X[1:5,])
```

---

```
print.cv.grpnet      print a cross-validated grpnet object
```

---

## Description

Print a summary of the results of cross-validation for a grpnet model.

## Usage

```
## S3 method for class 'cv.grpnet'
print(x, digits = max(3, getOption("digits") - 3), ...)
```

## Arguments

x	fitted 'cv.grpnet' object
digits	significant digits in printout
...	additional print arguments

## Author(s)

James Yang, Trevor Hastie, and Balasubramanian Narasimhan  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

## References

Yang, James and Hastie, Trevor. (2024) A Fast and Scalable Pathwise-Solver for Group Lasso and Elastic Net Penalized Regression via Block-Coordinate Descent. arXiv [doi:10.48550/arXiv.2405.08631](https://doi.org/10.48550/arXiv.2405.08631).

## See Also

grpnet, predict and coef methods.

## Examples

```
x = matrix(rnorm(100 * 20), 100, 20)
y = rnorm(100)
fit1 = cv.grpnet(x, glm.gaussian(y))
print(fit1)
```

---

print.grpnet                    *print a grpnet object*

---

### Description

Print a summary of the grpnet path at each step along the path.

### Usage

```
## S3 method for class 'grpnet'  
print(x, digits = max(3, getOption("digits") - 3), ...)
```

### Arguments

x	fitted grpnet object
digits	significant digits in printout
...	additional print arguments

### Details

The call that produced the object x is printed, followed by a three-column matrix with columns Df, %Dev and Lambda. The Df column is the number of nonzero coefficients (Df is a reasonable name only for lasso fits). %Dev is the percent deviance explained (relative to the null deviance).

### Value

The matrix above is silently returned

### References

Yang, James and Hastie, Trevor. (2024) A Fast and Scalable Pathwise-Solver for Group Lasso and Elastic Net Penalized Regression via Block-Coordinate Descent. arXiv [doi:10.48550/arXiv.2405.08631](https://arxiv.org/abs/10.48550/arXiv.2405.08631).

### See Also

grpnet, predict, plot and coef methods.

### Examples

```
x = matrix(rnorm(100 * 20), 100, 20)  
y = rnorm(100)  
fit1 = grpnet(x, glm.gaussian(y))  
print(fit1)
```

---

set_configs	<i>Set configuration settings.</i>
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**Description**

Set configuration settings.

**Usage**

```
set_configs(name, value = NULL)
```

**Arguments**

name	Configuration variable name.
value	Value to assign to the configuration variable.

**Value**

Assigned value.

**Examples**

```
set_configs("hessian_min", 1e-6)  
set_configs("hessian_min")
```

# Index

- \* **group**
  - plot.cv.grpnet, 30
  - print.cv.grpnet, 35
- \* **lasso**
  - plot.cv.grpnet, 30
  - print.cv.grpnet, 35
- \* **models**
  - plot.cv.grpnet, 30
  - plot.grpnet, 31
  - predict.cv.grpnet, 32
  - predict.grpnet, 33
  - print.cv.grpnet, 35
  - print.grpnet, 36
- \* **regression**
  - plot.cv.grpnet, 30
  - plot.grpnet, 31
  - predict.cv.grpnet, 32
  - predict.grpnet, 33
  - print.cv.grpnet, 35
  - print.grpnet, 36

coef.cv.grpnet (predict.cv.grpnet), 32  
coef.grpnet (predict.grpnet), 33  
cv.grpnet, 2

gaussian\_cov, 5  
glm.binomial, 7  
glm.cox, 8  
glm.gaussian, 9  
glm.multigaussian, 10  
glm.multinomial, 11  
glm.poisson, 12  
grpnet, 13

io.snp\_phased\_ancestry, 16  
io.snp\_unphased, 17

matrix.block\_diag, 18  
matrix.concatenate, 19  
matrix.dense, 20  
matrix.eager\_cov, 21  
matrix.interaction, 21  
matrix.kronecker\_eye, 22  
matrix.lazy\_cov, 23  
matrix.one\_hot, 24  
matrix.snp\_phased\_ancestry, 25  
matrix.snp\_unphased, 26  
matrix.sparse, 27  
matrix.standardize, 28  
matrix.subset, 29

plot.cv.grpnet, 30  
plot.grpnet, 31  
predict.cv.grpnet, 32  
predict.grpnet, 33  
print.cv.grpnet, 35  
print.grpnet, 36

set\_configs, 37