Package 'ILSM'

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Title Analyze Interconnection Structure of Multilayer Interaction Networks

Version 1.0.3.2

Description In view of the analysis of the structural characteristics of the multilayer network has been complete, however, there is still a lack of a unified operation that can quickly obtain the corresponding characteristics of the multilayer network.
To solve this insufficiency, 'ILSM' was designed for supporting calculating such metrics of multilayer networks by functions of this R package.

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Contents

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build_net   *Generating tripartite network*

Description

Generating a network of three layers. All layers of network contain `lay_0`, `lay_1` and `lay_2` nodes respectively.

Usage

```
build_net(lay_0, lay_1, lay_2, C_lay, asmatrices = FALSE)
```

Arguments

`lay_0`	The number of nodes in the first layer.
`lay_1`	The number of nodes in the second layer.
`lay_2`	The number of nodes in the third layer.
`C_lay`	The probability of each node interact with the other one. It ranges from 0 to 1.
`asmatrices`	Logical. whether to output the overall adjacency matrix of the network and the corresponding interaction matrix of the respective subnetworks. Defaults to FALSE.

Value

Return a tripatite network of direction. The network contains three groups of species and interactions within layers, and there is no link among each group of nodes within one layer.

Examples

```
set.seed(12)
d <- build_net(11,15,16,0.2)
plot(d)

set.seed(12)
N <- build_net(11,15,16,0.2,asmatrices=FALSE)
```

N

---

coid   *Correlation of Interaction Degree: CoID*

Description

Calculating correlation of interaction degree among subnetworks ("CoID_~").

Usage

```
coid(network.or.subnet_mat1, subnet_mat2 = NULL, weighted = FALSE)
```

Arguments

network.or.subnet_mat1

> Either a multilayer(tripartite) network of 'igraph' class which contains three groups of species and interactions within layers without interactions between each group of species, or a numeric matrix(or data.frame) representing interactions between two groups of species. Each row and column of matrix represents single species in the second and first groups of the tripartite network respectively. Elements of matrix are non-zero numbers if the two groups of species are connected, and 0 otherwise.

subnet_mat2   A numeric matrix(or data.frame) representing interactions between two groups of species. Each row and column of matrix represents single species in the second and third groups of the tripartite network respectively. Elements of matrix are non-zero numbers if the two groups of species are connected, and 0 otherwise. If network.or.subnet_mat1 is "igraph", subnet_mat2 defaults to NULL.

weighted   Logical. should elements of matrix be fractional? Default to FALSE. Generally, 'igraph' network represent a spare matrix, so weighted is FALSE. While elements of matrix represent interaction strength, weighted is TRUE.

Details

weighted

If the weighted = FALSE, the input for the parameter can be:

- network.or.subnet_mat1: input a 'igraph' of network data independently or input sparse matrix together with subnet_mat2.

If the weighted = TRUE, the input for the parameter can be:

- network.or.subnet_mat1: must input matrix(or data.frame) together with subnet_mat2. the matrix can be sparse matrix and matrix of interaction strength.

network.or.subnet_mat1 and **subnet_mat2**

There are two types of `network.or.subnet_mat1` that can be processed:

- (1). Input in a network of type "igraph" alone.
- (2). Must be entered as data frame or matrix with `subnet_mat2`.

If the type of inputting is data frame or matrix, please make sure the row of `network.or.subnet_mat1` and `subnet_mat2` correspond with the second group of species that both belong to two subnetworks and interact with other groups of species.

- Try to make the rows of both matrices have the same attributes. Or we default:
- When the two matrices can have different numbers of rows:
    - (1). If both matrices have row names, then the function counts all row names to produce two new matrices with the same row names.
    - (2). If at most one matrix has row names, the function assigns new row names to both matrices on a row-to-row basis (any extra row names are assigned a new value) and then counts all row names to produce two new matrices with the same row names.
- When the two matrices can have the same numbers of rows:
    - No matter how the row names of the two matrices are arranged, as long as the row names are exactly the same; But we don't handle matrices with empty row names (the function will give an error).
- The two matrices can have different numbers of rows, but read our default handling carefully to make sure the calculation is accurate when using this function!!!

About a network of type "igraph", It can be obtained from the connection matrices of subnetworks by the function `igraph_from_matrices`.

Value

Return a numeric value representing correlation of interaction degree: CoID.

If `weighted = FALSE`, the results will show "CoID= ;" and If `weighted = TRUE`, the results will show "CoID_weight= ;"

References

Sauve, A. M., Thébault, E., Pocock, M. J., & Fontaine, C. (2016). How plants connect pollination and herbivory networks and their contribution to community stability. Ecology, 97(4), 908-917.

Examples

```
set.seed(12)
d <- build_net(11,15,17,0.2)
coid(d)

md1<-matrix(sample(c(0,1),110,replace=TRUE),10,11)
md2<-matrix(sample(c(0,1),120,replace=TRUE),10,12)
coid(md1,md2)
coid(md1,md2,weighted=TRUE)
```

```
md1<-matrix(sample(c(0,1),80,replace=TRUE),8,10)
md2<-matrix(sample(c(0,1),120,replace=TRUE),10,12)
coid(md1,md2)

mdw1<-matrix(runif(110,0,1),10,11)
mdw2<-matrix(runif(120,0,1),10,12)
coid(mdw1,mdw2,weighted=TRUE)

set.seed(1)
mdw1<-matrix(runif(80,0,1),8,10)
mdw2<-matrix(runif(120,0,1),10,12)
coid(mdw1,mdw2,weighted=TRUE)
```

---

cois   *Correlation of Interaction Similarity for Shared species: CoIS*

Description

Calculating correlation of interaction similarity for shared species("COis_ ~") in two subnetworks.

Usage

```
cois(network.or.subnet_mat1, subnet_mat2 = NULL, weighted = FALSE)
```

Arguments

network.or.subnet_mat1

Either a multilayer(tripartite) network of 'igraph' class which contains three groups of species and interactions within layers without interactions between each group of species, or a numeric matrix(or data.frame) representing interactions between two groups of species. Each row and column of matrix represents single species in the second and first groups of the tripartite network respectively. Elements of matrix are non-zero numbers if the two groups of species are connected, and 0 otherwise.

subnet_mat2   A numeric matrix(or data.frame) representing interactions between two groups of species. Each row and column of matrix represents single species in the second and third groups of the tripartite network respectively. Elements of matrix are non-zero numbers if the two groups of species are connected, and 0 otherwise. If network.or.subnet_mat1 is "igraph", subnet_mat2 defaults to NULL.

weighted   Logical. should elements of matrix be fractional? Default to FALSE. Generally, 'igraph' network represent a spare matrix, so weighted is FALSE. While elements of matrix represent interaction strength, weighted is TRUE.

Details

weighted

If the `weighted = FALSE`, the input for the parameter can be:

- `network.or.subnet_mat1`: input a 'igraph' of network data independently or input sparse matrix together with `subnet_mat2`.

If the `weighted = TRUE`, the input for the parameter can be:

- `network.or.subnet_mat1`: must input matrix(or data.frame) together with `subnet_mat2`. the matrix can be sparse matrix and matrix of interaction strength.

network.or.subnet_mat1 and **subnet_mat2**

There are two types of `network.or.subnet_mat1` that can be processed:

- (1). Input in a network of type "igraph" alone.
- (2). Must be entered as data frame or matrix with `subnet_mat2`.

If the type of inputting is data frame or matrix, please make sure the row of `network.or.subnet_mat1` and `subnet_mat2` correspond with the second group of species that both belong to two subnetworks and interact with other groups of species.

- Try to make the rows of both matrices have the same attributes. Or we default:
- When the two matrices can have different numbers of rows:
    - (1). If both matrices have row names, then the function counts all row names to produce two new matrices with the same row names.
    - (2). If at most one matrix has row names, the function assigns new row names to both matrices on a row-to-row basis (any extra row names are assigned a new value) and then counts all row names to produce two new matrices with the same row names.
- When the two matrices can have the same numbers of rows:
    - No matter how the row names of the two matrices are arranged, as long as the row names are exactly the same; But we don't handle matrices with empty row names (the function will give an error).
- The two matrices can have different numbers of rows, but read our default handling carefully to make sure the calculation is accurate when using this function!!!

About a network of type "igraph", It can be obtained from the connection matrices of subnetworks by the function `igraph_from_matrices`.

Value

Return a numeric value representing correlation of interaction similarity for shared species among subnetworks .

If `weighted = FALSE`, the results will show "CoIS= ;" and If `weighted = TRUE`, the results will show "CoIS_weight= ;"

References

Sauve, A. M., Thébault, E., Pocock, M. J., & Fontaine, C. (2016). How plants connect pollination and herbivory networks and their contribution to community stability. Ecology, 97(4), 908-917.

Examples

```
set.seed(12)
d <- build_net(11,15,17,0.2)
cois(d)

md1<-matrix(sample(c(0,1),110,replace=TRUE),10,11)
md2<-matrix(sample(c(0,1),120,replace=TRUE),10,12)
cois(md1,md2)
cois(md1,md2,weighted=TRUE)

md1<-matrix(sample(c(0,1),80,replace=TRUE),8,10)
md2<-matrix(sample(c(0,1),120,replace=TRUE),10,12)
cois(md1,md2)

mdw1<-matrix(runif(110,0,1),10,11)
mdw2<-matrix(runif(120,0,1),10,12)
cois(mdw1,mdw2,weighted=TRUE)

set.seed(1)
mdw1<-matrix(runif(80,0,1),8,10)
mdw2<-matrix(runif(120,0,1),10,12)
cois(mdw1,mdw2,weighted=TRUE)
```

---

hc   *Counting the degree hub of multilayer network*

Description

This function counts degree hub that the proportion of interconnecting species serving as the core node of the network degree.

Usage

```
hc(network.or.subnet_mat1, subnet_mat2 = NULL)
```

Arguments

network.or.subnet_mat1

> Either a multilayer(tripartite) network of 'igraph' class which contains three groups of species and interactions within layers without interactions between each group of species, or a numeric matrix(or data.frame) representing interactions between two groups of species. Each row and column of matrix represents

single species in the second and first groups of the tripartite network respectively. Elements of matrix are non-zero numbers if the two groups of species are connected, and 0 otherwise.

subnet_mat2   A numeric matrix(or data.frame) representing interactions between two groups of species. Each row and column of matrix represents single species in the second and third groups of the tripartite network respectively. Elements of matrix are non-zero numbers if the two groups of species are connected, and 0 otherwise. If network.or.subnet_mat1 is "igraph", subnet_mat2 defaults to NULL.

Details

network.or.subnet_mat1 and subnet_mat2

There are two types of network.or.subnet_mat1 that can be processed:

- (1). Input in a network of type "igraph" alone.
- (2). Must be entered as data frame or matrix with subnet_mat2.

If the type of inputting is data frame or matrix, please make sure the row of network.or.subnet_mat1 and subnet_mat2 correspond with the second group of species that both belong to two subnetworks and interact with other groups of species.

- Try to make the rows of both matrices have the same attributes. Or we default:
- (1). If both matrices have row names, then the function counts all row names to produce two new matrices with the same row names.
- (2). If at most one matrix has row names, the function assigns new row names to both matrices on a row-to-row basis (any extra row names are assigned a new value) and then counts all row names to produce two new matrices with the same row names.
- The two matrices can have different numbers of rows, but read our default handling carefully to make sure the calculation is accurate when using this function!!!

About a network of type "igraph", It can be obtained from the connection matrices of subnetworks by the function igraph_from_matrices.

Value

Print a "hc= ;" and Return a numeric value representing the degree hub of network.

References

Battiston, F., Nicosia, V. & Latora, V. (2014) Structural measures for multiplex networks. Physical Review E, 89, 032804.

Domínguez-García, V., & Kéfi, S. (2024). The structure and robustness of ecological networks with two interaction types. PLOS Computational Biology, 20(1), e1011770.

Guimera, R. & Amaral, L.A.N. (2005) Cartography of complex networks: modules and universal roles. Journal of Statistical Mechanics: Theory and Experiment, 2005, P02001.

Examples

```
set.seed(15)
d <- build_net(11,15,17,0.2)
hc(d)

md1<-matrix(sample(c(0,1),80,replace=TRUE),8,10)
md2<-matrix(sample(c(0,1),120,replace=TRUE),10,12)
hc(md1,md2)

mdw1<-matrix(sample(c(rep(0,60),runif(60,0,1))),12,10)
mdw2<-matrix(sample(c(rep(0,40),runif(80,0,1))),10,12)
hc(mdw1,mdw2)
```

---

icmotif_count   *Calculating the number of 48 motifs*

Description

Calculating the number of 48 motifs from a tripartite interaction network.

Usage

```
icmotif_count(network.or.subnet_mat1, subnet_mat2 = NULL)
```

Arguments

network.or.subnet_mat1

> Either a multilayer(tripartite) network of 'igraph' class which contains three groups of species and interactions within layers without interactions between each group of species, or a numeric matrix(or data.frame) representing interactions between two groups of species. Each row and column of matrix represents single species in the second and first groups of the tripartite network respectively. Elements of matrix are non-zero numbers if the two groups of species are connected, and 0 otherwise.

subnet_mat2   A numeric matrix(or data.frame) representing interactions between two groups of species. Each row and column of matrix represents single species in the second and third groups of the tripartite network respectively. Elements of matrix are non-zero numbers if the two groups of species are connected, and 0 otherwise. If network.or.subnet_mat1 is "igraph", subnet_mat2 defaults to NULL.

Details

network.or.subnet_mat1 and **subnet_mat2**

There are two types of network.or.subnet_mat1 that can be processed:

- (1). Input in a network of type "igraph" alone.

- (2). Must be entered as data frame or matrix with `subnet_mat2`.

If the type of inputting is data frame or matrix, please make sure the row of `network.or.subnet_mat1` and `subnet_mat2` correspond with the second group of species that both belong to two subnetworks and interact with other groups of species.

- Try to make the rows of both matrices have the same attributes. Or we default:
- When the two matrices can have different numbers of rows:
    - (1). If both matrices have row names, then the function counts all row names to produce two new matrices with the same row names.
    - (2). If at most one matrix has row names, the function assigns new row names to both matrices on a row-to-row basis (any extra row names are assigned a new value) and then counts all row names to produce two new matrices with the same row names.
- When the two matrices can have the same numbers of rows:
    - No matter how the row names of the two matrices are arranged, as long as the row names are exactly the same; But we don't handle matrices with empty row names (the function will give an error).
- The two matrices can have different numbers of rows, but read our default handling carefully to make sure the calculation is accurate when using this function!!!

About a network of type "igraph", It can be obtained from the connection matrices of subnetworks by the function `igraph_from_matrices`.

Value

Return a numeric vector with the number of 48 motifs: M111, M112, M113, M114, M211, M212, M213, M311, M312, M411, M121_1, M122_1, M122_2, M122_3, M123_1, M123_2, M123_3, M123_4, M123_5, M221_1, M221_2, M221_3, M222_1, M222_2, M222_3, M222_4, M222_5, M222_6, M222_7, M222_8, M222_8, M321_1, M321_2, M321_3, M321_4, M321_5, M131, M132-1, M132-2, M132-3, M132-4, M132-5, M231-1, M231-2, M231-3, M231-4, M231-5, M141.

References

Pilosof, S., Porter, M. A., Pascual, M., & Kéfi, S. (2017). The multilayer nature of ecological networks. Nature Ecology & Evolution, 1(4), 0101.

Simmons, B. I., Sweering, M. J., Schillinger, M., Dicks, L. V., Sutherland, W. J., & Di Clemente, R. (2019). bmotif: A package for motif analyses of bipartite networks. Methods in Ecology and Evolution, 10(5), 695-701.

Examples

```
set.seed(12)
d <- build_net(11,22,21,0.2)
m <- icmotif_count(d)
m

set.seed(12)
d <- build_net(11,22,21,0.2,asmatrices=TRUE)
```

```
MAT<-d
icmotif_count(MAT[[3]],MAT[[4]])

md1<-matrix(sample(c(0,1),120,replace=TRUE),8,15)
md2<-matrix(sample(c(0,1),120,replace=TRUE),10,12)
icmotif_count(md1,md2)

R<-rownames(MAT[[4]])[12]
MR<-MAT[[4]][12,]
MAT[[4]]<-MAT[[4]][-12,]
MAT[[4]]<-rbind(MAT[[4]],MR)
rownames(MAT[[4]])[22]<-R

icmotif_count(MAT[[3]],MAT[[4]])
```

---

icmotif_role   *Analyzing role of interconnecting node in motifs*

Description

Counting the number of 70 roles about interconnecting species in multilayer network motifs.

Usage

```
icmotif_role(network.or.subnet_mat1, subnet_mat2 = NULL)
```

Arguments

network.or.subnet_mat1

Either a multilayer(tripartite) network of 'igraph' class which contains three groups of species and interactions within layers without interactions between each group of species, or a numeric matrix(or data.frame) representing interactions between two groups of species. Each row and column of matrix represents single species in the second and first groups of the tripartite network respectively. Elements of matrix are non-zero numbers if the two groups of species are connected, and 0 otherwise.

subnet_mat2   A numeric matrix(or data.frame) representing interactions between two groups of species. Each row and column of matrix represents single species in the second and third groups of the tripartite network respectively. Elements of matrix are non-zero numbers if the two groups of species are connected, and 0 otherwise. If network.or.subnet_mat1 is "igraph", subnet_mat2 defaults to NULL.

Details

network.or.subnet_mat1 and **subnet_mat2**

There are two types of `network.or.subnet_mat1` that can be processed:

- (1). Input in a network of type "igraph" alone.
- (2). Must be entered as data frame or matrix with `subnet_mat2`.

If the type of inputting is data frame or matrix, please make sure the row of `network.or.subnet_mat1` and `subnet_mat2` correspond with the second group of species that both belong to two subnetworks and interact with other groups of species.

- Try to make the rows of both matrices have the same attributes. Or we default:
- When the two matrices can have different numbers of rows:
  - (1). If both matrices have row names, then the function counts all row names to produce two new matrices with the same row names.
  - (2). If at most one matrix has row names, the function assigns new row names to both matrices on a row-to-row basis (any extra row names are assigned a new value) and then counts all row names to produce two new matrices with the same row names.
- When the two matrices can have the same numbers of rows:
  - No matter how the row names of the two matrices are arranged, as long as the row names are exactly the same; But we don't handle matrices with empty row names (the function will give an error).
- The two matrices can have different numbers of rows, but read our default handling carefully to make sure the calculation is accurate when using this function!!!

About a network of type "igraph", It can be obtained from the connection matrices of subnetworks by the function `igraph_from_matrices`.

Value

Returns a matrix of 70 columns representing the roles of interconnecting species in the motifs. Columns names are Role1, Role2, Role3 ... Role70.

Each row of matrix corresponds to a interconnecting species in the second layer of network. If a interconnecting species is linked to both the second and third level species, the elements in this row are not all zero, otherwise the elements are all zero.

References

Simmons, B. I., Sweering, M. J., Schillinger, M., Dicks, L. V., Sutherland, W. J., & Di Clemente, R. (2019). bmotif: A package for motif analyses of bipartite networks. Methods in Ecology and Evolution, 10(5), 695-701.

Examples

```
set.seed(12)
d <- build_net(11,22,21,0.2)
icmotif_role(d)
```

```
set.seed(12)
MAT <- build_net(11,22,21,0.2,asmatrices=TRUE)

icmotif_role(MAT[[3]],MAT[[4]])

md1<-matrix(sample(c(0,1),88,replace=TRUE),8,11)
md2<-matrix(sample(c(0,1),120,replace=TRUE),10,12)
icmotif_role(md1,md2)

R<-rownames(MAT[[4]])[12]
MR<-MAT[[4]][12,]
MAT[[4]]<-MAT[[4]][-12,]
MAT[[4]]<-rbind(MAT[[4]],MR)
rownames(MAT[[4]])[22]<-R

icmotif_role(MAT[[3]],MAT[[4]])
```

---

igraph_from_matrices   *Transforming matrices into network*

Description

Two matrices contain three groups of tropical level species. A multilayer network can be transformed from existing matrices data.

Usage

```
igraph_from_matrices(mat1, mat2, isDirected1 = TRUE, isDirected2 = TRUE)
```

Arguments

mat1   A numeric matrix(or data.frame) representing interactions between two groups
                of species.Each row and column of matrix represents single species in the second
                and first groups of the tripartite network respectively. Elements of matrix are
                non-zero numbers if the two groups of species are connected, and 0 otherwise.

mat2   A numeric matrix(or data.frame) representing interactions between two groups
                of species.Each row and column of matrix represents single species in the second
                and third groups of the tripartite network respectively. Elements of matrix are
                non-zero numbers if the two groups of species are connected, and 0 otherwise.

isDirected1   Logical. Whether the interaction between the two groups of species in mat1 is
                unidirectional.Default to TRUE, such as Predation and Herbivory. Otherwise it
                is bidirectional, such as Mutualism.

isDirected2   Logical. Whether the interaction between the two groups of species in mat2 is
                unidirectional.Default to TRUE, such as Predation and Herbivory. Otherwise it
                is bidirectional, such as Mutualism.

Details

mat1 and **mat2**

The type of inputting is data frame or matrix, please make sure the row of mat1 and mat2 correspond with the second group of species that both belong to two subnetworks and interact with other groups of species.

- Try to make the rows of both matrices have the same attributes. Or we default:
- When the two matrices can have different numbers of rows:
  - (1). If both matrices have row names, then the function counts all row names to produce two new matrices with the same row names.
  - (2). If at most one matrix has row names, the function assigns new row names to both matrices on a row-to-row basis (any extra row names are assigned a new value) and then counts all row names to produce two new matrices with the same row names.
- When the two matrices can have the same numbers of rows:
  - No matter how the row names of the two matrices are arranged, as long as the row names are exactly the same; But we don't handle matrices with empty row names (the function will give an error).
- The two matrices can have different numbers of rows, but read our default handling carefully to make sure the calculation is accurate when using this function!!!

The columns of mat1 and mat2 could be empty. If empty, the function also defaults to the suggested assignment.

Value

Return a network of type "igraph".

Examples

```
set.seed(12)
MAT <- build_net(11,22,21,0.2,asmatrices=TRUE)
MAT[[1]]

tmat<-t(MAT[[3]])
colnames(tmat)<-NULL
igraph_from_matrices(MAT[[3]],MAT[[4]])
M <- igraph_from_matrices(tmat,MAT[[4]])
M
```

Multi_motif   *Defined multilayer motifs*

Description

Acquiring each or all of 48 motifs of definition of multilayer network.

Usage

```
Multi_motif(
  type = c("M111", "M112", "M113", "M114", "M211", "M212", "M213", "M311", "M312",
    "M411", "M121", "M122-1", "M122-2", "M122-3", "M123-1", "M123-2", "M123-3", "M123-4",
    "M123-5", "M221-1", "M221-2", "M221-3", "M222-1", "M222-2", "M222-3", "M222-4",
    "M222-5", "M222-6", "M222-7", "M222-8", "M222-9", "M321-1", "M321-2", "M321-3",
     "M321-4", "M321-5", "M131", "M132-1", "M132-2", "M132-3", "M132-4", "M132-5",
      "M231-1", "M231-2", "M231-3", "M231-4", "M231-5", "M141", "all")
)
```

Arguments

type   Character. 49 values representing each and all types of multilayer motifs.

Value

If type is one of 48 motifs of definition, function returns a corresponding motif of "igraph".

If type is "all", function returns a list containing 48 corresponding motifs of "igraph".

Examples

```
type<-c("M111","M112","M113","M114","M211","M212","M213","M311",
"M312","M411","M121","M122-1","M122-2","M122-3","M123-1",
"M123-2","M123-3","M123-4","M123-5","M221-1","M221-2",
"M221-3","M222-1","M222-2","M222-3","M222-4","M222-5",
"M222-6","M222-7","M222-8","M222-9","M321-1","M321-2",
"M321-3","M321-4","M321-5","M131","M132-1","M132-2",
"M132-3","M132-4","M132-5","M231-1","M231-2","M231-3",
"M231-4","M231-5","M141")

m<-Multi_motif("M222-4")
plot(m,main="M222-4")

mr <- par(mfrow=c(6,8),mar=c(1,1,3,1))
for(i in 1:48){
    plot(Multi_motif("all")[[i]],
    vertex.size=30, vertex.label=NA,
    vertex.color="blue",main=type[i])
}
par(mr)
```

---

node_cv   *Measuring node versatility of multilayer network*

Description

The versatility of nodes is revealed by several centrality measures that have now been applied to multilayer networks, such as Degree, Pagerank, Hub, Authority, Katz, Eigenvector, and Closeness centrality.

Usage

```
node_cv(
  network.or.subnet_mat1,
  subnet_mat2 = NULL,
  isDirected1 = TRUE,
  isDirected2 = TRUE,
 type = c("degree", "pagerank", "hub", "authority", "katz", "eigenvector", "closeness",
    "all")
)
```

Arguments

network.or.subnet_mat1

> Either a multilayer(tripartite) network of 'igraph' class which contains three groups of species and interactions within layers without interactions between each group of species, or a numeric matrix(or data.frame) representing interactions between two groups of species. Each row and column of matrix represents single species in the second and first groups of the tripartite network respectively. Elements of matrix are non-zero numbers if the two groups of species are connected, and 0 otherwise.

subnet_mat2

> A numeric matrix(or data.frame) representing interactions between two groups of species. Each row and column of matrix represents single species in the second and third groups of the tripartite network respectively. Elements of matrix are non-zero numbers if the two groups of species are connected, and 0 otherwise. If `network.or.subnet_mat1` is "igraph", `subnet_mat2` defaults to NULL.

isDirected1

> Logical. Whether the interaction between the two groups of species in `mat1` is unidirectional.Default to TRUE, such as Predation and Herbivory. Otherwise it is bidirectional, such as Mutualism.

isDirected2

> Logical. Whether the interaction between the two groups of species in `mat2` is unidirectional.Default to TRUE, such as Predation and Herbivory. Otherwise it is bidirectional, such as Mutualism.

type

> Character. Including "degree", "pagerank", "hub", "authority", "katz", "eigenvector", "closeness", and "all".

Details

network.or.subnet_mat1 and **subnet_mat2**

There are two types of `network.or.subnet_mat1` that can be processed:

- (1). Input in a network of type "igraph" alone.
- (2). Must be entered as data frame or matrix with `subnet_mat2`.

If the type of inputting is data frame or matrix, please make sure the row of `network.or.subnet_mat1` and `subnet_mat2` correspond with the second group of species that both belong to two subnetworks and interact with other groups of species.

- Try to make the rows of both matrices have the same attributes. Or we default:

- When the two matrices can have different numbers of rows:
    - (1). If both matrices have row names, then the function counts all row names to produce two new matrices with the same row names.
    - (2). If at most one matrix has row names, the function assigns new row names to both matrices on a row-to-row basis (any extra row names are assigned a new value) and then counts all row names to produce two new matrices with the same row names.
- When the two matrices can have the same numbers of rows:
    - No matter how the row names of the two matrices are arranged, as long as the row names are exactly the same; But we don't handle matrices with empty row names (the function will give an error).
- The two matrices can have different numbers of rows, but read our default handling carefully to make sure the calculation is accurate when using this function!!!

About a network of type "igraph", It can be obtained from the connection matrices of subnetworks by the function `igraph_from_matrices`.

type

type "degree", "pagerank", "hub", "authority", "katz", "eigenvector", and "closeness" correspond to Degree, PageRank, Hub, Authority, Katz, Eigenvector, and Closeness centrality. type "all" integrates the above centrality.

Value

Return a data frame with the first row "node" for each node of network representing each species.

- If `type` is either of "degree", "pagerank", "hub", "authority", "katz", "eigenvector", "closeness", the data frame has two columns, and the second column corresponds to either of "Degree", "Pagerank_versatility", "Hub_versatility", "Authority_versatility", "Katz_versatility", "Eigenvector_versatility", "Closeness_versatility".
- If `type` is "all", the data frame has eight columns, and columns form the second to the eighth correspond to "Degree", "Pagerank_versatility", "Hub_versatility", "Authority_versatility", "Katz_versatility", "Eigenvector_versatility", "Closeness_versatility".

References

De Domenico, M., Nicosia, V., Arenas, A., & Latora, V. (2015). Structural reducibility of multilayer networks. Nature communications, 6(1), 6864.

De Domenico, M., Solé-Ribalta, A., Omodei, E., Gómez, S., & Arenas, A. (2013). Centrality in interconnected multilayer networks. arXiv preprint arXiv:1311.2906.

De Domenico, M. (2022). Multilayer Networks: Analysis and Visualization. Introduction to muxViz with R. Cham: Springer.

Page, L., Brin, S., Motwani, R., & Winograd, T. (1999). The pagerank citation ranking: Bringing order to the web.

Magnani, M., Micenkova, B., & Rossi, L. (2013). Combinatorial analysis of multiple networks. arXiv preprint arXiv:1303.4986.

Examples

```
set.seed(12)
d <- build_net(11,22,21,0.2,asmatrices=TRUE)
d
node_cv(d[[1]])

MAT<-d
tmat<-t(MAT[[3]])
colnames(tmat)<-NULL
node_cv(MAT[[3]],MAT[[4]])
node_cv(tmat,MAT[[4]])
node_cv(MAT[[3]],MAT[[4]],type="pagerank")

node_cv(MAT[[3]],MAT[[4]],isDirected2=FALSE)
```

---

null_model   *Null model of multilayer network*

Description

The null model could be generated according to different matrix scrambling algorithms for inter-connection patterns in the multilayer network

Usage

```
null_model(
  network,
  number = NULL,
  null_type = c("subnetwork1", "subnetwork2", "all", "Savue")
)
```

Arguments

network	A multilayer(tripartite) network of 'igraph' class. The network contains three groups of species and interactions within layers without interactions between each group of species.
number	A numeric value. The number of null model. Default to NULL representing number 1.
null_type	Logical. Four matrix scrambling algorithms. If null_type = NULL, default to "all".

Details

null_type

- For each of the four types of null models, there are corresponding algorithms. The first type, "subnetwork1", involved scrambling the adjacency matrix of the first and second groups of the multilayer network.

- The second type, "subnetwork2", focused on scrambling the adjacency matrix of the second and third groups.

- Comprehensively, the third type, "all", blended the approaches of the first two to disarrange the entire network's adjacency matrix, achieving a thorough perturbation of the network's structure.

- The last type named "Savue" that disarranged inherent structure in terms of the groups of species connected by each interconnecting species of every subnetworks, thus exhibiting different interconnection patterns.

network

About a network of type "igraph", It can be obtained from the connection matrices of subnetworks by the function `igraph_from_matrices`

Value

Return a list contains one or more elements. Each element represent a null model of multilayer network.

References

Vázquez, D. P., C. J. Melian, N. M. Williams, N. Blüthgen, B. R. Krasnov, and R. Poulin. 2007. Species abundance and asymmetric interaction strength in ecological networks. Oikos 116: 1120-1127.

Sauve, A. M., Thébault, E., Pocock, M. J., & Fontaine, C. (2016). How plants connect pollination and herbivory networks and their contribution to community stability. Ecology, 97(4), 908-917.

Examples

```
set.seed(12)
d <- build_net(11,22,21,0.2)

set.seed(123)
null_model(d)
set.seed(123)
null_model(d,null_type="subnetwork1")
set.seed(123)
null_model(d,null_type="Savue")
set.seed(123)
null_model(d,number=2,null_type="Savue")
```

---

pc   *Participation ratio of interconnecting code*

Description

Counting participation ratio that the difference in the degree of interconnecting nodes within two subnetworks.

Usage

```
pc(network.or.subnet_mat1, subnet_mat2 = NULL)
```

Arguments

network.or.subnet_mat1

> Either a multilayer(tripartite) network of 'igraph' class which contains three groups of species and interactions within layers without interactions between each group of species, or a numeric matrix(or data.frame) representing interactions between two groups of species. Each row and column of matrix represents single species in the second and first groups of the tripartite network respectively. Elements of matrix are non-zero numbers if two groups of species are connected, and 0 otherwise.

subnet_mat2   A numeric matrix(or data.frame) representing interactions between two groups of species. Each row and column of matrix represents single species in the second and third groups of the tripartite network respectively. Elements of matrix are non-zero numbers if the two groups of species are connected, and 0 otherwise. If network.or.subnet_mat1 is "igraph", subnet_mat2 defaults to NULL.

Details

network.or.subnet_mat1 and **subnet_mat2**

There are two types of network.or.subnet_mat1 that can be processed:

- (1). Input in a network of type "igraph" alone.
- (2). Must be entered as data frame or matrix with subnet_mat2.

If the type of inputting is data frame or matrix, please make sure the row of network.or.subnet_mat1 and subnet_mat2 correspond with the second group of species that both belong to two subnetworks and interact with other groups of species.

- Try to make the rows of both matrices have the same attributes. Or we default:
- (1). If both matrices have row names, then the function counts all row names to produce two new matrices with the same row names.
- (2). If at most one matrix has row names, the function assigns new row names to both matrices on a row-to-row basis (any extra row names are assigned a new value) and then counts all row names to produce two new matrices with the same row names.

- The two matrices can have different numbers of rows, but read our default handling carefully to make sure the calculation is accurate when using this function!!!

About a network of type "igraph", It can be obtained from the connection matrices of subnetworks by the function `igraph_from_matrices`.

Value

Print a "pc= ;" and Return a numeric value representing difference in the degree of interconnecting nodes within two subnetworks of multialyer network.

References

Battiston, F., Nicosia, V. & Latora, V. (2014) Structural measures for multiplex networks. Physical Review E, 89, 032804.

Domínguez-García, V., & Kéfi, S. (2024). The structure and robustness of ecological networks with two interaction types. PLOS Computational Biology, 20(1), e1011770.

Guimera, R. & Amaral, L.A.N. (2005) Cartography of complex networks: modules and universal roles. Journal of Statistical Mechanics: Theory and Experiment, 2005, P02001.

Examples

```
set.seed(15)
d <- build_net(11,15,17,0.2)
pc(d)

md1<-matrix(sample(c(0,1),80,replace=TRUE),8,10)
md2<-matrix(sample(c(0,1),120,replace=TRUE),10,12)
pc(md1,md2)

mdw1<-matrix(sample(c(rep(0,60),runif(60,0,1))),12,10)
mdw2<-matrix(sample(c(rep(0,40),runif(80,0,1))),10,12)
pc(mdw1,mdw2)
```

---

poc   *Proportion of interconnection*

Description

Calculating the proportion of species sharing with other species of two subnetworks in intermediate layer.

Usage

```
poc(network.or.subnet_mat1, subnet_mat2 = NULL)
```

Arguments

`network.or.subnet_mat1`

Either a multilayer(tripartite) network of 'igraph' class which contains three groups of species and interactions within layers without interactions between each group of species, or a numeric matrix(or data.frame) representing interactions between two groups of species. Each row and column of matrix represents single species in the second and first groups of the tripartite network respectively. Elements of matrix are non-zero numbers if two groups of species are connected, and 0 otherwise.

`subnet_mat2`   A numeric matrix(or data.frame) representing interactions between two groups of species. Each row and column of matrix represents single species in the second and third groups of the tripartite network respectively. Elements of matrix are non-zero numbers if the two groups of species are connected, and 0 otherwise. If `network.or.subnet_mat1` is "igraph", `subnet_mat2` defaults to NULL.

Details

network.or.subnet_mat1 and **subnet_mat2**

There are two types of `network.or.subnet_mat1` that can be processed:

- (1). Input in a network of type "igraph" alone.
- (2). Must be entered as data frame or matrix with `subnet_mat2`.

If the type of inputting is data frame or matrix, please make sure the row of `network.or.subnet_mat1` and `subnet_mat2` correspond with the second group of species that both belong to two subnetworks and interact with other groups of species.

- Try to make the rows of both matrices have the same attributes. Or we default:
- (1). If both matrices have row names, then the function counts all row names to produce two new matrices with the same row names.
- (2). If at most one matrix has row names, the function assigns new row names to both matrices on a row-to-row basis (any extra row names are assigned a new value) and then counts all row names to produce two new matrices with the same row names.
- The two matrices can have different numbers of rows, but read our default handling carefully to make sure the calculation is accurate when using this function!!!

About a network of type "igraph", It can be obtained from the connection matrices of subnetworks by the function `igraph_from_matrices`.

Value

Print a "poc= ;" and Return a numeric value representing the proportion of sharing species in intermediate layer.

References

Battiston, F., Nicosia, V. & Latora, V. (2014) Structural measures for multiplex networks. Physical Review E, 89, 032804.

Domínguez-García, V., & Kéfi, S. (2024). The structure and robustness of ecological networks with two interaction types. PLOS Computational Biology, 20(1), e1011770.

Guimera, R. & Amaral, L.A.N. (2005) Cartography of complex networks: modules and universal roles. Journal of Statistical Mechanics: Theory and Experiment, 2005, P02001.

Examples

```
set.seed(15)
d <- build_net(11,15,17,0.2)
poc(d)

md1<-matrix(sample(c(0,1),80,replace=TRUE),8,10)
md2<-matrix(sample(c(0,1),120,replace=TRUE),10,12)
poc(md1,md2)

mdw1<-matrix(sample(c(rep(0,40),runif(60,0,1))),10,10)
mdw2<-matrix(sample(c(rep(0,40),runif(80,0,1))),10,12)
poc(mdw1,mdw2)

mdw1<-matrix(sample(c(rep(0,60),runif(60,0,1))),12,10)
mdw2<-matrix(sample(c(rep(0,40),runif(80,0,1))),10,12)
poc(mdw1,mdw2)
```

PPH_Coltparkmeadow   *A pollinator-plant-herbivore network from Villa-Galaviz et. al. 2020. Journal of Animal Ecology*

Description

A pollinator-plant-herbivore network from Villa-Galaviz et. al. 2020. Journal of Animal Ecology

Usage

```
data(PPH_Coltparkmeadow)
```

Details

A list with "igraph". This is a classical example of multilayer interaction network.

References

Villa-Galaviz, E., S. M. Smart, E. L. Clare, S. E. Ward, and J. Memmott. 2021. Differential effects of fertilisers on pollination and parasitoid interaction networks. Journal of animal ecology 90:404-414.

Examples

```
data(PPH_Coltparkmeadow)
```

---

role_sim   *Similarity of roles of interconnecting species*

Description

The average of Similarity of 65 roles of interconnecting species of multilayer network.

Usage

```
role_sim(spe_role_mat)
```

Arguments

spe_role_mat   A matrix of 65 columns representing the roles of interconnecting species in the
                motifs. Columns names are Role1, Role2, Role3 ... Role70.

Details

spe_role_mat

Should acquire from function `motif_role`.

Value

Return a numeric value.

Examples

```
set.seed(12)
d <- build_net(11,22,21,0.2)
mr <- icmotif_role(d)
role_sim(mr)

set.seed(1)
D <- build_net(11,22,21,0.2)
role_sim(icmotif_role(D))
```

---

subnet_cor	*Correlation of the Structural indices between Subnetworks*

Description

Calculating correlation of interconnecting species generalism among Subnetworks ("general_'~'cor") and correlation between similarities of interconnecing species interaction partners in two subnetworks ("similar_'~'cor").

Usage

```
subnet_cor(network.or.subnet_mat1, subnet_mat2 = NULL, weighted = FALSE)
```

Arguments

network.or.subnet_mat1

Either a multilayer(tripartite) network of 'igraph' class which contains three groups of species and interactions within layers without interactions between each group of species, or a numeric matrix(or data.frame) representing interactions between two groups of species. Each row and column of matrix represents single species in the second and first groups of the tripartite network respectively. Elements of matrix are non-zero numbers if the two groups of species are connected, and 0 otherwise.

subnet_mat2   A numeric matrix(or data.frame) representing interactions between two groups of species. Each row and column of matrix represents single species in the second and third groups of the tripartite network respectively. Elements of matrix are non-zero numbers if the two groups of species are connected, and 0 otherwise. If network.or.subnet_mat1 is "igraph", subnet_mat2 defaults to NULL.

weighted   Logical. should elements of matrix be fractional? Default to FALSE. Generally, 'igraph' network represent a spare matrix, so weighted is FALSE. While elements of matrix represent interaction strength, weighted is TRUE.

Details

weighted

If the weighted = FALSE, the input for the parameter can be:

- network.or.subnet_mat1: input a 'igraph' of network data independently or input sparse matrix together with subnet_mat2.

If the weighted = TRUE, the input for the parameter can be:

- network.or.subnet_mat1: must input matrix(or data.frame) together with subnet_mat2. the matrix can be sparse matrix and matrix of interaction strength.

network.or.subnet_mat1 and subnet_mat2

There are two types of network.or.subnet_mat1 that can be processed:

- (1). Input in a network of type "igraph" alone.
- (2). Must be entered as data frame or matrix with `subnet_mat2`.

If the type of inputting is data frame or matrix, please make sure the row of `network.or.subnet_mat1` and `subnet_mat2` correspond with the second group of species that both belong to two subnetworks and interact with other groups of species.

- Try to make the rows of both matrices have the same attributes. Or we default:
- When the two matrices can have different numbers of rows:
    - (1). If both matrices have row names, then the function counts all row names to produce two new matrices with the same row names.
    - (2). If at most one matrix has row names, the function assigns new row names to both matrices on a row-to-row basis (any extra row names are assigned a new value) and then counts all row names to produce two new matrices with the same row names.
- When the two matrices can have the same numbers of rows:
    - No matter how the row names of the two matrices are arranged, as long as the row names are exactly the same; But we don't handle matrices with empty row names (the function will give an error).
- The two matrices can have different numbers of rows, but read our default handling carefully to make sure the calculation is accurate when using this function!!!

About a network of type "igraph", It can be obtained from the connection matrices of subnetworks by the function `igraph_from_matrices`.

Value

Return a numeric vector of two elements representing correlation of interconnecting species generalism among Subnetworks and correlation between similarities of interconnecing species interaction partners in two subnetworks.

If `weighted = FALSE`, the results will show "general_cor= ;similar_cor= ;" and If `weighted = TRUE`, the results will show "general_weight_cor= ;similar_weight_cor= ;"

References

Sauve, A. M., Thébault, E., Pocock, M. J., & Fontaine, C. (2016). How plants connect pollination and herbivory networks and their contribution to community stability. Ecology, 97(4), 908-917.

Examples

```
set.seed(12)
d <- build_net(11,15,17,0.2)
subnet_cor(d)

md1<-matrix(sample(c(0,1),110,replace=TRUE),10,11)
md2<-matrix(sample(c(0,1),120,replace=TRUE),10,12)
subnet_cor(md1,md2)
subnet_cor(md1,md2,weighted=TRUE)

md1<-matrix(sample(c(0,1),80,replace=TRUE),8,10)
```

```
md2<-matrix(sample(c(0,1),120,replace=TRUE),10,12)
subnet_cor(md1,md2)

mdw1<-matrix(runif(110,0,1),10,11)
mdw2<-matrix(runif(120,0,1),10,12)
subnet_cor(mdw1,mdw2,weighted=TRUE)

set.seed(1)
mdw1<-matrix(runif(80,0,1),8,10)
mdw2<-matrix(runif(120,0,1),10,12)
subnet_cor(mdw1,mdw2,weighted=TRUE)
```

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