Package: enet (via r-universe)

October 31, 2026

Type Package

Title Network Analysis for Exposomics

Version 0.1.0

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Description Network analysis for exposomics including generation of exposures-metabolites network, metabolites-metabolites network and gatekeeper metabolites discovery for non-targeted high resolution mass spectrometry data. It can be used to discover gatekeepers.

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Encoding UTF-8

LazyData true

Imports igraph, impute, limma, stats

Depends R (>= 2.10)

RoxygenNote 7.1.1

Suggests knitr, rmarkdown, ggnetwork, genefilter

VignetteBuilder knitr

Config/pak/sysreqs libglpk-dev libxml2-dev

Repository https://ymgroup.r-universe.dev

Date/Publication 2022-02-17 18:07:18 UTC

RemoteUrl https://github.com/yufree/enet

RemoteRef HEAD

RemoteSha 24eddc9ab11d6070b95e468d1091ca498a49aeb6

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asthma *A vector with asthma condition for 1198 samples*

Description

A vector with asthma condition for 1198 samples

Usage

```
data(asthma)
```

Format

asthma condition for 1198 samples

1 means asthma and 0 means non-asthma. Raw data are from Exposome Data Challenge 2021.

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expo *A dataset with 7 exposures from 1198 samples*

Description

A dataset with 7 exposures from 1198 samples

Usage

```
data(expo)
```

Format

A data frame with 7 rows and 1198 columns:

7 exposures from 1198 samples. Raw data are from Exposome Data Challenge 2021.

getcf *Get correlation cutoff by max network clusters*

Description

Get correlation cutoff by max network clusters

Usage

```
getcf(mat, cutoff = seq(0, 1, 0.02), ...)
```

Arguments

mat	dataframe with row as feature and column as samples
cutoff	correlation coefficient cutoff
...	other parameters for 'cor'

Value

list with cutoff

Examples

```
data(meta)
cf <- getcf(t(meta))
```

geteenet *Generate exposures-exposures network*

Description

Generate exposures-exposures network

Usage

```
geteenet(expo, cutoff = 0.9, nacf = 0.2, e = NULL, name = NULL, ...)
```

Arguments

expo	exposures dataframe with row as exposures/peaks and column as samples
cutoff	correlation coefficient cutoff
nacf	NA cutoff for exposure, exposure with NA percentage larger than cutoff will be removed and others will be imputed by knn methods, default 0.2
e	value or vector, specific exposure or peak to its export network
name	export gml file for Cytoscape
...	other parameters for 'cor'

Value

list with index of exposures clusters, exposures clusters data and edge table

Examples

```
data(expo)
ee <- geteenet(expo)
```

`getemnet` *Generate metabolites-exposures network*

Description

Generate metabolites-exposures network

Usage

```
getemnet(meta, expo, cutoffm = 0.9, cutoffe = 0.6, nacf = 0.2, ...)
```

Arguments

`meta`	metabolites dataframe with row as metabolites/peaks and column as samples
`expo`	exposures dataframe with row as exposures/peaks and column as samples
`cutoffm`	correlation coefficient cutoff for metabolites-metabolites network
`cutoffe`	correlation coefficient cutoff for exposures-exposures network
`nacf`	NA cutoff for exposure, exposure with NA percentage larger than cutoff will be removed and others will be imputed by knn methods, default 0.2
`...`	other parameters for 'cor'

Value

list with table of metabolites-exposures, metabolites-exposures network clusters data and edge table

Examples

```
data(expo)
data(meta)
me <- getemnet(exp(meta),expo)
```

getgk *Gatekeeper discovery*

Description

Gatekeeper discovery

Usage

```
getgk(meta, expo, cutoff = 0.9, multiple = FALSE, ...)
```

Arguments

meta	metabolites dataframe with row as metabolites/peaks and column as samples
expo	exposures dataframe with row as exposures/peaks and column as samples
cutoff	correlation coefficient cutoff for metabolites-metabolites network
multiple	logical, only output gatekeeper with multiple exposures
...	other parameters for 'cor'

Value

list with table of metabolites-exposures, metabolites-exposures network clusters data and edge table

Examples

```
data(expo)
data(meta)
gk <- getgk(exp(meta),expo)
```

getmmnet *Generate metabolites-metabolites network*

Description

Generate metabolites-metabolites network

Usage

```
getmmnet(meta, cutoff = 0.9, m = NULL, name = NULL, ...)
```

Arguments

meta	metabolites dataframe with row as metabolites/peaks and column as samples
cutoff	correlation coefficient cutoff
m	value or vector, specific metabolite or peak to its export network
name	export gml file for Cytoscape
...	other parameters for 'cor'

Value

list with index of metabolites clusters, metabolites clusters data and edge table

Examples

```
data(meta)
mm <- getmmnet(meta)
```

---

meta *A dataset 177 peaks/metabolites from 1198 samples*

Description

A dataset 177 peaks/metabolites from 1198 samples

Usage

```
data(meta)
```

Format

A data frame with 177 rows and 1198 columns:

177 peaks/metabolites from 1198 samples. Raw data are from Exposome Data Challenge 2021.

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