

# Package ‘pareg’

October 18, 2022

**Title** Pathway enrichment using a regularized regression approach

**Version** 1.0.0

**Description** Compute pathway enrichment scores while accounting for term-term relations. This package uses a regularized multiple linear regression to regress differential expression p-values obtained from multi-condition experiments on a pathway membership matrix. By doing so, it is able to incorporate additional biological knowledge into the enrichment analysis and to estimate pathway enrichment scores more robustly.

**URL** <https://github.com/cbg-ethz/pareg>

**BugReports** <https://github.com/cbg-ethz/pareg/issues>

**biocViews** Software, StatisticalMethod, GraphAndNetwork, Regression, GeneExpression, DifferentialExpression, NetworkEnrichment, Network

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---

as.data.frame.pareg    *as.data.frame for an object of class pareg.*

---

### Description

Retrieve dataframe with enrichment information.

### Usage

```
## S3 method for class 'pareg'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

### Arguments

x	An object of class pareg.
row.names	Optional character vector of rownames.
optional	Allow optional arguments.
...	Additional arguments.

**Value**

Dataframe containing enrichment score and name for each pathway.

**Examples**

```
df_genes <- data.frame(
  gene = paste("g", 1:20, sep = ""),
  pvalue = c(
    rbeta(10, .1, 1),
    rbeta(10, 1, 1)
  )
)
df_terms <- rbind(
  data.frame(
    term = "foo",
    gene = paste("g", 1:10, sep = "")
  ),
  data.frame(
    term = "bar",
    gene = paste("g", 11:20, sep = "")
  )
)
fit <- pareg(df_genes, df_terms, max_iterations = 10)
as.data.frame(fit)
```

---

as\_dense\_sim

*Convert matrices.*

---

**Description**

Convert sparse similarity matrix from package data to a dense version with 1 on its diagonal. This matrix can then be used by pareg.

**Usage**

```
as_dense_sim(mat_sparse)
```

**Arguments**

mat\_sparse      Sparse matrix.

**Value**

Dense matrix

**Examples**

```
transform_y(c(0, 0.5, 1))
```

---

as\_enrichplot\_object *Convert object of class pareg to class enrichResult.*

---

### Description

The resulting object can be passed to any method from the enrichplot package and thus allows for nice visualizations of the enrichment results. Note: term similarities are included if available.

### Usage

```
as_enrichplot_object(x, pvalue_threshold = 0.05)
```

### Arguments

x                      An object of class pareg.  
pvalue\_threshold        Threshold to select genes for count statistics.

### Value

Object of class enrichResult.

### Examples

```
df_genes <- data.frame(  
  gene = paste("g", 1:20, sep = ""),  
  pvalue = c(  
    rbeta(10, .1, 1),  
    rbeta(10, 1, 1)  
  )  
)  
df_terms <- rbind(  
  data.frame(  
    term = "foo",  
    gene = paste("g", 1:10, sep = "")  
  ),  
  data.frame(  
    term = "bar",  
    gene = paste("g", 11:20, sep = "")  
  )  
)  
fit <- pareg(df_genes, df_terms, max_iterations = 10)  
as_enrichplot_object(fit)
```

---

compute\_term\_similarities  
*Term similarity computation.*

---

**Description**

Generate similarity matrix for input terms.

**Usage**

```
compute_term_similarities(  
  df_terms,  
  similarity_function = jaccard,  
  max_similarity = 1  
)
```

**Arguments**

df\_terms            Dataframe storing pathway database.  
similarity\_function            Function to compute similarity between two sets.  
max\_similarity    Value to fill diagonal with.

**Value**

Symmetric matrix of similarity scores.

**Examples**

```
df_terms <- data.frame(  
  term = c("A", "A", "B", "B", "C", "C", "C"),  
  gene = c("a", "b", "a", "b", "c", "a", "c", "d")  
)  
compute_term_similarities(df_terms)
```

---

create\_model\_df            *Create design matrix.*

---

**Description**

Store term membership for each gene.

**Usage**

```
create_model_df(df_genes, df_terms, pvalue_threshold = 0.05)
```

**Arguments**

df\_genes            Dataframe storing gene names and DE p-values.  
df\_terms            Dataframe storing pathway database.  
pvalue\_threshold    P-value threshold to create binary columns 'pvalue\_sig' and 'pvalue\_notsig'.

**Value**

Dataframe.

**Examples**

```
df_genes <- data.frame(
  gene = c("g1", "g2"),
  pvalue = c(0.1, 0.2)
)
df_terms <- data.frame(
  term = c("A", "A", "B", "B", "C"),
  gene = c("g1", "g2", "g1", "g2", "g2")
)
create_model_df(df_genes, df_terms)
```

---

cv\_edgenet

*Find the optimal shrinkage parameters for edgenet*


---

**Description**

Finds the optimal regularization parameters using cross-validation for edgenet. We use the BOBYQA algorithm to find the optimal regularization parameters in a cross-validation framework.

**Usage**

```
cv_edgenet(
  X,
  Y,
  G.X = NULL,
  G.Y = NULL,
  lambda = NA_real_,
  psigx = NA_real_,
  psigy = NA_real_,
  thresh = 1e-05,
  maxit = 1e+05,
  learning.rate = 0.01,
  family = gaussian,
  optim.thresh = 0.01,
  optim.maxit = 100,
  lambda_range = seq(0, 2, length.out = 10),
```

```
    psigx_range = seq(0, 500, length.out = 10),
    psigy_range = seq(0, 500, length.out = 10),
    nfolds = 2,
    cv_method = c("grid_search", "optim")
)

## S4 method for signature 'matrix,numeric'
cv_edgenet(
  X,
  Y,
  G.X = NULL,
  G.Y = NULL,
  lambda = NA_real_,
  psigx = NA_real_,
  psigy = NA_real_,
  thresh = 1e-05,
  maxit = 1e+05,
  learning.rate = 0.01,
  family = gaussian,
  optim.thresh = 0.01,
  optim.maxit = 100,
  lambda_range = seq(0, 2, length.out = 10),
  psigx_range = seq(0, 500, length.out = 10),
  psigy_range = seq(0, 500, length.out = 10),
  nfolds = 2,
  cv_method = c("grid_search", "optim")
)

## S4 method for signature 'matrix,matrix'
cv_edgenet(
  X,
  Y,
  G.X = NULL,
  G.Y = NULL,
  lambda = NA_real_,
  psigx = NA_real_,
  psigy = NA_real_,
  thresh = 1e-05,
  maxit = 1e+05,
  learning.rate = 0.01,
  family = gaussian,
  optim.thresh = 0.01,
  optim.maxit = 100,
  lambda_range = seq(0, 2, length.out = 10),
  psigx_range = seq(0, 500, length.out = 10),
  psigy_range = seq(0, 500, length.out = 10),
  nfolds = 2,
  cv_method = c("grid_search", "optim")
)
```

)

**Arguments**

X	input matrix, of dimension (n x p) where n is the number of observations and p is the number of covariables. Each row is an observation vector.
Y	output matrix, of dimension (n x q) where n is the number of observations and q is the number of response variables. Each row is an observation vector.
G.X	non-negativ affinity matrix for X, of dimensions (p x p) where p is the number of covariables. Providing a graph G.X will optimize the regularization parameter $\psi_{i.gx}$ . If this is not desired just set G.X to NULL.
G.Y	non-negativ affinity matrix for Y, of dimensions (q x q) where q is the number of responses Y. Providing a graph G.Y will optimize the regularization parameter $\psi_{i.gy}$ . If this is not desired just set G.Y to NULL.
lambda	numerical shrinkage parameter for LASSO. Per default this parameter is set to NA_real_ which means that lambda is going to be estimated using cross-validation. If any numerical value for lambda is set, estimation of the optimal parameter will <i>not</i> be conducted.
psigx	numerical shrinkage parameter for graph-regularization of G.X. Per default this parameter is set to NA_real_ which means that psigx is going to be estimated in the cross-validation. If any numerical value for psigx is set, estimation of the optimal parameter will <i>not</i> be conducted.
psigy	numerical shrinkage parameter for graph-regularization of G.Y. Per default this parameter is set to NA_real_ which means that psigy is going to be estimated in the cross-validation. If any numerical value for psigy is set, estimation of the optimal parameter will <i>not</i> be conducted.
thresh	numerical threshold for the optimizer
maxit	maximum number of iterations for the optimizer (integer)
learning.rate	step size for Adam optimizer (numerical)
family	family of response, e.g. <i>gaussian</i> or <i>binomial</i>
optim.thresh	numerical threshold criterion for the optimization to stop. Usually 1e-3 is a good choice.
optim.maxit	the maximum number of iterations for the optimization (integer). Usually 1e4 is a good choice.
lambda_range	range of lambda to use in CV grid.
psigx_range	range of psigx to use in CV grid.
psigy_range	range of psigy to use in CV grid.
nfolds	the number of folds to be used - default is 10.
cv_method	which cross-validation method to use.



**Value**

An object of class cv\_edgenet

parameters	the estimated, optimal regularization parameters
lambda	optimal estimated value for regularization parameter lambda (or, if provided as argument, the value of the parameter)
psigx	optimal estimated value for regularization parameter psigx (or, if provided as argument, the value of the parameter)
psigy	optimal estimated value for regularization parameter psigy (or, if provided as argument, the value of the parameter)
estimated.parameters	names of parameters that were estimated
family	family used for estimated
fit	an edgenet object fitted with the optimal, estimated parameters
call	the call that produced the object

**Examples**

```
X <- matrix(rnorm(100 * 10), 100, 10)
b <- matrix(rnorm(100), 10)
G.X <- abs(rWishart(1, 10, diag(10))[, , 1])
G.Y <- abs(rWishart(1, 10, diag(10))[, , 1])
diag(G.X) <- diag(G.Y) <- 0

# estimate the parameters of a Gaussian model
Y <- X %*% b + matrix(rnorm(100 * 10), 100)

## dont use affinity matrices and estimate lambda
fit <- cv_edgenet(
  X = X,
  Y = Y,
  family = gaussian,
  maxit = 1,
  lambda_range = c(0, 1)
)
## only provide one matrix and estimate lambda
fit <- cv_edgenet(
  X = X,
  Y = Y,
  G.X = G.X,
  psigx = 1,
  family = gaussian,
  maxit = 1,
  lambda_range = c(0, 1)
)
## estimate only lambda with two matrices
fit <- cv_edgenet(
  X = X,
  Y = Y,
```

```

    G.X = G.X,
    G.Y,
    psigx = 1,
    psigy = 1,
    family = gaussian,
    maxit = 1,
    lambda_range = c(0, 1)
  )
  ## estimate only psigx
  fit <- cv_edgenet(
    X = X,
    Y = Y,
    G.X = G.X,
    G.Y,
    lambda = 1,
    psigy = 1,
    family = gaussian,
    maxit = 1,
    psigx_range = c(0, 1)
  )
  ## estimate all parameters
  fit <- cv_edgenet(
    X = X,
    Y = Y,
    G.X = G.X,
    G.Y,
    family = gaussian,
    maxit = 1,
    lambda_range = c(0, 1),
    psigx_range = c(0, 1),
    psigy_range = c(0, 1)
  )
  ## if Y is vectorial, we cannot use an affinity matrix for Y
  fit <- cv_edgenet(
    X = X,
    Y = Y[, 1],
    G.X = G.X,
    family = gaussian,
    maxit = 1,
    lambda_range = c(0, 1),
    psigx_range = c(0, 1),
  )

```

---

edgenet

*Fit a graph-regularized linear regression model using edge-based regularization. Adapted from <https://github.com/dirmeier/netReg>.*

---

### Description

Fit a graph-regularized linear regression model using edge-penalization. The coefficients are computed using graph-prior knowledge in the form of one/two affinity matrices. Graph-regularization

is an extension to previously introduced regularization techniques, such as the LASSO. See the vignette for details on the objective function of the model: `vignette("edgenet", package="netReg")`

### Usage

```
edgenet(  
  X,  
  Y,  
  G.X = NULL,  
  G.Y = NULL,  
  lambda = 0,  
  psigx = 0,  
  psigy = 0,  
  thresh = 1e-05,  
  maxit = 1e+05,  
  learning.rate = 0.01,  
  family = gaussian  
)  
  
## S4 method for signature 'matrix,numeric'  
edgenet(  
  X,  
  Y,  
  G.X = NULL,  
  G.Y = NULL,  
  lambda = 0,  
  psigx = 0,  
  psigy = 0,  
  thresh = 1e-05,  
  maxit = 1e+05,  
  learning.rate = 0.01,  
  family = gaussian  
)  
  
## S4 method for signature 'matrix,matrix'  
edgenet(  
  X,  
  Y,  
  G.X = NULL,  
  G.Y = NULL,  
  lambda = 0,  
  psigx = 0,  
  psigy = 0,  
  thresh = 1e-05,  
  maxit = 1e+05,  
  learning.rate = 0.01,  
  family = gaussian  
)
```

**Arguments**

X	input matrix, of dimension (n x p) where n is the number of observations and p is the number of covariables. Each row is an observation vector.
Y	output matrix, of dimension (n x q) where n is the number of observations and q is the number of response variables. Each row is an observation vector.
G.X	non-negativ affinity matrix for X, of dimensions (p x p) where p is the number of covariables
G.Y	non-negativ affinity matrix for Y, of dimensions (q x q) where q is the number of responses
lambda	numerical shrinkage parameter for LASSO.
psigx	numerical shrinkage parameter for graph-regularization of G.X
psigy	numerical shrinkage parameter for graph-regularization of G.Y
thresh	numerical threshold for optimizer
maxit	maximum number of iterations for optimizer (integer)
learning.rate	step size for Adam optimizer (numerical)
family	family of response, e.g. <i>gaussian</i> or <i>binomial</i>

**Value**

An object of class edgenet

beta	the estimated (p x q)-dimensional coefficient matrix B.hat
alpha	the estimated (q x 1)-dimensional vector of intercepts
parameters	regularization parameters
lambda	regularization parameter lambda
psigx	regularization parameter psigx
psigy	regularization parameter psigy
family	a description of the error distribution and link function to be used. Can be a <a href="#">pareg::family</a> function or a character string naming a family function, e.g. <i>gaussian</i> or "gaussian".
call	the call that produced the object

**References**

Cheng, Wei and Zhang, Xiang and Guo, Zhishan and Shi, Yu and Wang, Wei (2014), Graph-regularized dual Lasso for robust eQTL mapping.  
*Bioinformatics*

**Examples**

```

X <- matrix(rnorm(100 * 10), 100, 10)
b <- matrix(rnorm(100), 10)
G.X <- abs(rWishart(1, 10, diag(10))[, , 1])
G.Y <- abs(rWishart(1, 10, diag(10))[, , 1])
diag(G.X) <- diag(G.Y) <- 0

# estimate the parameters of a Gaussian model
Y <- X %*% b + matrix(rnorm(100 * 10), 100)
## dont use affinity matrices
fit <- edgenet(X = X, Y = Y, family = gaussian, maxit = 10)
## only provide one matrix
fit <- edgenet(
  X = X,
  Y = Y,
  G.X = G.X,
  psigx = 1,
  family = gaussian,
  maxit = 10
)
## use two matrices
fit <- edgenet(X = X, Y = Y, G.X = G.X, G.Y, family = gaussian, maxit = 10)
## if Y is vectorial, we cannot use an affinity matrix for Y
fit <- edgenet(X = X, Y = Y[, 1], G.X = G.X, family = gaussian, maxit = 10)

```

---

family

*Family objects for models*


---

**Description**

Family objects provide a convenient way to specify the details of the models used by `pareg`. See also `stats::family` for more details.

**Usage**

```

family(object, ...)

gaussian(link = c("identity"))

bernoulli(link = c("logit", "probit", "log"))

beta(link = c("logit", "probit", "log"))

beta_phi_lm(link = c("logit", "probit", "log"))

beta_phi_var(link = c("logit", "probit", "log"))

```

**Arguments**

object	a object for which the family should be returned (e.g. edgenet)
...	further arguments passed to methods
link	name of a link function

**Value**

An object of class <code>pareg.family</code>	
family	name of the family
link	name of the link function
linkinv	inverse link function
loss	loss function

**Examples**

```
gaussian()  
bernoulli("probit")$link  
beta()$loss
```

---

```
generate_similarity_matrix  
      Similarity matrix generation.
```

---

**Description**

Generate block-structured similarity matrices corresponding to cluster structures.

**Usage**

```
generate_similarity_matrix(cluster_sizes)
```

**Arguments**

`cluster_sizes` List of cluster sizes.

**Value**

Similarity matrix with samples as row-/colnames.

**Examples**

```
generate_similarity_matrix(c(1, 2, 3))
```

---

jaccard	<i>Jaccard similarity.</i>
---------	----------------------------

---

**Description**

Compute Jaccard similarity between two sets.

**Usage**

```
jaccard(x, y)
```

**Arguments**

x	First set.
y	Second set.

**Value**

Jaccard similarity between set x and y.

**See Also**

Other pathway similarity methods: [overlap\\_coefficient\(\)](#)

**Examples**

```
jaccard(c(1, 2, 3), c(2, 3, 4))
```

---

overlap_coefficient	<i>Overlap coefficient.</i>
---------------------	-----------------------------

---

**Description**

Compute overlap coefficient between two sets.

**Usage**

```
overlap_coefficient(x, y)
```

**Arguments**

x	First set.
y	Second set.

**Value**

Overlap coefficient between set x and y.

**See Also**

Other pathway similarity methods: [jaccard\(\)](#)

**Examples**

```
overlap_coefficient(c(1, 2, 3), c(2, 3, 4))
```

---

pareg

*Pathway enrichment using a regularized regression approach.*

---

**Description**

Run model to compute pathway enrichments. Can model inter-pathway relations, cross-validation and much more.

**Usage**

```
pareg(  
  df_genes,  
  df_terms,  
  lasso_param = NA_real_,  
  network_param = NA_real_,  
  term_network = NULL,  
  cv = FALSE,  
  family = beta,  
  response_column_name = "pvalue",  
  max_iterations = 1e+05,  
  lasso_param_range = seq(0, 2, length.out = 10),  
  network_param_range = seq(0, 500, length.out = 10),  
  ...  
)
```

**Arguments**

df_genes	Dataframe storing gene names and DE p-values.
df_terms	Dataframe storing pathway database.
lasso_param	Lasso regularization parameter.
network_param	Network regularization parameter.
term_network	Term similarity network as adjacency matrix.
cv	Estimate best regularization parameters using cross-validation.
family	Distribution family of response.



```

response_column_name      Which column of model dataframe to use as response.
max_iterations             How many iterations to maximally run optimizer for.
lasso_param_range         LASSO regularization parameter search space in grid search of CV.
network_param_range       Network regularization parameter search space in grid search of CV.
...                       Further arguments to pass to '(cv.)edgenet'.

```

**Value**

An object of class `pareg`.

**Examples**

```

df_genes <- data.frame(
  gene = paste("g", 1:20, sep = ""),
  pvalue = c(
    rbeta(10, .1, 1),
    rbeta(10, 1, 1)
  )
)
df_terms <- rbind(
  data.frame(
    term = "foo",
    gene = paste("g", 1:10, sep = "")
  ),
  data.frame(
    term = "bar",
    gene = paste("g", 11:20, sep = "")
  )
)
pareg(df_genes, df_terms, max_iterations = 10)

```

---

`pathway_similarities` *Collection of pathway similarity matrices.*

---

**Description**

Contains matrices for various pathway databases and similarity measures. Note that the matrices are sparse, upper triangular and subsampled to a maximum size of \$1000x1000\$ if necessary. They can be transformed to a dense representation using `pareg::as_dense_sim`.

**Usage**

```
pathway_similarities
```

**Format**

A list of lists of matrices. \* Pathway database 1 \* Similarity measure 1 \* Similarity measure 2 \* ...  
 \* Pathway database 2 \* ...

---

plot.pareg	<i>Plot pareg object.</i>
------------	---------------------------

---

**Description**

Check pareg::plot\_pareg\_with\_args for details. Needed because of WARNING in "checking S3 generic/method consistency"

**Usage**

```
## S3 method for class 'pareg'
plot(x, ...)
```

**Arguments**

x	An object of class pareg.
...	Parameters passed to pareg::plot_pareg_with_args

**Value**

ggplot object.

---

plot_pareg_with_args	<i>Plot result of enrichment computation.</i>
----------------------	---

---

**Description**

Visualize pathway enrichments as network.

**Usage**

```
plot_pareg_with_args(x, show_term_names = TRUE, min_similarity = 0)
```

**Arguments**

x	An object of class pareg.
show_term_names	Whether to plot node labels.
min_similarity	Don't plot edges for similarities below this value.

**Value**

ggplot object.

**Examples**

```
df_genes <- data.frame(  
  gene = paste("g", 1:20, sep = ""),  
  pvalue = c(  
    rbeta(10, .1, 1),  
    rbeta(10, 1, 1)  
  )  
)  
df_terms <- rbind(  
  data.frame(  
    term = "foo",  
    gene = paste("g", 1:10, sep = "")  
  ),  
  data.frame(  
    term = "bar",  
    gene = paste("g", 11:20, sep = "")  
  )  
)  
fit <- pareg(df_genes, df_terms, max_iterations = 10)  
plot(fit)
```

---

similarity\_sample      *Sample elements based on similarity structure.*

---

**Description**

Choose similar object more often, depending on ‘similarity\_factor’.

**Usage**

```
similarity_sample(sim_mat, size, similarity_factor = 1)
```

**Arguments**

sim_mat	Similarity matrix with samples as row/col names.
size	How many samples to draw.
similarity_factor	Uniform sampling for 0. Weights mixture of uniform and similarity vector for each draw.

**Value**

Vector of samples.

**Examples**

```
similarity_sample(matrix(runif(100), nrow = 10, ncol = 10), 3)
```

---

transform\_y

*Transform vector from [0, 1] to (0, 1).*

---

**Description**

Make (response) vector conform to Beta assumptions as described in section 2 of the betareg vignette <https://cran.r-project.org/web/packages/betareg/vignettes/betareg.pdf>.

**Usage**

```
transform_y(y)
```

**Arguments**

y                    Numeric vector in  $[0, 1]^N$

**Value**

Numeric vector in  $(0, 1)^N$

**Examples**

```
transform_y(c(0, 0.5, 1))
```

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