

# Package ‘BNrich’

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**Type** Package

**Title** Pathway Enrichment Analysis Based on Bayesian Network

**Version** 0.1.1

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## Description

Maleknia et al. (2020) <[doi:10.1101/2020.01.13.905448](https://doi.org/10.1101/2020.01.13.905448)>. A novel pathway enrichment analysis package based on Bayesian network to investigate the topology features of the pathways. firstly, 187 kyoto encyclopedia of genes and genomes (KEGG) human non-metabolic pathways which their cycles were eliminated by biological approach, enter in analysis as Bayesian network structures. The constructed Bayesian network were optimized by the Least Absolute Shrinkage Selector Operator (lasso) and the parameters were learned based on gene expression data. Finally, the impacted pathways were enriched by Fisher’s Exact Test on significant parameters.

**biocViews** NetworkEnrichment, GeneExpression, Pathways, Bayesian, KEGG

**License** GPL (>= 2)

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.0

**Imports** bnlearn, corpcor, glmnet, graph, stats, utils

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**URL** <https://github.com/Samaneh-Bioinformatics/BNrich>

**BugReports** <https://github.com/Samaneh-Bioinformatics/BNrich/issues>

**NeedsCompilation** no

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BNrich	<i>Analysis of significant final BNs</i>
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### Description

Fisher's exact test applied to PEA on final BNs

### Usage

```
BNrich(Ttest_Results, Pathway.id1, PathName_Final, fdr.value = 0.05)
```

### Arguments

Ttest\_Results A data frame contains T-test results for all parameters  
 Pathway.id1 A vector contains modified KEEG pathway IDs  
 PathName\_Final A data frame contains is IDs and names of KEEG pathways  
 fdr.value A numeric threshold to determine significant parameters

### Value

A data frame contains fisher test results for any final pathways

### Examples

```
#All the 187 preprocessed signaling pathways can be entered in analysis by fetch_data_file().
#But here you enter a subset of those pathways to see how this package works.
files <- system.file("extdata", "test_files_to_start.RData", package = "BNrich", mustWork = TRUE)
load(files)
Data <- system.file("extdata", "Test_DATA.RData", package = "BNrich", mustWork = TRUE)
load(Data)
uni_Result <- unify_path(dataH, dataD, MapkG = sub_mapkG, Pathway.id = path.id)
M1 <- uni_Result$mapkG1
BN <- BN_struct(M1)
data_h1 <- uni_Result$data_h
data_d1 <- uni_Result$data_d
LASSO_Result <- LASSO_BN(BN = BN , data_h = data_h1 , data_d = data_d1)
```

```

BN_h1 <- LASSO_Result$BN_h
BN_d1 <- LASSO_Result$BN_d
esti_result <- esti_par(BN_H = BN_h1, BN_D = BN_d1, data_h = data_h1, data_d = data_d1)
BNs_H <- esti_result$BNs_h
BNs_D <- esti_result$BNs_d
coef_h <- esti_result$coef_h
coef_d <- esti_result$coef_d
var_result <- var_mat(data_h1, coef_h, BNs_H, data_d1, coef_d, BNs_D)
Var_H = var_result$var_mat_Bh
Var_D = var_result$var_mat_Bd
path.id1 <- uni_Result$pathway.id1
Ttest_result <- parm_Ttest(data_h1, coef_h, BNs_H, data_d1, coef_d, BNs_D, Var_H, Var_D, path.id1)
BNrich_result <- BNrich(Ttest_result, path.id1, Path.Name)

```

---

BN\_struct

*Construct Bayesian networks structures*


---

### Description

Construct BNs structures using unified signaling pathways

### Usage

```
BN_struct(mapkG1)
```

### Arguments

mapkG1            A list contains unified signaling pathways

### Value

A list contains Bayesian networks structures

### Examples

```

#All the 187 preprocessed signaling pathways can be entered in analysis by fetch_data_file().
#But here you enter a subset of those pathways to see how this package works.
files <- system.file("extdata", "test_files_to_start.RData", package = "BNrich", mustWork = TRUE)
load(files)
Data <- system.file("extdata", "Test_DATA.RData", package = "BNrich", mustWork = TRUE)
load(Data)
uni_Result <- unify_path(dataH, dataD, MapkG = sub_mapkG, Pathway.id = path.id)
M1 <- uni_Result$mapkG1
BN <- BN_struct(M1)

```

---

 esti\_par

*Estimate parameters of BNs in control and disease states*


---

### Description

Estimate parameters of BNs in control and disease states

### Usage

```
esti_par(BN_H, BN_D, data_h, data_d)
```

### Arguments

BN_H	A list contains simplified BNs structures for control objects
BN_D	A list contains simplified BNs structures for disease objects
data_h	A list contains data frames related to control objects for any BN
data_d	A list contains data frames related to disease objects for any BN

### Value

A list contains four lists BNs\_h, BNs\_d, coef\_h and coef\_d

### Examples

```
#All the 187 preprocessed signaling pathways can be entered in analysis by fetch_data_file().
#But here you enter a subset of those pathways to see how this package works.
files <- system.file("extdata", "test_files_to_start.RData", package = "BNrich", mustWork = TRUE)
load(files)
Data <- system.file("extdata", "Test_DATA.RData", package = "BNrich", mustWork = TRUE)
load(Data)
uni_Result <- unify_path(dataH, dataD, MapkG = sub_mapkG, Pathway.id = path.id)
M1 <- uni_Result$mapkG1
BN <- BN_struct(M1)
data_h1 <- uni_Result$data_h
data_d1 <- uni_Result$data_d
LASSO_Result <- LASSO_BN(BN = BN , data_h = data_h1 , data_d = data_d1)
BN_h1 <- LASSO_Result$BN_h
BN_d1 <- LASSO_Result$BN_d
esti_result <- esti_par(BN_H = BN_h1, BN_D = BN_d1, data_h = data_h1, data_d = data_d1)
```

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fetch_data_file	<i>Download data file</i>
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---

**Description**

Download necessary data file to start BNrich

**Usage**

```
fetch_data_file(destfile, verbose = FALSE)
```

**Arguments**

destfile	A directory in user's own computer for save preprocessed data file
verbose	A logical argument to show verbose results

**Value**

A list contain mapkG, PathName\_final and pathway.id. The mapkG is a list contains imported 187 preprocessed signaling pathways, PathName\_final is a data.frame includes names and IDs of all 187 pathways and pathway.id is a character vector of pathways IDs

**Examples**

```
destfile = tempfile("files", fileext = ".rda")
files <- fetch_data_file()
load(destfile)
```

---

LASSO_BN	<i>LASSO regression</i>
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---

**Description**

LASSO regression – second step of simplification of BNs structures

**Usage**

```
LASSO_BN(BN, data_h, data_d)
```

**Arguments**

BN	A list of Bayesian networks achieved by BN_struct function
data_h	A list contains data frames related to control objects
data_d	A list contains data frames related to disease objects

**Value**

A list contains two lists. BN\_h and BN\_d are simplified BNs

**Examples**

```
#All the 187 preprocessed signaling pathways can be entered in analysis by fetch_data_file().
#But here you enter a subset of those pathways to see how this package works.
files <- system.file("extdata", "test_files_to_start.RData", package = "BNrich", mustWork = TRUE)
load(files)
Data <- system.file("extdata", "Test_DATA.RData", package = "BNrich", mustWork = TRUE)
load(Data)
uni_Result <- unify_path(dataH, dataD, MapkG = sub_mapkG, Pathway.id = path.id)
M1 <- uni_Result$mapkG1
BN <- BN_struct(M1)
data_h1 <- uni_Result$data_h
data_d1 <- uni_Result$data_d
LASSO_Result <- LASSO_BN(BN = BN , data_h = data_h1 , data_d = data_d1)
```

---

 parm\_Ttest

*Testing the equality regression coefficients*


---

**Description**

t-test for equality the corresponding parameters in any BN

**Usage**

```
parm_Ttest(
  Data_h,
  coef_H,
  BNs_H,
  Data_d,
  coef_D,
  BNs_D,
  Var_mat_Bh,
  Var_mat_Bd,
  Pathway.id1
)
```

**Arguments**

Data_h	A list contains data frames related to control objects for any BN
coef_H	A list contains parameters of BN_h
BNs_H	A list contains BNs learned by control objects data
Data_d	A list contains data frames related to disease objects for any BN
coef_D	A list contains parameters of BN_d

BNs_D	A list contains BNs learned by disease objects data
Var_mat_Bh	A list contains covariance matrixes for any node of BN_h
Var_mat_Bd	A list contains covariance matrixes for any node of BN_d
Pathway.id1	A vector contains modified KEEG pathway IDs

**Value**

A data frame contains T-test results for all parameters in final BNs

**Examples**

```
#All the 187 preprocessed signaling pathways can be entered in analysis by fetch_data_file().
#But here you enter a subset of those pathways to see how this package works.
files <- system.file("extdata", "test_files_to_start.RData", package = "BNrich", mustWork = TRUE)
load(files)
Data <- system.file("extdata", "Test_DATA.RData", package = "BNrich", mustWork = TRUE)
load(Data)
uni_Result <- unify_path(dataH, dataD, MapkG = sub_mapkG, Pathway.id = path.id)
M1 <- uni_Result$mapkG1
BN <- BN_struct(M1)
data_h1 <- uni_Result$data_h
data_d1 <- uni_Result$data_d
LASSO_Result <- LASSO_BN(BN = BN , data_h = data_h1 , data_d = data_d1)
BN_h1 <- LASSO_Result$BN_h
BN_d1 <- LASSO_Result$BN_d
esti_result <- esti_par(BN_H = BN_h1, BN_D = BN_d1, data_h = data_h1, data_d = data_d1)
BNs_H <- esti_result$BNs_h
BNs_D <- esti_result$BNs_d
coef_h <- esti_result$coef_h
coef_d <- esti_result$coef_d
var_result <- var_mat(data_h1, coef_h, BNs_H, data_d1, coef_d, BNs_D)
Var_H = var_result$var_mat_Bh
Var_D = var_result$var_mat_Bd
path.id1 <- uni_Result$pathway.id1
Ttest_result <- parm_Ttest(data_h1, coef_h, BNs_H, data_d1, coef_d, BNs_D, Var_H, Var_D, path.id1)
```

---

unify\_path

*Simplification networks – applied to unifying nodes*


---

**Description**

Unifying nodes based imported signaling pathways and GE data

**Usage**

```
unify_path(dataH, dataD, MapkG, Pathway.id)
```

**Arguments**

dataH	A data frame contains (healthy) control objects data
dataD	A data frame contains disease objects data
MapkG	A list contains imported 187 signaling pathways
Pathway.id	A vector contains 187 KEEG pathway IDs

**Value**

A list contain data\_h,data\_d,mapkG1 and pathway.id1

**Examples**

```
#All the 187 preprocessed signaling pathways can be entered in analysis by fetch_data_file().
#But here you enter a subset of those pathways to see how this package works.
files <- system.file("extdata", "test_files_to_start.RData", package = "BNrich", mustWork = TRUE)
load(files)
Data <- system.file("extdata", "Test_DATA.RData", package = "BNrich", mustWork = TRUE)
load(Data)
uni_Result <- unify_path(dataH, dataD, MapkG = sub_mapkG, Pathway.id = path.id)
```

---

var\_mat

*Estimate variance-covariance matrixes for any parameters of BNs*


---

**Description**

Estimate variance-covariance matrixes for any parameters of

**Usage**

```
var_mat(Data_h, coef_H, BNs_H, Data_d, coef_D, BNs_D)
```

**Arguments**

Data_h	A list contains data frames related to control objects for any BN
coef_H	A lists of parameters of BN_h achieved
BNs_H	A list of BNs learned by control objects data
Data_d	A list contains data frames related to disease objects for any BN
coef_D	A lists of parameters of BN_d
BNs_D	A list of BNs learned by disease objects data

**Value**

A listcontains two lists var\_mat\_Bh and var\_mat\_Bd



**Examples**

```
#All the 187 preprocessed signaling pathways can be entered in analysis by fetch_data_file().
#But here you enter a subset of those pathways to see how this package works.
files <- system.file("extdata", "test_files_to_start.RData", package = "BNrich", mustWork = TRUE)
load(files)
Data <- system.file("extdata", "Test_DATA.RData", package = "BNrich", mustWork = TRUE)
load(Data)
uni_Result <- unify_path(dataH, dataD, MapkG = sub_mapkG, Pathway.id = path.id)
M1 <- uni_Result$mapkG1
BN <- BN_struct(M1)
data_h1 <- uni_Result$data_h
data_d1 <- uni_Result$data_d
LASSO_Result <- LASSO_BN(BN = BN , data_h = data_h1 , data_d = data_d1)
BN_h1 <- LASSO_Result$BN_h
BN_d1 <- LASSO_Result$BN_d
esti_result <- esti_par(BN_H = BN_h1, BN_D = BN_d1, data_h = data_h1, data_d = data_d1)
BNs_H <- esti_result$BNs_h
BNs_D <- esti_result$BNs_d
coef_h <- esti_result$coef_h
coef_d <- esti_result$coef_d
var_result <- var_mat(data_h1, coef_h, BNs_H, data_d1, coef_d, BNs_D)
```

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