

# Package ‘netprioR’

July 21, 2025

**Title** A model for network-based prioritisation of genes

**Description** A model for semi-supervised prioritisation of genes integrating network data, phenotypes and additional prior knowledge about TP and TN gene labels from the literature or experts.

**Imports** stats, Matrix, dplyr, doParallel, foreach, parallel, sparseMVN, ggplot2, gridExtra, pROC

**Depends** methods, graphics, R(>= 3.3)

**Suggests** knitr, BiocStyle, pander

**VignetteBuilder** knitr

**biocViews** ImmunoOncology, CellBasedAssays, Preprocessing, Network

**Type** Package

**Lazyload** yes

**LazyData** true

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**License** GPL-3

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Contents

|                                      |           |
|--------------------------------------|-----------|
| netprioR-package . . . . .           | 2         |
| bandwidth . . . . .                  | 3         |
| cmn . . . . .                        | 3         |
| conjugate_gradient . . . . .         | 4         |
| cuthill_mckee . . . . .              | 4         |
| fit . . . . .                        | 5         |
| laplacian . . . . .                  | 6         |
| learn . . . . .                      | 6         |
| netprioR-class . . . . .             | 7         |
| norm_kern . . . . .                  | 9         |
| plot.netprioR . . . . .              | 9         |
| ranks . . . . .                      | 10        |
| ROC . . . . .                        | 11        |
| simulate_labels . . . . .            | 11        |
| simulate_network_random . . . . .    | 12        |
| simulate_network_scalefree . . . . . | 13        |
| simulate_phenotype . . . . .         | 13        |
| simulation . . . . .                 | 14        |
| weights . . . . .                    | 15        |
| <b>Index</b>                         | <b>16</b> |

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|                  |                   |
|------------------|-------------------|
| netprioR-package | Package: netprioR |
|------------------|-------------------|

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Description

This package provides a model for semi-supervised prioritisation of genes integrating network data, phenotypes and additional prior knowledge about TP and TN gene labels.

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References

Fabian Schmich et. al (2016).

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|           |                  |
|-----------|------------------|
| bandwidth | <i>bandwidth</i> |
|-----------|------------------|

---

**Description**

Compute the bandwidth of a matrix

**Usage**

bandwidth(x)

**Arguments**

x                      Input matrix

**Value**

Bandwidth

**Author(s)**

Fabian Schmich

---

|     |                                                             |
|-----|-------------------------------------------------------------|
| cmn | <i>Class Mass Normalization (CMN) from Zhu et al., 2003</i> |
|-----|-------------------------------------------------------------|

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**Description**

Class Mass Normalization (CMN) from Zhu et al., 2003

**Usage**

cmn(yhat, l, u)

**Arguments**

yhat                      Response for labeled (l) and unlabeled (u) genes  
l                          Indices of labeled genes  
u                          Indices of unlabeled genes

**Value**

Class normalized yhat

**Author(s)**

Fabian Schmich

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|                    |                                  |
|--------------------|----------------------------------|
| conjugate_gradient | <i>Conjugate Gradient Solver</i> |
|--------------------|----------------------------------|

---

**Description**

Solves linear equation systems iteratively

**Usage**

```
conjugate_gradient(A, b, x0 = rep(0, ncol(A)), threshold = 1e-15,  
  verbose = FALSE)
```

**Arguments**

|           |                         |
|-----------|-------------------------|
| A         | Matrix                  |
| b         | Coefficients            |
| x0        | Starting solution       |
| threshold | Termination threshold   |
| verbose   | Show iterative progress |

**Value**

Solution for equation system

**Author(s)**

Fabian Schmich

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|               |                                     |
|---------------|-------------------------------------|
| cuthill_mckee | <i>Cuthill McKee (CM) algorithm</i> |
|---------------|-------------------------------------|

---

**Description**

Transform sparse matrix into a band matrix

**Usage**

```
cuthill_mckee(x)
```

**Arguments**

|   |              |
|---|--------------|
| x | Input matrix |
|---|--------------|

**Value**

Band matrix

**Author(s)**

Fabian Schmich

---

fit

*Fit netprioR model*

---

**Description**

Fit [netprioR](#) model

**Usage**

```
fit(object, ...)  
  
## S4 method for signature 'netprioR'  
fit(object, refit = FALSE, ...)
```

**Arguments**

|        |                                        |
|--------|----------------------------------------|
| object | A <a href="#">netprioR</a> object      |
| ...    | Additional arguments                   |
| refit  | Flag whether to overwrite existing fit |

**Value**

A [netprioR](#) object with fitted model

**Author(s)**

Fabian Schmich

**Examples**

```
data(simulation)  
np <- netprioR(networks = simulation$networks,  
               phenotypes = simulation$phenotypes,  
               labels = simulation$labels.obs,  
               model.fit = FALSE)  
  
summary(np)  
np <- fit(np, nrestarts = 1, verbose = FALSE)  
summary(np)
```

---

|           |                        |
|-----------|------------------------|
| laplacian | <i>Graph Laplacian</i> |
|-----------|------------------------|

---

**Description**

Compute the Laplacian matrix of a graph given its adjacency matrix

**Usage**

```
laplacian(x, norm = c("none", "sym", "asym"))
```

**Arguments**

|      |                       |
|------|-----------------------|
| x    | Adjacency matrix      |
| norm | Type of normalisation |

**Value**

Laplacian matrix

**Author(s)**

Fabian Schmich

---

|       |                           |
|-------|---------------------------|
| learn | <i>Fit netprioR model</i> |
|-------|---------------------------|

---

**Description**

Infer parameters and hidden data using the EM algorithm of netprioR

**Usage**

```
learn(Yobs, X, G, l, u, a = 0.1, b = 0.1, sigma2 = 1, tau2 = 10,  
      eps = 1e-11, max.iter = 500, thresh = 0.001, use.cg = TRUE,  
      thresh.cg = 1e-05, nrestarts = 5, max.cores = detectCores(),  
      verbose = FALSE)
```

**Arguments**

|           |                                                                                     |
|-----------|-------------------------------------------------------------------------------------|
| Yobs      | Observed labels (NA, if not observed)                                               |
| X         | Phenotypes                                                                          |
| G         | Graph Laplacians                                                                    |
| l         | Indices of labelled instances                                                       |
| u         | Indices of unlabelled instances                                                     |
| a         | Shape parameter of Gamma prior for W                                                |
| b         | Scale parameter of Gamma prior for W                                                |
| sigma2    | Cariance for Gaussian labels                                                        |
| tau2      | Variance for Gaussian prior for beta                                                |
| eps       | Small value added to diagonal of Q in order to make it non-singular                 |
| max.iter  | Maximum number of iterations for EM                                                 |
| thresh    | Threshold for termination of EM with respect to change in parameters                |
| use.cg    | Flag whether to use conjugate gradient instead of exact computation of expectations |
| thresh.cg | Threshold for the termination of the conjugate gradient solver                      |
| nrestarts | Number of restarts for EM                                                           |
| max.cores | Maximum number of cores to use for parallel computation                             |
| verbose   | Print verbose output                                                                |

**Value**

List containing: Predicted labels Yhat and inferred parameters W and beta

**Author(s)**

Fabian Schmich

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|                |                 |
|----------------|-----------------|
| netprioR-class | <i>netprioR</i> |
|----------------|-----------------|

---

**Description**

Class that represents a netprioR model.

**Usage**

```
netprioR(networks, phenotypes, labels, ...)

## S4 method for signature 'list,matrix,factor'
netprioR(networks, phenotypes, labels,
  fit.model = FALSE, a = 0.1, b = 0.1, sigma2 = 0.1, tau2 = 100,
  eps = 1e-10, max.iter = 500, thresh = 1e-06, use.cg = FALSE,
  thresh.cg = 1e-06, nrestarts = 5, max.cores = detectCores(),
  verbose = TRUE, ...)
```

**Arguments**

|            |                                                                                     |
|------------|-------------------------------------------------------------------------------------|
| networks   | List of NxN adjacency matrices of gene-gene similarities                            |
| phenotypes | Matrix of dimension NxP containing covariates                                       |
| labels     | Vector of Nx1 labels for all genes (NA if no label available)                       |
| ...        | Additional arguments                                                                |
| fit.model  | Indicator whether to fit the model                                                  |
| a          | Shape parameter of Gamma prior for W                                                |
| b          | Scale parameter of Gamma prior for W                                                |
| sigma2     | Cariance for Gaussian labels                                                        |
| tau2       | Variance for Gaussian prior for beta                                                |
| eps        | Small value added to diagonal of Q in order to make it non-singular                 |
| max.iter   | Maximum number of iterations for EM                                                 |
| thresh     | Threshold for termination of EM with respect to change in parameters                |
| use.cg     | Flag whether to use conjugate gradient instead of exact computation of expectations |
| thresh.cg  | Threshold for the termination of the conjugate gradient solver                      |
| nrestarts  | Number of restarts for EM                                                           |
| max.cores  | Maximum number of cores to use for parallel computation                             |
| verbose    | Print verbose output                                                                |

**Value**

A [netprioR](#) object

**Slots**

|            |                                                               |
|------------|---------------------------------------------------------------|
| networks   | List of NxN adjacency matrices of gene-gene similarities      |
| phenotypes | Matrix of dimension NxP containing covariates                 |
| labels     | Vector of Nx1 labels for all genes. NA if no label available. |
| is.fitted  | Flag indicating if model is fitted                            |
| model      | List containing estimated parameters and imputed missing data |

**Author(s)**

Fabian Schmich

**Examples**

```
# runs long-ish
data(simulation)
np <- netprioR(networks = simulation$networks,
               phenotypes = simulation$phenotypes,
               labels = simulation$labels.obs,
               fit.model = TRUE)
summary(np)
```



---

|           |                         |
|-----------|-------------------------|
| norm_kern | <i>Normalise kernel</i> |
|-----------|-------------------------|

---

**Description**

adopted from GeneMania, Mostafavi et al, 2009

**Usage**

```
norm_kern(x)
```

**Arguments**

|   |        |
|---|--------|
| x | kernel |
|---|--------|

**Value**

Normalised kernel

**Author(s)**

Fabian Schmich

---

|               |                                                         |
|---------------|---------------------------------------------------------|
| plot.netprioR | <i>Plot method for <a href="#">netprioR</a> objects</i> |
|---------------|---------------------------------------------------------|

---

**Description**

Plot method for [netprioR](#) objects

**Usage**

```
## S3 method for class 'netprioR'  
plot(x, which = c("all", "weights", "lik", "scores"), ...)
```

**Arguments**

|       |                                                                         |
|-------|-------------------------------------------------------------------------|
| x     | A <a href="#">netprioR</a> object                                       |
| which | Flag for which plot should be shown, options: weights, lik, scores, all |
| ...   | Additional paramters for plot                                           |

**Value**

Plot of the weights, likelihood, ranks, or all three

**Author(s)**

Fabian Schmich

**Examples**

```
data(simulation)
plot(simulation$model)
```

---

ranks

*Retrieve ranked prioritisation list*

---

**Description**

Retrieve ranked prioritisation list

**Usage**

```
ranks(object)

## S4 method for signature 'netpriorR'
ranks(object)
```

**Arguments**

object            A [netpriorR](#) object

**Value**

Ranked list of prioritised genes

**Author(s)**

Fabian Schmich

**Examples**

```
data(simulation)
ranks(simulation$model)
```

---

ROC*Compute ROC curve from netprioR model and true labels*

---

**Description**

Compute ROC curve from netprioR model and true labels

**Usage**

```
ROC(object, ...)
```

```
## S4 method for signature 'netprioR'  
ROC(object, true.labels, plot = FALSE, ...)
```

**Arguments**

|             |                                    |
|-------------|------------------------------------|
| object      | A <a href="#">netprioR</a> object  |
| ...         | Additional arguments               |
| true.labels | True full set of underlying labels |
| plot        | Flag whether to plot the AUC curve |

**Value**

ROC curve with AUC

**Author(s)**

Fabian Schmich

**Examples**

```
data(simulation)  
ROC(simulation$model, true.labels = simulation$labels.true)
```

---

simulate\_labels*Simulate labels*

---

**Description**

Simulate labels

**Usage**

```
simulate_labels(values, sizes, nobs)
```

**Arguments**

|        |                                               |
|--------|-----------------------------------------------|
| values | Vector of labels for groups                   |
| sizes  | Vector of group sizes                         |
| nobs   | Vector of number of observed labels per group |

**Value**

List of Y, Yobs and indices for labeled instances

**Author(s)**

Fabian Schmich

**Examples**

```
labels <- simulate_labels(values = c("Positive", "Negative"),
  sizes = c(10, 10),
  nobs = c(5, 5))
```

---

```
simulate_network_random
```

*Simulate random networks with predefined number of members for each of the two groups and the number of neighbours for each node*

---

**Description**

Simulate random networks with predefined number of members for each of the two groups and the number of neighbours for each node

**Usage**

```
simulate_network_random(nmemb, nnei = 1)
```

**Arguments**

|       |                                            |
|-------|--------------------------------------------|
| nmemb | Vector of number of members for each group |
| nnei  | Number of neighbours for each node         |

**Value**

Adjacency matrix of graph

**Author(s)**

Fabian Schmich

**Examples**

```
network <- simulate_network_random(nmemb = c(10, 10), nnei = 1)
```

---

```
simulate_network_scalefree
```

*Simulate scalefree networks*

---

**Description**

Simulate scale free networks for predefined number of members for each of two groups and a parameter pclus that determines how strictly distinct the groups are

**Usage**

```
simulate_network_scalefree(nmemb, pclus = 1)
```

**Arguments**

|       |                                                               |
|-------|---------------------------------------------------------------|
| nmemb | Vector of numbers of members per group                        |
| pclus | Scalar in [0, 1] determining how strictly distinct groups are |

**Value**

Adjacency matrix

**Author(s)**

Fabian Schmich

**Examples**

```
network <- simulate_network_scalefree(nmemb = c(10, 10), pclus = 0.8)
```

---

```
simulate_phenotype
```

*Simulate phenotypes correlated to labels pivoted into two groups*

---

**Description**

Simulate phenotypes correlated to labels pivoted into two groups

**Usage**

```
simulate_phenotype(labels.true, meandiff, sd)
```

**Arguments**

|             |                                                          |
|-------------|----------------------------------------------------------|
| labels.true | Vector of labels                                         |
| meandiff    | difference of means between positive and negative groups |
| sd          | Standard deviation of the phenotype                      |

**Value**

Simulated phenotype

**Author(s)**

Fabian Schmich

**Examples**

```
data(simulation)
phenotypes <- simulate_phenotype(labels.true = simulation$labels.true, meandiff = 0.5, sd = 1)
```

---

|            |                                                                                   |
|------------|-----------------------------------------------------------------------------------|
| simulation | <i>Example data: Simulated networks, phenotypes and labels for N = 1000 genes</i> |
|------------|-----------------------------------------------------------------------------------|

---

**Description**

The data set contains simulated data for  $N = 1000$  genes and  $P = 1$  (univariate) phenotypes. The list of networks contains 2 low noise networks and two high noise networks. The class labels are "Positive" and "Negative".

**Usage**

```
data(simulation)
```

**Details**

The code used to simulate the data can be found in `system.file("example", "data_simulation.R", package = "netprioR")`

**Value**

List of simulated networks, phenotypes and labels for 1000 genes

---

|         |                                 |
|---------|---------------------------------|
| weights | <i>Retrieve network weights</i> |
|---------|---------------------------------|

---

**Description**

Retrieve network weights

**Usage**

```
weights(object, ...)
```

```
## S4 method for signature 'netprioR'  
weights(object)
```

**Arguments**

|        |                                   |
|--------|-----------------------------------|
| object | A <a href="#">netprioR</a> object |
| ...    | Additional arguments              |

**Value**

Estimated network weights

**Author(s)**

Fabian Schmich

**Examples**

```
data(simulation)  
weights(simulation$model)
```

# Index

- \* **package**
  - netprioR-package, [2](#)
- bandwidth, [3](#)
- cmn, [3](#)
- conjugate\_gradient, [4](#)
- cuthill\_mckee, [4](#)
- fit, [5](#)
- fit, netprioR-method (fit), [5](#)
- laplacian, [6](#)
- learn, [6](#)
- netprioR, [5](#), [8–11](#), [15](#)
- netprioR (netprioR-class), [7](#)
- netprioR, list, matrix, factor-method (netprioR-class), [7](#)
- netprioR-class, [7](#)
- netprioR-package, [2](#)
- norm\_kern, [9](#)
- plot.netprioR, [9](#)
- ranks, [10](#)
- ranks, netprioR-method (ranks), [10](#)
- ROC, [11](#)
- ROC, netprioR-method (ROC), [11](#)
- simulate\_labels, [11](#)
- simulate\_network\_random, [12](#)
- simulate\_network\_scalefree, [13](#)
- simulate\_phenotype, [13](#)
- simulation, [14](#)
- weights, [15](#)
- weights, netprioR-method (weights), [15](#)